IFLRC VI & ICLGG VII

6th International Food Legume Research Conference

7th International Conference on Legume Genetics and Genomics

PROGRAM & ABSTRACT BOOK

TCU Place

Saskatoon, Saskatchewan, Canada

July 7-11, 2014

UNIVERSITY OF SASKATCHEWAN

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Sunday, July 6, 2014

15:00 – 18:30	Registration Open
	Open Forum: Science in Grain Legumes (Coordinated by Noel Ellis, CGIAR)
19:00 – 21:00	Welcome and Networking Reception for IFLRC VI & ICLGG VII delegates and Canadian Special Crops Association Convention (CSCA) delegates

Monday, July 7, 2014

Fundamental and Applied Genetics and Genomics

Location: Salons A, B, C (Upper Level)

7:30	Registration Open
7:30– 8:45	Breakfast (Grand Salon - Upper Level)
9:00– 10:30	**Plenary Session IFLRC VI & ICLGG VII** Co-chairs: Doug Cook (University of California Davis, USA) Tom Warkentin (University of Saskatchewan, Canada)
9:00– 9:45	**Nevin D. Young** (University of Minnesota, USA) **Exploring Nodulation through Genome Resequencing and Association Genetics in *Medicago***
9:45– 10:30	**Judith Burstin** (INRA, Dijon, FRANCE) **Recent pea genomic resources will enhance complementary improvement strategies in this crop**
10:30- 11:00	Refreshment Break
11:00- 12:30	Concurrent Sessions

ICLGG **Gallery A, B (Main Level)**	**IFLRC** **Gallery C, D (Main Level)**
Fundamental Genomics	**Applied Genetics & Genomics**
Chair: Doug Cook (University of California Davis, USA)	Chair: Tom Warkentin (University of Saskatchewan, Canada)

11:00-11:30 **Scott Jackson** (Univ. of Georgia, USA) "Genetic and epigenetic variation in legumes: focus on *Glycine max* and *Phaseolus vulgaris"*	11:00-11:30 **Noel Ellis** (CGIAR, Hyderabad, India) Shifting the focus: populations, genetics and genomics
11:30-11:50 **Stig Andersen** (Aarhus University, Denmark) *Lotus japonicus* natural variation and LORE1 insertion mutants	11:30-11:45 **Rachit K. Saxena** (ICRISAT, India) Whole genome re-sequencing based classification of heterotic pools for accelerating hybrid breeding in pigeonpea
11:50-12:10 **Greg Perry** (University of Guelph, Canada) Using SNP genotyping to identify regions of *Phaseolus acutifolius* introgression in OAC-Rex, a CBB resistant variety of *Phaseolus vulgaris*	11:45-12:00 **Ping Wan** (Beijing University of Agriculture) A high-density SNP genetic map and QTL mapping for yield and other agronomic traits in adzuki bean (*Vigna angularis*)
12:10-12:30 **Stephan Schröder** (North Dakota State University, USA) Optimization of Genotyping by Sequencing (GBS) Data in Common Bean (*Phaseolus vulgaris* L.)	12:00-12:15 **Trupti Joshi** (University of Missouri, Columbia, USA) Next Generation Resequencing of Soybean Germplasm for Trait Discovery
	12:15-12:30 Gilles Boutet (INRA, Rennes, France) SNP discovery in pea: A powerful tool for academic research and breeding

12:30 - 14:00 Lunch Break (Grand Salon - Upper Level)

14:00 - 15:30 Concurrent Sessions

ICLGG **Gallery A, B (Main Level)** **Evolution** Chair: Sachiko Isobe (Kazusa DNA Research Institute, Japan)	**IFLRC** **Gallery C, D (Main Level)** **Applied Genetics & Genomics; Disease Resistance** Chair: N.P. Singh (IIPR, Kanpur, India)
14:00-14:30 **Peter Tiffin** (University of Minnesota, USA) Targets of selection in the *Medicago* genome	14:00-14:15 **Janila Pasupuleti** (ICRISAT, India) Identification of introgression lines with superior pod yield and improved rust resistance in peanut (*Arachis hypogaea* L.)
14:30-15:00 **Maren Friesen** (Michigan State University, USA) Symbiotic Dimensions of Trifolium Biodiversity	14:15-14:30 **Ehsan Sari** (University of Saskatchewan) Genotype-dependent interaction of lentil lines with *Ascochyta lentis*
15:00-15:20 **Steven Cannon** (USDA-ARS) Multiple incidents of polyploidy and nodule evolution near the origin of the legumes	14:30-14:45 **Judith Lichtenzveig** (Curtin University, Australia) Pathogenomics of the *Didymella* spp. causal agents of Ascochyta blights in legumes
15:20-15:40 **Elisa Bellucci** (Università Politecnica delle Marche, Ancona, Italy) Decreased nucleotide and expression diversity and modified co-expression patterns characterize domestication in the common bean	14:45-15:00 **Jagmeet Kaur** (Punjab Agricultural University, Ludhiana, India) Moisture stress induced changes in metabolites and cellular functions of chickpea (*Cicer arietinum* L.) genotypes
	15:00-15:15 **Renu Singh** (CCS Haryana Agricultural University, India) Mapping micronutrients using recombinant inbred lines (RILs) in Mung bean (*Vigna radiata* L.)

	15:15-15:30 **Larn McMurray** (SARDI, Adelaide, Australia) Improved weed control in Australian pulse production through advancements in genetic and agronomic research

15:40 - 16:00 Refreshment Break

16:00 – 18:00 Concurrent Sessions

ICLGG Gallery A, B (Main Level) **Development** Chair: Sachiko Isobe (Kazusa DNA Research Institute, Japan)	**IFLRC Gallery C, D (Main Level)** **Applied Genetics and Genomics; Abiotic Stress Tolerance** Chair: Ashutosh Sarker (ICARDA, India)
16:00-16:30 **Catherine Rameau** (INRA, Versailles , France) Strigolactones and other long distances signals regulating shoot branching	16:00-16:30 **Steve Beebe** (CIAT, Cali, Colombia) Breeding for tolerance to low soil phosphorus: the example of common bean
16:30-17:00 **Jim Weller** (University of Tasmania, Australia) Genetic control of flowering in temperate legumes	16:30-16:45 **Shane Rothwell** (Lancaster University, UK) Liming (to recommended rates) limits legume growth and gas exchange by increasing root-to-shoot signalling of the phytohormone abscisic acid
17:00-17:20 **Jianxin Ma** (Purdue University, USA) Molecular Basis of Soybean Stem Architecture	16:45-17:00 **Ralf Metzner** (Institute of Plant Sciences, Jülich, Germany) Monitoring roots, nodule and pod development in vivo: New perspectives on legume development
17:20-17:40 **Julie Hofer** (ICRISAT, Patancheru, India) Sequence analysis of a pea (*Pisum sativum*) fast neutron mutant population identifies the gene corresponding to *Stipules reduced*	17:00-17:15 **Jens Berger** (CSIRO Plant Industry) Chickpea phenology and evolution
17:40-18:00 **Jocelyn Ozga** (University of Alberta, Canada) Role of gibberellins in seed coat development and photoassimilate partitioning in developing pea (*Pisum sativum* L.) seeds	17:15-17:30 **Shiv Kumar** (ICARDA) Extra short duration lentils for rice-based cropping systems in the Indo-Gangetic Plains of South Asia
	17:30-17:45 **Imran Malik** (University of Western Australia) Variation in physiological responses in pea and lentil to soil waterlogging
	17:45-18:00 **Hari D. Upadhyaya** (ICRISAT, India) Capturing Variations for Multiple Stress and Agronomic Traits for Improvement of Grain Legumes

18:30 – 22:00 Evening Event, **Wanuskewin Heritage Park**

Tuesday, July 8, 2014

Seeds and Nutrition

Location: Salons A, B, C (Upper Level)

7:30– 8:25	Breakfast (Grand Salon - Upper Level)
8:30– 10:30	**Plenary Session IFLRC VI & ICLGG VII** Co-Chairs: Georgina Hernandez (Universidad Nacional Autónoma de México, Mexico) Albert Vandenberg (University of Saskatchewan, Canada)
8:30– 9:15	**Murad Al-Katib** (President and CEO of *Alliance Grain Traders Inc.*) **Changing Face of Global Agriculture**
9:15– 10:00	**Richard Thompson** (INRA, Dijon, France) **Use of translational genomics to identify genes important for legume seed development**
10:00– 10:45	**Michael Grusak** (USDA-ARS, Baylor College of Medicine, Houston, Texas, USA) **Nutritional Enhancement of Food Crops: Recent Conceptual Developments and Strategic Targets for Common Bean**
10:45– 11:00	Refreshment Break
11:00 - 12:30	Concurrent Sessions

ICLGG **Gallery A, B (Main Level)**	**IFLRC** **Gallery C, D (Main Level)**
Seeds and Nutrition Chair: Georgina Hernandez (Universidad Nacional Autónoma de México, Mexico)	**Seeds and Nutrition** Chair: Albert Vandenberg (University of Saskatchewan, Canada)
11:00-11:30 **Jerome Verdier** (Shanghai Institutes of Biological Sciences, CAS, China) Deciphering regulation of legume seed nutritional composition	11:00-11:30 **Francesca Sparvoli** (IBBA, CNR, Milan, Italy) Iron biofortification in common bean
11:30-11:50 **Claire Domoney** (John Innes Centre, Norwich, UK) The wild side of seed quality improvement: discovering novel genetic variation that impacts on the control of visual traits and composition in *Pisum sativum* L. (pea)	11:30-11:45 **William Erskine** (University of Western Australia) Selenium biofortification of lentil in Australia and Bangladesh
11:50-12:10 **Mitch Lucas** (University of California Riverside, USA) Using SNPs to Breed Cowpeas with Large Seeds	11:45-12:00 **Peter Zahradka (**Canadian Centre for Agri-Food Research in Health and Medicine) The structural properties of arteries are altered by consumption of pulses: Implications for treatment of atherosclerotic disease
Biotic Stress 12:10-12:30 **Vijai Bhadauria** (University of Saskatchewan, Canada) Regulation of hemibiotrophy in the lentil anthracnose pathogen *Glomerella truncata*	12:00-12:15 **Laura McBreairty** (University of Saskatchewan) A pulse-based diet and exercise training in women with polycystic ovarian syndrome: Effects on body composition, blood lipids and reproductive measures
	12:15-12:30 **Susan Arntfield** (University of Manitoba,

	Canada) Changes in levels of antioxidant and selected antinutritional factors in peas and beans due to the application of heat

12:30 - 14:00 Lunch Break (Grand Salon - Upper Level)

12:45 - 14:00 Legume data integration meeting (Coordinated by Steven Cannon) – open forum

14:00 – 15:30 Concurrent Sessions

ICLGG **Gallery A, B (Main Level)** **Biotic Stress** Chair: Scott Jackson (Univ. of Georgia, USA)	**IFLRC** **Gallery C, D (Main Level)** **Seeds and Nutrition** Chair: Khalid Daoui (Centre Régional de la Recherche Agronomique de Mèknes, Morocco)
14:00-14:30 **Kiran Mysore** (The Samuel Roberts Noble Foundation, USA) Identification of novel sources of resistance in a nonhost plant, *Medicago truncatula*, against Asian Soybean Rust caused by *Phakopsora pachyrhizi*	14:00-14:30 **C.L. Laxmipathi Gowda** (ICRISAT, India) Impact-Oriented Legume Seed Systems in developing countries of Sub-Saharan Africa and Asia
14:30-15:00 **Nadine Ilk** (The Sainsbury Laboratory, Norwich, UK) Translational research at The Sainsbury Laboratory – from the laboratory to the farm	14:30-14:45 **Felix Dapare Dakora** (Tshwane University of Technology, South Africa) Role of symbiotic cowpea (*Vigna unguiculata L. Walp*.) as a major food legume for nutritional security in Africa
15:00-15:20 **Marie-Laure Pilet-Nayel** (INRA, Rennes, France) Translational genomics for resistance to *Aphanomyces euteiches* between *Medicago truncatula* and pea	14:45-15:00 **Ramakrishnan Nair** (AVRDC – The World Vegetable Center South Asia, India) Enhancing production and consumption of mungbean
15:20-15:40 **Zenglu Li** (University of Georgia, USA) An Integrated Molecular Breeding Approach for Breeding Nematode Resistance in Soybean	15:00-15:15 **Jenny Wood** (NSW Department of Primary Industries, Australia) Imaging of grain legume seeds: understanding what is where and the influence on nutritive value, health benefits and quality traits
	15:15-15:30 **Arun Shunmugam** (University of Saskatchewan) Biochemical and molecular characterization of low phytate pea lines

15:40 – 16:00 Refreshment Break

16:00 – 18:00 **Poster Session (Odd number)**

8:30 – 22:00 Banquet Reception, **Delta Bessborough Gardens**

Wednesday, July 9, 2014

Location: Salons A, B, C (Upper Level)

Nitrogen Fixation, Plant Nutrition and Legume Mega Projects

7:30– 8:45 Breakfast (Grand Salon - Upper Level)

9:00– 10:30 **Plenary Session IFLRC VI & ICLGG VII**
Co-Chairs:
Jens Stougaard (Aarhus University, Denmark)
C.L. Laxmipathi Gowda (ICRISAT, India)

9:00– 9:45 **Kirstin Bett** (University of Saskatchewan, Canada)
Lentil genome sequencing: establishing a comprehensive platform for molecular breeding

9:45– 10:30 **Ken Giller** (Plant Production Systems, Wageningen University, The Netherlands)
N2Africa: Putting nitrogen fixation to work for smallholder farmers in Africa

10:30– 11:00 Refreshment Break

11:00- 12:30 Concurrent Sessions

ICLGG **Gallery A, B (Main Level)** **Legume Mega Projects** Chair: Jens Stougaard (Aarhus University, Denmark)	**IFLRC** **Gallery C, D (Main Level)** **N Fixation and Plant Nutrition** Chair: C.L. Laxmipathi Gowda (ICRISAT, India)
11:00-11:30 **Tim Close** (University of California Riverside, USA) Innovation Lab on Climate Resilient Cowpea	11:00-11:30 **Endalkachew Wolde-meskel** (Hawassa University, Ethiopia) Exploiting indigenous rhizobial biodiversity resources and symbiotic N2-fixation to benefit small-holder farmers: the case of Ethiopia
11:30-12:00 **Doug Cook** (University of California Davis, USA) Taking a walk on the wild side: prospecting for climate resilience and nitrogen fixation traits in the wild progenitors of cultivated chickpea	11:30-11:45 **Matthew Denton** (University of Adelaide, Australia) A national survey of farmers in Australia to understand rhizobial inoculant use for pulse and pasture legumes
12:00-12:30 **Suk-Ha Lee** (Seoul National University, Korea) Genome Sequence of Mungbean and Vigna Speciation	11:45-12:00 **Adriana Navarro-Borrell** (Agriculture and Agri-Food Canada, Swift Current) Managing soil microbial resources and wheat yield through crop rotation in 4-year systems in the Canadian Prairie
	12:00-12:**15** **Fran Walley** (University of Saskatchewan) Assessment of Arbuscular Mycorrhizal Fungal Inoculants for Pulse Production Systems
	12:15-12:30 **Navid Bazghaleh** (University of Saskatchewan) Genotypic variation in the response of chickpea to arbuscular mycorrhiza and fungal endophytes

12:30 - 13:15 Lunch Break (Grand Salon - Upper Level)

13:15 - 16:30	**Pulse Breeding Field Tour**
13:15 – 17:00	**Visit a Hutterite Colony**
13:15 – 15:00	**Canadian Light Source**
13:15 – 16:00	**Pulse Cooking Class with Local Chef**
13:15 – 18:30	**Weed Research Plots at Scott**
17:30 – 19:00	Join the "**Fun Run** or **Fun Walk"**

Free evening

Thursday, July 10, 2014 — Location: Salons A, B, C (Upper Level)

Biotic Stress and Plant Microbe Interactions

7:30– 8:45	Breakfast (Grand Salon - Upper Level)
9:00– 10:30	**Plenary Session IFLRC VI & ICLGG VII** Co-Chairs: Kirstin Bett (University of Saskatchewan, Canada) Phil Davies (SARDI, Adelaide, Australia)
9:00– 9:45	**Jens Stougaard** (Department of Molecular Biology, Aarhus University, Denmark) **Bacterial infection of epidermal cells is controlled by a two-step recognition process**
9:45– 10:30	**Alain Baranger** (INRA, Rennes, France) **Plant architecture and development to control aerial disease epidemics in legumes: the case of Ascochyta blight in pea**
10:30– 11:00	Refreshment Break
11:00 - 12:30	Concurrent Sessions

ICLGG Gallery A, B (Main Level) **Symbiosis** Chair: Kirstin Bett (University of Saskatchewan, Canada)	**IFLRC** Gallery C, D (Main Level) **Disease and Pest Resistance** Chair: Carlota Vaz Patto (Universidade Nova de Lisboa, Portugal)
11:00-11:30 **Pascal Ratet** (Institut des Sciences du végétal CNRS, Gif sur Yvette, France) Identification of *Medicago truncatula* genes preventing development of plant defenses during symbiosis	11:00-11:30 **Weidong Chen** (USDA/ARS, Washington State University, USA) What roles do fungal secondary metabolites play in interactions between Ascochyta fungi and cool season food legumes?
11:30-11:50 **Georgina Hernandez** (Universidad Nacional Autónoma de México, Mexico) MicroRNAs from common bean (*Phaseolus vulgaris*) in the rhizobia symbiosis and in the response to abiotic stress	11:30-11:45 **Aurore Desgroux** (INRA, Rennes, France) Identification of pea lines resistant to *Aphanomyces euteiches* and related root architecture traits
11:50-12:10 **Jeremy Murray** (John Innes Centre, Norwich, UK)	11:45-12:00 **Beybin Bucak** (Harran University, Sanliurfa, Turkey)

The Rhizobial Infectome: Uncovering the Genes that Control the Early Steps of the Legume-Rhizobia Interaction	Transfer of resistance to broomrape (*Orobanche crenata*) from *Lens ervoides* to cultivated lentil.
12:10-12:30 **Hongyan Zhu** (University of Kentucky, USA) Genetic control of symbiosis specificity in the legume-rhizobial mutualism	12:00-12:15 **Kristy Hobson** (NSW Department of Primary Industries, Australia) Developing superior chickpea varieties by improving chickpea Phytophthora resistance using wild relatives
	12:15-12:30 **Diego Rubiales** (Institute for Sustainable Agriculture, Cordoba, Spain) Exploitation of wild relatives in pea breeding for disease and pest resistance

12:30 - 14:00 Lunch Break (Grand Salon - Upper Level)

14:00 – 15:30 Concurrent Sessions

ICLGG **Gallery A, B (Main Level)** **Symbiosis** Chair: Jeremy Murray (John Innes Centre, Norwich, UK)	**IFLRC** **Gallery C, D (Main Level)** **Disease and Pest Resistance** Chair: Sabine Banniza (University of Saskatchewan, Canada)
14:00-14:30 **Krzysztof Szczyglowski** (Agriculture and Agri-Food Canada, London, Ontario, Canada) Turning on the nitrogen tap: how legumes keep the nutrient flowing	14:00-14:30 **Hari Sharma** (ICRISAT, India) Potential of host plant resistance to insects for pest management in grain legumes: Progress and limitations
14:30-15:00 **Masayoshi Kawaguchi** (National Institute for Basic Biology, Okazaki, Japan) Two kinds of mobile signals mediate long-distance control of nodulation	14:30-14:45 **Mustapha El-Bouhssini** (ICARDA, Rabat, Morocco) Progress in host plant resistance in chickpea to Leaf miner, *Liriomyza cicerina* (Rondani)
15:00-15:30 **Christine Lelandais-Brière** (Université Paris Diderot- France) MicroRNA networks involved in root architecture and environmental interactions in the model legume *Medicago truncatula*	14:45-15:00 **Lars Kamphuis** (CSIRO Plant Industry, Wembley, Australia) Resistance to aphids in the model legume *Medicago truncatula*
	15:00-15:15 **Kiran Sharma** (ICRISAT, India) Transgenic pigeonpea for resistance to legume pod borer: moving towards product development
	15:15-15:30 **Ashutosh Sarker** (ICARDA, Beirut, Lebanon) Adaptation of lentil and grasspea under various cropping systems in South Asia

15:30 – 16:00 Refreshment Break

16:00 – 18:00 **Poster Session (Even number)**

16:00 – 17:30 Mini symposium: **Root Diseases in Legumes (Coordinated by Clare Coyne)**
Gallery C, D (Main Level)

18:30 – 21:00 Evening Event, **Western Development Museum**

Friday, July 11, 2014 **Location: Salons A, B, C (Upper Level)**

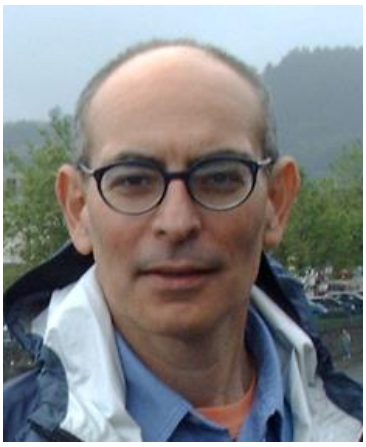
Abiotic Stress and Crop Management

7:30– 8:45	Breakfast (Grand Salon - Upper Level)
9:00- 10:30	**Plenary Session IFLRC VI & ICLGG VII** Co-Chairs: Noel Ellis (CGIAR, Hyderabad, India) Felix Dapare Dakora (Tshwane University of Technology, South Africa)
9:00– 9:45	**Rajeev Varshney** (CEG, ICRISAT, India) **The 1000 Pulse Genome Sequencing Initiative: Connecting Genes to Traits**
9:45– 10:30	**Kadambot Siddique** (University of Western Australia) **Abiotic Stress in Cool Season Grain Legumes: Genetic and Agronomic Approaches**
10:30- 11:00	Refreshment Break
11:00- 12:30	Concurrent Sessions

ICLGG **Gallery A, B (Main Level)** **Applied Genomics** Chair: Noel Ellis (CGIAR, Hyderabad, India)	**IFLRC** **Gallery C, D (Main Level)** **Abiotic stress** Chair: Kadambot Siddique (University of Western Australia)
11:00-11:30 **Maria Monteros** (The Samuel Roberts Noble Foundation, USA) Opportunities for Genomics-Assisted Breeding Approaches in Alfalfa (*Medicago sativa* L.)	11:00-11:30 **Pooran Gaur** (ICRISAT, India) High temperature tolerance in grain legumes
11:30-11:50 **Sachiko Isobe** (Kazusa DNA Research Institute, Japan) *In silico* SNP and SSRP discovery in horsegram genome sequences	11:30-11:45 **Phil Davies** (SARDI, Adelaide, Australia) Selecting pulses tolerant to temperature extremes: frost and heat stress tolerance in field pea and faba bean
11:50-12:10 **Sujan Mamidi** (North Dakota State University, USA) Genome-wide association studies to identify major QTL responsible for Iron Deficiency chlorosis in soybean (*Glycine max*)	11:45-12:00 **Rosalind Bueckert** (University of Saskatchewan) Cool leaf traits to reduce heat stress in pea
12:10-12:30 **Hamid Khazaei** (University of Helsinki, Finland) Synteny-based mapping of morphological, agronomic and quality traits in faba bean (*Vicia faba* L.)	12:00-12:15 **Maryse Bourgault** (University of Melbourne, Australia) Field Pea growth and yield response to elevated CO2 in the Australian Grains Free Air CO2 enrichment facility (AGFACE)
	12:15-12:30 **Janine Croser** (University of Western Australia) Recombinant inbred line populations in less than a year? A novel system for combining accelerated breeding with screening for abiotic stress in grain legumes.

12:30 – 12:45	**Closing remarks**
12:45 - 14:00	Lunch (Grand Salon - Upper Level)

Keynote Speaker: **Fundamental and Applied Genetics and Genomics (ICLGG)**



Nevin Young is a Distinguished McKnight University Professor at the University of Minnesota with joint appointments in the Department of Plant Pathology and the Department of Plant Biology. Previously, Dr. Young was director of the Plant Molecular Genetics Institute (PMGI) at Minnesota. Dr. Young received his B.A. at Indiana University in 1977 and Ph.D. at Yale University in 1984, followed by a NSF Postdoctoral Fellowship at Cornell University. He is author or co-author of more than 270 scientific publications, including 105 refereed publications and 18 book chapters with an overall h-index score of 57. His research highlights include the first mapping of a plant disease resistance gene using DNA markers, the first comparative genetic mapping of plant developmental genes, and the first bioinformatic analysis of plant disease resistance gene families. In 2003, Dr. Young became principal investigator on the NSF initiative to sequence the genome of the model legume, *Medicago truncatula*, which was published in *Nature* magazine in 2011.

Exploring Nodulation through Genome Resequencing and Association Genetics in *Medicago*

Young, N.D.[1*]. [1]University of Minnesota. *(neviny@umn.edu)

Genome resequencing enables the discovery of candidate loci and provides insights into the genomic architecture of complex traits. The Medicago Hapmap Consortium (University of Minnesota, National Center for Genome Resources, Boyce Thompson, J. Craig Venter Institute, Hamline University) is resequencing the genome of *Medicago truncatula* to explore the genomics of nodulation. Previously, we resequenced 320 diverse accessions of *M. truncatula* and related taxa to discover >6,000,000 single nucleotide polymorphisms (SNPs). Subsequent genome-wide association studies (GWAS) of nodulation uncovered previously reported genes (eg, CaML3, NFP, SERK2) plus novel candidates associated with DNA repair, ubiquination, molecular chaperones and other nodule-upregulated loci of unknown function. Functional genomics experiments are now underway to validate these novel candidates. A subset of 30 lines from the GWAS panel are now being deeply sequenced and assembled independently from the published A17 reference. This approach is essential for the discovery of DNA elements not found in the reference sequence as well as for high confidence prediction of structural variants (SVs). Our resequencing work has already produced a reference quality assembly for R108, a *M. truncatula* genotype widely used in functional genomics. These independent *M. truncatula* genome assemblies also lay a foundation for creating a *Medicago* "pan-genome". Multiple lines of evidence indicate that dynamic gene families, including NBS-LRRs and nodule-specific cysteine-rich peptides (NCRs), play key roles in nodulation. Genome resequencing is beginning to reveal the evolution and architecture of these important gene families.

Keynote Speaker: **Fundamental and Applied Genetics and Genomics (IFLRC)**

Dr. Judith BURSTIN is Director of research at INRA UMR1347 Agroecology Dijon-F. With an initial background in agronomy, quantitative genetics and breeding, she has acquired competencies in genomics and post-genomics. Her research focuses on pea and aims at deciphering the control of seed yield and quality in the context of climate change. A major scope of her research is the molecular understanding of plant adaptation. She leads a group working on the genetics and genomics of protein crops (mainly pea and fababean). She has been coordinating large multi-disciplinary projects in the field of pea quantitative molecular genetics, translational genomics and proteomics, and of development of molecular tools and plant material. She co-authored more than 30 papers in peer-reviewed international journals and 5 book chapters. She is expert for the French variety registration office and has been vice-president of the former European association of grain legumes.

Recent pea genomic resources will enhance complementary improvement strategies in this crop

Burstin, J.[1*], Alves-Carvalho, S.[1], Tayeh, N.[1], Aluome, C.[2], Bourion, V.[1], Klein, A.[1], Carrère, S.[3], Brochot, A.L.[1], Salloignon, P.[4], Siol, M.[1], Delaitre, C.[1], Cruaud, C.[5], Kreplak, J.[1], Truntzer, C.[4], Balzergue, S.[6], Wincker, P.[5], Le Paslier, M.C.[2], Brunel, D.[2], Gouzy, J.[3], Lejeune-Hénaut, I.[7], Duc, G.[1], and Aubert, G.[1]. [1]UMR1347 Agroecology, INRA, 17 rue de Sully, 21065 Dijon cedex; [2]EPGV, INRA, CEA, Evry, France; [3]LIPM, INRA, Auzeville, France; [4]CLIPP, U. Bourgogne, Dijon, France; [5]Genoscope, CEA, Evry, France; [6]URGV, INRA, Evry, France; [7]SADV, INRA, Mons en Chaussée, France. *(judith.burstin@dijon.inra.fr)

Pea has lagged behind many other crops in terms of dedicated genomic tools for several reasons including its large genome size (ca. 4.5 Gb). The recent development of high-throughput sequencing and genotyping technologies has permitted pea genomics to catch up and enter into the genomic era. We will present the development of functional and structural genomic resources in pea and their application in pea breeding. We developed a pea Unigene expression atlas that allows visualization of expression profiles for any gene of interest in various tissues subjected to different conditions. This was the basis for generating a high density microarray for functional genomics and a high-throughput genotyping BeadChip array for genotyping. These tools will be extremely useful in three breeding strategies followed by the team: (i) ideotype breeding, which pursue an ideal plant model that is expected to meet the desired yield and quality requirements of producers and users; (ii) targeted breeding, which chase the good combinations of genetic factors controlling traits of interest; and (iii) genome-wide breeding, which models phenotypes from high density marker genotypes.

Murad Al-Katib, as President and CEO of Alliance Grain Traders Inc., is the guiding vision in all aspects of the business, also serving on the Board of Directors. After completing a Masters from Thunderbird School of Global Management in Arizona and a Bachelor of Commerce from the University of Saskatchewan, Murad worked in international trade promotion for the Government of Saskatchewan before founding Saskcan Pulse Trading in 2001, providing the nucleus for Alliance Grain Traders. Over the next decade, the company has grown to become a world leader in value-added pulses, staple foods and ingredients selling to over 100 countries around the globe and with 29 manufacturing plants in 5 continents.Murad has served on the Board of Directors of the Canadian Special Crops Association and Pulse Canada and served as Chair of the Advisory Board for Small and Medium Enterprise for the Canadian Minister of International Trade. Murad also served as a member of the Panel for the Renewal of Canada's Global Commerce Strategy. Murad is also the recipient of a number of prestigious awards including the 2012 Pulse Promoter Award from BASF and Saskatchewan Pulse Growers, the 2004 Ernst and Young Emerging Entrepreneur of the Year and one of 2005's Canada's "Top 40 under 40" by the Caldwell Partners and the Globe and Mail.

Changing Face of Global Agriculture

Al-Katib, M.[1*]. [1]Alliance Grain, Regina, SK, Canada. *(Murad@saskcan.com)

As the world population rises, global demand for protein is rising in emerging markets and consumer tastes and preferences in non-traditional markets for pulses such as North America and Europe are leading to robust new demand. The discussion will examine these trends and explore the role of innovation, product development and R&D in meeting the new opportunities ahead in the global pulses industry. The speaker will use AGT as a case study in discussing regional development of the global pulses industry and discuss current and future trends that will drive the consumption of pulses.

Keynote Speaker: **Seeds and Nutrition (ICLGG)**

Richard D. Thompson. After a Ph.D. in Molecular Biology U. Edinburgh (1979) and periods at the PBI Cambridge UK, and the MPI for Plant Breeding Research, Köln, currently researcher in the INRA Agroecology Unit, Dijon, (2002-present, Grain Legumes Unit Director 2002-2010), focussing on the genetic control of seed development and composition in legumes, using the *Medicago truncatula* model, and more recently, Pea (*Pisum sativum*). By applying proteomics and transcriptomics approaches, gene expression profiles for isolated tissues of the seed have been obtained and clusters of co-regulated genes acting during discrete stages in seed filling identified. To narrow down candidate genes for the control of seed composition and yield, we have selected genes that co-locate with QTLs for these traits and are analysed the phenotypes of corresponding TILLING and TnT1 insertion mutants. Also coordinating the EU project LEGATO (Legumes for the Agriculture of Tomorrow (2014-2017)), aimed at increasing grain legume cultivation in Europe.

Use of translational genomics to identify genes important for legume seed development

Noguero, M.[1], Le Signor, C.[1], Vernoud, V.[1], D'Erfurth, I.[2], Verdier, J.[3], Aubert, G.[4], Gouzy, J.[5], Prosperi, J-M.[6], Huguet, T.[7], Burstin, J.[8], Gallardo, K.[8], and Thompson, R.D.[8]*. [1]INRA, UMR Agroécologie, DIJON, FRANCE; [2]INRA, UMR1347 Agroecologie, DIJON FRANCE; [3]Shanghai Center for Plant Stress Biology, Shanghai Institutes of Biological Sciences, Chinese Academy of Sciences, Shanghai, PR China; [4]INRA, UMR1347 Agroécologie DIJON, FRANCE; [5]INRA, Lab. Interactions Plantes - Microoganismes, TOULOUSE; [6]UMR Diversité et adaptation des plantes cultivées, MONTPELLIER; [7]ENSAT, TOULOUSE; [8]INRA, UMR1347 Agroécologie, DIJON, FRANCE. *(thompson@dijon.inra.fr)

We have been using genomics approaches with *Medicago truncatula* as a tool to identify key genes determining seed yield and composition in Medicago and in closely related legumes. Analyses of the proteome and transcriptome of the component tissues of the developing seed revealed extensive compartmentalization of gene expression and metabolic activities (Gallardo et al, 2007). Using a TF (Transcription Factor) qRT-PCR platform (Verdier et al., 2008) the Affymetrix Gene Chip (Benedito et al, 2008), and more recently, Nimblegen arrays (Buitink et al. submitted), putative regulatory genes specific for each seed tissue were identified, along with putative target genes of transcription factors (TFs). These genes have been located on the *M. truncatula* genetic map and correlations between map positions of TF loci and QTLs for protein quantities and other seed phenotypes were detected. These correlations were confirmed in certain cases by the existence of similar QTLs at syntenic positions in pea. This approach has enabled us to attribute roles to two genes, both specifically expressed in the developing endosperm of *M. truncatula* and present in pea. One encodes a DOF class transcription factor, whose mutant phenotype severely affects endosperm development. The second gene encodes an endosperm-specific subtilase (*SBT1.1*), which affects final seed weight in both species (D'Erfurth et al, 2012). The importance of the endosperm in determining legume seed size and composition will be discussed.

The research leading to these results has received funding from the European Community FP7 grant agreements FP7 KBBE-613551, LEGATO, and FP7 KBBE-289562, ABSTRESS, from the ANR (QualityLegSeed and GenoPea), and from the Burgundy Regional Council.

Keynote Speaker: **Seeds and Nutrition (IFLRC)**

Dr. Grusak is a Plant Physiologist at the USDA-ARS Children's Nutrition Research Center (CNRC), Houston, TX and a Professor of Pediatrics, Baylor College of Medicine. He joined the CNRC in 1990 to develop an interdisciplinary program to link crop science and production agriculture with human nutrition concerns. His research involves understanding the molecular mechanisms and regulation of nutrient transport within plants, with the long-term goal of enhancing the nutritional quality of plant foods for human consumption. Dr. Grusak serves on the Editorial Boards of the journals: Plant and Soil, Crop Science, Plant Foods for Human Nutrition, and Rice Journal. He serves on the Board of Directors of the Texas Academy of Science and is the 2015 President-Elect for the Crop Science Society of America. He was recently appointed as the Scientific Officer for the Office of Scientific Quality Review, which conducts peer review of all USDA-ARS research projects.

Nutritional Enhancement of Food Crops: Recent Conceptual Developments and Strategic Targets for Common Bean

Grusak, M.A.[1*]. [1]USDA-ARS Children's Nutrition Research Center, Department of Pediatrics, Baylor College of Medicine, Houston, TX. *(mike.grusak@ars.usda.gov)

Food crops are an important source of nutritional and health-beneficial compounds for humans. Unfortunately, mineral deficiencies abound in certain population groups due to food insecurity or to the inadequate nutritional composition of staple foods. In recent years, crop scientists have realized that agriculture could be used to impact human health and have worked to enhance nutritional density in staple crops through breeding approaches or management strategies. Our group has focused on several grain legumes to understand the whole-plant dynamics and temporal patterns that control mineral allocation to seeds. We are interested in how the delivery of minerals to aerial tissues is controlled by root and soil processes, and in the crosstalk that occurs between shoots and roots. We also wish to know how mineral trafficking to seeds is regulated by processes in source tissues, which themselves require minerals. In this talk, results will be presented on whole-plant regional and temporal patterns of mineral partitioning in common bean, which are being used to assess where the rate-limiting steps are occuring in the trafficking of various minerals throughout the plant. We will discuss which processes might be the best targets for increasing seed mineral levels, and will provide data on the extent to which these enhancements might be achievable in light of current source tissue pool sizes. Lastly, we will present a framework for setting target levels and assessing dietary impact of a given enhancement strategy. This work was funded by USDA-ARS (Agreement 58-6250-0-008) and by USAID (Feed the Future Grain Legumes Project).

Keynote Speaker: **Legume Mega Projects (ICLGG)**

Kirstin Bett is Professor of Plant Breeding and Genetics in the Department of Plant Sciences, University of Saskatchewan in Canada. She teaches courses at the graduate and undergraduate level in plant breeding and plant genetics. She is currently responsible for a common bean breeding program and genomic and genetic research in pulse crops. Three of her pinto bean cultivars and a yellow bean cultivar are now being grown commercially in western Canada. She has also established a complementary genetics program that uses classical and molecular techniques to better understand the traits that lead to the development of superior pulse crop cultivars. This has included work in seed quality, disease resistance and cold tolerance and has extended to the use of wild species as a source of useful variability. She has been involved in the development of genomic resources for pulse crops and is currently leading the effort to sequence the lentil genome.

Lentil genome sequencing: establishing a comprehensive platform for molecular breeding

Kirstin Bett, Larissa Ramsay, Andrew Sharpe, Douglas Cook, R. Varma Penmetsa, Neha Verma, Melissa Wong, Crystal Chan, Albert Vandenberg, Allen VanDeynze, Clarice Coyne, Rebecca McGee, Dorrie Main, Jaroslav Doezel, Dave Edwards, Sukhijwan Kaur, Shiv Kumar Agrawal, Sripada Udupa

While global production of lentil (*Lens culinaris*) is on the rise, breeding programs are limited in their ability to implement marker-assisted selection (MAS) due to a lack of genomic resources. Large steps have been taken lately to develop SNP-based markers but the availability of a reference genome sequence will provide a basis for further crop improvement. With the common bean and chickpea draft genome sequences now available, it is time to tackle the larger pulse crop genomes such as lentil. Through funding from the Saskatchewan Pulse Growers we have been able to carry out large amounts of next-generation sequencing on CDC Redberry, a small red cultivar from Saskatchewan. An initial draft of 23x coverage produced scaffolds covering over half the genome (2.7 Gb of the expected 4.3 Gb) and recent additional 125x coverage is currently being assembled. Long reads based on PacBio sequencing are being used to assemble smaller scaffolds into larger assemblies. Genotype by sequencing (GBS) in key mapping populations is being used to anchor scaffolds as well as select individuals for resequencing. Collaborations with labs in Australia, Czech Republic, USA and ICARDA will facilitate further assembly and annotation of the genome as well as add to the growing database of genotypic diversity in the global lentil germplasm. The sequence data from the initial 23x coverage was sufficient for the identification of gene sequences for traits of interest in the lentil breeding program and derived SNP markers are now being used in routine MAS.

Keynote Speaker: **Nitrogen Fixation and Plant Nutrition (IFLRC)**

Ken Giller is Professor Plant Production Systems (http://www.pps.wur.nl), within ***WaCASA*** (the **Wa**geningen **C**entre for **A**groecology and **S**ystems **A**nalysis - http://www.wacasa.wur.nl) at Wageningen University. He leads a group of scientists with profound experience in applying systems analysis to explore future scenarios for land use with a focus on food production. Ken's research has focused on smallholder farming systems in sub-Saharan Africa, and in particular problems of soil fertility and the role of nitrogen fixation in tropical legumes, with emphasis on the temporal and spatial dynamics of resources within crop/livestock farming systems and their interactions. He is author of the standard text "*Nitrogen Fixation in Tropical Cropping Systems*" published in second edition in 2001. He leads a number of initiatives such as N2Africa (Putting Nitrogen Fixation to Work for Smallholder Farmers in Africa - http://www.n2africa.org/). Ken joined Wageningen University in 2001 after holding professorships at Wye College, University of London, and the University of Zimbabwe.

N2Africa: Putting nitrogen fixation to work for smallholder farmers in Africa

Ken E. Giller
Plant Production Systems, Wageningen University, P.O. Box 430, 6700AK Wageningen, The Netherlands.

N2Africa (http://www.n2africa.org/) is a large development-to-research project that focuses on tapping expertise from all around the world to ensure the best technologies find their way into the hands of smallholder farmers in Africa. The major output of the project is enhanced productivity, nitrogen fixation and production of the major grain legumes, common bean, groundnut, cowpea, soyabean, chickpea and faba bean is enhanced. We work across 11 countries in East and Central, West and southern Africa through a wide range of partnerships with research and development organisations.

Successful N_2-fixation by legumes in the field depends on the interaction: $(G_L \times G_R) \times E \times M$ that is (legume genotype × rhizobium genotype) × environment × management. Environment encompasses climate and soil stresses. Management includes aspects of agronomic management (use of rhizobial inoculum, mineral fertilizers, sowing dates, plant density, weeding). Although much legume research is focused on identifying best combinations of G_L and G_R, the E and M factors often override the potential of the legume/rhizobium symbiosis for N_2-fixation in the field. Our approach is to target nitrogen fixation technologies to 'socioecological niches' within the huge diversity of countries and agroecologies and farming systems in Africa.

In the second phase of N2Africa, which has just begun, we aim to increase inputs from N_2-fixation on more than 550,000 smallholder farms within the coming five years through: a) Increasing the area of land cropped with legumes; b) Increasing legume productivity through better agronomy and basal (P, K etc) fertilizer; c) Selecting and disseminating legume varieties with increased N_2-fixation; d) Selecting better rhizobium strains and promoting high quality inoculants; e) Linking farmers to markets and creating new enterprises to increase demand for legumes. N2Africa has already reached more than 250,000 farmers and the latest learning will be discussed.

Keynote Speaker: **Biotic Stress and Plant Microbe Interactions (ICLGG)**

Jens Stougaard is Professor of Molecular Biology and Genetics at Aarhus University and Director of the Centre for Carbohydrate Recognition and Signalling (CARB). Jens Stougaard leads a group studying genes regulating development of nitrogen fixing root nodules and mycorrhiza formation in legumes. Currently the mechanisms of Nod-factor perception, the function of receptors involved and the downstream signal transduction cascades are in focus. The plant model system used for this research is *Lotus japonicus* that is also used for investigating the long range signalling integrating root nodule development into the general developmental program of the plant. Genetics, genomics and biochemical methods are used to identify and characterise components of regulatory circuits. In order to improve the genetic analysis and to establish a system for reverse genetics, a large-scale insertion population based on the germ-line specific activity of the LORE1 retroelement is being established and made available to the community.

Bacterial infection of epidermal cells is controlled by a two-step recognition process

Stougaard, J.[1*]. [1]Centre for Carbohydrate Recognition and Signalling, Department of Molecular Biology and Genetics, Aarhus University, Gustav Wieds Vej 10, DK-8000 Denmark. *(stougaard@mb.au.dk)

Development of root nodules in legumes in response to signals secreted from rhizobiais an example of a regulated bacterial infection process that is synchronised with an inducible organ formation. Lipochito-oligosaccharides (Nod-factors), consisting of substituted b,1-4 N-acetylglucosamine (chitin) backbones are the major rhizobial signals triggering root hair deformation, initiation of the bacterial infection process and start of the cell divisions leading to formation of nodule primordia. An important determinant of bacterial recognition and host specificity is the interaction between Nod-factors and the plant receptors involved in signal perception and signal transduction initiating the plant developmental response. In *Lotus japonicus* there are seventeen LysM receptor kinases that could be involved in perception of Nod-factors or other chitin derived signal molecules. The possible role of these LysM type serine/threonine receptor kinases in plant-microbe interaction will be discussed. Biochemical experiments investigating the function of LysM receptors will be presented and the involvement of NFR1 and NFR5 receptor kinases in the earliest physiological and cellular responses will be illustrated. A second recognition step has recently been discovered and the molecular basis of this novel non-self recognition will be presented together with a model for two-step recognition of rhizobial bacteria at the initiation of infection.

Bek et al. (2010) Improved Characterization of Nod Factors and Genetically Based Variation in LysM Receptor Domains Identify Amino Acids Expendable for Nod Factor Recognition in *Lotus* spp. MPMI, 23, 58-66.

Broghammer et al (2012) Legume receptors perceive the rhizobial lipochitin oligosaccharide signal molecules by direct binding. PNAS 109, 13859-14864.

Keynote Speaker: **Biotic Stress and Plant Microbe Interactions (IFLRC)**

Alain Baranger is a geneticist at UMR IGEPP Institute, INRA Rennes, France. He leads a research group focusing on efficiency and durability of the control of pathogen epidemics in legumes, including ascochyta blight and aphanomyces root rot in pea, using standard as well as molecular-based methods. This involves the exploration of variability in the host response (quantitative resistance), of diversity and evolution of pathogen populations (adaptation), and of epidemic processes. Current considered issues are the potential role of plant and canopy architecture traits to control epidemics through various processes (spore dispersion, microclimate, senescence), and the relative and complementary role of plant/canopy architecture and plant resistance genetic factors to reduce disease severity and effects.

Plant architecture and development to control aerial disease epidemics in legumes: the case of Ascochyta blight in pea

Baranger, A.[1*], Giorgetti, C.[1], Jumel, S.[1], Langrume, C.[1], Moussart, A.[1,2], Onfroy, C.[1,2], Richard, B.[1], Rivière, J.P.[1], Vetel, P.[1], and Tivoli, B.[1]. [1]INRA, UMR1349 IGEPP, Le Rheu F-35653, France; [2]UNIP-CETIOM, 11 rue de Monceau, CS 60003, F-75378 Paris, France. *(Alain.Baranger@rennes.inra.fr)

Plant and canopy architecture can contribute to the control of aerial diseases by creating a less conducive environment to their development. This control involves the modification of specific processes such as plant ageing and senescence, microclimatic conditions (leaf wetness duration, temperature and light penetration) and spore dispersal. Ascochyta blight in pea, mainly due to *Didymella pinodes,* is the most encountered and damaging aerial disease worldwide. Available resistance to this pathogen is scarce, partial, and is not always fully expressed in the field. Alternative strategies based on plant and canopy architecture and development modifications have shown that internode length and plant height, as well as leaf area index and senescence are key factors in Ascochyta blight epidemics. The genetic control of such and other architectural and developmental variables (earliness, stipule size, aerial biomass) relies both on some major genes and QTL that often colocalize with known factors controlling partial resistance components. We thus developed different biparental recombinant inbred line populations segregating for these major genes and QTL, as well as near isogenic lines from heterogeneous inbred families segregating within colocalizing QTL confidence intervals. These populations were screened in controlled conditions, where architecture and development are not likely to interfere with epidemics, to define whether these colocalizations were due either to linkage or to pleiotropic genetic effects. First insights showed that linkage effects are involved.

Keynote Speaker: **Applied Genomics (ICLGG)**

Dr. Rajeev Varshney, an Indian national and Principal Scientist (Applied Genomics) is serving ICRISAT as a Research Program Director, Grain Legumes and Director - Center of Excellence in Genomics. In addition to serving ICRISAT, Rajeev, in his dual appointment also served CGIAR Generation Challenge Program based in Mexico as Theme Leader for six years. Before joining ICRISAT, he worked at Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), Germany for five years.

Rajeev has a basic background in molecular genetics and possess more than 15 years research experience in international agriculture. The primary contribution of Rajeev Varshney includes genome sequencing of pigeonpea and chickpea and first generation of molecular breeding products in chickpea and groundnut in addition to large-scale genomic resources like molecular markers, transcriptome assemblies and QTLs for a range of traits in legumes.
Rajeev has >200 publications in leading journals of international reputes including Nature (1), Nature Biotechnology (3), PNAS (1), etc., 10 edited books and Special Issues (as Guest Editor) for several journals to his credit. He has been a frequent invited speaker in several national/ international conferences including G-8 Conference on "Open Data for Agriculture", FAO conference on "Application of Biotechnologies in Developing Countries" and "Digital Design Meeting", chaired by Mr Bill Gates.

The 1000 Pulse Genome Sequencing Initiative: Connecting Genes to Traits

Varshney, RK.[1*]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India.
*(r.k.varshney@cgiar.org)

Chickpea (*Cicer arietinum*) and pigeonpea (*Cajanus cajan*) are playing a vital role in ensuring the nutritional food security in several countries of Asia and sub-Saharan Africa. Average productivity of these pulses is less than 1 t ha–1 due to their expousre to several biotic and abiotic stresses. Breeding efforts to elevate the yield levels and enhance crop productivity could not be achieved due to availability of limited genomic resources andlow level of genetic diversity present in the cultivated pools. ICRISAT genebank has >20,000 and >13,000 accessions of chickpea and pigeonpea, respectively. With an objective to 'explore this huge genetic diversity available to address the issue of low productivity and bottlenecks' associated with narrow genetic diversity, >1000 pulse genomes including 554 chickpea (reference set, elite varieties and parents of several mapping populations) and 526 pigeonpea (reference set, hybrid parental lines, wild species accession and parents of mapping populations) genomes were sequenced at 5X to 13X coverage. These genomes were aligned to their respective reference genomes for variant calling and structural variation analysis. Detailed analysis provided comprehenisve data on diversity features, gene loss, domestication and selection sweep. Multi-location phenotyping data for high priority traits for breeding is being assembled for undertaking genome-wide association studies. In brief, this initiative is expected to identify superior/novel alleles associated with the traits of interest for enhancing crop productivity of these pulse crops.

Keynote Speaker: **Abiotic Stress and Crop Management (IFLRC)**

Professor Kadambot Siddique is the Hackett Professor of Agriculture Chair and Director of The University of Western Australia's Institute of Agriculture. He has 30 years' experience in agricultural research, teaching and management in both Australia and overseas. He has developed a national and international reputation in agricultural science especially in the fields of crop physiology, production agronomy, farming systems, genetic resources, breeding research in cereal, grain and pasture legumes and oilseed crops. Professor Siddique's publications are considered as key papers in the above fields and are widely cited. As a result of Professor Siddique's personal research and with others with whom he collaborates, Australia has become one of the major grain legume exporting nations in the world. His pioneering research on chickpea has contributed enormously to the Australian chickpea industry which is currently valued at more than $300 million per annum.

Professor Siddique is winner of the **Western Australian Year of the Award 2014** (Professions Category) for his contribution to agricultural science and farming community. In September 2013 Professor Siddique was honoured with a prestigious **Dunhunag Award** by China's Gansu Provincial Government for his outstanding contribution to research and leadership within Gansu Province, especially at Lanzhou University. In 2013 Professor Siddique was elected as a **Fellow of the Australian Agricultural Institute** (FAAI) and the citation recognised his outstanding contribution to professional agriculture. In 2011 Professor Siddique was made **Member of the Order of Australia** (AM) in Queen's Birthday Honours List. The citation recognised his lifetime's work in advancing agricultural science as an academic and researcher in the area of crop improvement and agronomy and through contributions to professional associations. In 2005 he was elected as a **Fellow of the Australian Academy of Technological Sciences and Engineering** (FTSE). In 2009 he received a gold medal and citation from the former **President of India, Dr A.P.J. Abdul Kalam**, for his international contribution to agricultural science and education. In 2001, Professor Siddique received **the prestigious "Urrbrae Memorial Award"** for his contribution to Australian agricultural science and the industry. Professor Siddique has published more than 250 scientific papers and book chapters. Professor Siddique is on the Editorial Board of a number of international scientific journals. He has also trained numerous Honours, MSc and PhD students. He is a visiting Professor in a number of overseas universities.

ABIOTIC STRESS IN COOL SEASON GRAIN LEGUMES: GENETIC AND AGRONOMIC APPROACHES

Siddique, K.H.M.[1*], Pang, J.[1,2], and Khan, T.N.[1]. [1]The UWA Institute of Agriculture, University of Western Australia; [2]School of Plant Biology, University of Western Australia. *(kadambot.Siddique@uwa.edu.au)

Among the cool season grain legume species, chickpea, field pea, lentil and faba beans are the most important. They are grown on a range of soil types and environments experiencing various abiotic stresses. Drought at early developmental stages, flowering and pollination and pod andseed set stages may adversely affect yield. High temperatures often combined with drought may also inhibit pollination and pod/seed development. Excess water while causing transient water logging damage may also lead to salinity in the soil. Low temperatures may lead to freezing injury at all stages and less than optimum temperature at flowering affects pollination and pod set. Oftenenvironmental factors interact, e. g. high temperature and drought; salinity and waterlogging. Grain legumes vary in their sensitivity and this may help to choose the appropriate species to address the abiotic constraint identified. Progress has been made in understanding physiological and genetic mechanism and developing tools for selection of key traits for drought resistance and salinity tolerance but such research on low temperature/freezing tolerance or water logging tolerance is sparse. Agronomic management such as time of sowing, no-till technology, weed management and adequate fertilizer application has also been successfully applied to alleviate abiotic stresses. Major breakthroughs in understanding abiotic factors, breeding for tolerance to abiotic stress and their agronomic management continues to offer formidable challenges.

Concurrent Session Abstracts

Monday, July 7, 2014

Fundamental and Applied Genetics and Genomics

ICLGG Fundamental Genomics
Chair: Doug Cook (University of California Davis, USA)

11:00-11:30 Presenter: Scott Jackson (Univ. of Georgia, USA)

Genetic and epigenetic variation in legumes: focus on Glycine max and Phaseolus vulgaris.

Jackson, S.A.[1*], Kim, K-D.[1], ElBaidouri, M.[1], Schmitz, R.[1], Libault, M.[2], Schmutz, J.[3], Qiu, L.[4], and Li, Y-H.[4]. [1]University of Georgia; [2]University of Oklahoma; [3]Hudson Alpha Institute for Biotechnology; [4]Chinese Academy of Agricultural Sciences. *(sjackson@uga.edu)

Reference genome sequences are available for soybean (Glycine max) and common bean (Phaseolus vulgaris). However, these reference genome sequences do not represent the array of variation contained within a species. In order to explore this variation, we created a pan-genome for undomesticated soybean (Glycine soja) and resequenced more than 100 landraces and wild relatives of common bean. Both data sets provide differing levels of insight into sequence and structural variation within a species and provide a framework for examining genetic variation as a tool for crop improvement. In addition, epigenetic variation, that cause by DNA packaging, is a potential source of variation that is being explored to understand its evolution and role variation that is available, or has been used for improvement.

11:30-11:50 Presenter: Stig Andersen (Aarhus University, Denmark)

***Lotus japonicus* natural variation and LORE1 insertion mutants**

Gupta, V.[1], Malolepszy, A.[1], Shah, N.[1], Hirakawa, H.[2], Fukai, E.[3], Jin, H.[1], Mun, T.[1], Urbanski, D.[1], Kawaharada, Y.[1], Markmann, K.[1], Sandal, N.[1], Umehara, Y.[3], Soyana, T.[3], Miyahara, A.[3], Schierup, M.[4], Hayashi, M.[3], Busch, W.[5], Sato, S.[2,6], Stougaard, J.[1], and Andersen, S. U.[1*]. [1]Centre for Carbohydrate Recognition and Signalling, Department of Molecular Biology and Genetics, Aarhus University, Gustav Wieds Vej 10, DK-8000 Aarhus C, Denmark; [2]Kazusa DNA Research Institute, 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818 Japan; [3]Division of Plant Sciences, National Institute of Agrobiological Sciences, Tsukuba 305-8602, Japan; [4]Bioinformatics Research Centre, C. F. Møllers Allé 8, Aarhus University, DK-8000 Aarhus C, Denmark; [5]Gregor Mendel Institute of Molecular Plant Biology, Dr. Bohr-Gasse 3, 1030 Vienna, Austria; [6]Graduate School of Life Sciences, Tohoku University, Katahira 2-1-1, Aoba-ku, Sendai, 980-8577, Japan. *(sua@mb.au.dk)

We are in the process of transforming the genomic resources of the model legume *L. japonicus* to allow QTL and genome-wide association studies of multigene inherited traits to be combined with efficient validation by reverse genetics. These approaches will facilitate study of a wide range of traits, including interactions with symbionts and other microbes, but require a complete and well-annotated genome, a catalog of natural variation, accurate phenotyping methods, and a comprehensive mutant collection. To provide the genotype data needed, we have updated the genome assembly and annotation and re-

sequenced 124 Japanese *L. japonicus* accessions. In order to generate accurate phenotype data, we have developed high-throughput image-based methods for root growth trait quantification. The results of genome-wide association studies based on combined use of these datasets will be described. Testing of the resulting candidate genes is greatly facilitated by access to LORE1 insertion mutants, and the status of the LORE1 collection, which now includes more than 340,000 annotated insertions, will be presented (www.carb.au.dk/lore1).

11:50-12:10 Presenter: Greg Perry (University of Guelph, Canada)

Using SNP genotyping to identify regions of *Phaseolus acutifolius* introgression in OAC-Rex, a CBB resistant variety of *Phaseolus vulgaris*

Perry, GE.[1*], Xie, W.[2], Castro, ED.[1], Cooper, D.[1], Turner, F.[1], Reinprecht, Y.[1], Dinatale, C.[3], Munholland, S.[3], Crosby, WC.[3], and Pauls, KP.[1]. [1]University of Guelph, Department of Plant Agriculture; [2]AAFC, University of Guelph; [3]University of Windsor, Department of Biology. *(perryg@uoguelph.ca)

OAC-Rex was the first variety of dry bean released in North America that was resistant to Common Bacterial Blight (CBB), caused by *Xanthomonas axonopodis* pv. *phaseoli*. Although some resistance to CBB has been detected in the vulgaris germplasam, strong resistance has only been achieved using interspecific crosses between P. vulgaris and species such as *Phaseolus coccineus*, and *Phaseolus acutifolius*. In the case of OAC-Rex, the CBB resistance was the result of an interspecific hybridization with the *P. acutifolius* line PI440795. As part of the Applied Bean Genomics and Bioproducts Project, the genomic sequence for OAC-Rex and PI440795 is being sequenced using the Illumina HiSeq platform. Although the full-length chromosomal sequence is not available at this time, contigs and scaffolds allow us to interrogate both lines using BLAST. Using the SNP markers from the BeanCAP project, we identified over 6000 markers present in OAC-Rex, and 3800 in PI440795. Markers which were shared between the two lines were examined for alleles which could be considered as acutifolius specific by comparing them to G19833, an Andean *P. vulgaris* line, whose genomic sequence has been previously published. By identifying regions with potential *P. acutifolius*-derived sequence, we will be able to better understand the rearrangement of the *P. vulgaris* and *P. acutifolius* genetic information during the interspecific cross.

12:10-12:30 Presenter: Stephan Schröder (North Dakota State University, USA)

Optimization of Genotyping by Sequencing (GBS) Data in Common Bean (*Phaseolus vulgaris* L.)

Schröder, S.[1*], Mamidi, S.[1], Lee, R.[1], Osorno, J.M.[1], and McClean, P.E.[1]. [1]North Dakota State University, Department of Plant Sciences, Dept. 7670, PO Box 6050, Fargo, ND 58108-6050. *(stephan.schroder@ndsu.edu)

The standard version of the Genotyping by Sequencing (GBS) method uses a relatively large fragment pool and is typically sequenced at low coverage (1X). This often results in misscoring of heterozygotes as homozygotes and a high rate (≥ 30%) of missing data points. Common bean has a haploid genome size of 550 Mb. We are interested in improving quality and coverage of GBS data in order to: i) accurately estimate genetic diversity in a drought diversity panel and ii) find associations with traits of agronomic importance using a Genome-Wide Association approach. With these two considerations in mind, we developed an improved GBS method, which utilizes an *in silico* digest of the bean genome to predict

fragment density and length, a double digest of genomic DNA, ligation of a barcoded and a common Y-adapter, and DNA fragment size selection to achieve a reduced fragment pool that can be sequenced at higher coverage. In our pilot study consisting of 6 diverse Middle American dry bean lines, we obtained reads that were present at a coverage ≥ 3X in all six lines. More than 14,000 high quality SNPs were identified, with an average of one SNP every 36 Kb and the maximum distance between adjacent SNPs of 1.75MB. These preliminary results provide us with a high marker density which will enable us to address the questions mentioned above.

IFLRC Applied Genetics & Genomics
Chair: Tom Warkentin (University of Saskatchewan, Canada)

11:00-11:30 Presenter: Noel Ellis (CGIAR, Hyderabad, India)

Shifting the focus: populations, genetics and genomics

Ellis, T.H.N.[1*]. [1]CGIAR Research Program on Grain Legumes, ICRISAT, Patancheru 502 324, Andhra Pradesh, India. *(n.ellis@cgiar.org)

For many legume species whole genome sequence information is either available or; being generated, this resource can provide many tools for genome analysis. Extensive germplasm collections for legumes, held in a variety of institutions, have been characterised in terms of their genomic diversity enabling targeted access to accessions tailored to a variety of needs. These can be accessed, for example, by searching for maximally different genomes, or by comprehensive searches within a sub-population. The generation of transgenic plants is also feasible in many legume species, as is the analysis of gene function in transient assays such as VIGS. All of these should provide a rich resource for understanding and deploying appropriate genes in breeding programmes. However, two additional resources are required: systematic mutant populations and consensus genetic linkage maps.

Systematically curated mutant populations provide an alternative to VIGS and transgenesis for analysis of gene function. These have been generated in several species, but are not yet available for all legume crops.

Genetic maps are not made redundant by genome sequence: they describe the distribution of alleles in populations and this is essential for connecting genotype and phenotype. In order to exploit mutant populations and genomic tools we need robust genetic analysis. The efficient application of genomics to breeding requires the sharing of both genotypic and phenotypic data: a lesson to be learnt from the rapid progress in genomics that was driven by data sharing. The time is ripe for a re-emphasis on the use of genetics to dissect and understand traits in terms of their discrete determinants.

11:30-11:45 Presenter: Rachit K. Saxena (ICRISAT, India)

Whole genome re-sequencing based classification of heterotic pools for accelerating hybrid breeding in pigeonpea

Saxena, RK.[1*], Patel, K.[1], Obarley, Yu.[2], Kumar, V.[1], Kim, C.[3], Singh, V.[1], Shaun, An.[2], Kuruvinashetti,

MS.[4], Rhee, H.[3], Kim, B.[3], Zhang, W.[2], Sameerkumar, CV.[1], Karwa, A.[4], and Varshney, RK.[1]. [1]Inetrnational Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Millennium Genomics Inc., Shenzhen, China; [3]MACROGEN Inc., Seoul, South Korea; [4]Krishidhan Seeds Pvt Ltd, Jalna, India. *(r.saxena@cgiar.org)

Hybrid technology has potential to elevate the yield levels in pigeonpea. Recently, the world's first grain legume hybrid of pigeonpea ICPH 2671 has been released for commercial cultivation in India, which showed 47% yield advantage over the check varieties. To develop such hybrids, breeders make thousands of random crosses between cytoplasmic male sterile (CMS) lines and tester lines. Genomic diversity along with the phenotyping data have been used for predicting best possible combinations and defining heterotic pools in many crop species such as maize, rice, sunflower and rapeseeds. In order to define heterotic pools in pigeonpea, a set of 104 parental lines (10 CMS, 12 maintainers and 82 restorers) have been re-sequenced following whole genome re-sequencing (WGRS) approach. WGRS yielded 511 GB sequence data with the coverage ranging from 5X to 10X. A total of 3.4 million SNPs could be identified across 104 lines, while comparing individual genotypes with the reference genome and SNPs ranged from a minimum of 15,388 to a maximum of 84, 851. Structural variations such as copy number and presence/ absence variations are being identified. In parallel, these parental lines are being used to develop testcrosses in factorial mating design. F1 hybrids along with parental lines will be phenotyped for yield and yield related traits. In brief, the availability of genome-wide SNP variations combined with the phenotypic data should provide clues on candidate genomic regions associated with yield and yield related traits as well as those associated with heterosis and hetereotic pools in pigeonpea for accelerating hybrid improvement.

11:45-12:00 Presenter: Ping Wan (Beijing University of Agriculture)

A high-density SNP genetic map and QTL mapping for yield and other agronomic traits in adzuki bean (*Vigna angularis*)

Wan, PING.[1*], Ai, Danjiao.[1], Yang, Kai.[1], Zhao, Bo.[1], and Li, Yisong.[1]. [1]College of Plant Science and Technology, Beijing University of Agriculture. *(pingwan3@163.com)

Cultivar ass001, wild adzuki bean CWA108 and one hundred fifty F2 individuals derived from the cross of them were sequenced by RAD-seq technology. In total, 133.93G base sequences and 379024 SNPs were obtained. 3617 segregated SNPs were used to mapping, a SNPs genetic map of adzuki bean was firstly constructed. The genetic map is composed of 1571 SNP markers, spanned over the distance of 1031.171 cM with an average distance between markers of 0.656 cM and covered 11 linkage groups.

The important agronomic trait QTLs of bloomin and ripening time, leaf length and width, stem tickness, pod width, 100-seed weight and the number of seeds per pod were mapped by SNPs markers. Three flowering time (FLD) QTLs on chromosome 3, 4 and 5 explained 8.5%、10.6% and 9.4% of phenotypic variance. Five QTLs controlling mature stage were mapped on chromosome 2, 3 and 4, and phenotypic variances were 12.9%, 9.9%, 15.9% ,18% and 11.2%. QTLs of FLD qFLD50 4, maturity qPDDM 50 4 and qPDDM100 4 have the same co-segregated SNP marker s58_ 238422. QTLs of leaf length, stem tickness and pod width were mapped on different region of chromosome 10, and explained 12.7%、13.7% and 11.3% of phenotypic variance. Two leaf width QTLs were mapped on chromosome 2 and 6, which explained of 7.3% and 7.2%. phenotypic variance. Two 100-seed weight (SD100WT) QTLs of chromosome 6 and 10 were identified with the phenotypic variance of 13.3% and 11.0%. QTLs of

SD100WT 10 and stem tickness STT 10 have the same co-segregated SNP marker s41_311101. one major QTL of seed number per pod SDNPPD 6 was mapped on chromosome 6, explained 11.9% phenotypic variance. The QTLs of SDNPPD 6, 100-seed weight SD100WT 6, leaf width LFMW 6 located in common SNP marker interval of s768_70977 and s85_114079, and were co-segregated with s130_56874.

This work was supported by fund from National Natural Science Foundation of China (Project Number 31071474)

12:00-12:15 Presenter: Trupti Joshi (University of Missouri, Columbia, USA)

Next Generation Resequencing of Soybean Germplasm for Trait Discovery

Joshi, T.[1,2,3*], Khan, S.M.[4], Liu, Y.[4], Maldonado dos Santos, J.V.[5], Wang, J.[1], Rynge, M.[6], Mehta, N.[7], Valliyodan, B.[3,5], Xu, D.[1,2,3], and Nguyen, H.T.[2,3,5]. [1]Department of Computer Science, University of Missouri, Columbia; [2]Christopher S. Bond Life Sciences Center; [3]National Center of Soybean Biotechnology; [4]Informatics Institute; University of Missouri, Columbia; [5]Division of Plant Sciences, University of Missouri, Columbia; [6]Information Sciences Institute, University of Southern California; [7]iPlant Collaborative, University of Arizona. *(joshitr@missouri.edu)

With the advances in next generation sequencing (NGS) technology and significant reduction in sequencing costs it is now possible to sequence large sets of crop germplasm and generate whole genome scale structural variations and genotypic data. In depth informatics analysis of the genotypic data can provide better understanding of the links with the observed phenotypic changes. This approach can be used to further understand and study different traits for the improvement of crops by design.

We have conducted resequencing of several soybean germplasm lines selected for major traits including oil, protein, soybean cyst nematode resistance (SCN), abiotic stress resistance (drought, heat and salt) and root system architecture. We have done bioinformatics analysis and identified SNPs and insertion, deletions using GATK3.0 software. We have also conducted copy number variations (CNV) analysis and SNP annotations with SnpEff. We conducted 25 genomes case study for analysis of SCN resistance and classified them into four different categories of resistance and susceptibility levels. GWAS analysis identified major SNPs associated with the phenotypic changes between these lines. We have performed linkage disequilibrium and haplotype analysis using Haploview. We have also applied generalized linear models (GLM) and mixed linear models (MLM) using TASSEL for identifying SNPs significant for phenotypic changes.

Analysis was conducted using XSEDE as the computing infrastructure, iPlant as the data and cloud infrastructure, and the Pegasus workflow systems to control and coordinate the data management and computational tasks. All data including GWAS, SNP annotations can be accessed through Soybean Knowledge Base (SoyKB) at http://soykb.org.

12:15-12:30 Presenter: Gilles Boutet (INRA, Rennes, France)

SNP discovery in pea: A powerful tool for academic research and breeding

Boutet, G.[1*], Duarte, J.[2], Alves Carvalho, S.[1], Lavaud, C.[1], Uricaru, R.[1,3], Peterlongo, P.[3], Pilet-Nayel, M-L.[1], Baranger, A.[1], and Rivière, N.[2]. [1]UMR1349 IGEPP INRA AGROcampus-Ouest Université Rennes1, 35653 LE RHEU France; [2]BIOGEMMA, Upstream Genomics Team, 63720 CHAPPES France; [3]INRIA

Rennes - Bretagne Atlantique/IRISA, EPI GenScale, Rennes, France. *(gboutet@rennes.inra.fr)

Pea has a 4.3 Gb complex genome for which only limited genomic and sequencing resources are available to date. In order to answer to an increasing demand from French breeders for a breakthrough in Marker Assisted Selection, we carried out a massive development of markers in pea.

We sequenced eight cDNA normalized libraries from genotypes representative of modern pea breeding material, assembled a large set of 10,000 cDNA contigs, and identified over 35,000 reliable SNP markers. A SNP subset was genotyped with the Golden Gate assay to generate a high density reference composite genetic map covering 1255 cM and comprising 2070 markers including 1340 newly developed SNPs, anchored to the *M. truncatula* physical map. Developed SNPs furthermore showed efficiency in structuring diversity in a collection of pea cultivars, even using a proposed reduced subset of 297 most informative SNPs (Duarte *et al.*, 2014).

A complementary approach of SNP "genotyping by sequencing" ran on genomic DNA libraries from a 48 RILs mapping population. It has developed to date more than 100,000 SNPs, among which approximately 60,000 will undergo mapping (unpublished).

This work gives a comprehensive knowledge for the selection of choice subsets of SNP markers useful for polymorphism, mapping and hierarchical information purposes. These new resources publicly delivered by the PEAPOL project will thus help as tools in cumulating alleles at QTLs for traits of interest, directing the creation of new pea ideotypes adapted to various climates and cropping systems, with stabilized and high yields.

Duarte *et al.* (2014) *BMC Genomics* 15:126

ICLGG Evolution
Chair: Sachiko Isobe (Kazusa DNA Research Institute, Japan)

14:00-14:30 Presenter: Peter Tiffin (University of Minnesota, USA)

Targets of selection in the *Medicago* genome

Tiffin, PETER.[1*]. [1]University of Minnesota. *(ptiffin@umn.edu)

Population genomic data provide opportunities to identify the genes that contribute to naturally occurring phenotypic variation and to characterize how selection has shaped the evolution of those genes. I will present results from three series of analyses that made use of full genome sequence data from more than 200 accessions of M. truncatula. These analyses: i) identify targets of selection and how expression, genomic location, and recombination affects genome-wide diversity, ii) characterize the role of local adaptation, and iii) compare whether selection has acted differently on genes identified through forward genetic screens and association genetic analyses. The results from these analyses identify legume genes that may be most likely to contribute to phenotypic variation (and thus most amenable for crop improvement), the evolutionary history of nodulation genes, and the evolutionary stability of symbiotic interactions.

14:30-15:00 Presenter: Maren Friesen (Michigan State University, USA)

Symbiotic Dimensions of Trifolium Biodiversity

Maren L. Friesen[1], Sharon Y. Strauss[2], Brain L. Anacker[2], Joseph P. Dunham[3], Prateek Shetty[1].
1: Department of Plant Biology, Michigan State University; 2: Department of Evolution and Ecology, University of California, Davis; 3: Section of Molecular and Computational Biology, University of Southern California

Understanding the biodiversity of natural plant communities has twofold relevance for agriculture. First, this diversity underlies the genetic variation drawn upon by breeders. Second, plants in both ecological and agronomic communities compete with one another for resources and structure the soil microbial communities important for plant performance. Diverse North American *Trifolium-Rhizobium* communities are an exemplar system in which the roles of positive and negative feedbacks in coexistence can be dissected at molecular, functional, and taxonomic levels. We find that plants make more large nodules in their home soils and that nodulation correlates with performance, demonstrating that rhizobia are an important part of the niche. Competition experiments show that plants allocate more to nodules when competing against members of their own species, suggesting that symbiotic interactions play a role in species coexistence. Nodule genotyping shows widespread sharing of rhizobium strains across *Trifolium* species with the majority of structuring occuring between different soils rather than species. Using 16S amplicon sequencing, we find that nodules harbor a small but diverse community of bacteria that is largely conserved; however, species structure this community to a small extent as does the soil from which they presumably originate. A de novo transcriptome assembly of one species is underway; preliminary results suggest that a high fraction of transcripts belong to root-colonizing fungi and thus fungal members of the microbiome may also play key roles in performance. The overarching goal of this work is to bridge organismal and community scales to predict coexistence and inform variation in biological nitrogen fixation.

15:00-15:20 Presenter: Steven Cannon (USDA-ARS)

Multiple incidents of polyploidy and nodule evolution near the origin of the legumes

Cannon, S.B.[1*], McKain, M.[2,3], Harkess, A.[3], Doyle, J.J.[4], and 1kp_project_consortium, .[5]. [1]USDA-Agricultural Research Service; [2]Donald Danforth Plant Sciences Center; [3]University of Georgia; [4]Cornell University; [5]multiple institutions. *(steven.cannon@ars.usda.gov)

As part of the Thousand Plant Transcriptomes (1kp) project, we have evaluated the transcriptomes and genomic proteomes from 20 diverse legumes and 16 outgroup species. We reconstructed and analyzed thousands of phylogenetic trees calculated from transcriptomes and genomic proteomes to identify patterns consistent with whole genome duplications (polyploidy events). We find that the papilionoid whole genome duplication (WGD) occurred in the common ancestor of the entire Papilionoideae. The earliest diverging lineages of the subfamily include both non-nodulating and nodulating taxa. Among the latter are the familiar lineages of the subfamily: genistoids (e.g. lupin) and dalbergioids (e.g. peanut), phaseolids (e.g. beans), galegoids (e.g. clovers). Thus, the ancestral WGD likely influenced the evolution of all papilionoid species. We also find evidence for several independent WGDs near the base of other major legume lineages: in the Mimosoid-Cassiinae-Caesalpinieae (MCC) clade (the classical Mimosoideae clade and elements of the caesalpinioid grade that includes it), and in the two other sampled clades (Detarieae and Cercideae) that comprise the remainder of the caesalpinioid grade. We note that nodulation arose in

two clades that experienced WGD near their origins (the MCC and Papilionoid clades), but also that there are numerous non-nodulating lineages in both clades.

15:20-15:40 Presenter: Elisa Bellucci (Università Politecnica delle Marche, Ancona, Italy)

Decreased nucleotide and expression diversity and modified co-expression patterns characterize domestication in the common bean

Bellucci, E.[1], Bitocchi, E.[1], Ferrarini, A.[2], Benazzo, A.[3], Biagetti, E.[1], Rau, D.[4], Rodriguez, M.[4], Attene, G.[4], Jackson, S.A.[5], Nanni, L.[1], Fernie, A.R.[6], Nikoloski, Z.[7], Bertorelle, G.[3], Delledonne, M.[2], and Papa, R.[1]*. [1]Department of Agricultural, Food and Environmental Sciences, Università Politecnica delle Marche, Via Brecce Bianche, 60131 Ancona (Italy); [2]Department of Biotechnology, University of Verona, Strada le Grazie 15, 37134 Verona (Italy); [3]Department of Life Sciences and Biotechnology, University of Ferrara, Via Luigi Borsari 46, 44100 Ferrara (Italy); [4]Department of Agriculture, University of Sassari, Via E. de Nicola, 07100 Sassari (Italy); [5]Center for Applied Genetic Technologies, University of Georgia, 111 Riverbend Road, 30602 Athens (USA); [6]Central Metabolism Group, Max-Planck-Institute of Molecular Plant Physiology, 14476 Potsdam-Golm, Germany; [7]Systems Biology and Mathematical Modeling Group, Max Planck Institute of Molecular Plant Physiology, Potsdam-Golm, 14476, Germany. *(r.papa@univpm.it)

Using RNA sequencing technology and *de novo* transcriptome assembly, we compared representative sets of wild and domesticated accessions of *Phaseolus vulgaris* from Mesoamerica. RNA was extracted at the first true-leaf stage, and *de novo* assembly was used to develop a reference transcriptome; the final dataset consists of ~190,000 SNPs from 27,243 contigs in expressed genomic regions. A drastic reduction in nucleotide diversity (~60%) is evident for the domesticated form, compared to the wild form, and almost 50% of the contigs that are polymorphic were brought to fixation by domestication. In parallel, the effects of domestication decreased the diversity of gene expression (18%). While the co-expression networks for the wild and domesticated accessions demonstrate similar seminal network properties, they show distinct community structures that are enriched for different molecular functions. After simulating the demographic dynamics during domestication, we found that 9% of the genes were actively selected during domestication. We also show that selection induced a further reduction in the diversity of gene expression (26%) and was associated with five-fold enrichment of differentially expressed genes. While there is substantial evidence of positive selection associated to domestication, in a few cases, this selection has increased the nucleotide diversity in the domesticated pool at target loci associated to abiotic stress responses, flowering time, and morphology.

IFLRC Applied Genetics & Genomics; Disease Resistance
Chair: Ashutosh Sarker (ICARDA, India)

14:00-14:15 Presenter: Janila Pasupuleti (ICRISAT, India)

Identification of introgression lines with superior pod yield and improved rust resistance in peanut (*Arachis hypogaea* L.)

Pasupuleti, JANILA.[1*], Pandey, MK.[1], Manohar, SS.[1], Sudini, H.[1], Upadhyaya, HD.[1], and Varshney, RK.[1].

[1]ICRISAT. *(p.janila@cgiar.org)

A major QTL explaining up to 82.62% of phenotypic variation for rust resistance was introgressed into three popular peanut varieties (TAG 24, ICGV 91114, JL 24) using marker-assisted backcrossing (MABC) approach. The donor parent, GPBD 4 derived its resistance from one of its interspecific parent, ICGV 86855 (CS 16), which in turn received from a diploid wild species, *Arachis cardenasii.* Four linked markers (IPAHM103, GM2079, GM1536, and GM2301) present in the QTL region were employed for foreground selection.

Preliminary yield evaluation of 51 introgression lines (ILs) (17 of TAG 24, 13 of ICGV 91114 and 21 of JL 24) along with parents and checks showed significant differences among the lines for yield parameters and rust resistance. The pod yield of ILs was up to 56-96% higher than recurrent parents. The superior pod yield in ILs is in part attributed to pod yield protection offered by resistance. The ILs were resistant to rust with a disease score of 2.0 or 2.5 at 90 DAS (on 1-9 scale) similar to donor parent, while the recurrent parents had higher score (5.0 in TAG 24, 6.5 in ICGV 91114, 7.0 in JL 24). Disease progress from 75 to 90 days was slower in ILs. The differences were not significant for days to flowering between ILs and their respective recurrent parents. Combining disease resistance and early maturity in peanut varieties is the most significant outcome. Further evaluations and promotion of promising ILs to multi location evaluation will facilitate nominations to varietal release trials.

14:15-14:30 Presenter: Ehsan Sari (University of Saskatchewan)

Genotype-dependent interaction of lentil lines with *Ascochyta lentis*

Sari, E.[1]*, Banniza, S.[1], and Vandenberg, A.[1]. [1]Department of Plant Sciences/Crop Development Centre, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada. *(ehsan.sari@usask.ca)

Previous genetic studies suggested that resistance genes in the well-known ascochyta blight resistant lentil lines CDC Robin, ILL 7537, 964a-46, ILL 1704 are non-allelic. To understand how different resistance genes manifest resistance in these genotypes, cellular and molecular defense responses were compared after inoculation with the causal pathogen *Ascochyta lentis*. Histological tests suggested that cell-death inhibition might be mechanism of resistance in CDC Robin. By contrast, limited colonization by *A. lentis* of epidermal cells of 964a-46 was suggested as a mechanism of resistance in this line. Comparing the expression of key genes in the major signaling pathways of CDC Robin and 964a-46, the salicylic acid signaling pathway was only triggered in 964a-46. The jasmonic acid pathway was triggered in both resistant genotypes, however at a lower expression level in 964a-46 than in CDC Robin. These observations confirmed the existence of separate ascochyta blight resistance mechanisms in different lentil lines supporting the hypothesis of different resistance genes.

14:30-14:45 Presenter: Judith Lichtenzveig (Curtin University, Australia)

Pathogenomics of the *Didymella* spp. causal agents of Ascochyta blights in legumes

Lichtenzveig, J.[1]*, Turo, C. J.[1], Williams, Angela.[2], and Hane, J.[1]. [1]Department of Environment & Agriculture, and Centre for Crop Disease Management, Curtin University, Western Australia; [2]Plant-Industry, CSIRO, Floreat, Western Australia. *(Judith.Lichtenzveig@curtin.edu.au)

The *Didymellaceae* family includes some of the most important pathogens of legume crops: the causal agents of Ascochyta blight in chickpea, pea, lentil, and faba beans among others (Aveskamp et al 2010). Despite their substantial economic impact, little is known about the molecular aspects of pathogenicity in these closely related species. At this meeting, the first genome assemblies and comparative analyses of eight legume pathogens, *Ascochyta rabiei* (chickpea), *Peyronellaea pinodes* (*syn*. *Mycosphaerella pinodes*), *P. pinodella, A.pisi* and *Phoma koolunga* (field pea), *A. lentis* (lentil), *A. fabae* (faba bean) and *Phoma medicaginis* (pathogen of the model legume *Medicago truncatula*) will be presented and discussed. Untrained *ab-initio* annotation resulted in the identification of 9,000-12,000 genes per species, of which 91-97% are complete gene models. The sequence data is serving to: pinpoint areas of synteny and clusters of genes associated with reproduction and adaptation; identify pathogenicity-related gene-candidates through proteomic, transcriptomic and *in silico* comparative analyses; and design DNA makers for diagnostics and studies in population structure. Among the pathogenicity related genes, we have identified potential necrotrophic effectors that seem to operate similarly to those found other fungal pathogens of the order of the Pleosporales. Detailed understanding of the molecular mechanism involved in fungal adaptation in general, and pathogenicity in particular, is facilitating the development of novel tools and strategies in crop protection.

This project is co- funded by Grains Research and Development Corporation and Curtin University.

14:45-15:00 Presenter: Jagmeet Kaur (Punjab Agricultural University, Ludhiana, India)

Moisture stress induced changes in metabolites and cellular functions of chickpea (*Cicer arietinum* L.) genotypes

Randhawa, Navkiran.[1], Kaur, JAGMEET.[1*], Kaur, S.[2], Singh, S.[1], and Singh, I.[1]. [1]Department of Plant Breeding and Genetics, Punjab Agricultural University, Ludhiana, India; [2]Department of Biochemistry, Punjab Agricultural University, Ludhiana, India. *(jagskaur@gmail.com)

The present investigation was aimed to study moisture stress induced changes in metabolites and cellular functions in *in vitro* identified tolerant (GL28151, RSG963, PDG3) and sensitive (GL22044, GNG1861, PBG1) chickpea genotypes. Moisture stress was induced during crop development by restricting irrigation at different growth stages viz. one pre-sowing irrigation (WSVFP), restricted irrigation at flower initiation (WSF), restricted irrigation at pod-initiation (WSP). Cellular functions (leaves) viz membrane permeability index, relative water content and lipid peroxidation and osmolytes (seeds) viz. total soluble sugars, starch, sucrose, proline, nitrogen content along with protein profiling were estimated in under control and stressed conditions. Antioxidative enzymes (peroxidase, catalase, superoxide dismutase and glutathione reductase) were assessed in seeds at pod filling stage. RSG963 was the most tolerant genotype in terms of minimal damage caused to cellular functions and attainment of maximum yield under stress conditions whereas GL22044 emerged as highly sensitive genotype with disruption in cellular functions and minimum yield. The least deterioration of cellular functions and higher accumulation of osmolytes, nitrogen and enhanced activities of anti oxidative enzymes in RSG963 might be responsible for rendering tolerance to moisture induced stress. The pronounced cellular damage and lesser alleviation in the content of osmolytes, nitrogen and activities of antioxidant enzymes was observed in sensitive genotype GL22044 under stress treatments. High molecular weight protein bands were found to be either absent or of low intensity in sensitive genotypes (GL22044, GNG1861 and PBG1) under severe stress treatment (WSVFP), sown with one pre-sowing irrigation.

15:00-15:15 Presenter: Renu Singh (CCS Haryana Agricultural University, India)

Mapping micronutrients using recombinant inbred lines (RILs) in Mung bean (*Vigna radiata* L.)

Singh, RENU.[1,2*], (Sjaak) Heusden, A. W.[1], Kumar, R.[3], Visser, R.G.F.[1], and Yadav, R. C.[2]. [1]Laboratory of Plant Breeding, Plant Research International (PRI), Wageningen University, The Netherlands; [2]Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar, Haryana, India; [3]Department of Plant Breeding, College of Agriculture, CCS Haryana Agricultural University, Hisar, Haryana, India. *(renuboora@gmail.com)

Malnutrition, particularly among women, children and adolescents living in developing world, is an emergency that needs immediate attention. Vegetarian Indian diets are qualitatively deficient in micro-nutrients such as iron, calcium, vitamin A and zinc, which have direct impact on growth, metabolism and reproduction in human. One of the methods to mitigate micro-nutrient deficiencies is to develop food crop cultivars with higher levels of essential micro-nutrients. As such, the food legumes are of major nutritional importance, especially in developing countries, because they have high protein contents with biological values. Mung bean is one of the major food legumes consumed by people in Indian sub-continent. As an initial step, available mung bean genotypes were assessed for genetic diversity of selected micro-nutrient and protein contents. Marker analysis (AFLP & ISSR) shows moderate genetic diversity ranging from 65 to 87 %. Chemical analysis showed a fair range of micro-nutrient and protein variation (Fe content ranging from 1.6 to 9.3 mg/100g; Zn content ranging from 1.5 to 3.9 mg/100g and total protein content ranging from21.1 to 30 %). Fe and Zn content showed a positive correlation (r = 0.469) along with fair heritability values (h2 = 0.259 for Fe and 0.727 for (Zn). The existing genetic diversity provides an opportunity to make indirect selection for both the traits. Results of RIL analysis are being used for developing new mung bean lines with higher contents of these micro-nutrients. The micronutrient content varied between individuals of the populations and values show transgressive segregation, but there was no significant association between the markers and the phenotypic traits.

15:15-15:30 Presenter: Larn McMurray (SARDI, Adelaide, Australia)

Improved weed control in Australian pulse production through advancements in genetic and agronomic research

McMurray, L.S.[1*], Paull, J.[2], Lines, M.D.[1], Mao, D.[1], Sherriff, S.A.[1], Rodda, M.[3], Hobson, K.[4], Kennedy, P.[3], Preston, C.[2], Oldach, K.[1], Yang, S.Y.[2], and Brand, J.[3]. [1]South Australian Research and Development Institute; [2]The University of Adelaide; [3]Department of Environment and Primary Industries, Victoria; [4]NSW Department of Primary Industries. *(larn.mcmurray@sa.gov.au)

Australian winter pulse production of chickpea, lentil, faba bean and field pea is in excess of 1.0 M ha annually and offers rotational and cash crop benefits to growers (1). Successful and profitable pulse production is reliant on the use of modern, innovative and broad acre mechanized systems. Weeds are a major production constraint in these systems due to inherent low levels of crop competitive ability, limited availability of registered herbicides, low levels of crop herbicide safety and the increasing occurrence of herbicide resistant weeds (2). Pulse Breeding Australia and the Southern Region Pulse Agronomy

program are attempting to address these limitations in pulses through combining outputs from both breeding and agronomic research. This presentation will outline recent progress made by these programs in the areas of novel herbicide tolerance development (imidazolinone and metribuzin), agronomic herbicide management strategies for improved weed control and the development of varieties better suited to the agronomic practice of "crop-topping" herbicide resistant weeds. It will also discuss the current limitations to effective weed control in the Australian system, the current use of innovative agronomic production methods to improve weed control and future research and regulatory needs required in this area to help sustain Australian pulse production.

ICLGG Development
Chair: Sachiko Isobe (Kazusa DNA Research Institute, Japan)

16:00-16:30 Presenter: Catherine Rameau (INRA, Versailles , France)

Strigolactones and other long distances signals regulating shoot branching

Rameau, C.[1*], de Saint Germain, A.[1], Ligerot, Y.[1], Clavé, G.[2], Pillot, J.P.[1], Dalmais, M.[3], Bendahmane, A.[3], Bonhomme, S.[1], and Boyer, F.D.[2]. [1]Institut Jean-Pierre Bourgin, UMR1318 Institut National de la Recherche Agronomique (INRA)-AgroParisTech, Route de Saint-Cyr (RD 10), F-78026 Versailles Cedex, France; [2]Centre de Recherche de Gif, Institut de Chimie des Substances Naturelles, UPR2301 Centre National de la Recherche Scientifique (CNRS), 1 avenue de la Terrasse, F-91198 Gif-sur-Yvette Cedex, France; [3]Unité de Recherche en Génomique Végétale, INRA/CNRS, CP5708, 91057 Evry Cedex, France. *(rameau@versailles.inra.fr)

Shoot branching results from the tight regulation of axillary bud outgrowth at most leaf axils. For each axillary bud along the stem, endogenous and environmental signals (e.g. light, nutrition status) are integrated for maintaining the bud in a dormant state or inducing its outgrowth. The use of pea branching mutants and grafting experiments demonstrated the existence of a novel signal acting as a branching inhibitor, now identified as strigolactones (SL). Here several advantages of pea as a model species will be presented for elucidating several aspects of SL signaling pathway. Its simple architecture with easy access to axillary buds allows both precise phenotyping and comparison of shoot branching in the different mutants screened by forward or reverse genetics (TILLING). The possibility to apply SL onto the pea plant in several ways is very powerful for Structure-Activity-Relationships studies and for the use of labelled SL. Tritiated-labeled SLs and fluorescent SLs are being synthesized and their fate within the plant is analyzed. Different types of grafting are very easy to perform in pea for identifying and characterizing long distance signals. Evidences for further long distance signals, with a strong influence on shoot branching will be shown here, such as the *RMS3*-dependent graft-transmissible signal which can partially suppress branching, independently of SLs. The cloning of this gene demonstrates that *RMS3* encodes an α/β-hydrolase identified as the SL-receptor and very likely moving in the phloem sap.

16:30-17:00 Presenter: Jim Weller (University of Tasmania, Australia)

Genetic control of flowering in temperate legumes

Weller, JL.[1*], Hecht, V.[1], Liew, LC.[1], Ridge, S.[1], Sussmilch, FC.[1], Vander Schoor, JK.[1], Rajandran, V.[1], Rubenach, A.[1], Ortega-Martínez, R.[1], and Macknight, RC.[2]. [1]School of Biological Sciences, University of Tasmania, Australia; [2]Department of Biochemistry, University of Otago, Dunedin, New Zealand. *(Jim.Weller@utas.edu.au)

We are using a comparative approach to explore the genetic network controlling flowering time across a number of temperate legumes. We have performed comprehensive isolation/annotation of flowering-related gene families in several legume species and are identifying genes with a role in flowering processes using forward and reverse screening and analysis of natural variation. In pea, we have cloned seven photoperiod-response loci. These include the *SN*, *DNE*, *HR* and *PPD* loci, which all inhibit flowering through a primary effect on circadian clock function. The *PHYA* photoreceptor, the *GIGANTEA* ortholog *LATE1*, and the newly identified *LATE2* gene all promote flowering specifically under long days. Progress on understanding the interactions of these genes, and on the isolation of other flowering time loci will be reported. Systematic analysis of the six-member *FT* family of floral integrators in pea and Medicago has shown that specific *FT* genes are targets of photoperiod and vernalization regulation and have distinct expression patterns and developmental roles. In addition, QTL analyses of flowering time in several other legumes also implicate *FT* genes in control of flowering time. Overall, our results suggest that both clock and *FT* genes are important in legume flowering time adaptation, and that both groups of genes affect not only flowering time but also other aspects of development including growth habit. A better understanding of these genes should accelerate work on flowering and related traits across a wide range of legume species.

17:00-17:20 Presenter: Jianxin Ma (Purdue University, USA)

Molecular Basis of Soybean Stem Architecture

Ping, J.[1], Liu, Y.[1], Sun, L.[1], Zhao, M.[1], Nguyen, H.[2], Li, Y.[3], Qiu, L.[3], Nelson, R.L.[4], Clemente, T.E.[2], Specht, J.E.[2], and Ma, J.[1*]. [1]Department of Agronomy, Purdue University; [2]Department of Agronomy and Horticulture, University of Nebraska; [3]Institute of Crop Sciences, Chinese Academy of Agricultural Sciences; [4]Soybean/Maize Germplasm, Pathology, and Genetics Research Unit, US Department of Agriculture–Agricultural Research Service, and Department of Crop Sciences, University of Illinois. *(maj@purdue.edu)

Soybean (*Glycine max*) stem growth habit is a critical agronomic trait that affects the plant's yield potential and adaptability. Based on the timing of the termination of apical stem growth, soybeans can be classified into indeterminate, semi-determinate, and determinate types. Similar to *Arabidopsis*, the wild soybean (*Glycine soja*) and many cultivars exhibit indeterminate stem growth controlled by a shoot identity gene *Dt1,* the functional counterpart of the *Arabidopsis TFL1,* a floral suppressor gene primarily expressed in SAMs. Mutations in *TFL1* and *Dt1* result in the shoot apical meristem (SAM) switching from vegetative to reproductive state to initiate terminal flowering and thus show determinate stem growth. A second soybean gene (*Dt2*) regulating the stem growth habit was identified, which, in the presence of *Dt1,* produces semi-determinate plants with terminal racemes similar to those observed in determinate plants. Our recent work demonstrates that *Dt2* was a dominant MADS domain factor gene homologous to the *Arabidopsis* floral meristem (FM) identity gene *AP1*. However, unlike *AP1*, whose expression is limited to FMs in which the expression of *TFL1* is repressed, *Dt2* appears to repress the expression of *Dt1* in the SAMs to promote early conversion of the SAMs into reproductive inflorescences, resulting in semi-determinate stems. Given that *Dt2* is not among several soybean genes most closely related to *AP1*, as revealed by phylogenetic

analysis, and that semi-determinacy is rarely seen in wild soybeans, *Dt2* appears to be a recent gain-of-function mutation that has re-shaped the regulatory networks in the palaeopolyploid soybean.

17:20-17:40 Presenter: Julie Hofer (ICRISAT, Patancheru, India)

Sequence analysis of a pea (*Pisum sativum*) fast neutron mutant population identifies the gene corresponding to *Stipules reduced*

Hofer, J.M.I.[1,2*], Moreau, C.[3], Ambrose, M.J.[3], Eléouët, M.P.[1], Hegarty, M.J.[1], Blackmore, T.[1], Swain, M.T.[1], and Ellis, T.H.N.[1,2]. [1]IBERS, Aberystwyth University, Aberystwyth SY23 3EE, UK; [2]current address: ICRISAT, Patancheru 502 324, Andhra Pradesh, India; [3]John Innes Centre, Norwich, NR4 7UH, UK. *(j.hofer@cgiar.org)

A fast neutron mutant population developed in *Pisum sativum* (pea) for gene discovery has been used to identify eight morphology genes, two pigmentation genes and four seed metabolism genes to date. These previous studies showed that a range of deletion sizes exists in the population and that individual lines are expected to carry seven deletions, on average. The population is therefore suitable for both forward and reverse genetics, whereby high throughput sequence data is searched systematically for deleted sequences. As a test of the utility of the population for forward genetics, we screened Restriction Site Associated DNA (RAD) sequence data and identified a genetic determinant of stipule organ size, the *Stipules-reduced* (*St*) gene. A total of 994 sequence read tags were identified as absent from a *st*/*st* FN mutant line, compared to tags present with a read depth of at least 150 in isogenic *St*/*St* lines. Absent tags were used to identify 498 pea transcript contigs, which were filtered by BLAST against all sequence tags from the *st*/*st* line. This identified 43 candidate *St* transcripts, which were mapped in silico in Medicago. Genomic regions with clusters of adjacent-mapped candidates were investigated further using PCR assays and sequence analysis on mutant and wild type lines. A transcription factor on Chromosome 5 was identified as *St* and five pre-existing mutant alleles were characterized. This gene identification approach is readily applicable to any genome, even where extensive sequence is not available.

17:40-18:00 Presenter: Jocelyn Ozga (University of Alberta, Canada)

Role of gibberellins in seed coat development and photoassimilate partitioning in developing pea (*Pisum sativum* L.) seeds

Waduthanthri, K.[1], Ozga, J.A.[1*], Kaur, H.[1], and Reinecke, D.M.[1]. [1]Plant BioSystems Group, Department of Agricultural, Food, and Nutritional Science, University of Alberta, Edmonton, AB, Canada T6G 2P5. *(jocelyn.ozga@ualberta.ca)

Gibberellins (GAs) are known to play a key role in early seed development. To understand the involvement of GAs as a sink strength determinant during rapid embryo growth and the early seed storage phase (8 to 20 days after anthesis [DAA]) of pea (*Pisum sativum* L.), seed coat and cotyledon development were histologically compared among the GA biosynthesis mutant lines *lh-2* and *lh-1* (mutant alleles of the LH gene that codes for the GAbiosynthesis enzyme ent-kaurene oxidase), and their wild-type line LH. *lh-2*and *lh-1* reduce GA1 levels (54% and 84%, respectively) in young pea seeds. The *lh-2* mutation reduces seed size, but the *lh-1* mutation only hasa transient effect on seed size during development (Swain et al., 1993, Planta 191:482). In our study, we observed marked differences in celldifferentiation and expansion in the

seed coats of the *lh* mutants compared to the wild-type LH line. Development of the seed coat layers in *lh-2* was affected to a greater extent than *lh-1* when compared to LH. With respect to photoassimilate partitioning, the mobilization of starch from the seed coat to the embryo at the initiation of the storage phase in the embryo (14-16 DAA) was delayed by approximately 2 days in the *lh-1* mutant, and greater than 4 days in the more severe *lh-2* mutant. These data support that GAs regulate specific aspects of seed coat development, and as a result, can modify photoassimilate partitioning into the developing embryo.

IFLRC Applied Genetics and Genomics; Abiotic Stress Tolerance
Chair: Ashutosh Sarker (ICARDA, India)

16:00-16:30 Presenter: Steve Beebe (CIAT, Cali, Colombia)

Breeding for tolerance to low soil phosphorus: the example of common bean

Beebe, S.[1*], and Rao, I.M.[1]. [1]International Center for Tropical Agriculture (CIAT). *(s.beebe@cgiar.org)

Abiotic stress limits crop yields across the tropics. Poor soil fertility is widespread, especially low soil phosphorus (P) availability. The wild ancestor of common bean evolved in an environment in which abiotic stress was seldom intense, and thus the domesticated common bean is not inherently well adapted to poor soil conditions. In spite of this, there is sufficient genetic variability to improve adaptation, based on multiple tolerance mechanisms. Large seed size can supply greater nutrients and carbon for early plant growth when roots for nutrient uptake are still not well developed. Several root traits can contribute to better P acquisition from soil. Translocation of resources to grain is inhibited under stress and but is also subject to improvement. Crop phenology influences nutrient acquisition, and a longer growth cycle favors greater nutrient capture. Different mechanisms may be relatively more effective under different levels of stress, contributing to GxE. Interactions of drought with low P can result in more severe yield losses than with individual stresses. Experience with common bean suggests that under combined stress of low soil P and drought, addressing nutritional constraints may be the first line of defense, while some genotypes respond well in spite of multiple stresses.

16:30-16:45 Presenter: Shane Rothwell (Lancaster University, UK)

Liming (to recommended rates) limits legume growth and gas exchange by increasing root-to-shoot signalling of the phytohormone abscisic acid

Rothwell, SA.[1*], and Dodd, IC.[1]. [1]Centre for Sustainable Agriculture, Lancaster Environment Centre, Lancaster University. *(s.rothwell1@lancaster.ac.uk)

Soil acidification is a natural process that can be hastened by intensive agricultural practices such as excessive use of mineral nitrogen fertilisers. If unchecked, these may negatively affect crop yield via altered nutrient availability and aluminium toxicity. Impacts of low soil pH are traditionally managed by applying lime (calcium carbonate) to target soil pH ranges (often 6-6.5) that optimise nutrient availability and subsequent yield. However, recommended rates of liming can decrease crop yields in susceptible soil types, possibly by reducing phosphorous availability though there is little mechanistic information on how plant physiological responses limit yield. Shoot dry weight of pot grown pea (*Pisum sativum* L. cv.

Alderman) amended with lime to target pH 6.5 (recommended rate) was reduced by 38% and gas exchange (stomatal conductance and photosynthesis) was inhibited by 50% and 32% respectively when compared to un-limed control plants (pH 5.7). Although lime increases rhizospheric calcium concentrations to levels significantly higher than that required for adequate crop nutrition, xylem calcium concentrations (a potential antitranspirant) were not increased (Rothwell & Dodd 2014; *Plant & Soil* in press). Instead, xylem sap and tissue analysis suggest that reduced gas exchange is caused by an increase in the plant hormone abscisic acid (ABA) which decreases stomatal conductance. The ABA deficient mutant pea '*wilty*' showed an attenuated stomatal response to liming, apparently confirming that increased ABA is mediating legume responses to low phosphorus availability under recommended rates of liming.

16:45-17:00 Presenter: Ralf Metzner (Institute of Plant Sciences, Jülich, Germany)

Monitoring roots, nodule and pod development in vivo: New perspectives on legume development

Metzner, R.[1*], Windt, C.W.[1], van Dusschoten, D.[1], and Jahnke, S.[1]. [1]Forschungszentrum Jülich, Institute of Plant Sciences (IBG-2), Jülich, Germany. *(R.Metzner@fz-juelich.de)

Seed filling, root and nodule development are some of the key processes involved in abiotic stress resistance. However, these are complex processes hidden either by pod tissue (seed filling) or by soil (roots and nodules), so studying them quantitatively in-vivo is challenging. Non-invasive (3D) imaging techniques such as magnetic resonance imaging (MRI) can be used to investigate hidden structural development both above- and belowground. Co-registered positron emission tomography (PET) allows the acquisition of functional information by mapping of recent carbon investment of the plant and its dynamics e.g. in response to stress. For tasks not requiring spatial (volumetric) resolution, such as monitoring changes in pod water and dry-matter content, low field nuclear magnetic resonance relaxometry with portable devices (pNMR) can be applied. Such devices allow sensor-like applications in the greenhouse and the field. In the current contribution we will demonstrate the application of MRI to follow the development of root system architecture in soil grown pea and bean genotypes and monitor the progress of nodulation by repeated 3D mapping of nodule distribution. By correlating these maps with PET, monitoring carbon import, we get first insights into the functionality of nodules in the soil. Additionally we will demonstrate monitoring changes of bean pod water and dry-matter contents over the course of several weeks with pNMR. We discuss the potential and challenges of all three techniques (MRI, PET and pNMR) for application in legume research.

17:00-17:15 Presenter: Jens Berger (CSIRO Plant Industry)

Chickpea phenology and evolution

Berger, J. D.[1*]. [1]CSIRO Plant Industry. *(Jens.Berger@csiro.au)

Among broad-acre crops, chickpea has had a unique evolutionary trajectory through a series of bottlenecks that have selected for environment-specific phenological controls, adaptive strengths and weaknesses that still define where the crop is grown today. Originally a narrowly distributed, vernalization-responsive Mediterranean winter annual (*Cicer reticulatum*) from SE Anatolia, chickpea is now a widely distributed crop predominantly grown in warmer South Asian or spring-sown Mediterranean/temperate systems. The advent of Mediterranean spring-sowing in the Bronze Age and subsequent spread to

warmer climates in the south and southeast (South Asia) modified chickpea selection pressures: elevating the role of terminal drought and high temperature stress, and reducing the role of low winter temperatures. This led to the evolution of regionally-appropriate regulation of phenology through 3 distinct mechanisms:

The loss of the vernalization response, an unreliable regulator of flowering time in warmer, variable climates.An increase in temperature response as vegetative phase temperatures increased from north to south.Temperature-photoperiod compensation. Inverse relationships between temperature and photoperiod responses in Mediterranean germplasm provided the plasticity to facilitate expansion to warmer southern climes.
These mechanisms allow chickpea to match phenology with growing season length and avoid its principal stresses: the almost ubiquitous terminal drought, and winter cold, damaging at the vegetative phase largely in Mediterranean climates, but delaying pod set and exacerbating terminal drought almost universally. The move from north to south, and associated phenological changes have had wider ramifications for chickpea adaptation. While high temperature tolerance is comparatively common in chickpea, reproductive chilling tolerance is extremely rare, and more likely to reside in its Mediterranean winter annual wild relatives. For further chickpea improvement it is essential to understand the interplay between phenology and specific adaptation, so that we focus on adaptive traits that augment, rather than oppose the crop's principal strategy of stress avoidance.

17:15-17:30 Presenter: Shiv Kumar (ICARDA)

Extra short duration lentil for rice-based cropping systems in the Indo-Gangetic Plain of South Asia

Kumar, S.[1*], Kumar, J.[2], Dikshit, H.K.[3], Zaman, S.[4], Nath, R.[5], and Sarker, A.[6]. [1]International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat-Office, Morocco; [2]Indian Institute of Pulses Research, Kanpur, India; [3]Indian Agricultural Research Institute, New Delhi, India; [4]Pulses Research Centre, Bangladesh Agricultural Research Institute, Gazipur, Bangladesh; [5]Bidhan Chandra Krishi Viswavidyalaya, Mohanpur, India; [6]South Asia and China Regional Office of ICARDA, New Delhi, India. *(s.agrawal@cgiar.org)

Lentil (*Lens culinaris* Medik. ssp. *culinaris*) has been an integral part of rice-based cropping system in the Indo-Gangetic plain (IGP) of South Asia, mainly because of its ability to thrive comparatively well under water-limiting environments. The expansion of productive boro-rice system, particularly in irrigated region of Bangladesh and northeastern India, has emerged as a threat to lentil cultivation in the absence of appropriate lentil varieties, which can fit in the system. The rice-rice system provides a short-season window of 100-110 days in which an extra short duration lentil variety (90-100 days) can successfully be grown. We have developed short duration breeding lines which can mature in 90-100 days in South Asia and are under testing in preliminary yield trials for their yield performance. Similar opportunity also exists for extra short duration lentil in the rainfed rice growing areas of South Asia dominated by medium to long duration varieties of rice and termed as rice fallows. The top soil layer generally dries completely at the time of the rice harvest and thus planting of a post-rainy season crop is not feasible. Under such conditions, extra-short duration lentil lines can convert these mono-cropped areas into double cropped areas and thus increase lentil production and sustain productivity of the rice-based system. Increased adaptability of these lines to marginal soil conditions will help increase the overall cropping intensity, system productivity, sustainability and profitability.

17:30-17:45 Presenter: Imran Malik (University of Western Australia)

Variation in physiological responses in pea and lentil to soil waterlogging

Malik, A.I.[1*], Ailewe, T.I.[2], and Erskine, W.[1]. [1]Centre for Plant Genetics and Breeding, School of Plant Biology, Institute of Agriculture, Faculty of Sciences, The University of Western Australia, Australia; [2]School of Plant Biology and Institute of Agriculture, Faculty of Sciences, The University of Western Australia, Australia. *(imran.malik@uwa.edu.au)

Pea (*Pisum sativum* L.) and lentil (*Lens culinaris* subsp. culinaris Medik) are grown under rainfed conditions after rice in South Asia. However, production of these legumes in rice-based cropping systems is difficult due to their susceptibility to waterlogging. A pea and a lentil cultivar from Australia and a germplasm accession from each of Bangladesh and Pakistan were evaluated for waterlogging tolerance in glasshouse and in laboratory experiments. In the laboratory, O2-consumption rates at germination were measured under aerated conditions or after 72 h under water. O2-consumption rate differed significantly among genotypes and increased up to 6-fold after 72 h under water. Waterlogging tolerance at early developmental stage and their recovery was evaluated in pot soil system. With increasing severity of waterlogging treatment germination rate decreased; in waterlogged-10 (water level 10 mm below soil surface) germination rates were 100 % for peas; however, it was 75% for lentils. In waterlogged+10 (water level 10 mm above soil surface), at the end of the experimental period (14 d treatment) all seeds of Australian pea cultivar were moulded and the germination rate of the other genotypes was reduced to 50 - 66%. Root length and root porosity differed significantly between pea and lentil genotypes during waterlogging, and differences in tolerance to waterlogging and recovery during the vegetative stage were also demonstrated. These observations of marked differences in waterlogging tolerance within a restricted sample of pea and lentil germplasm from different origins indicate that selection within a broader germplasm sample is clearly warranted.

17:45-18:00 Presenter: Hari D. Upadhyaya (ICRISAT, India)

Capturing Variations for Multiple Stress and Agronomic Traits for Improvement of Grain Legumes

Upadhyaya, H D.[1*], Dwivedi, SL .[1], Sharma, Shivali .[1], Pattanashetti, SK.[1], Vetriventhan, M.[1], Lalitha, N.[1], Varshney, RK .[1], and Singh, Sube.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India. *(h.upadhyaya@cgiar.org)

Grain legumes are the primary sources of oil, fiber, and protein-rich food and feed. Crops adaptation to climate change is one of the major challenges to scientific community in the 21st century. Grain legumes have narrow genetic base due to bottlenecks associated with domestication. Genes for desirable traits are embedded in biodiversity. ICRISAT genebank holds 49,819 accessions of its mandate grain legumes. Core/mini core collections have been suggested as resource to discover new sources of variations for enhanced use of germplasm in crop breeding. Using mini core approach trait-specific genetically diverse germplasm for resistance to drought, salinity, water logging, heat stress, pest, diseases, herbicide, and for agronomic and nutritional traits have been identified. The evidence to date suggests increased use of germplasm in legumes breeding at ICRISAT since formation of mini core collections. The crops have moved from orphan to genomic resources rich crops. The chickpea and pigeonpea genomes have been decoded. Resistance to some pest and diseases has been successfully transferred from wild relatives to

cultivated species. Synthetics in groundnut are recycled for capturing diversity lost during domestication. Increased use of agrobiodiversity together with modern genomics tools is crucial to coping with new challenges to agricultural production. Germplasm and breeding lines with unique traits are being sequenced, and comparison of sequence information of these unique germplasm with reference genomes will enable us to detect variation at nucleotide level. This will provide researchers opportunity to relate these differences with beneficial traits for enhancing trait value in breeding programs.

Tuesday, July 8, 2014

Seeds and Nutrition

ICLGG Seeds and Nutrition
Chair: Georgina Hernandez (Universidad Nacional Autónoma de México, Mexico)

11:00-11:30 Presenter: Jerome Verdier (Shanghai Institutes of Biological Sciences, CAS, China)

Deciphering regulation of legume seed nutritional composition

Huang, Z.[1], Wagnon, P.[1], Chen, C.[1], Li, M.[1], Sun, Y.[1], Wang, M.[2], Buitink, J.[3], Liu, R.[1], She, Y.M.[1], Young, N.[4], Udvardi, M.K.[2], and Verdier, J.[1*]. [1]Shanghai Institute for Plant Stress Biology, Shanghai Institutes of Biological Sciences, Chinese Academy of Sciences, Shanghai, P.R. China; [2]The Samuel Roberts Noble Foundation, Ardmore OK, USA; [3]INRA IRHS, Angers, France; [4]University of Minnesota, St Paul MN, USA. *(javerdier@sibs.ac.cn)

Legume seeds are a primary source of proteins, lipids, carbohydrates, secondary metabolites, and minerals. Few regulatory genes have been discovered that control legume seed storage metabolism. Therefore, we have initiated a systems biology approach to decipher seed storage metabolism in the model legume, *Medicago truncatula.* To unravel these mechanisms, we have been using different approaches to model the seed development. An *in silico* gene regulatory network during seed development was built, which linked transcription factor genes to their potential target genes, enzymatic genes to metabolites and proteins, hormones to signaling genes and small RNA to transcription factors. In parallel, a genome-wide association study using resources developed by the *Medicago* HapMap project has been initiated and should reveal sequence polymorphisms associated with distinct seed composition phenotypes such as carbohydrate, protein, lipid, secondary metabolite and mineral contents. Finally, a comparative genomics study between legumes with contrasting seed storage composition has been conducted to highlight common and different mechanisms within legume seed development. The combination of these approaches will lead to the discovery of genes controlling seed nutritional composition and seed quality in legumes. In a near future, it should lead to new ways to improve the nutritional quality of legume seeds.

11:30-11:50 Presenter: Claire Domoney (John Innes Centre, Norwich, UK)

The wild side of seed quality improvement: discovering novel genetic variation that impacts on the control of visual traits and composition in *Pisum sativum* L. (pea)

Domoney, C.[1*], Chinoy, C.[1], Knox, M.[1], Bilham, L.[1], Bell, A.[1], Spanner, B.[1], Rayner, T.[1], Warkentin, T.[2], Ellis, N.[3], and Isaac, P.[4]. [1]John Innes Centre, Norwich Research Park, Norwich NR4 7UH, UK; [2]University of Saskatchewan, Saskatoon, Saskatchewan S7N 5A8, Canada; [3]International Crops Research Institute for the Semi-Arid Tropics, Hyderabad, Andhra Pradesh, Patancheru, India; [4]IDna Genetics Ltd, Norwich Research Park, Norwich NR4 7UH, UK. *(claire.domoney@jic.ac.uk)

Germplasm resources of *Pisum*, including natural variants, EMS and fast neutron mutagenised populations, harbor novel variants of genes that impact on seed metabolism, nutritional quality and additional traits of economic importance. Our studies of variation within genes that control chlorophyll metabolism during late stages of seed maturation show the considerable allelic variation that exists outside standard breeding genetic resources. The role of retro-elements in shaping the diversity of variation for this biochemical process will be discussed, alongside the potential of novel genetic variants to stabilize desirable seed visual traits. Mutations in genes involved in the control of seed composition enable the profile of seed constituents to be altered dramatically. Allelic variants of genes encoding starch-branching enzyme, ADP-glucose pyrophosphorylase and other genes involved in sucrose metabolism lead to different contents of starch and profiles of sugars within seeds. Mutations in genes encoding albumin 2, trypsin inhibitor and lectin have been identified and combinations of null mutations for these offer prospects for increasing the yield of digestible protein. The high-throughput screening and characterization of *Pisum* resources will assist greatly with the adoption and selection of superior alleles of genes relevant to the breeding of legume food and feed crops for improved yield and quality.

11:50-12:10 Presenter: Mitch Lucas (University of California Riverside, USA)

Using SNPs to Breed Cowpeas with Large Seeds

Lucas, M.R.[1*], Huynh, B.L.[2], Vinholes, P.S.[2], Cisse, N.[3], Drabo, I.[4], Ehlers, J.D.[1], Roberts, P.A.[2], and Close, T.J.[1]. [1]Department of Botany and Plant Sciences, University of California Riverside; USA; [2]Department of Nematology, University of California Riverside; USA; [3]Senegalese Institue of Agricultural Research; Thies, Senegal; [4]Institute of Environmental and Agricultural Research; Ouagadougou, Burkina Faso. *(mluca002@gmail.com)

Seed size distinguishes most crops from their wild relatives and is an important quality trait for the grain legume cowpea. In order to breed cowpea varieties with larger seeds we associated SNP markers from a 1,536-plex GoldenGate assay with seed size by studying 7 RIL populations, a subset of the USDA core collection, and synteny to the related legume soybean. These QTL discovery and characterization efforts described SNP haplotypes and their predicted effects in different pedigrees such that marker-assisted breeding schemes could be designed for cowpea with larger or smaller seeds. Parents for crosses were chosen based on genotype calls with a goal of pyramiding large seed haplotypes into different seed types. Foreground and background selection were performed during two cycles of backcrossing based on the KASP genotype calls of a genome-wide set of polymorphic markers. Progeny with very large seeds (up to 35g/100 seed) were developed through introgression of one QTL from IT82E-18 (18.5g/100 seed) into CB27 (22g/100 seed). Field testing for performance and enabling partner institutions for the deployment of markers is a continuing effort that will be enhanced later this year by the availability of a 60,000 SNP iSelect genotyping platform. This will be a core resource for collaboration with partners from Burkina Faso, Ghana, Nigeria, and Senegal. Coupling high-density genotyping with knowledge of physical and genetic maps provides excellent opportunities to identify genetic determinants underlying traits relevant to breeding objectives.

Biotic Stress

12:10-12:30 Presenter: Vijai Bhadauria (University of Saskatchewan, Canada)

Regulation of hemibiotrophy in the lentil anthracnose pathogen *Glomerella truncata*

Bhadauria, V.[1*], Wei, Y.[2], and Banniza, S.[1]. [1]Crop Development Center, University of Saskatchewan, Saskatoon SK Canada; [2]Department of Biology, University of Saskatchewan, Saskatoon SK Canada. *(vijai.bhadauria@usask.ca)

Anthracnose caused by *Glomerella truncata* is one of the most devastating fungal diseases on lentil. This pathogen exploits a hemibiotrophic infection strategy to colonize lentil plants, and the lifestyle transition from biotrophy to necrotrophy (the hemibiotrophic switch) is critical in anthracnose development. Mining of *G. truncata*-infected lentil transcriptome coupled with quantitative real-time PCR and Northern blot analysis identified a hemibiotrophic switch-specific gene *CtNUDIX* (*Colletotrichum truncatum* NUcleoside DIphosphate linked to moiety X). Nudix hydrolases are known to hydrolyze inositol pyrophosphates (IPs), and some IPs are involved in endocytotic trafficking in plants. Western blot analysis and *in planta* expression assays revealed that CtNUDIX is an effector protein and secreted in lentil cells to induce cell death. Green fluorescent protein tagged CtNUDIX was localized in endocytotic vesicles located at the plasma membrane, suggesting that CtNUDIX perturbs the plant cell surface dynamics to trigger a hypersensitive cell death like response. Furthermore, overexpression of *CtNUDIX* in *G. truncata* and heterologous expression in the model pathogen *Magnaporthe oryzae* blocked the hemibiotrophic switch and resulted in incompatibility with hosts lentil and barley, respectively. A hypersensitive cell death response was also observed in infected host cells associated with the biotrophic invasive hyphae. Taken together, these results provide compelling evidence that *G. truncata* secretes CtNUDIX in lentil cells to shut down the biotrophic phase by inducing cell death and to initiate the destructive necrotrophic phase resulting in anthracnose lesions. CtNUDIX can therefore serve as an excellent target to control diseases caused by hemibiotrophic fungal pathogens.

IFLRC Seeds and Nutrition
Chair: Albert Vandenberg (University of Saskatchewan, Canada)

11:00-11:30 Presenter: Francesca Sparvoli (IBBA, CNR, Milan, Italy)

Iron biofortification in common bean

Sparvoli, F.[1*], Cominelli, E.[1], Bollini, R.[1], and Nielsen, E.[2]. [1]Institute of Agricultural Biology and Biotechnology, CNR, Milan, Italy; [2]Department of Biology and Biotechnology, University of Pavia, Pavia, Italy. *(sparvoli@ibba.cnr.it)

Iron deficiency anaemia is the most prevalent micronutrient deficiency affecting more than 2 billion people throughout of the world. Iron bioavailability may be strongly reduced by the presence in the seeds of iron absorption inhibitors, such as phytic acid (IP6) and polyphenols (PP). In different crop species low PP

genotypes can be easily identified, conversely natural variability in IP6 content is not very high and the best way to gain significant IP6 reduction is by obtaining low phytic acid (*lpa*) mutants. Although such type of mutants have been identified in several grain crops, often IP6 reduction is associated with negative agronomic traits, such as lower seed viability and emergence, reduced plant growth rate and grain yield. These findings may limit the use of *lpa* mutants for iron biofortification, since acceptable agronomic performance should be guaranteed to small farmers and poor populations that would benefit from biofortified crops.

Due to its worldwide consumption and nutritional qualities, common bean has been identified as a strategic target crop for iron biofortification. We have isolated a bean *lpa* mutant having a 90% seed IP6 reduction and showed it is defective in a MRP type ATP-binding cassette transporter (Pvmrp1) specific for IP6. Agronomic analyses of the original *lpa* mutant and of derived *lpa* lines have shown that seedling emergence, seed yield and plant growth were not affected. *In vitro* and *in vivo* analyses confirmed significant increases of iron bioavailability in bean *lpa* seeds.

11:30-11:45 Presenter: William Erskine (University of Western Australia)

Selenium biofortification of lentil in Australia and Bangladesh

Rahman, M.M.[1,2], Erskine, W.[1,2*], Siddique, K.H.M.[2], Thavarajah, P.[3], Thavarajah, D.[3], Zaman, M.S.[4], Materne, M.A.[5], and Mcmurray, L.M.[6]. [1]Centre for Plant Genetics and Breeding, School of Plant Biology, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia; [2]The UWA Institute of Agriculture, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia; [3]Pulse Quality and Nutrition, North Dakota State University, 208 Harris Hall, Fargo, ND 58105, USA; [4]Pulses Research Centre, Bangladesh Agricultural Research Institute, Ishurdi, Pabna, Bangladesh; [5]Department of Primary Industries, 110 Natimuk Road, Horsham, Victoria 3400, Australia; [6]South Australian Research and Development Institute, Clare, South Australia 5453, Australia.
*(William.erskine@uwa.edu.au)

A low concentration of micronutrients in the diet causes micronutrient malnutrition. Biofortification by agronomic management or plant breeding approaches can reduce such malnutrition in rural areas of developing countries. Globally over one billion people suffer from selenium (Se) deficiency. Lentil can be an effective food to supply dietary Se to affected populations. This study used a baseline survey in farmers' lentil fields in Bangladesh and conducted field experiments in Bangladesh and Australia to unravel genotypic and environmental effects on seed Se concentration and to evaluate foliar Se application.

A farmers' field survey and evaluation of seven lentil genotypes at four locations were conducted in Bangladesh in 2010/11. Soil and lentil seed Se concentration in farmers' fields averaged 163 and 312 µg/kg, respectively. There were significant genotype and location differences for seed Se and seed yield. But the genotype-location interaction was non-significant for seed Se concentration.

In Australia trials on Se foliar application at two locations and an evaluation of 12 genotypes at seven locations were undertaken in 2011. Foliar application of 40 g/ha of Se as K2SeO4 increased seed Se concentration from 200 to 2772 µg/kg, but did not affect seed size or yield. The genotypic evaluation, as in Bangladesh, showed significant genotype and location effects for seed Se, but the interaction was non-significant.

In summary, foliar Se application is an efficient approach to improve lentil seed Se concentration. With clear genetic differences in Se uptake in lentil exhibited, there is scope to breed lentil for an improved Se

seed content.

11:45-12:00 Presenter: Peter Zahradka (Canadian Centre for Agri-Food Research in Health and Medicine)

The structural properties of arteries are altered by consumption of pulses: Implications for treatment of atherosclerotic disease

Zahradka, P.[1,2*], Hanson, M.G.[1,2], and Taylor, C.G.[1,2]. [1]Canadian Centre for Agri-Food Research in Health and Medicine, St. Boniface Hospital; [2]Depts of Physiology and Human Nutritional Sciences, University of Manitoba, Winnipeg, Canada. *(pzahradka@sbrc.ca)

A human study was conducted to evaluate the effects of eating ½ cup per day of a mixture of pulses (beans, peas, chickpeas, lentils) over an 8 week period on vascular function in persons with peripheral artery disease (PAD), a manifestation of atherosclerosis in which blood flow to the legs is reduced. A cohort of 26 men and women was provided with pulse-rich foods (14 different items to provide variety) to incorporate into their usual diet. This study revealed that consuming pulses above the normal amounts usually eaten by Canadians could improve the ankle-brachial index, the primary tool for diagnosis of PAD, by increasing blood flow to the legs. No pharmaceutical drug currently available exhibits this capability. Furthermore, these results suggest that dietary pulses affect the physical properties of blood vessels. We therefore conducted an animal study to investigate the effects of individual pulses on arterial structure and function. Spontaneously hypertensive rats were randomly assigned (n=8/group) to diets containing 30% (wt/wt) cooked and freeze-dried beans, peas, lentils, chickpeas, a pulse mixture or no pulses for 4 weeks. Blood pressure (BP) and pulse wave velocity were measured weekly, and morphometry was performed at termination. Arterial stiffness assessed by pulse wave velocity was unchanged, however, lentils decreased BP and reduced the aortic media:lumen ratio. Our results are the first to show that eating a specific food can reverse the main cause of atherosclerotic disease, and that the amount of pulses providing this benefit can be reasonably incorporated into our regular diet.

12:00-12:15 Presenter: Laura McBreairty (University of Saskatchewan)

A pulse-based diet and exercise training in women with polycystic ovarian syndrome: Effects on body composition, blood lipids and reproductive measures

McBreairty, L.E.[1*], Zello, G.A.[1], Rooke, J.J.[2], Serrao, S.[3], Pierson, R.A.[3], Chizen, D.R.[3], and Chilibeck, P.D.[2]. [1]Colleges of Pharmacy and Nutrition, University of Saskatchewan; [2]College of Kinesiology, University of Saskatchewan; [3]College of Medicine, University of Saskatchewan. *(l.mcbreairty@usask.ca)

Polycystic ovarian syndrome (PCOS) is an endocrine disorder that predisposes women to increased risk of heart disease, diabetes, infertility and endometrial cancer with annual cost of $4 billion in the United States. We hypothesized a pulse-based diet (e.g. beans, lentils) would have a positive effect on body composition, reproductive measures and serum lipid profiles. Thirty-one women with PCOS aged 18-35y with a mean body mass index of 33 were randomly assigned to groups receiving a pulse-based diet (n=17) or the National Cholesterol Education Program (NCEP) therapeutic lifestyle changes (TLC) diet (n=14) for 16 wks while participating in an exercise program. During the intervention, both groups lost body mass ($p<0.001$; Pulse -3.6 vs TLC -3.0 kg), percent fat mass ($p=0.0013$;Pulse -1.0 vs TLC -1.5 %),

trunk fat mass (p=0.0005 Pulse -1.0 vs TLC -1.5 kg) as well as lean body mass (p<0.02; Pulse -1.3 vs TLC -0.4 kg). Both dietary interventions also resulted in more women exhibiting regular menstrual patterns (p<0.01) and a decreased antral follicle count in the right ovary (p=0.04); however, only the pulse diet reduced total cholesterol to HDL ratio (4.1 to 3.7 p<0.005). The pulse-based diet and TLC diet reduced body fat, and improved reproductive endpoints; however,the pulse-based diet appeared to provide additional benefits by improving lipid profile. Diet and exercise are important in alleviating the personal health and economic costs associated with PCOS.

Supported by Agriculture and Agri-Food Canada and the Saskatchewan Pulse Growers

12:15-12:30 Presenter: Susan Arntfield (University of Manitoba, Canada)

Changes in levels of antioxidant and selected antinutritional factors in peas and beans due to the application of heat

Arntfield, S.D.[1*]. [1]Department of Food Science, University of Manitoba, Winnipeg, MB, Canada. *(susan.arntfield@umanitoba.ca)

Increased consumption of legumes offers many nutritional advantages including high levels of antioxidants but antinutritional compounds such as phytic acid and trypsin inhibitors can limit legume consumption. This work represents an overview of changes in antioxidants based on a DPPH analysis (AOX) and total phenolics (TP) as well as the antinutritional factors phytic acid (PA) and trypsin inhibitors (TI) due to micronization (infrared heat) and roasting (convection heat). Changes in whole seeds as well as changes during the preparation of noodles, flat breads and extruded snack foods have been investigated. Both infrared and convection heating reduced PA (40-60%) and TI (88-100%) in whole seeds with greater reductions with roasting. For beans, there were also decreases in TP (up to 25%) and AOX (up to 55%), but for peas both TP and AOX increased. When these materials (peas specifically) were dehulled and milled prior to use, the effects of heat were greatly reduced. Noodles prepared from flour containing navy bean and yellow pea had reduced levels of PA and TP compared to the raw blend, but TIs were unchanged. When preparing tortillas from flours that included varying levels of peas and beans, PA and TI were again reduced but TP increased by 40-75%; however AOX activity decreased slightly. The high temperatures used in extrusion eliminated TI and reduced all other parameters. The temperature and type of heating influence both antinutritional and antioxidant activity; however conditions can found to reduce antinutritional factors while minimizing loss of antioxidants.

ICLGG Biotic Stress
Chair: Scott Jackson (Univ. of Georgia, USA)

14:00-14:30 Presenter: Kiran Mysore (The Samuel Roberts Noble Foundation, USA)

Identification of novel sources of resistance in a nonhost plant, *Medicago truncatula*, against Asian Soybean Rust caused by *Phakopsora pachyrhizi*.

Ishiga, Y.[1], Gill, U.S.[1], Mittal, S.[1], Uppalapati, S.R.[1], and Mysore, K.S.[1*]. [1]The Samuel Roberts Noble Foundation. *(ksmysore@noble.org)

Asian soybean rust (ASR) caused by *Phakopsora pachyrhizi* is a devastating foliar disease affecting soybean production worldwide. Identification of genes in another legume species that confer nonhost resistance against ASR will provide an avenue to engineer soybean for durable resistance against ASR. We found that *Medicago truncatula,* a model legume, conferred nonhost resistance against ASR. Tobacco retrotransposon, *Tnt1*, has been used to mutagenize and tag the whole genome of *M. truncatula*. A forward genetics approach using *Tnt1* tagged *M. truncatula* lines has been established to identify genes that confer nonhost resistance to *P. pachyrhizi*. Several *M. truncatula Tnt1* mutants with altered response to *P. pachyrhizi* have been identified and being characterized. *irg1* (inhibitor of rust germ-tube differentation1) mutant inhibited pre-infection structure differentiation of *P. pachyrhizi* and several other biotrophic pathogens. *IRG1* encodes a Cys(2)His(2) zinc finger transcription factor, PALM1 that also controls dissected leaf morphology in *M. truncatula*. Characterization of other mutants will also be presented.

14:30-15:00 Presenter: Nadine Ilk (The Sainsbury Laboratory, Norwich, UK)

Translational research at The Sainsbury Laboratory– from the laboratory to the farm–

Ilk, N.[1*]. [1]The Sainsbury Laboratory, Norwich, UK. *(nadine.ilk@tsl.ac.uk)

The coming century poses some formidable challenges for agriculture. We must increase food and feed production from the same amount of land 50% by 2030, against a backdrop of climate change, a reduction in water availability and rising energy costs. In addition, we want to accomplish these goals with respect for the environment, a reduction of chemical pesticides and increased food safety. Plant diseases cause severe crop losses worldwide with devastating effects on food and feed production. Over the past decades the understanding of how plant pathogens cause disease and how plants defend themselves against them has been refined. Within TSL we not only aim to further this understanding through fundamental research, but we also aim to improve current methods of disease control via translational research.
The Soybean Rust research group within TSL performs such translational research in collaboration with the 2Blades foundation, the Universidade Federal Viçosa and our commercial partner DuPont-Pioneer. The strong combination of expertise of team members and collaborators in various aspects of host-pathogen interactions enables us to make disproportionate gains in speed of discovery and deployment. Using this know-how, we are making inroads in understanding the basic biology of the causal agent of Asian Soybean Rust, the obligate biotrophic fungus *Phakopsora pachyrhizi*, and into the development of plant disease resistance against this pathogen.

15:00-15:20 Presenter: Marie-Laure Pilet-Nayel (INRA, Rennes, France)

Translational genomics for resistance to *Aphanomyces euteiches* between *Medicago truncatula* and pea

Pilet-Nayel, M-L.[1*], Bonhomme, M.[2], André, O.[2], Hajri, A.[1], Boutet, G.[1], Badis, Y.[2], Chantret, N.[3], Ronfort, J.[3], Young, N.D.[4], Baranger, A.[1], and Jacquet, C.[2]. [1]INRA, UMR IGEPP, Le Rheu F-35653, France; [2]UPS-CNRS, LRSV, F-31326 Castanet-Tolosan, France; [3]INRA, UMR AGAP, Montpellier F-34060, France; [4]University of Minnesota, Saint Paul, MN 55108, USA. *(Marie-Laure.Pilet@rennes.inra.fr)

Common root rot, due to *Aphanomyces euteiches,* is a very damaging disease of legumes, especially pea,

in many countries. Several consistent quantitative trait loci controlling partial resistance were identified in different pea genetic pools. Genomic basis of resistance to *A. euteiches* was investigated in the model legume *Medicago truncatula* in order to identify candidate genes underlying Aphanomyces resistance loci and analyze synteny of resistance loci between pea and *M. truncatula*. High density genome-wide association mapping was conducted in a collection of 179 *M. truncatula* accessions, for resistance to five reference *A. euteiches* isolates of main pea and alfalfa pathotypes. Two main genomic regions carrying candidate SNPs were associated with resistance. The first one corresponded to an F-box protein encoding gene at the *prAe1/AER1* loci on chromosome 3 and the second one to a NBS-LRR resistance protein encoding gene underlying a new resistance locus on chromosome 4. The candidate genomic regions identified in *M. truncatula* were projected to a pea consensus genetic map carrying 1250 SNP markers anchored to *M. truncatula* genome. The F-box gene syntenic region co-located with the minor QTL *Ae-Ps3.2* on pea LGIII and the NBS-LRR gene syntenic region was positioned about 50 cM far from the major QTL *Ae-Ps7.6* on pea LGVII. Work is in progress to precise synteny between Aphanomyces resistance loci in pea and *M. truncatula* and to search for pea genes orthologous to the *M. truncatula* candidate genes identified.

15:20-15:40 Presenter: Zenglu Li (University of Georgia, USA)

An Integrated Molecular Breeding Approach for Breeding Nematode Resistance in Soybean

Li, Z.[1*], Pham, A.[1], Shi, Z.[1], Noe, J.[1], and Boerma, H. R.[1,2]. [1]University of Georgia; [2]Georgia Seed Development Commission. *(zli@uga.edu)

Soybean nematodes including soybean cyst nematode (SCN), root-knot nematode (RKN) are one of the most destructive pests in soybean production in the world. These nematodes are able to live in the soilfor years and cause a significant loss of soybean yield. Phenotyping for nematode resistance is labor-intensive and time-consuming. Development of nematode resistance soybean cultivars is the most effective way to controlling nematodes in soybean production. PI 96354 was identified having a high level of resistance to RKN galling and egg production. Two QTLs were found to condition the resistance in PI 96354, a major *and minor QTL*on chromosome 10 and 8, respectively. Using the recombinants derived from the cross of PI 96354 x Bossier as well as soybean reference genome sequence, we have identified four candidate genes with cell-wall modification function responsible for RKN resistance. These candidate genes have several mutations in promoter, exon, 5', and 3'UTR regions, which were confirmed with sequencing and RT-PCR. Two mutant SNPs were selected to develop KASP assays to detect the resistant alleles. Based on the SNP assays, we have developed a high-throughput procedure for seed and leaf samples to select the progeny for RKN resistance in our breeding program. Two genes, *Rhg1* and *Rhg4* have been widely used for breeding SCN resistance. Based on the published sequences, we have also developed SNP assays to select for SCN resistance. The genotyping and selection workflow will be presented.

IFLRC Seeds and Nutrition
Chair: Khalid Daoui (Centre Régional de la Recherche Agronomique de Mèknes, Morocco)

14:00-14:30 Presenter: C.L. Laxmipathi Gowda (ICRISAT, India)

Impact-Oriented Legume Seed Systems in developing countries of Sub-Saharan Africa and Asia

Laxmipathi Gowda, C L.[1*], Jukant, Aravind.[2], Rubyogo, J C.[3], Gaur, Pooran.[1], and Monyo, E S.[4]. [1]ICRISAT, Patancheru, Hyderabad-502324, Andhra Pradesh, India; [2]Central Arid Zone Research Institute (CAZRI), Jodhpur - 342003, Rajasthan, India; [3]CIAT Arusha, P.O. Box 2704, Arusha, Tanzania; [4]ICRISAT-Nairobi, PO Box 39063, Nairobi, Kenya. *(c.gowda@cgiar.org)

Seed is the most important input for increasing crop productivity globally, especially for the smallholder farmers of Sub-Saharan Africa and Asia. Timely availability of quality seeds of improved crop varieties even at remote locations, at affordable prices, and required quantity, is essential for smallholder farmers to adopt improved varieties. During the past two decades several high yielding varieties of different legume crops have been developed, but only a few have been widely adopted. One of the main reasons for slow rate of adoption of these varieties is due to inadequacy of the seed production and delivery systems. Many international research centers, national systems, donor agencies, and development projects have been working together to strengthen the seed systems in the national programs, and also regionally. There are many bottlenecks in legumes seed systems due to (i) low multiplication ratio, (ii) bulkiness and reduced storability of seeds, (iii) fragmented seed demand (agro-ecology/market based) and (iv) inadequacy of national policy support, coupled with limited interest by the private sector. Basically, two types of seed systems operate: (i) formal seed system (supplying 5%) – organised sector with production, processing and delivery of quality seeds (ii) informal system (supplying 95%) – less organised but working reasonably in developing countries of Asia and Africa. Several successful models have been studied in different countries to strengthen both seed systems, but it is clear that each system needs to be fine-tuned to suit local situations.

14:30-14:45 Presenter: Felix Dapare Dakora (Tshwane University of Technology, South Africa)

Role of symbiotic cowpea (*Vigna unguiculata L. Walp.*) as a major food legume for nutritional security in Africa

Dakora, F.D.[1*], Belane, A.K.[2], and Pule-Meulenberg, F.[2]. [1]Chemistry Department, Tshwane University of Technology, Private Bag X680, Pretoria 0001, South Africa; [2]Department of Crop Sciences, Tshwane University of Technology, Private Bag X680, Pretoria 0001, South Africa. *(DakoraFD@tut.ac.za)

Cowpea (*Vigna unguiculata* L. Walp.) is the most important grain legume in Africa. It meets the food and nutritional security of about 1.1 billion people in the African continent. Studies of its grain yield and food quality are therefore crucial for the human nutrition and health of many Africans. The leaves and grain of cowpea are consumed in large quantities in Africa and elsewhere in the world. The grain yield of high performing cowpea varieties can be as high as 2000-3000 kg.ha-1 in South Africa, and 2500 kg.ha-1 in Ghana. Protein levels in the edible leaves are high and range from 29 to 40%, while grain protein also ranges from 23 to 40% depending on the variety and its symbiotic functioning. In fact, the grain protein of farmer-selected cowpea varieties such as Soronko and Bengpla can be as high as 40%, a level comparable to that of soybean. Both leaves and grain also contain very high concentrations/amounts of macronutrients and trace elements, the latter needed for overcoming micronutrient deficiency in rural Africa. Evidence from field and glasshouse studies has shown that, as with leaf and grain protein, the accumulation of mineral nutrients by cowpea is symbiosis-dependent. In the field, cowpea varieties with high N2-fixing ability accumulated more nutrient elements than low fixers, while in nodulation assays,

rhizobia with high N2-fixing efficiency generally elicited greater mineral accumulation in cowpea shoots when compared to strains with low symbiotic efficacy. These findings on the symbiosis-induced mineral accumulation in cowpea offer an additional explanation for the benefits of legume/cereal rotations beyond the known N contribution by the legume, and further validate cowpea as an important food legume for nutritional security in Africa.

14:45-15:00 Presenter: Ramakrishnan Nair (AVRDC – The World Vegetable Center South Asia, India)

Enhancing production and consumption of mungbean

Nair, R.M.[1*], Schafleitner, R.[2], Yang, R-Y.[2], Kenyon, L.[2], Srinivasan, R.[2], Hanson, P.[2], Ebert, A.W.[2], Easdown, W.[1], Hughes, J. d'A.[2], and Keatinge, J.D.H. (Dyno).[2]. [1]AVRDC – The World Vegetable Center South Asia, ICRISAT Campus, Patancheru 502 324, Hyderabad, India; [2]AVRDC – The World Vegetable Center, P.O. Box 42 Shanhua, Tainan 74199, Taiwan. *(ramakrishnan.nair@worldveg.org)

Mungbean is a short duration (55-70 days) grain legume that fits well into the cereal cropping systems prevalent in the tropics and is currently being grown on more than 6 million hectares worldwide. Mungbean is consumed by boiling whole dried seeds or split seeds, as *dhal* (porridge), bean sprouts or bean paste, or processed into high-value noodles or confectionery. Owing to its palatable taste and nutritional quality, mungbean has been used as an iron-rich whole food source for baby food. Broadening the genetic base of mungbean is a priority and breeding programs increasingly use crosses between unrelated parents and interspecific hybridization. This is important to tackle problems such as mungbean yellow mosaic disease, for which currently available sources of resistance are insufficient to cope with disease pressure in certain locations. Resistance to Cercospora leaf spot, powdery mildew and bruchids are other traits of importance to improve productivity. Among abiotic stresses, tolerance to heat stress and salinity are desirable. There is scope for improvement in starch, iron and zinc content and protein quality through plant breeding, which will lead to further enhancement of the nutritional value of the crop. Active promotion of the nutritional value of mungbean with its proven agronomic advantages will support the case for further expansion in Asia and other parts of the world, including sub-Saharan Africa. The availability and accessibility of new mungbean cultivars with improved nutrient content and higher productivity will also help to reduce malnutrition, especially among women and children in developing countries.

15:00-15:15 Presenter: Jenny Wood (NSW Department of Primary Industries, Australia)

Imaging of grain legume seeds: understanding what is where and the influence on nutritive value, health benefits and quality traits

Wood, J.A.[1*]. [1]Tamworth Agricultural Institute, NSW Department of Primary Industries, Australia. *(jenny.wood@dpi.nsw.gov.au)

Opportunities exist to add value to our grain legume crops through enhancing our understanding of their nutritive value, health benefits and other quality traits. It is also important to consider how these factors interact. Whilst there is a large amount of information available on the nutrient composition of the raw seeds, there is less detail available about the anatomical location of these nutrients and how these can affect quality traits like splitting and cooking.

Australian faba beans and chickpeas were investigated microscopically with preferential staining to highlight specific chemical components of the morphological structures within grain legume seeds. Differences were observed between varieties which help explain differences in nutritive value, ease of splitting, speed of cooking and potential benefits to human health.

This presentation will summarise the significant findings, dispel some industry myths and explain the relevance for breeding programs, grain legume processors, animal nutritionists, dieticians and consumers.

15:15-15:30 Presenter: Arun Shunmugam (University of Saskatchewan)

Biochemical and molecular characterization of low phytate pea lines

Shunmugam, A.S.K.[1*], Bock, C.[2], Arganosa, G.C.[1], Stonehouse, R.[1], Georges, F.[3], Gray, G.R.[4], Bett, K.E.[1], Tar'an, B.[1], and Warkentin, T.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK; [2]National Research Council of Canada, Saskatoon, SK; [3]National Research Council of Canada/Department of Biochemistry, University of Saskatchewan, Saskatoon, SK; [4]Department of Plant Sciences/Department of Biochemistry, University of Saskatchewan, Saskatoon, SK. *(s.ask@usask.ca)

Seeds of low phytic acid (*lpa*) pea lines are low in phytic acid (IP6) and high in inorganic phosphorus (Pi). The present study was aimed at biochemical and molecular characterization of two *lpa* pea lines, 1-150-81, 1-2347-144, and their progenitor CDC Bronco. The *lpa* lines did not significantly differ from CDC Bronco in the agronomic traits assessed except for lower grain yield. No inositol polyphosphates (IP1, IP3, IP4, IP5) other than phytic acid were detected in cotyledons of CDC Bronco and the *lpa* lines at different seed developmental stages analyzed through HPLC. Total phosphorus concentration was similar in *lpa* lines and CDC Bronco throughout seed development. To understand the genetic basis of the *lpa* mutation in pea, a 1530 bp open reading frame of *myo*-inositol phosphate synthase (MIPS) (EC 5.5.1.4) was amplified from CDC Bronco and the *lpa* lines. Sequencing results showed no difference in coding sequence in MIPS between CDC Bronco and *lpa* lines. Transcription levels of both MIPS and *myo*-inositol penta*kis*phosphate 2-kinase (*IPK1*) were relatively lower at 49 DAF than at 14 DAF for CDC Bronco and *lpa* lines. Recombinant inbred lines (RILs) developed from a cross between 1-2347-144 and CDC Meadow were evaluated in replicated field trials in Saskatchewan in 2011, 2012 and 2013. The RILs were genotyped using 1536 Single nucleotide polymorphic (SNP) markers in Illumina GoldenGate array and phenotyped using colorimetric assays. SNP marker associated with phytic acid phosphorus concentration was identified and mapped.

Wednesday, July 9, 2014

Nitrogen Fixation, Plant Nutrition and Legume Mega Project

ICLGG Legume Mega Projects
Chair: Jens Stougaard (Aarhus University, Denmark)

11:00-11:30 Presenter: Tim Close (University of California Riverside, USA)

Innovation Lab on Climate Resilient Cowpea

Close, T.J.[1*], Roberts, P.A.[1], Lonardi, S.[1], Cisse, N.[2], Drabo, I.[3], Tignegre de la Salle, JB.[3], Atokple, I.[4], Kusi, F.[4], and Boukar, Ousmane.[5]. [1]University of California, Riverside, California, USA; [2]Institut Senegalais Recherches Agricole (ISRA), Senegal; [3]Institut de l'Environnement et de Recherches Agricoles (INERA), Burkina Faso; [4]Council for Scientific & Industrial Research - Savanna Agricultural Research Institute (CSIR-SARI), Ghana; [5]International Institute of Tropical Agriculture (IITA), Nigeria.
*(timothy.close@ucr.edu)

This five-year project, "*USAID Feed the Future Innovation Lab for Climate Resilient Cowpea*" began September 2013. It is under the umbrella of the Feed the Future Global Hunger and Food Security Research Strategy: Climate Resilience, Nutrition, and Policy in the Program Area "High-Yielding, Climate Resilient Legumes". The focal theme is breeding and genetics for cowpea, with the aim of increasing the yield potential and providing solutions for major production constraints. The project involves partnership between the University of California at Riverside and the leading cowpea breeders in four West African nations (Burkina Faso, Ghana, Nigeria, Senegal) in the Sudano-Sahelian region, which is the main production zone for cowpea. The areas of emphasis for variety improvement are resistance to the drought-predisposed fungal pathogen *Macrophomina phaseolina*, drought tolerance at critical stages (early seedling, flowering, terminal) and heat tolerance during reproductive development. There are three basic objectives: 1) Foundation Development, 2) Training and 3) Implementation. Foundation Development includes the improvement of genotyping capabilities. In year 1 this includes the development of a 60,000 BeadAssay iSelect for SNP genotyping and its implementation to produce a higher density genetic map and baseline genetic knowledge about the breeding materials in each West African program. Drought tolerance of these same materials will be assessed in year 1 in sandbox assays to provide new baseline phenotypic data, supporting genotype-phenotype associations. A MAGIC population and diverse germplasm are also elements of this project. Training and implementation activities will occur through the life of the project.

11:30-12:00 Presenter: Doug Cook (University of California Davis, USA)

Taking a walk on the wild side: prospecting for climate resilience and nitrogen fixation traits in the wild progenitors of cultivated chickpea

R. Varma Penmetsa[1], Alex Greenspan[1], Peter Chang[1,2], Noelia Carrasquilla[1], Bullo Mamo[1], Lisa Vance[1], Reyaz Mir[1], Susan Moenga[1], Eleanor A. Siler[3], Janna L. Rose[4], Asnake Fikre[5], Bunyamin Tar'an[6], Maren Friesen[3], Sergey Nuzhdin[2], Bekir Bukun[7], Abdulkadir Aydogan[8], Jens D. Berger[9], Abdullah Kahraman[10], Eric von Wettberg[4] and Douglas R. Cook*[1],

[1]University of California, Davis, CA, [2]University of Southern California, Los Angeles, CA, [3]Michigan State University, East Lansing, MI, [4]Florida International University, Miami, FL, [5]Ethiopian Institute of Agricultural Research, Addis Ababa, Ethiopia, [6]University of Saskatchewan, Saskatoon, Canada, [7]Dicle University, Diyarbakir, Turkey, [8]Central Institute for Field Crops Research, Ankara, Turkey, [9]Plant Industry, CSIRO, Floreat, WA, Australia, [10]Harran University, Sanliurfa, Turkey. drcook@ucdavis.edu.

Crops are impacted in unintended, often negative ways during their domestication and breeding. Loss of adaptive alleles, fixation of deleterious alleles, and low genetic diversity in cultivated species constrains our ability to expand their cultivation into more extreme climates, marginal soils, or to situations with reduced agricultural inputs. We are addressing this need in chickpea, the world's second most important pulse legume, by harnessing the capacity of wild relatives to survive in harsh environments. Effective use

of wild germplasm in chickpea improvement requires new and systematic surveys of genotypes from natural environments, identification of adaptive alleles to environmental extremes, and incorporation of the diversity of wild alleles into purpose driven populations for trait analysis and breeding. We focus on climate resilience, nitrogen fixation and seed nutrient density, with the goal of more sustainable and stable production systems. We combine upstream ecology and genomics to assemble and characterize wild germplam; population development to remove barriers to use of wild alleles for trait assessment and breeding; and phenotyping and modeling of trait-gene associations to enhance the precision and rate with which wild alleles are applied to crop improvement. To date we have completed ecological characterization and genetic resource collection for ~1,100 novel accessions, used genotyping by sequencing and bioinformatics to deduce population genetic parameters, initiated whole genome re-sequencing, collected co-occurring bacterial symbionts, surveyed seed and flowering phenotypes, and initiated development of nested association mapping panels. We will present these results along with our vision for restructuring cultivated germplasm with wild alleles.

12:00-12:30 Presenter: Suk-Ha Lee (Seoul National University, Korea)

Genome Sequence of Mungbean and Vigna Speciation

Suk-Ha Lee
Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea.

Mungbean (*Vigna radiata*) is a fast-growing, warm-season legume crop that is primarily cultivated in developing countries of Asia. We constructed a draft genome sequence of mungbean to facilitate genome research into the subgenus *Ceratotropis* and to enable a better understanding of the evolution of leguminous species. The draft genome sequence covers 80% of the estimated genome, of which 50.1% consists of repetitive sequences. In total, 22,427 high confidence protein-coding genes were predicted. Based on the *de novo* assembly of additional wild mungbean species, the divergence of what was eventually domesticated and the sampled wild mungbean species appears to have predated domestication. Moreover, the *de novo* assembly of a tetraploid *Vigna* species (*Vigna reflexo-pilosa* var*. glabra*) provided genomic evidence of a recent allopolyploid event. To further study speciation, we compared *de novo* RNA-seq assemblies of 22 accessions of 18 *Vigna* species and protein sets of *Glycine max* and *Cajanus cajan*. The species tree was constructed by a Bayesian Markov chain Monte Carlo method using highly confident orthologs shared by all 24 accessions. The present assembly of *V. radiata* var. *radiata* will facilitate genome research and accelerate molecular breeding of the subgenus *Ceratotropis.*

IFLRC N Fixation and Plant Nutrition
Chair: C.L. Laxmipathi Gowda (ICRISAT, India))

11:00-11:30 Presenter: Endalkachew Wolde-meskel (Hawassa University, Ethiopia)

Exploiting indigenous rhizobial biodiversity resources and symbiotic N2-fixation to benefit small-holder farmers: the case of Ethiopia

Welde-meskel, E.[1,2*], Degefu, T.[3], Frostegåard, A.[4], Tena, W.[2], and Walley, F.[5]. [1]N2Africa Project-Ethiopia, International Livestock Research Institute (ILRI), P.O.Box 5689, Addis Ababa, Ethiopia; [2]Hawassa University, School of Plant and Horticultural Sciences, P.O. Box 5, Hawassa, Ethiopia; [3]Hawassa University, Department of Applied Biology, P.O. Box 5, Hawassa, Ethiopia; [4]Department of Chemistry, Biotechnology and Food Sciences, Norwegian University of Life Sciences, Ås, Norway; [5]University of Saskatchewan, Department of Soil Science, 51 Campus Drive, Saskatoon, S7N 5A8, Saskatchewan, Canada. *(E.Woldemeskel@cgiar.org)

Rhizobia are key resources as they strongly contribute to the nitrogen budget in many agricultural systems due to their nitrogen fixing capacity. Through North-South collaborative projects during last decade, we have isolated a large number of rhizobia (>500 strains) from different legume species growing in diverse agroecological zones in Ethiopia. Phylogenetic analyses revealed that the bulk of the Ethiopian strains are distinct from the hitherto known taxa of the family Rhizobiaceae. Recently, several new genospecies within this collection have been reported, including seven novel lineages within *Ensifer*, four within *Rhizobium and* three new species within *Mesorhizobium (M. hawassense, M. shonense, M. abyssinicae)*. Cross inoculation experiments in the greenhouse and farmers' fields, involving inoculation treatments on shrub and crop legumes indicated that some of the indigenous isolates excel (over +N control, elite national and imported inoculum strains) in their symbiotic performances. Also, "need for inoculation" studies indicated that legume crops markedly differ in their nodulation at various locations, demonstrating differences in the occurrence of compatible rhizobia at various locations and benefits from inoculation. These results, while suggesting the enormous untapped rhizobial resources resident in Ethiopian soils, indicate ample opportunities for selecting elite strains to enhance effective *Rhizobium*-legume symbiosis in agro-ecosystems. This work has formed the basis for expansion of N2Africa (www.n2africa.org) and intensification of efforts to enhance symbiotic nitrogen fixation in the farming systems of Ethiopia.

11:30-11:45 Presenter: Matthew Denton (University of Adelaide, Australia)

A national survey of farmers in Australia to understand rhizobial inoculant use for pulse and pasture legumes

Ryder, M.H.[1], and Denton, M.D.[1*]. [1]The University of Adelaide, School of Agriculture, Food and Wine. *(matthew.denton@adelaide.edu.au)

Inoculation of legumes with rhizobia is crucial to improving nitrogen fixation by pulse and pasture legumes but there is very little information on the inoculation practices of Australian farmers. A survey was conducted in 2013 to explore grower knowledge and practice in relation to rhizobial inoculation. The survey was completed by 405 growers, and represented a farmed area of just over 1 million hectares, across major cropping regions in Australia. Results showed that approximately 90% of mungbean and chickpea areas sown were inoculated. In contrast, less than 50% of lentil crops were inoculated. For pasture legumes, 85% of lucerne area was inoculated, while less than 50% of vetch, subterranean clover and annual medic pastures were typically inoculated. Peat formulation was by far the most common method of application (82% of respondents). Other formulations were also important, including granules (19%) and freeze-dried formulations (14%). A substantial proportion of farmers used more than one type of formulation. Farmers generally had a reasonable knowledge about rhizobia and their use, although ten per cent did not understand rhizobial specificity for particular legumes. Areas of concern are the acceptance of mixing inoculant with fertilisers (22% of farmers) or pesticides (9%). Ninety percent of

survey respondents reported that they had used inoculants on legumes in recent years. The key reasons provided for using inoculants related to perceived soil nitrogen benefits, improvements in yield and the influence of agronomic advisers. Of the ten per cent that did not inoculate, over half specified that inconvenience was a reason and also that the benefits of inoculation were not clear.

11:45-12:00 Presenter: Adriana Navarro-Borrell (Agriculture and Agri-Food Canada, Swift Current)

Managing soil microbial resources and wheat yield through crop rotation in 4-year systems in the Canadian Prairie

Navarro-Borrell, A.[1,2*], Hamel, C.[1,2], Gan, Y.[2], and Germida, J.[1]. [1]Department of Soil Science, University of Saskatchewan, Saskatoon, SK, S7N 5A8; [2]Semiarid Prairie Agricultural Research Centre, Agriculture and Agri-Food Canada, Swift Current, SK, S9H 3X2. *(adriana.navarroborrell@agr.gc.ca)

Crop rotation is a key component of enhancing agroecosystems performance, but it is unknown how different legume-cereal rotation systems may impact soil fungal communities and crop productivity. In this study, (1) we determined the relative efficiency of eight crop rotation systems involving pea, lentil, chickpea and wheat, based on crop performance, and (2) defined the contribution of plant-associated fungi to system performance. Pea-wheat-lentil-wheat, lentil-wheat-lentil-wheat, and pea-wheat-pea-wheat best promoted wheat seed yield and increased seed carbon content. In the lentil-wheat-lentil-wheat, and pea-wheat-pea-wheat systems, non-AM fungal colonization was positively correlated with wheat yield. Wheat monoculture and chickpea-wheat-wheat-wheat were the least productive systems. In year 3, diversified rotations had higher levels of mycorrhizal root colonization than rotations involving growing wheat on wheat. However, in year 4, wheat roots were similarly colonized by AM and non-AM fungi in all rotation systems.

The influence on plant growth of the soil microbiota selected under the first three phases of the rotation systems tested in the field was evaluated in an inoculation study, in the greenhouse. The microbiota selected under the rotation lentil-wheat-chickpea best promoted plant biomass and yield. Inoculation with soil from the plots under chickpea-wheat-chickpea and lentil-wheat-chickpea also increased wheat biomass, but the microbiota selected under wheat monoculture did not promote wheat growth; rather, it led to the lowest wheat biomass production. Yield was higher than the control in all the treatments, except pea-wheat-wheat-wheat and wheat monoculture.

We conclude that more diversified rotations promote AM fungal associations in the field and can enhance wheat productivity.

12:15-12:30 Presenter: Navid Bazghaleh (University of Saskatchewan)

Genotypic variation in the response of chickpea to arbuscular mycorrhiza and fungal endophytes

Bazghaleh, N.[1,2*], Hamel, C.[1,2], Knight, J.D.[1], and Gan, Y.[2,3]. [1]Department of Soil Science, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8; [2]Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada S9H 3X2; [3]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8. *(navid.bazghaleh@usask.ca)

Chickpea roots form symbioses with arbuscular mycorrhizal (AM) fungi and non-AM fungal endophytes

that influence its growth and productivity. Evidence shows that the genotype of the host plant can impact the outcome of root symbioses on plant growth, suggesting that intraspecific variations in the functionality of root symbioses may exist in chickpea. Here, we tested 13 cultivars of chickpea on the function of root symbioses formed by the AM, and non-AM endophytic fungi inoculated individually or co-inoculated. The AM symbiosis increased the biomass and nitrogen fixation activity of most cultivars of chickpea, whereas non-AM fungal endophytes had negative to positive influences. The genotype of both the chickpea and the fungal colonizer influenced the function of the symbioses. The root symbioses promoted plant growth most effectively in CDC Cory, CDC Anna and CDC Frontier and stimulated nitrogen fixation in CDC Corrine. Co-inoculation had additive effects on CDC Corrine, CDC Anna and CDC Cory but non-AM fungal endophytes reduced the positive effect of AM fungi on Amit and CDC Vanguard. Our results indicate that there is genetic variation in the response of chickpea to AM and non-AM fungal symbiosis. This variation could allow the selection of genotypes that form efficient symbioses with the AM and non-AM fungal endophytes, using conventional breeding techniques.

Thursday, July 10, 2014

Biotic Stress and Plant Microbe Interactions

ICLGG Symbiosis
Chair: Kirstin Bett (University of Saskatchewan, Canada)

11:00-11:30 Presenter: Pascal Ratet (Institut des Sciences du végétal CNRS, Gif sur Yvette, France)

Identification of *Medicago truncatula* genes preventing development of plant defenses during symbiosis

Berrabah, F.[1], Cayrel, A.[1], Eschstruth, A.[1], Bourcy, M.[1], Wen, .[2], Mysore, K.[2], Gourion, B.[1], and Ratet, P.[1]*.
[1]Institut des Sciences du végétal CNRS, 91198 Gif sur Yvette, France; [2]Samuel Roberts Noble Foundation, Ardmore, OK, USA. *(Pascal.Ratet@isv.cnrs-gif.fr)

The symbiosis between *Rhizobium* bacteria and legume plants results in the formation of nitrogen-fixing nodules on the roots of the host plant. In these nodules host large amount of bacteria that fix nitrogen for the benefit of the plant. How the plant can accommodate the chronic infection without eliciting defense reactions and how rhizobia can be distinguished from pathogenic bacteria during the post infection stages is not well understood. We have characterized the *dnf2* and *symCRK M. truncatula* mutants blocked in the symbiotic process after bacterial infection of the nodule symbiotic cells (Bourcy et al., 2013, New Phytol 197, 1250-61; Berrabah et al., 2014, submited). Nodules formed by the mutants contain only few layers of infected cells. Furthermore, they exhibit defense-like reactions which clearly contrast with premature senescence frequently observed during inefficient symbioses. The defense reactions are supported by the induction of molecular markers, the accumulation of phenolic compounds in the nodules and the death of the bacterial partner. In contrast to *symCRK*, the *dnf2* mutant phenotype is conditional suggesting a control of the symbiotic organ immunity by the environment. The description of these two mutants constitutes a significant step toward the elucidation of the mechanisms responsible for the establishment of the chronic infection during symbiosis.

11:30-11:50 Presenter: Georgina Hernandez (Universidad Nacional Autónoma de México, Mexico)

MicroRNAs from common bean (*Phaseolus vulgaris*) in the rhizobia symbiosis and in the response to abiotic stress

Hernandez, G.[1*], Nova-Franco, B.[1], Mendoza-Soto, A.B.[1], Formey, D.[1], Íñiguez, L.P.[1], Naya, L.[1], Paul, S.[1], Fuentes, S.I.[1], Leija, A.[1], Valdés-López, O.[2], Girard, L.[1], and Reyes, J.L.[3]. [1]Centro de Ciencias Genómicas, Universidad Nacional Autónoma de México (UNAM); [2]Facultad de Estudios Superiores-Iztacala, UNAM; [3]Instituto de Biotecnología, UNAM. *(gina@ccg.unam.mx)

Common bean (*Phaseolus vulgaris*) is the most important grain legume for human consumption; it establishes N-fixing symbiosis (SNF) with rhizobia. Plant microRNAs (miRNAs) (21-22 nt non-coding RNAs) are key post-transcriptional regulators of different processes. Our goal is to contribute deciphering common bean miRNA functions.

High-throughput sequence led to identify 114 known miRNAs in *P. vulgaris* (Peláez et al.2012). We are mapping these miRNAs in the *Phaseolus* genome (www.phytozome.net, v.1.0) and predicting novel MiRNA genes.

Aluminum toxicity (Al-t) is widespread in acidic soils where the common bean is produced and it is a limiting factor for crop production and for SNF. We have identified some 30 miRNAs that respond to Al-t in roots and nodules of SNF bean plants and have performed target gene expression analysis (Mendoza-Soto et al. submitted).

We have selected common bean miRNAs for functional analysis. The regulation of copper homeostasis and biotic interactions by miR398b has been demonstrated. The two validated miR398b target genes: CSD and novel Nod19 are up-regulated, while miR398b is down-regulated, under oxidative stress resulting from Cu toxicity, early interaction with rhizobia or infection of pathogenic fungi (Naya et al. 2014). Also we demonstrated the crucial role of miR172c and AP2-1 target gene in bean root and nodule development and in nodule function during effective N-fixing symbiosis. The over-expression of bean miR172c results in increased root growth, earlier nodulation, increased nodule number and higher nitrogenase activity (Nova-Franco et al. submitted).

11:50-12:10 Presenter: Jeremy Murray (John Innes Centre, Norwich, UK)

The Rhizobial Infectome: Uncovering the Genes that Control the Early Steps of the Legume-Rhizobia Interaction.

Breakspear, A.[1], Liu, C.[1], Wang, M.[2], He, J.[2], Cerri, M.R.[3], Guan, D.[1], Roy, S.[1], Stacey, N.[1], Rogers, C.[1], Trick, M.[1], Morieri, G.[1], Oldroyd, G.E.D.[1], Niebel, A.[3], Downie, J.A.[1], de Carvalho-Niebel, F.[3], and Murray, J.D.[1*]. [1]John Innes Centre, Norwich Research Park, Norwich, NR4 7UH, United Kingdom; [2]Cancer Genomics Research Laboratory, NCI Leidos Biomedical Research, Inc. 8717 Grovemont Circle Gaithersburg, MD 20877, USA; [3]LIPM, INRA-CNRS, Unité Mixte de Recherche 441/2594, 31326 Castanet-Tolosan, France. *(jeremy.murray@jic.ac.uk)

Sinorhizobium meliloti infects its host *Medicago truncatula* through root hairs which is essential for the

eventual development of nitrogen-fixing nodules. This process depends on flavonoids released from the plant roots that induce the production of signalling molecules called Nod factors by the rhizobia. These Nod factors are host-symbiont specific and essential throughout the infection process. To gain insight into the early-stage interactions we isolated and transcriptionally profiled root hairs from WT seedlings at different time points during infection. We also profiled several mutants: *sickle* which is hyperinfected, and *nin*, *ern1* and *nfya1*, that have defects in infection thread formation. The data indicate that that plant likely produces and secretes a large spectrum of compounds from root hairs including specific Nod factor inducing molecules, but also Nod factor degrading enzyme, strigolactones, phytoalexins, and potentially glucose. The data also provided insights into specific processes that are involved in infection thread growth and development, in particular the regulation of hormone biosynthesis and signalling. A gene regulatory network based on a larger data set that included the mutants was constructed which provided specific insights into how some of these components are controlled.

12:10-12:30 Presenter: Hongyan Zhu (University of Kentucky, USA)

Genetic control of symbiosis specificity in the legume-rhizobial mutualism

Zhu, H.[1*]. [1]University of Kentucky. *(hzhu4@uky.edu)

Legume plants are able to engage in root nodule symbiosis with nitrogen-fixing soil bacteria, collectively called rhizobia. This mutualistic association is highly specific, such that each rhizobial species/strain interacts with only a specific group of legumes, and vice versa. Symbiosis specificity can occur at multiple phases of the interaction, ranging from initial bacterial attachment and infection to late nodule development associated with nitrogen fixation. Genetic control of symbiosis specificity is complex, involving fine-tuned signal communication between the symbiotic partners. We will present our recent work on positional cloning of the soybean genes that control nodulation specificity with different rhizobial strains. We will also report our progress in cloning genes in Medicago that regulate symbiosis specificity at the nitrogen-fixing phase.

IFLRC Disease and Pest Resistance
Chair: Carlota Vaz Patto (Universidade Nova de Lisboa, Portugal)

11:00-11:30 Presenter: Weidong Chen (USDA/ARS, Washington State University, USA)

What roles do fungal secondary metabolites play in interactions between *Ascochyta* fungi and cool season food legumes?

Kim, W.[1], Peever, T.[1], Vandemark, G.[2], and Chen, W.[2*]. [1]Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA; [2]USDA ARS, Grain Legume Genetics and Physiology Research Unit, Washington State University, Pullman, WA 99164, USA. *(w-chen@wsu.edu)

Fungal plant pathogens produce many secondary metabolites including many that are toxic to plants (phytotoxins). Some of these phytotoxins are host-selective (toxic only to particular genotypes of host

plants) and required for pathogenicity, while many others are non host-selective and toxic to many different plants. The Ascochyta blight pathogens of cool season food legumes produce an array of non host-selective toxins. Although Ascochyta blight pathogens are generally host-specific, their phytotoxins are not. Nevertheless, these phytotoxins have often been proposed to be virulence/pathogenicity factors without conclusive evidence. We are currently investigating the roles of secondary metabolites produced by the Ascochyta blight pathogens in their pathogenicity and ecology. We found that each *Ascochyta* species produces a unique set of secondary metabolites, which is highly correlated to evolutionary relationships inferred among the species. For the chickpea blight pathogen, all isolates of *Ascochyta rabiei* produce solanapyrone toxins, which are unique among *Ascochyta* species, but identical to those produced by the potato pathogen, *Alternaria solani*. During studying the roles of solanopyrones in pathogenesis, the solanapyrone synthase gene in both *Ascochyta rabiei* and *Alternaria solani* was disrupted through targeted gene replacement. The resulting mutants do not produce solanapyrones, but accumulate the precursor presolanopyrone which is not toxic to plants. Surprisingly, these solanapyrone-deficient mutants are equally pathogenic, if not more pathogenic, than the wild-type strains, on their respective hosts. Results show that the solanapyrone toxins are not required for pathogenicity, but may play important roles in the biology of these fungi including competition and survival in nature.

11:30-11:45 **Presenter:** Aurore Desgroux (INRA, Rennes, France)

Identification of pea lines resistant to *Aphanomyces euteiches* and related root architecture traits

Desgroux, A.[1*], Baudais, V.[1], Rivière, J-P.[1], Mangin, P.[2], Roux-Duparque, M.[3,4], Moussart, A.[1,5], Duc, G.[6], Manzanares-Dauleux, M.[1,7], Bourion, V.#.[6], and Pilet-Nayel, M-L.#.[1]. [1]INRA, UMR1349 IGEPP, Domaine de la Motte, Le Rheu F-35653, France; [2]INRA, Domaine Expérimental Epoisses, UE0115, Bretenières F-21110, France; [3]GSP, Domaine Brunehaut, Estrées-Mons 80200, France; [4]Current address : Chambre d'Agriculture de l'Aisne, Laon Cedex 02007, France; [5]UNIP-CETIOM, 11 rue de Monceau, CS 60003, F-75378 Paris, France; [6]INRA, UMR 1347 Agroécologie, F-21065 Dijon cedex, France; [7]AGROCAMPUS Ouest, UMR1349 IGEPP, 65 rue de Saint Brieuc, 35042 Rennes, France; # The two last co-authors contributed equally to this study. *(adesgroux@rennes.inra.fr)

Common root rot caused by *Aphanomyces euteiches*, is a major soil borne disease of pea in many countries. Genetic resistance is considered to be the main way to control the disease. The role of plant root architecture in Aphanomyces root rot resistance is not well known. This study aimed at identifying pea lines with high levels of resistance in a collection of 175 accessions enriched with sources of resistance and root architectural traits harbored by resistant lines. The collection was assessed for resistance to *A. euteiches* on the roots and on the aerial plant parts, both in controlled conditions and in a four-year and multi-location field disease network. The collection was also described for root architectural traits on healthy and infested plants in controlled conditions at young plant stage. Lines with higher levels of resistance than partially resistant controls were identified. Susceptible and partially resistant plants mostly showed a decrease of lateral root density and dry weight when compared to healthy controls. However, some resistant lines maintained both root density and dry weight, suggesting their ability to preserve the root system in response to infection. These results will be confirmed in the field using a set of contrasted genotypes. Genome wide association analysis will be performed to compare the genetic control of Aphanomyces root rot resistance and of root architecture traits in response to infection.

11:45-12:00 Presenter: Beybin Bucak (Harran University, Sanliurfa, Turkey)

Transfer of resistance to broomrape (*Orobanche crenata*) from *Lens ervoides* to cultivated lentil.

Bucak B[1], Bett KE[2], Banniza S[2] and Vandenberg A[2]. [1]Harran University, Sanliurfa, Turkey. [2] Dept. of Plant Sciences/Crop Development Centre, University of Saskatchewan, Canada.

The parasitic plant *Orobanche crenata* has been a threat to legume crops since antiquity and remains an important biotic stress for lentil production in the Mediterranean Basin regions. The objectives of the study were to determine if broomrape resistance could be identified and transferred to cultivated lentil using specific parental genotypes of *Lens ervoides* which had been previously used to develop interspecific RIL populations for investigation of resistance to fungal pathogens. RILs are a good tool for constructing linkage maps to identify quantitative characters such as broomrape resistance which may be controlled by many genes. We initially screened for resistance to crenate broomrape under *in vitro* conditions using a single accessions of each of the wild lentil species (*L. nigricans*, *L. ervoides*, *L. orientalis*, *L. odemensis*, *L. tomentosus*, *L. lamottei*), and a single RIL plus parents from the LR-59 population (*Lens culinaris* 'Eston' x *Lens ervoides* L-01-827A). *Lens ervoides* accessions and the single RIL had resistance to broomrape. Later, two larger sets of RIL populations derived from 'Eston x *L. ervoides* were grown in the field in Southeastern Anatolia in 2012-2013. A wide range of responses in the RILs was observed, from complete resistance like the *L. ervoides* parents to high susceptibility like 'Eston'. The field study provided the first evidence interspecific transfer of resistance to broomrape from wild lentil to cultivated lentil.

12:00-12:15 Presenter: Kristy Hobson (NSW Department of Primary Industries, Australia)

Developing superior chickpea varieties by improving chickpea Phytophthora resistance using wild relatives.

Hobson, K.[1*], Knights, T.[1], Moore, K.[1], Bithell, S.[1], Douglas, C.[2], Ryan, M.[2], Ryley, M.[3], and Sutton, T.[4]. [1]NSW Department of Primary Industries, 4 Marsden Park Rd, Tamworth NSW 2340; [2]Department of Agriculture, Fisheries and Forestry, Hermitage Research Facility, 604 Yangan Road, Warwick, Qld 4370; [3]formerly Department of Agriculture, Fisheries and Forestry, 203 Tor St, Toowoomba, Qld 4350; [4]Australian Centre for Plant Functional Genomics, University of Adelaide, Hartley Grove, Urrbrae, SA 5064. *(kristy.hobson@dpi.nsw.gov.au)

Australian chickpea production expanded from 7,000 ha in 1984 to peak at 560,000 ha in 2012 with desi chickpea accounting for approximately 85 % of the crop. The Pulse Breeding Australia (PBA) chickpea program breeds desi and kabuli types adapted to major chickpea growing areas in Australia with the primary focus on improved yield reliability and stability. Improved disease resistance is an essential component of this aim.

Phytophthora root rot (PRR), caused by *Phytophthora medicaginis,* is a major disease constraint in north eastern Australia. Accessions of *Cicer echinospermum* were previously identified as having higher levels of resistance to this pathogen than *C. arietinum* (chickpea) germplasm. In 2000, a concerted breeding effort was initiated to incorporate this resistance into adapted desi and kabuli backgrounds. Following a number of backcrosses, high levels of resistance to PRR has been transferred into adapted breeding lines with acceptable agronomic characteristics and seed quality attributes. Under higher PRR disease pressure the improved resistance resulted in higher yields of inter-specific breeding lines compared to commercial

varieties. The most advanced desi lines have also been evaluated in multi-site yield trials in northern Australia and in addition to their superior PRR resistance, have demonstrated a yield advantage over the current industry standard, PBA HatTrick.

Future research will utilise inter-specific recombinant inbred populations to develop breeding tools aimed at providing rapid incorporation of the superior PRR resistance of *C. echinospermum* into the breeding program.

12:15-12:30 Presenter: Diego Rubiales (Institute for Sustainable Agriculture, Cordoba, Spain)

Exploitation of wild relatives in pea breeding for disease and pest resistance

Rubiales, D.[1*], Barilli, E.[1], Bani, M.[1], Rispail, N.[1], Aznar, T.[1], and Fondevilla, S.[1]. [1]Institute for Sustainable Agriculture, CSIC, Cordoba, Spain. *(diego.rubiales@ias.csic.es)

Unfortunately, for some pathogens and pests, there genetic resistance in pea (*Pisum sativum* ssp. *sativum*) germplasm and cultivars is scarce. In occasions, we can exploit them for related *P. sativum* ssp. germplasm, or even from the most distant *P. fulvum*. Examples of the breeding activities performed at CSIC-Cordoba will be mentioned. Germplasm collections of *Pisum* have been throroughtly screened for resistance to ascochyta blight, powdery mildew, rust, broomrape, and more recently fusarium wilt, aphid and weevil, yielding the identification of valuable sources of resistance that are being introduced in our breeding program. Inheritance of some of the identified resistances has been studied and underlaying mechanisms characterized. As an example, a new gene (*Er3*) for powdery mildew resistance was identified in *P. fulvum* and introduced in pea, with a resistant cultivar being released. Similarly, the first two broomrape resistant cultivars are now being realeased. Breeding for ascochyta, rust, aphid and weevil resistance is in progress

ICLGG Symbiosis
Chair: Jeremy Murray (John Innes Centre, Norwich, UK)

14:00-14:30 Presenter: Krzysztof Szczyglowski (Agriculture and Agri-Food Canada, London, Ontario, Canada)

Turning on the nitrogen tap: how legumes keep the nutrient flowing

Szczyglowski, K.[1,2*], Hou, H.[1], Miri, M.[1,2], Ross, L.[1], Sato, S.[3], Tabata, Satoshi.[3], Perry, J.[4], Wang, T.[4], Torres-Jerez, I.[5], Murray, J.[4,5], Udvardi, M.[5], and Held, M.[1,2]. [1]Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, London, Ontario, N5V 4T3 Canada; [2]Department of Biology, University of Western Ontario, London, Ontario, N6A 5BF Canada; [3]Kazusa DNA Research Institute, 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818 Japan; [4]John Innes Centre, Norwich Research Park Colney, Norwich NR4 7UH, United Kingdom; [5]The Samuel Roberts Noble Foundation, Ardmore, Oklahoma 73401. *(Krzysztof.Szczyglowski@agr.gc.ca)

Almost 80 percent of Earth's atmosphere is nitrogen. Yet, only a very limited number of plants, mainly

legumes like pea, soybean or alfalfa, can efficiently tap into this abundant natural resource to support their growth. They do so through cooperation with prokaryotic partners by building new organs that host the bacteria while providing appropriate conditions for symbiotic nitrogen fixation to occur.

Looking at leguminous plants "soaking up" atmospheric nitrogen, it is hard not to question whether this beneficial process could be instilled into other crop plants. During my presentation, I will discuss aspects of current knowledge and steps that are being taken in my laboratory and others to unlock the secret behind the ability of legumes to build nodules. The primary focus will be on cytokinin signaling and its role in mediating nodule formation. Understanding and possibly transferring this ability to non-legume crops could support a greener revolution, where agricultural production is more 'in tune' with the natural environment.

14:30-15:00 Presenter: Masayoshi Kawaguchi (National Institute for Basic Biology, Okazaki, Japan)

Two kinds of mobile signals mediate long-distance control of nodulation

Kawaguchi, M.[1*]. [1]Division of Symbiotic Systems, National Institute for Basic Biology, Okazaki 444-8585, Japan. *(masayosi@nibb.ac.jp)

Legume-*Rhizobium* symbiosis is one of the most beneficial interactions on earth. In this symbiosis, rhizobia supply ammonia to the host plants through symbiotic nitrogen fixation. In return, the host plants provide the rhizobia with their photosynthetic products. To keep the symbiotic balance with rhizobia, legumes evolved specific mechanisms to control the nodule number. An important internal cue is a feedback regulatory system involving long-distance signaling also known as autoregulation of nodulation (AON). AON is believed to consist of two presumptive long-distance signals, i.e., the root-derived signal and shoot-derived inhibitor. The root-derived signal is thought to be generated in roots in response to rhizobial Nod factors and then translocated to the shoot, while the shoot-derived inhibitor is generated in shoots and then translocated to the root to restrict further nodulation. Mutants defective in AON display a 'hyper-nodulation' phenotype.

Using *Lotus japonicus*, we have isolated *har1, klavier*, *too much love* (*tml*) and *plenty* hyper-nodulation mutants. Grafting experiments revealed that HAR1and KLAVIER function in the shoot, while TML and PLENTY in the root. Two CLE peptides (LjCLE-RS1, -RS2) are strong candidates of the root-derived signal. Over-expression of *CLE-RS1/2* inhibits nodulation systemically in HAR1, KLAVIER and TML-dependent manner. Then, we identified candidates of shoot-derived signal that is activated by rhizobial infection in shoots, and found that exogenous application of the candidates to shoots can inhibit nodulation in a TML-dependent manner. Based on the findings, we propose a model for AON mediated by two kinds of long-distance mobile signal molecules.

15:00-15:30 Presenter: Christine Lelandais-Brière (Université Paris Diderot- France)

MicroRNA networks involved in root architecture and environmental interactions in the model legume *Medicago truncatula*

Lelandais-Brière, C.[1,2*], Bazin, J.[2], Formey, D.[3], Sallet, E.[3], Combier, J.P.[3,3], Roux, C.[3], Niebel, A.[3], Bustos, P.[2], Hartmann, C.[1,2], Genzbittel, L.[4], Gouzy, J.[3], and Crespi, M.[2]. [1]Université Paris Diderot- France; [2]ISV-CNRS-Gif/Yvette-France; [3]LIPM-CNRS-Toulouse-France; [4]ENSAT-Toulouse-France.

*(christine.lelandais@isv.cnrs-gif.fr)

Root systems are crucial for crop productivity and acquisition of soil resources and present a large plasticity in response to environmental constraints. Since 10 years, microRNAs have emerged as key players in regulatory networks that control root development and adaptation to the environment. We sequenced smallRNA libraries from roots under a variety of abiotic and biotic interactions, including salt stress, pathogens, rhizobia and endomycorrhizal fungi. We identified 416 miRNAs (and their targets), among which 52 are novel and some are legume-specific. miRNAs responsive to one or several stresses were identified. In addition, by comparing 26 *M. truncatula* accessions, an unsuspected level of variation inside conserved miRNA genes was observed in comparison to novel miRNAs. We studied in detail miR396, a conserved miRNA induced by salt stress. This miRNA regulates leaf development by repressing transcription factors of the Growth Regulating Factor family (GRF). We showed that mtr-miR396 regulates 6 *MtGRF* genes but also bHLH transcription factors in *M. truncatula*. miR396 genes are differentially expressed in roots and nodules, suggesting a possible diversification and a complex regulatory network. Over-expression of miR396 in roots led to reduced growth and cell division activity, while its inactivation using a mimicry construct strongly enhanced root biomass. Finally, this miRNA appears to positively control AM fungus infection. Finally, in the European ABSTRESS project, we are investigating the impact of combined abiotic and pathogenic stresses on the small RNAome. Our results highlight new putative regulatory networks involved in root plasticity in response to environmental interactions in legumes.

IFLRC Disease and Pest Resistance
Chair: Sabine Banniza (University of Saskatchewan, Canada)

14:00-14:30 Presenter: Hari Sharma (ICRISAT, India)

Potential of host plant resistance to insects for pest management in grain legumes: Progress and limitations

HC Sharma*, Mandeep Pathania, AR War, S Srinivasan and PM Gaur.[1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India. *Email: h.sharma@cgiar.org. *(h.sharma@cgiar.org)

Grain legumes such as chickpea, pigeonpea, cowpea, field pea, lentil, faba bean, black gram, green gram, grass pea, and *Phaseolus* beans play an important role in food and nutritional security, and sustainable crop production. Several insect pests damage these crops, of which pod borer, *Helicoverpa armigera*; spotted pod borer, *Maruca vitrata*; pod fly, *Melanagromyza obtusa*; stem fly, *Ophiomyia phaseoli*; white fly, *Bemisia tabaci*; defoliators, *Spodoptera litura* and *S. exigua*; leafhoppers, *Empoasca* spp., thrips, *Megaleurothrips dorsalis*, and *Caliothrips indicus*;and the bruchids, *Collasobruchus chinensis* and *Bruchus pisorum* cause extensive losses. Infester row, no-choice cage, detached leaf assay, and diet incorporation assay to evaluate germplasm, mapping populations, and transgenic plants for resistance to insect pests have been developed. Considerable progress has been made in identification and utilization of sources of resistance to insect pests, development of cultivars with resistance/tolerance to major pests. The levels of resistance to some insect species, particularly the pod borers, *Helicoverpa*, *Maruca* and *Spodoptera* in the cultivated germplasm are quite low. However, the wild relatives of many crops have shown very high

levels of resistance to insects. There is a need for identification of morphological and biochemical traits and the molecular markers associated with insect resistance for developing cultivars with resistance to insects for use in IPM.

14:30-14:45 Presenter: Mustapha El-Bouhssini (ICARDA, Rabat, Morocco)

Progress in host plant resistance in chickpea to Leaf miner, *Liriomyza cicerina* (Rondani)

El Bouhssini, M.[1*], Malhotra, R.S.[2], Imtiaz, M. .[3], Ali, L.[4], Hamwieh, A.[5], Murad, S.[6], Ibrahim, Z.[7], Lhaloui, S.[8], and Sabraoui, A. .[9]. [1]International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box: 6299- Rabat Instituts, Rabat, Morocco; [2]Consultant, Florida, USA; [3]International Maize and Wheat Improvement Centre (CIMMYT) Pakistan Office, NARC, Park Road, Islamabad 44000, Pakistan; [4]Plant protection department, Faculty of Agriculture, Aleppo University, Aleppo, Syria; [5]ICARDA, Cairo, Egypt; [6]ICARDA, Terbol, Lebanon; [7]ICARDA, Aleppo, Syria; [8]INRA-CRRA,Settat, PO Box 589, Settat, Morocco; [9]ICARDA, Rabat, Morocco. *(M.Bohssini@cgiar.org)

Leaf miner (*Liriomyza cicerina* R.) is an important pest affecting chickpea in West Asia and North Africa. Grain yield losses caused by this pest could be as high as 45% in susceptible cultivars. Breeding efforts to develop resistant varieties to this pest started in 1999 when the first five crosses were made at ICARDA, Aleppo, Syria. As a result, seven lines which possessed good agronomic background, seed quality and relatively high yielders were registered as sources of resistance in Crop science in 2007. Six new crosses were made recently to combine Leaf miner resistance with better agronomic characters and resistance to key diseases such as Aschochyta blight. In 2013, a total of 200 F3 chickpea single plants were selected at Khemis Zemamra station in Morocco with good level of resistance to the chickpea leaf miner and high number of pods/plant. This material is being tested in 2014 for agronomic characters and disease resistance in several stations in Morocco. In a study conducted in 2011 and 2012 using eight lines with different levels of resistance/susceptibility to Leaf miner, we examined the role of oxalic acid concentration in resistance to Leaf miner, using High Performance Liquid Chromatography (HPLC). We found significant negative correlation between the concentration of oxalic acid and leaf miner damage, indicating that this acid plays a role in resistance to this pest. Efforts are also underway to develop molecular markers associated with resistance to Leaf miner and thus facilitating selection for resistance.

14:45-15:00 Presenter: Lars Kamphuis (CSIRO Plant Industry, Wembley, Australia)

Resistance to aphids in the model legume *Medicago truncatula*

Kamphuis, L.G.[1,2*], Zulak, K.[1], Guo, S.[1], Gao, L.-L.[1], and Singh, K.B.[1,2]. [1]CSIRO Plant Industry, Private Bag 5, Wembley, WA 6913, Australia; [2]The UWA Institute of Agriculture, University of Western Australia, Crawley, WA 6009, Australia. *(lars.kamphuis@csiro.au)

Aphids are probably the largest group of sap-sucking insects causing serious damage to agriculture and natural ecosystems. Resistance to aphids has been identified in a number of plant species, yet the molecular mechanisms underlying aphid resistance remain largely unknown. Australian breeders have introgressed BGA resistance into three popular cultivars and generated three new resistant linesin the model legume *M. truncatula*. Further characterization showed that each resistance line operates against a number of major legume aphid species. However, the magnitude of resistance varied depending on the *M.*

truncatula line and/or aphid species. We have focused on one pair of near isogenic lines, A17 (susceptible) and Jester (resistant) in which single dominant genes condition resistance to bluegreen, pea and spotted alfalfa aphid. All three aphid resistance genes have been fine-mapped and cloning and complementation of these genes is underway.

We have generated very near isogenic lines of *M. truncatula* A17 harbouring these aphid resistance genes, which are powerful tools that essentially eliminate background noise in our transcriptomics and metabolomics experiments. Using these resources, we are making considerable progress on deciphering downstream signalling and defence mechanisms against these aphid species including terpenoid profiling and the identification of transcription factors that may control a successful plant response to aphid attack.

15:00-15:15 Presenter: Kiran Sharma (ICRISAT, India)

Transgenic pigeonpea for resistance to legume pod borer: moving towards product development

Sharma, K.K.[1*], and Bhatnagar-Mathur, P.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, Andhra Pradesh, India. *(k.sharma@cgiar.org)

In pigeonpea, the annual losses due to the legume podborer (*Helicoverpa armigera)* have been estimated at US$ 317 million worldwide. Current statistics indicate that the pigeonpea farmers resort to three to six insecticidal sprays to control *H. armigera* in India, posing not only a significant health and environmental risk but also resulting in resistance built-up. To address these constraints, efforts are being made to develop transgenic plants of pigeonpea engineered for resistance to this important insect using different insecticidalgene constructs. Over 150 transgenic events have been produced using different gene-promoter combinations using single or gene stacks for effective *Cry* gene expression. The transgenic events showing higher transgene expression based on ELISA are selected and subjected to insect bioassays using detached leaf, flower and pods along with the untransformed control and resistant checks. While the flower twig bioassays usually form the basis of preliminary screening for phenotyping, prominence is given to pod bioassay results for conclusiveness. We have made advances in identifying few promising events with optimal *cry1Ac*and *cry2Aa* gene expression which are currently in T4-T5 generations, selected based on significant reduction in larval weights in flower twig bioassays followed by pod bioassays. Pod bioassays of such T4 generation plants carried out using mid to late 3rd instars larvae indicated >90% mortality in6 events that showed considerable reduction in damage, larval survival and weight gain compared to their untransformed control counterparts. The results of these studies and the status of the technology will be discussed in detail.

15:15-15:30 Presenter: Ashutosh Sarker (ICARDA, Beirut, Lebanon)

Adaptation of lentil and grasspea under various cropping systems in South Asia

Sarker, A.[1*], Kumar, J.[2], Nath, R.[3], Zaman, S.[4], Roy, S.[4], Gharti, D.B.[5], Derai, R.[5], and Ali, A.[6]. [1]ICARDA, Beirut, Lebanon; [2]Indian Institute of Pulses Research, Kanpur, India; [3]Bidhan Chandra Krishi Visvidyala, Kalyani, India; [4]Bangladesh Agricultural Research Institute, Joydebpur, Bangladesh; [5]Nepal Agricultural Research Council, Rampore, Nepal; [6]National Agricultural Research Center, Islamabad, Pakistan. *(A.Sarker@cgiar.org)

Lentil (*Lens culinaris* Medikus subsp. *culinaris*) and grasspea (*Lathyrus sativus* L.) are among important pulse crops grown under various cropping systems in South Asia. Their importance in food and feed and for sustainable cereal-based cropping systems is well documented. They constitute an important component of daily diet and contribute to nutritional security of the people of South Asia. Plant residues are valued animal feed. However, traditional cultivars are low and unstable in yield, mainly due to numerous stresses including diseases and frequent drought. These crops are cultivated as sole crop, mixed- and intercrop, relay crop, and thus appropriate varieties with improved production technologies under these niches are essential for farmers.

To address these issues, the International Center for Agricultural Research in the Dry Areas (ICARDA) in collaboration with national research programs of South Asia have successfully disseminated improved lentil and grasspea varieties and their matching production technologies. For example, lentil varieties, Barimasur-4, Barimasur-5, Barimasur-6, Barimasur-7 and Blinamasur-7 in Bangladesh; Khajurah-3, Shekhar, Sagun, MP Bharati and Shital in Nepal; Moitree, NDL-1, PL-6, VL507, IPL-406 and IPL316 in India; and Masoor-93, Masoor-4, NIAB Masoor-06 in Pakistan have substantially increased lentil production. Some of the varieties with early maturity are suitable for relay cropping, and yielded up to 1.7 t/ha compared to <0.9 t/ha average productivity in the region. Super-early lentils with maturity <90 days have been developed for rice-lentil-rice systems. Low-toxin grasspea varieties (Nirmal, Ratan, Mahatiwara, Pateek and Barikhesari-2) with low-ODAP content and inherent drought tolerance have been adopted by farmers.

Friday, July 11, 2014

Abiotic Stress and Crop Management

ICLGG Applied Genomics
Chair: Noel Ellis (CGIAR, Hyderabad, India)

11:00-11:30 Presenter: Maria Monteros (The Samuel Roberts Noble Foundation, USA)

Opportunities for Genomics-Assisted Breeding Approaches in Alfalfa (*Medicago sativa* L.)

Monteros, MARIA J.[1*], Brummer, E.C.[2], Motes, C.[1], Wei, Y.[1], and Li, X.[1]. [1]The Samuel Roberts Noble Foundation; [2]University of California, Davis. *(mjmonteros@noble.org)

Alfalfa is a high yielding perennial forage legume species that can be harvested multiple times per year during the growing season. In addition to its broad economic value in agriculture, alfalfa contributes to the reduction of soil erosion and has the capacity to fix nitrogen for its own use as well as for a subsequent crop in a crop-rotation system. New technologies have revolutionized biological inquiry and now have the potential to transform plant improvement strategies. The availability of genotyping-by-sequencing and other SNP genotyping approaches, the generation of a draft genome assembly, the manipulation of mechanisms of post-transcriptional gene regulation and the ability to accurately phenotype plant growth in a variety of conditions can facilitate the development and implementation of genomics-assisted breeding approaches for alfalfa improvement. Target traits for improvement using these technologies include maximizing water and nutrient use efficiency, increasing tolerance to stress conditions and enhancing

nutritional value. Consolidating the results of basic discoveries in plant science with genotypic and phenotypic data from breeding programs into a user-friendly alfalfa breeder's toolbox will enable the development of enhanced cultivars to more effectively address current and future challenges to crop productivity.

11:30-11:50 Presenter: Sachiko Isobe (Kazusa DNA Research Institute, Japan)

***In silico* SNP and SSRP discovery in horsegram genome sequences**

ISOBE, S.N.[1*], Hirakawa, H.[1], Chahota, R.[2], Shirasawa, K.[1], and Sharma, T.[2]. [1]Kazusa DNA Research Institute; [2]CSK Himachal Pradesh Agricultural University. *(sisobe@kazusa.or.jp)

Horsegram (*Macrotyloma uniflorum*) is wildly cultivated in tropical, sub-tropical and wet temperate regions of the world. It is a self-fertilizing plant (2n=2X=20, genome size= ca. 400Mb) and the only cultivated species of genus *Macrotyloma*. Insufficient number of DNA markers has been developed in horsegram because of the low genetic diversity of the species. Hence, we have tried *in silico* SNP (single nucleotide polymorphism) and SSRP (simple sequence repeat polymorphism) discovery by comparison of assembled Illumina genome sequences of two horsegram inbred lines, 'K_Ho1' and 'K_Ho2'. A total of 375M paired end reads of 'K_Ho1' were obtained and subjected to genome assembly by the SOAPdenovo2 r223. The number of assembled scaffolds was 237,662 (Kmer=81) consisting of 314 Mb with N50=97,711 bp. After masking repeat regions, 'K_Ho2' reads were mapped onto the 'K_Ho1' scaffolds by using the Bowtie2 2.1.0 program. As a result, a total of 4,686 candidate SNPs were discovered between the two lines. In parallel, a total of 23,305 SSR sequences were identified on the 'K_Ho1' scaffolds, of which repeat regions were masked. Of these, 6,418 SSRs were successfully used to designing primers on the flanking regions. BLAST searches of the designed primer sequences was performed against the 'K_Ho2' sequences and a total of 5,754 (89.7%) corresponding SSRs were identified on the 'K_Ho2' scaffolds. Only 27 SSRPs were identified between the two lines by comparisons of the corresponding SSRs. The discovered candidate SNPs and SSRPs are expected to be useful resources for genetic analysis and breeding applications in horsegram.

11:50-12:10 Presenter: Sujan Mamidi (North Dakota State University, USA)

Genome-wide association studies to identify major QTL responsible for Iron Deficiency chlorosis in soybean (*Glycine max*)

Mamidi, S.[1,2*], Lee, R.K.[1,2], Goos, R.J.[3], and McClean, P.E.[1,2]. [1]Genomics and Bioinformatics Program, North Dakota State University, Fargo, ND, USA; [2]Department of Plant Sciences, North Dakota State University, Fargo, ND, USA; [3]Department of Soil Science, North Dakota State University, Fargo, ND, USA. *(sujan.mamidi@gmail.com)

Iron deficiency chlorosis (IDC) is an important yield-limiting factor for soybeans (*G. max*) grown on soils with a high levels of calcium carbonate and soluble salts. These calcareous soils are common in the north-central regions of the United States. The interactions of high pH, carbonate and high field moisture content at planting leads to early IDC symptoms in these soils. It is estimated that the current revenue losses due to IDC in soybean are $260 million. Genome-wide association study (GWAS) was performed using 35,000 SNP discovered by genotype by sequencing to discover significant markers, QTL and candidate genes

associated with IDC trait variation. These markers defined seven major QTL on six chromosomes. Thirteen candidate genes known to be associated with iron metabolism mapped near these QTL supporting the polygenic nature of IDC. A non-synonymous substitution in a major QTL region suggests soybean orthologs of *FRE1* on Gm03 is a major gene associated with trait variation. NAS3, a gene that encodes the enzyme nicotianamine synthase also maps to the same QTL region. Allelic combinations of ten major markers can be used for marker assisted selection.

12:10-12:30 Presenter: Hamid Khazaei (University of Helsinki, Finland)

Synteny-based mapping of morphological, agronomic and quality traits in faba bean (*Vicia faba* L.)

Khazaei, H.[1*], O'Sullivan, D.M.[2], Sillanpää, M.J.[3], and Stoddard, F.L.[1]. [1]Department of Agricultural Sciences, P O Box 27 (Latokartanonkaari 5), FIN-00014, University of Helsinki, Finland; [2]School of Agriculture, Policy and Development, University of Reading, Whiteknights, P O Box 237, Reading, UK; [3]Department of Mathematical Sciences, Department of Biology and Biocenter Oulu, P O Box 3000, FIN-90014, University of Oulu, Finland. *(hamid.khazaei@helsinki.fi)

The faba bean (*Vicia faba* L.) is a valuable food and feed crop, but it is reputed to be sensitive to several abiotic and biotic stresses (*e.g.* drought), and its consumption is limited by anti-nutritional factors (*e.g.* vicine-convicine, VC). Its large and complex genome (~13000 Mbp) has slowed progress toward molecular breeding in this species, and an indirect approach using synteny with the model legume species *Medicago truncatula* may help to bridge this gap. An F5 RIL population of 211 individuals was derived from the cross Mélodie/2 × ILB938/2. It was genotyped using 222 polymorphic SNPs and phenotyped for several morpho-physiological traits related to drought adaptation and VC content. The genetic map covered ~928 cM of faba bean genome in nine linkage groups, seven of which were assigned to chromosomes. The map showed a high degree of synteny with the genome of *M. truncatula*. Most of the detected QTLs for stomatal morphology and function were in a single region of faba bean chromosome 2 syntenic with a segment of *M. truncatula* chromosome 4 that harbours Receptor-like protein kinase. Furthermore, a strong QTL (R2=0.765) for VC content was detected on faba bean chromosome 1, 6.6 cM from hilum colour. In the same chromosome, we mapped a novel locus (*ssp1*) for stipule pigmentation in a well conserved region of *M. truncatula* chromosome 5 containing some candidate Myb and bHLH transcription factor genes. These results confirm that genomic information from *M. truncatula* can be translated to the faba bean genome.

IFLRC Abiotic stress
Chair: Kadambot Siddique (University of Western Australia)

11:00-11:30 Presenter: Pooran Gaur (ICRISAT, India)

High temperature tolerance in grain legumes

Gaur, P.M.[1*], Samineni, S.[1], Krishnamurthy, L.[1], Varshney, R.K.[1], Kumar, S.[2], Ghanem, M.E.[2], Beebe, S.[3], Rao, I.[3], Chaturvedi, S.K.[4], Basu, P.S.[4], Nayyar, H.[5], Jayalakshmi, V.[6], and Babbar, A.[7]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Hyderabad 502 324, AP, India; [2]International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco; [3]International

Center for Tropical Agriculture (CIAT), A.A. 6713, Cali, Colombia; [4]Indian Institute of Pulses Research (IIPR), Kanpur 208024, UP, India; [5]Panjab University, Chandigarh 160 014, India; [6]Regional Agricultural Research Station, Nandyal 518 502, AP, India; [7]Jawaharlal Nehru Agricultural University, Jabalpur 482 004, MP, India. *(p.gaur@cgiar.org)

High temperature stress (or heat stress) during reproductive stages is becoming a serious constraint to productivity of grain legumes as their cultivation is expanding to warmer environments and temperature variability is increasing due to climate change. Heat stress adversely affects pollen viability, fertilization, pod set and seed development leading to abscission of flowers and pods and substantial losses in grain yield. Photosynthate remobilization has been identified to play an important role in heat tolerance. A high temperature of 35°C was found critical in differentiating heat tolerant and heat sensitive genotypes in chickpea, lentil and faba bean, while heat sensitive lines of common bean lose yield when night temperature is higher than 20°C. Field and laboratory screening techniques have been standardized for screening of genotypes for heat tolerance and sources of heat tolerance have been identified in most of the grain legumes. A heat tolerant chickpea line ICCV 92944 has been released in three countries (India, Myanmar and Kenya) and area under its cultivation is expanding rapidly. Several heat tolerant varieties of faba bean have been released in Sudan giving up to 2-fold increase in yield as compared to the sensitive cultivars. Interspecific crosses have been successfully used for enhancing heat tolerance in beans. Studies on physiological mechanisms and genetics of heat tolerance and identification of molecular markers and candidate genes for heat tolerance are in progress and would help in developing more efficient breeding strategies for heat tolerance in grain legumes.

11:30-11:45 Presenter: Phil Davies (SARDI, Adelaide, Australia)

Selecting pulses tolerant to temperature extremes: frost and heat stress tolerance in field pea and faba bean

Davies, P.A.[1*], Pham, T.[1], and Paull, J.G.[2]. [1]South Australian Research and Development Institute, GPO Box 397 Adelaide 5000, South Australia; [2]University of Adelaide, School of Agriculture Food and Wine, PMB1 Glen Osmond 5064, South Australia. *(phil.davies@sa.gov.au)

Both frost and heat stress at flowering and podding cause significant yield loss and deterioration of grain quality in pulse crops. A field-based method for selection of frost tolerance has been developed for field pea and a controlled environment method for heat stress tolerance has been developed for field pea and faba bean. The frost selection method uses replicated plantings of germplasm at a frost prone site. In the 48 hour period following a frost event, large numbers of young flowers and pods are tagged and the survival and damage to flowers and immature pods is recorded after plant maturity. Results over two seasons have shown consistent differences between control varieties and identified germplasm with putative reproductive frost tolerance. The heat stress selection method subjects podding plants to heat stress treatment of 40OC days/ 30OC nights, 14 hour photoperiod for a total of 72 hours. Plants are watered so that they do not suffer moisture stress during the heat stress treatment. Pod and seed survival from tagged pods is used as an indicator of heat stress tolerance. Both heat tolerant selections from field pea and faba bean have been identified.

11:45-12:00 Presenter Rosalind Bueckert (University of Saskatchewan)

Cool leaf traits to reduce heat stress in pea

Bueckert, R.A.[1*], Liu, Liping.[1], and Warkentin, T.[2]. [1]Department of Plant Sciences, University of Saskatchewan; [2]Crop Development Centre, University of Saskatchewan. *(rosalind.bueckert@usask.ca)

Heat stress in pea can occur when daytime air temperatures exceed 29°C to 32°C during vegetative and reproductive growth, and heat stress lowers yield. Irrigation or soil moisture availability appears to increase the temperature threshold to >32°C before heat stress occurs. When soil moisture is sufficient for crop evapotranspiration, crop canopies are usually cooler than daytime air temperatures. To date, our heat research has used daytime maximum temperature as a reference, but we know little of the actual canopy temperatures experienced by the crop. Our first objective was to characterize actual canopy temperatures in relation to air temperatures associated with heat stress. Our second objective, and ultimate goal, was to seek potential heat resistant parents through maintained cool canopy temperatures using traits such as leaf cuticular wax, leaf pigments, leaf size and shape, leaflet and stipule shape, and diameter of tendrils, peduncles and stems. In 2013 we sampled a 16-cultivar trial and the 94 diverse cultivars from the Pea Association Mapping Panel at two locations in Saskatchewan for leaf size, pigments and wax. Several times during reproductive growth canopy temperatures from plots were measured with a handheld Infrared thermometer. Preliminary results of wax and leaf traits will be presented with canopy temperature and yield.

12:00-12:15 Presenter: Maryse Bourgault (University of Melbourne, Australia)

Field Pea growth and yield response to elevated CO2 in the Australian Grains Free Air CO2 enrichment facility (AGFACE)

Bourgault, M.[1*], Fitzgerald, G.[2], Brand, J.[2], and Tausz, M.[3]. [1]Department of Agriculture and Food Systems, The University of Melbourne, 4 Water Street, Creswick, VIC, 3363, Australia; [2]Department of Environment and Primary Industries, Grains Innovation Park, 110 Natimuk Rd, Horsham, VIC, 3401, Australia; [3]Department of Forestry and Ecosystem Science, The University of Melbourne, 4 Water Street, Creswick, VIC, 3363, Australia. *(maryse.bourgault@unimelb.edu.au)

Atmospheric CO2 levels have been increasing from about 280 ppm to 399 ppm from the pre-industrial era until now. Our experiment aimed to determine the effects of elevated CO2 (eCO2) on the yield, biomass, and grain nitrogen content of field pea and the nitrogen contribution of field pea stubble. Plants were grown under Free Air CO2 Enrichment (FACE) at the Australian Grains FACE facility in Horsham, Victoria, Australia under eCO2 (550 ppm) or at ambient CO2 (390 ppm) from May to November during three seasons, 2010-2012. Yields were significantly increased by 26.4% under eCO2 due to an increase in the number of pods per area; grain size, the number of grains per pod and the harvest index remained unaffected by eCO2. Grain nitrogen concentration was slightly, but significantly, decreased by eCO2, on average from 3.71 to 3.61%. The total nitrogen contained in the straw was 25.9% greater under eCO2, increasing on average from 72 to 91 kg of N ha-1, due to the greater biomass. Implications for breeding and agronomy are discussed.

12:15-12:30 Presenter: Janine Croser (University of Western Australia)

Recombinant inbred line populations in less than a year? A novel system for combining

accelerated breeding with screening for abiotic stress in grain legumes.

Croser, J.[1*], Ribalta, F.[1], Munday, C.[1], Edwards, K.[1], Nelson, K.[1], Pazos, M.[1], Lulsdorf, M.[1], and Erskine, W.[1]. [1]Centre for Plant Genetics and Breeding (PGB), The University of Western Australia, 35 Stirling Hwy, Crawley 6009. *(renene@gmx.com)

Rapid development of recombinant inbred line (RIL) populations for exploitation of powerful new molecular technologies is just one benefit of new tools to accelerate generation turnover in grain legumes. We have developed assisted single seed descent (ASSD) technology to achieve a turnover of six to eight generations per year for field pea (*Pisum sativum* L.), chickpea (*Cicer arietinum* L.), lentil (*Lens culinaris* Medik.) and narrow-leaf lupin (*Lupinus angustifolius* L.). The ASSD technique is robust, cost-effective and enables the development of RIL populations in less than 12 months.

Our current research aims to integrate ASSD methodology with targeted screening for tolerance to abiotic traits of interest (*viz*. boron toxicity in pea and lentil; low pH and aluminium toxicity in lupin and chilling tolerance in chickpea). It is envisaged combining ASSD with abiotic stress screening will provide efficient selection of adapted germplasm for rapid incorporation into breeding programs and thus permit a timely response to emerging challenges.

LIST OF POSTERS

Session 1 (odd #) – Tuesday July 8, 16:00-18:00

Session 2 (even #) – Thursday July 10, 16:00-18:00

Poster #	Topic	Presenting Author	Poster Title
1	Development	Chen, Jianghua	The molecular mechanism of leaf movement in Medicago truncatula
2	Development	Eleouet, M.	Genetic Analysis of Leaf Development in Pisum sativum
3	Development	Hecht, V	Functional analysis of FT genes in pea
4	Development	Javier Mendiola, JM.	A set of marker lines for protein localization in Medicago truncatula for community use
5	Development	Li, W.L.	GmGBP1, a homolog of human ski interacting protein in soybean, regulates flowering stem elongation and heat tolerance
6	Development	Nelson, M.N.	What does it take to make lupins flower? Molecular and ecophysiological approaches to understanding phenology in Lupinus angustifolius L.
7	Development	Yang, Tianquan	Floral asymmetry in the model legume Medicago truncatula
8	Evolution	Coyne, C.C.	Phylogeography and genetic diversity of the Pisum genus, with inference to pea domestication
9	Evolution	Javadi, F.	Genetic diversity in wild and domesticated Azuki beans
10	Evolution	Kang, Y.J.	Genome sequence of mungbean and insights into evolution within Vigna species
11	Evolution	Pauls, K.P.	Comparisons between Bean and Soybean Genomes Lead to Insights into Gene Function and Evolution in Both Species
12	Evolution	Steele, K. P.	Genome Size Estimation in Medicago (Fabaceae): Independent Loss and Gain?
13	Evolution	Susek, K.	Cyto-molecular tracking of lupin chromosome evolution
14	Evolution	Wong, M.M.L.	A Whole Genome Duplication potentially drove diversification in Fabaceae
15	Genomics and Genetics	ABDI KETEMA, D.	Mapping QTLs for Days to Flowering, Photoperiod Sensitivity and Ascochyta Blight Reaction in a Chickpea Recombinant Inbred Population
16	Genomics and Genetics	Agunbiade, TA	Development of Reference Transcriptomes for the Major Field Insect Pests of Cowpea: A Toolbox for Insect Pest Management Approaches in West Africa
17	Genomics and	Ali, M.B.	Development and mapping of SNP markers associated with zt-1 and

	Genetics		zt-2 genes controlling zero tannin in faba bean (Vicia faba L.)
18	Genomics and Genetics	Araujo, S.S.	Unraveling grain filling mechanism in Phaseolus vulgaris L. under water deficit: transcriptomic and proteomic approaches
19	Genomics and Genetics	Bhatnagar-Mathur, P.	Drought tolerant transgenic peanut moves closer to reality
20	Genomics and Genetics	Buchwaldt, L.	Resistance in chickpea to Ascochyta rabiei is conferred by genes encoding pathogen recognition and other genes in basic defense pathways
21	Genomics and Genetics	Burstin, J.	PeaMUST, a large multidisciplinary project dedicated to pea improvement
22	Genomics and Genetics	Cannon, EKS	PeanutBase: The Genomic Data Portal for Arachis
23	Genomics and Genetics	Dastmalchi, M	Soybean chalcone isomerase: evolutionary history of the fold as told by sequence, expression and localization of the gene family
24	Genomics and Genetics	Deokar, A	QTL to Candidate Genes: Understanding Photoperiod Sensitivity and Flowering Time in Chickpea
25	Genomics and Genetics	Diapari, Marwan	Synteny analysis of markers associated with iron and zinc concentration in pea and chickpea with *Medicago truncatula*
26	Genomics and Genetics	Dickstein, R.	An improved genetic crossing method for Medicago truncatula
27	Genomics and Genetics	Guo, Y.	Developing a platform for allele mining in soybean (Glycine max) and its application to functional marker development and genotype identification
28	Genomics and Genetics	Gupta, P.	Genetic diversity at EST-SSR markers and its relationship to ODAP content under heat stress in grass pea (Lathyrus sativus L.)
29	Genomics and Genetics	Hamwieh, A.	Mapping QTLs across environments for heat related traits in Chickpea (Cicer arientinum L.)
30	Genomics and Genetics	Ibrahim, Hossam M.	Effectiveness of Breeding Methods for Production of Superior Genotypes and Maintenance of Genetic Variance in Fabe Bean (Vicia faba, L.)
31	Genomics and Genetics	Igrejas, G.	Can proteomic markers be used to evaluate genetic diversity in Portuguese populations of sweet chestnut (Castanea sativa Mill.)?
32	Genomics and Genetics	Igrejas, G.	SDS-PAGE of storage proteins as a way to discover genetic diversity of garbanzo beans (Cicer arietinum L.)
33	Genomics and Genetics	Jain, P.	Differential Expression of Acetohydroxyacid Synthase Genes and Response to Imazamox Herbicide in Chickpea
34	Genomics and Genetics	Joshi, T	Soybean Knowledge Base (SoyKB): Bridging the gap between soybean translational genomics and breeding
35	Genomics and Genetics	Kamphuis, L.G.	The narrow-leafed lupin genome assembly, transcriptome sequencing of different tissue types and generation of gene-based molecular markers
36	Genomics and Genetics	Kaur, P	First Genome Draft of subterranean clover (Trifolium subterraneum L.)
37	Genomics and Genetics	Kaur, S	Legume genomics – perspectives, progress and challenges
38	Genomics and Genetics	Khadke, S.G.	Development of Superior Mutants in Moth Bean (Vigna aconitifolia (Jacq.) Marechal) Through Induced Mutation Breeding
39	Genomics and Genetics	Khazaei, H.	The Faba bean Genome Sequencing Consortium
40	Genomics and Genetics	Kim, M.Y.	Genome-wide analysis of UV-B induced mutations in soybean (Glycine max (L.) Merr.)
41	Genomics and Genetics	Kisha, T.J.	Genetic Diversity of the Phaseolus acutifolius A. Gray Collection of the USDA National Plant Germplasm System Using Targeted Region Amplified Polymorphism (TRAP) Markers Designed form Genes Associated with Heat and Drought Stress

42	Genomics and Genetics	LAVAUD, L.C.	Constructing near-isogenic lines by Marker-Assisted-Selection to validate QTL for resistance to Aphanomyces euteiches in pea
43	Genomics and Genetics	Lightfoot, D.A.	Two decades of QTL analysis among Forrest, Essex, Hartwig and Flyer RILs and NILs
44	Genomics and Genetics	Lightfoot, D.A.	Why is resistance to soybean cyst nematode so complicated compared to sudden death syndrome?
45	Genomics and Genetics	Madrid, E	Large-scale transcriptome analysis in faba bean (Vicia faba L.)
46	Genomics and Genetics	Madrid, E	Candidate gene expression analysis of the genes located in the QTLAR3 in chickpea related with Ascochyta blight resistance
47	Genomics and Genetics	Marsolais, F.	Genomic analysis of polymorphisms conferrring storage protein deficiency in common bean
48	Genomics and Genetics	Mishra, N.	Exploiting potential of wild Cicer species for improving chickpea
49	Genomics and Genetics	Omar Idrissi, O.I	Assessment of genetic variation of lentil (Lens culinaris Medik) landraces from Morocco
50	Genomics and Genetics	O'Rourke, J.A.	Gene Expression Patterns in Soybean Fast Neutron Mutants
51	Genomics and Genetics	Pérez de la Vega, M.	A genetic map of lentil based on retrotransposon derived genetic markers.
52	Genomics and Genetics	Pérez de la Vega, M.	An annotated collection of EST sequences from lentil (Lens culinaris Medik.)
53	Genomics and Genetics	Porch, T.G.	Association mapping analysis of the response to Macrophomina phaseolina in the Andean Diversity Panel
54	Genomics and Genetics	Rajandran, V	Genetic control of early flowering in lentils
55	Genomics and Genetics	Ramsay, L.D.	Progress on the Lentil Draft Genome Assembly
56	Genomics and Genetics	RANA, J.C.	Developing trait specific sets of germplasm in selected grain legumes in India
57	Genomics and Genetics	Roorkiwal, M.	Prediction of breeding values using genome wide markers for yield related traits in chickpea
58	Genomics and Genetics	Saha, Shyamali	Wild Relatives of Lentil: Removing Obstacles to Increased Genetic Gain
59	Genomics and Genetics	Sameer kumar, C.V.	A unique hybrid parental line identification system using obcordate leaf shape marker in Pigeonpea
60	Genomics and Genetics	Sanderson, LA	KnowPulse: a breeder-focused web portal that integrates genetics and genomics of pulse crops with model genomes
61	Genomics and Genetics	Santalla, M.	Characterization of QTLs for flowering date in a mapping population of the legume species Phaseolus vulgaris
62	Genomics and Genetics	Saxena, R.K.	Fast forward genetic mapping provide candidate genes for resistance to fusarium wilt and sterility mosaic disease resistance in pigeonpea (Cajanus cajan L. Millsp.)
63	Genomics and Genetics	Schafleitner, R.	Next-Generation Genotyping of Mungbean (Vigna radiata)
64	Genomics and Genetics	Sen Gupta, D.	A validated source panel of SSR markers for effective discrimination of lentil species
65	Genomics and Genetics	Si, P.	Non-target-site mechanism of metribuzin tolerance in induced mutants of narrow-leafed lupin (Lupinus angustifolius L.)
66	Genomics and Genetics	Slater, SMH	An integrated breeding technology for accelerating generation advancement and trait introgression into dry bean (Phaseolus vulgaris).
67	Genomics and Genetics	Slater, SMH	Hardseededness in dry bean – effect of genotype, environment andmaturity.
68	Genomics and Genetics	Smitchger, J.A.	SSR AA122 is Linked to the Classical Morphological Mutation am2 in Pisum sativum

69	Genomics and Genetics	Smykal, P.	Establishment of wild pea Pisum fulvum chromosome segment substitution lines in cultivated P. sativum genetic background, as a tool to study domestication and to broaden genetic diversity.
70	Genomics and Genetics	Srinivasan, S	A major QTL identified for vernalization response in chickpea
71	Genomics and Genetics	Sudheesh S	SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (Pisum sativum L.)
72	Genomics and Genetics	Sudheesh, S.	Transcriptome atlas of field pea (Pisum sativum L.)
73	Genomics and Genetics	Thudi, M	CaTILL: A resource for novel alleles for chickpea (Cicer arietinum) improvement
74	Genomics and Genetics	Thudi, M	Fine mapping of a "QTL-hotspot" for drought tolerance in chickpea (Cicer arietinum L.)
75	Genomics and Genetics	Tikle, A.N.	Stability of male sterility and fertility restoration in pigeonpea(Cajanus cajan (L.) Millsp.) under different regimes of temperature and locations
76	Genomics and Genetics	Toker, C.	Induction and inheritance for Resistance to Herbicide in Cicer reticulatum Ladiz.
77	Genomics and Genetics	Trujillo, D.I.	Genomic characterization of the LEED..PEEDs, a gene family unique to Medicago species
78	Genomics and Genetics	Varshney, R.K.	Identification and validation of heat stress responsive genes in chickpea (Cicer arietinum L.)
79	Genomics and Genetics	Varshney, R.K.	Identification of internal housekeeping genes for studying gene expression in pigeonpea by quantitative real-time PCR
80	Genomics and Genetics	Varshney, RK	Selection of appropriate genomic selection model in an unstructured germplasm set of peanut (Arachis hypogaea L.)
81	Genomics and Genetics	Vaz Patto, M.C.	Take a walk on the bean side: The Portuguese genetic diversity
82	Genomics and Genetics	Wen, J.	Generation and Application of Medicago truncatula Tnt1 Mutants
83	Genomics and Genetics	Wolko, B.	Lupinus angustifolius gene copy number quantification
84	Genomics and Genetics	YANG, SY	Faba bean genomic study and its future application
85	Genomics and Genetics	Yuan, H. Y.	Developing a genomic in situ hybridization protocol for genomic studies of lentil
86	Genomics and Genetics	Yuan, H. Y.	Pubescence, can it be used to differentiate L. tomentosus from L. orientalis?
87	Genomics and Genetics	Zou, X.	Genome-wide SNP and InDel discovery and transcriptional profiling of CBB resistance in common bean
88	Nitrogen Fixation and Symbiosis	ARRIGHI, J.F.	Aeschynomene evenia, a model plant for studying the molecular genetics of the Nod-independent rhizobium-legume symbiosis
89	Nitrogen Fixation and Symbiosis	Gisiora, J. K.	Investigating the Development of M. truncatula Symbiosome Membrane Using ENOD16 and Vacuolar H+-ATPase
90	Nitrogen Fixation and Symbiosis	Maalouf, F.	Rhizobium nodulation of an Ethyl methanesulfonate (EMS) mutagenized faba bean population
91	Nitrogen Fixation and Symbiosis	Molla, M.M	Response of chickpea varieties to Rhizobium inoculation under different agro-ecological zones of Ethiopia.
92	Nitrogen Fixation and Symbiosis	TROMAS, A	Lotus japonicus AMP1 and HAR1 act synergistically to regulate root architecture
93	Nitrogen Fixation and Symbiosis	Wang, J.	Towards dissecting the genetic basis of peanut nodulation
94	Nitrogen Fixation and Symbiosis	Wijesinghe, M.A.K.	Commercial Arbuscular Mycorrhizal (AM) Inoculants Change the Diversity of AM Communities Associated with Roots and Rhizosphere of Field Pea
95	Nitrogen Fixation and Symbiosis	Woo, S.L.	Effects of microbe-legume interactions on agricultural production

96	Seeds and Nutrition	Adhikari, E.	Genetic and Environmental Effect on Mineral Nutrient Accumulation in Pea
97	Seeds and Nutrition	Adhikari, E.	Compositional Mineral Nutrient Variation in Lentil
98	Seeds and Nutrition	Bangar, P	Increasing iron concentration and bioavailability in field pea
99	Seeds and Nutrition	Boux, G.B.	Effects of Pre-milling Treatments of Yellow Peas on Spaghetti Quality
100	Seeds and Nutrition	Cichy, K.A.	Genome Wide Association Mapping of Cooking Time in Andean Dry Beans
101	Seeds and Nutrition	Dhaubhadel, S.	Seed coat RNAseq analysis of two Pinto bean cultivars that differ in post-harvest seed coat darkening
102	Seeds and Nutrition	Diederichsen, A.	Seed characteristics in cultivated Cicer arietinum and wild Cicer species preserved by Plant Gene Resources of Canada
103	Seeds and Nutrition	Emmrich, P.M.F.	Lifting the curse of the grass pea
104	Seeds and Nutrition	GAAD, D.	Morphological and Biometrical characterization of seeds of some Algerians lentil accessions: Quantitative and Qualitative characters.
105	Seeds and Nutrition	Gaikwad, N. B.	Trypsin inhibitor, Polyphenol and Lectin content in Soybean (Glycine max (L.) Merrill)
106	Seeds and Nutrition	Grusak, M. A.	Plant genotype, location, and their interaction effects on the concentrations of selected minerals in seed of kabuli chickpea breeding lines and cultivars examined in the US Pacific Northwest.
107	Seeds and Nutrition	Hu, J.	L-DOPA (L-3,4-dihydroxy phenylalanine) concentration variation in the leaf and flower tissues of six faba bean lines
108	Seeds and Nutrition	Joshi, J.	Analysis of candidate enzymes for the biosynthesis of S-methylcysteine in seed of common bean (Phaseolus vulgaris)
109	Seeds and Nutrition	Jaillais, B.	Phenotyping of internal structure of seeds of legume crops by imaging and chemometrics
110	Seeds and Nutrition	Kang, B.K.	The Effect of sprouting temperatures on Growth characteristics, Protein content and Antioxidant activity of Pea(Pisum sativum L.) sprouts
111	Seeds and Nutrition	Kim, S.U.	Variation of lignan content for sesame seed across origin and growing environments
112	Seeds and Nutrition	Kundu, Shudhangshu	Optimizing zinc analysis of seeds of wild lentil species
113	Seeds and Nutrition	Liu, X.	Iron bioavailability in low phytate pea
114	Seeds and Nutrition	Loader T.	Effect of Yellow Pea Flour Protein Content on End-Quality of Spaghetti
115	Seeds and Nutrition	Lu, JL	Starch morphology and compositions correlate with protein contents in field peas
116	Seeds and Nutrition	Mahla Mirali, M.M.	Polyphenols in whole seeds and seed coats of lentil market classes.
117	Seeds and Nutrition	Nayyar, H	Heat stress impairs reproductive function, sucrose metabolism and severely reduces seed yield in Chickpea and Lentil genotypes
118	Seeds and Nutrition	Pastor-Corrales, M.A.	Establishment of the Andean Diversity Panel and its implementation in screening for key dry edible bean production: constraints and nutrition traits for Sub-Saharan Africa
119	Seeds and Nutrition	Singh, Renu	To exploit genotype x environment interactions (G x E) for developing mung bean with increased micronutrients
120	Seeds and Nutrition	Smykal, P.	Structural, genetical and chemical analysis of the seed coat role in establishment of dormancy of the pea seed
121	Seeds and Nutrition	Thompson, R.D.	LEGumes for the Agriculture of TOmorrow (LEGATO project)
122	Seeds and Nutrition	Timmerman-Vaughan, G.M.	Candidate gene based association mapping of allelic polymorphisms associated with variation in seed starch chain length distribution
123	Seeds and Nutrition	Vasconcelos, M.W.	Development and characterization of a white lupin-enriched symbiotic yogurt
124	Seeds and Nutrition	Vasconcelos, M.W.	Potential of white lupins (Lupinus albus L.) to promote the growth of Bifidobacterium and Lactobacillus strains

125	Seeds and Nutrition	Wang, N.	Effect of variety and crude protein content on quality of gluten-free pasta prepared from lentil flour by high temperature extrusion
126	Seeds and Nutrition	Warkentin, T.D.	Towards biofortification of pea
127	Seeds and Nutrition	Wiesinger, J.A.	The Nutritive Value of Fast Cooking Dry Beans (Phaseolus vulgaris L)
128	Seeds and Nutrition	Yang, A.	Sensory Attributes of Soymilk and Tofu from Soybean Varieties Lacking Lipoxygenases
129	Abiotic Stress	Abbad Andaloussi, F.	Promote proven technologies for wheat – legume rotation systems under changing climate in Morocco
130	Abiotic Stress	Abd El-Rahman, R.	Identification of genetic variability for tolerance to metribuzin in faba bean
131	Abiotic Stress	Bueckert, R.A.	Controlled heat stress on pod and seed components in pea – ovule and pollination failure
132	Abiotic Stress	Coyne, C.J.	Screening chickpea for cold tolerance under controlled conditions
133	Abiotic Stress	Fevereiro, P.	Physiological responses toward water deficit of a M. truncatula homozigoustransgenic line expressing the oat Adc gene
134	Abiotic Stress	Ghanem, M.E.	Assessment of water-saving traits in terminal drought adaptation of contrasting lentil genotypes
135	Abiotic Stress	H. Mobini, S.	Shortening generation time in faba bean (Vicia faba) by application of cytokinin and cold stress
136	Abiotic Stress	He Yu Hua, H.Y.H	Early maturity innovation studying on Faba bean
137	Abiotic Stress	Huang, S	Characterizing the cross of CDC Sage and CDC Centennial field pea for heat resistance through flowering duration
138	Abiotic Stress	Jiang, Y	Heat stress on pollen development and seed-set in pea
139	Abiotic Stress	Jitendra, K.	Phenotyping for heat tolerance under field conditions in lentil
140	Abiotic Stress	Jogloy, S.	Nutrient uptakes and their contributions to yield in peanut genotypes with different levels of terminal drought resistance
141	Abiotic Stress	Kaur, Jagmeet	Identification of genetic variability for water logging and salinity tolerance in pigeonpea
142	Abiotic Stress	Maalouf, F.	Development of photoperiod insensitive faba bean breeding lines with tolerance to heat stress
143	Abiotic Stress	Maharjan, K.L.	Farmers' Decision in Land Allocation for Spring Season Crops: A Case Study in the Tarai Region of Nepal
144	Abiotic Stress	Meier, K.	Investigating the genetics of improved metribuzin herbicide tolerance in lentil
145	Abiotic Stress	Nath, Rajib	Comparative study on seedling performance due to imposed drought in lentil
146	Abiotic Stress	Omar Idrissi, O.I	Genetic variation of root and shoot traits at early stage in a lentil (Lens culinaris Medik) recombinant inbred lines population under drought: towards QTL mapping
147	Abiotic Stress	Rachaputi, R.C.N.	Genotype and environment interaction for resource use efficiency of chickpea (Cicer arietinum L) grown under water limited environments in subtropical Australia
148	Abiotic Stress	Singh, Sarvjeet	Identification of genetic variability for tolerance to Imazethapyr and Metribuzin in lentil (Lens culinaris)
149	Abiotic Stress	Singh, Sarvjeet	Identification of sources of post-emergence herbicide tolerance in chickpea and lentil
150	Abiotic Stress	Souter, J.R.	Ureide Accumulation and Abiotic Stress Resistance in a Population of Common Bean, Tepary Bean, and Interspecific Hybrids
151	Abiotic Stress	Vasconcelos, M.W.	Iron partitioning at an early growth stage impacts iron deficiency responses in soybean plants (Glycine max L.)
152	Abiotic Stress	Vasconcelos, M.W.	Evaluation of new iron (III)-chelates on mineral nutrition of soybean (Glycine max L.)
153	Abiotic Stress	von Wettberg, EJ	Microenvironmental variation in natural habitats of wild chickpea

154	Abiotic Stress	Yadava, H.S.	Genetic enhancement for biotic and abiotic stress resistance in chickpea: Achievements and perspectives in Madhya Pradesh, India
155	Abiotic Stress	Yoon, M.Y.	Whole transcriptome analysis of soybean in response to UV-B irradiation using RNA-seq.
156	Abiotic Stress	Youssef, C.	Cell elongation instead cell number becomes the predominant factor influencing genotypic differences in Medicago truncatula hypocotyl length under abiotic stress
157	Abiotic Stress	Yuliasti, YL	Response Of Mungbean Mutant Lines To Drought Stress And Genetic Relationships Using SSR Markers
158	Biotic Stress	Adhikari, K.N.	Breeding and genetic studies of rust (Uromyces viciae-fabae) resistance in faba bean (Vicia faba L.) in Australia
159	Biotic Stress	Armstrong-Cho, C.	The root of the problem: Aphanomyces and Fusarium in Saskatchewan pea and lentil fields.
160	Biotic Stress	Arwin, AW	BREEDING SOYBEAN SUPER EARLY MATURITY USING INDUCE MUTATION TECHNIQUE FOR HIGH YIELD, RESISTANCE TO LEAF RUST and SPOT DISEASE FOR ANTICIPATION CLIMATE CHANGE
161	Biotic Stress	Bazghaleh, N.	Effects of H2 oxidizing bacteria on plant growth and inhibition of fungal pathogens
162	Biotic Stress	Caudillo Ruiz, K. B.	Seed yield quantity, quality and seed infection caused by Stemphylium blight in lentil.
163	Biotic Stress	Chatterton, S.	Fusarium species composition and root rot incidence in Alberta pea fields in 2013
164	Biotic Stress	Chatterton, S.	Pathogen populations associated with root rot of field pea in western Canada
165	Biotic Stress	Conner, R.L.	Reactions of dry bean cultivars from western Canada to root rot.
166	Biotic Stress	Durkin, J.M.H.	A change in the Colletotrichumtruncatum population signals a need for new resistance in lentil
167	Biotic Stress	Hassan, F.	Development of Insect and Fungi Resistant Transgenic Pea (Pisum sativum L.)
168	Biotic Stress	Henriquez, M.A.	Fusarium species from soybean in Manitoba
169	Biotic Stress	Hou, A.	Combining resistance to common bacterial blight, anthracnose and bean common mosaic virus in drybean
170	Biotic Stress	Jendoubi, W.	Development of chickpea near-isogenic lines for Fusarium wilt race 0
171	Biotic Stress	Jha, A.B.	Identification of quantitative trait loci for mycosphaerella blight resistance in pea using an interspecific cross population
172	Biotic Stress	Jimenez-Lopez, J.C.	Lupin (Lupinus angustigolius L.) beta-conglutins as new bioactive seed proteins with fungal growth inhibitory activity
173	Biotic Stress	Jorge A. Acosta-Gallegos, J.A.A.G.	Pathogenic races of Fusarium oxysporum f. sp. ciceris attacking chickpeas at the Bajío region in Central Mexico
174	Biotic Stress	Jorge A. Acosta-Gallegos, J.A.A.G.	Resistance to Ascochyta rabiei is needed to expand the window frame for chickpea sowing in Central Mexico
175	Biotic Stress	Kahlon, J. G.	Efficacy of transgenic disease resistant peas against Fusarium root rot (F.solani and F. avenaceum) and Mycosphaerella blight (M. pinodes) in field.
176	Biotic Stress	Kumari, S.G.	Screening and selection of faba bean (Vicia faba L.) germplasm for resistance to Faba bean necrotic yellows virus
177	Biotic Stress	Le May, C.	Role of legume host species successions on Aphanomyces euteiches population structure
178	Biotic Stress	McLaren, D.L.	Fusarium species isolated from dry bean and field pea in Manitoba: Identification, pathogenicity and prognosis.
179	Biotic Stress	Miklas, P.N.	Characterizing quantitative resistance to halo bacterial blight in common bean population Rojo/CAL 143
180	Biotic Stress	Nyandoro, R.	Evaluation of soybean variety resistance to fusarium in the management of root rot of soybean in southern Alberta, Canada.

181	Biotic Stress	Ortega, P.F.	Blanoro: a new kabuli chickpea cultivar resistant to Fusarium oxysporum f. sp. ciceris
182	Biotic Stress	Pasche, J.S.	Comparison of Fusarium solani and F. avenaceum Inoculation Methods in Dry Pea
183	Biotic Stress	Podder, R.	Transfer of Stemphylium Blight Resistance from Lens ervoides to the Cultivated Lentil
184	Biotic Stress	Powell, T.K.	Bacterial auxin production facilitates resource conversion and carbon acquisition by the phyllosphere epiphyte Pantoea agglomerans on Phaseolus vulgaris leaves.
185	Biotic Stress	Rodda, M.S.	Establishment of screening methods and identification of resistant sources for stemphylium blight in lentil
186	Biotic Stress	Rodda, M.S.	Resistance to botrytis grey mould in Australian lentil breeding germplasm
187	Biotic Stress	Rubiales, D.	Legume breeding for broomrape resistance
188	Biotic Stress	Saraf, M	SUPPRESSION OF CHARCOAL ROT DISEASE BY TRICHODERMA spp.IN GLYCINE MAX
189	Biotic Stress	Saraf, M	Multifaceted beneficial microbes in rhizosphere to combat phytopathogens in Cicer arietinum.
190	Biotic Stress	Simons, K.J.	Seed to Seedling Transmission of Colletotrichum lindemuthianum Under Greenhouse Conditions
191	Biotic Stress	Sivachandra Kumar, NT	Seed-to-seedling transmission of Ascochyta pisi in field pea
192	Biotic Stress	Tenuta, M.	Results of the Manitoba soybean cyst nematode Survey
193	Biotic Stress	Tenuta, M.	The stem nematode (Ditylenchus weischeri) on grain pea and creeping thistle in the Canadian Prairie Provinces
194	Biotic Stress	Thompson, J.P.	Potential of wild chickpea species for improving the resistance of chickpea to root-lesion nematodes
195	Biotic Stress	Vaz Patto, M.C.	Chickling pea (Lathyrus cicera L.) resistance to rust and powdery mildew under QTLs scrutiny
196	Biotic Stress	Vijayan, P.	Evaluating secondary effects of strobilurin fungicides on cool season pulse crops in Canada.
197	Biotic Stress	Warale, R. R.	Phylogeny and pathogenicity of *Colletotrichum / Glomerella* species associated with anthracnose on leguminous hosts
198	Biotic Stress	Weeden, N.F.	A genetic analysis of the tolerance to Fusarium root rot in pea land races of the 'Afghanistan' type
199	Biotic Stress	Yang, Chao, Y.C.	Hydrogen oxidizing bacteria identified from Lentil field show the effects on plant growth
200	Biotic Stress	Zhang X	Evaluating new biological and chemical controls for soybean cyst nematode in dry bean
201	Biotic Stress	Zhou, Q.X.	Molecular identification of Fusarium species from soybean in Alberta
202	Crop management	Ahmed, S.	Effects of supplementary irrigation on Fusarium wilt epidemics and yield of lentil in northern Syria
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POSTER ABSTRACTS

Poster #	Topic	Presenting Author	Poster Title
1	Development	Chen, Jianghua	The molecular mechanism of leaf movement in Medicago truncatula

The molecular mechanism of leaf movement in Medicago truncatula

Chen, JIANGHUA.[1*], He, LiangLiang.[1], Yang, Tianquan.[1], Wang, Ruoruo.[1], Xu, Ronghua.[1], Wen, Jiangqi.[2], Cheng, Xiaofei.[2], Mysore, Kirankumar S.[2], Chen, Rujin.[2], and Xia, Yongmei.[1]. [1]Key Laboratory of Tropical Plant Resource and Sustainable Use, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, 88 Xuefu Road,Kunming 650223, Yunnan, P. R. China; [2]Plant Biology Division, Samuel Roberts Noble Foundation, Ardmore, OK 3401. *(jhchen@xtbg.ac.cn)

Legume and Oxalis plants have a special leaf motor organ, calling pulvinus, to control the leaf movement. Previous plant physiological studies had showed this kind of leaf movement is affected by the light signal, water transporter and potassium channel. However, the molecular mechanism was unclear for the determination of leaf motor organ. Recently, our work shows that one of the *Lateral Organ Domain*（*LOB*）family transcription factors determines the organ identity of legume plants. In this study, we will combine the transcriptomics and proteomics approaches to identify the differential expressed genes between the *elongated petiolule 1* （*elp1*） mutant and wild type of *M. truncatula*.

2	Development	Eleouet, M.	Genetic Analysis of Leaf Development in Pisum sativum

Genetic Analysis of Leaf Development in Pisum sativum

Eleouet, M.[1*], Hofer, J.[2], and Ellis, N.[2]. [1]Aberystwyth University; [2]ICRISAT-Patancheru. *(mpe@aber.ac.uk)

Compound leaf development is not fully understood and is studied in different model species, including pea (*Pisum sativum*). Several genetic regulators of leaf development, including *Crispa* (*Cri*, encoding a MYB-domain transcription factor), *Cochleata* (*Coch*, encoding a BTB/POZ-domain protein) and *Stipules-reduced* (*St*) have been identified by previous studies of leaf morphological mutants; however, the molecular mechanisms behind their roles are not well understood. The uncharacterized *crispoid* (*crd*) mutant and the *cri*, *coch* and *st* mutants are all maintained in the same genetic background, making them ideal for gene interaction and expression studies. These mutants have been crossed to study double mutant phenotypes indicative of gene interactions. Crosses between *cri* and *st*, *coch* and *cri, coch and st,* had already been done in previous studies, and will thus be studied in detail as well as any interactions with *crd.* Class1 *KNOX* genes have been shown to be involved in the maintenance of the meristematic state of cells,

and to play a role in organ development, however, their regulation during leaf development is not fully defined. The expression of several *KNOX1* genes, along with other genes, will thus be measured by RT-qPCR in the different mutant backgrounds in order to understand how they are regulated. Further characterisation of the relationship between *KNOX1* genes, *crd* and other leaf morphology genes will help to elucidate a model of gene interactions controlling legume compound leaf development. Comparison of our model with those of other specieswill provide a better insight into the genetics of leaf development.

3	Development	Hecht, V	Functional analysis of FT genes in pea

Functional analysis of FT genes in pea

Hecht, V.[1*], Dalmais, M.[2], Bendahmane, A.[2], and Weller, JL.[1]. [1]School of Biological Sciences, University of Tasmania, Australia; [2]UMR INRA-CNRS, Evry, France. *(valerie.hecht@utas.edu.au)

Genes in the *FLOWERING LOCUS T* (*FT*) family play important roles in integrating plant flowering responses to environmental variables. As part of ongoing studies of flowering in legumes, we have defined the *FT* gene family in pea and other legume species and are examining the regulation and function of its members. We previously showed that pea *FT* genes have distinctly different expression patterns with respect to developmental timing, tissue specificity, and response to photoperiod, and differ in their activity in transgenic Arabidopsis, suggesting they may have different functions. We also showed that *FTa1*/*GIGAS* is required for normal flowering under both long-day and short-day conditions but is not required for photoperiod responsiveness. Expression of the *FTb2* gene is leaf-specific and strongly correlated with photoperiod responsiveness. In contrast, *FTc* is only expressed in apical buds and its induction depends partly on *FTa1*. Here we will present a preliminary analysis of *FTb2* and *FTc* functions in pea using newly isolated TILLING mutants. In addition, we recently identified a sixth *FT* gene, *FTa3*, and are examining its regulation and contribution to natural variation for flowering time. Our results begin to outline how induction of flowering may result from interactions among several members of a diversified *FT* family.

4	Development	Javier Mendiola, JM.	A set of marker lines for protein localization in Medicago truncatula for community use

A set of marker lines for protein localization in Medicago truncatula for community use

JAVIER MENDIOLA, JM.[1*], Joan Mogire, .[2], and Janine Sherrier, .[3]. [1]Delaware Biotechnology Institute; [2]Department of Biology; [3]Delaware Biotechnology Institute, Department of Plant and Soil Science, Department of Biology, University of Delaware, Newark, Delaware, 19716, USA. *(mendiola@udel.edu)

The recent genome sequencing of the legume model *Medicago truncatula*, identified a number of genes encoding proteins with unknown biological function. Determining the intracellular location of uncharacterized proteins can be used to infer their biological function. Fluorescent molecules are routine tools used in studies for protein localization and interaction with other proteins. To contribute to such localization studies, we aim to develop a set of stably transformed plants that would serve as community resource for cell biological studies as part of a larger NSF-plant genome project on *Medicago truncatula*. The marker plant lines will encode organelle-specific proteins fused to citrine, a variant of yellow fluorescent protein (YFP) that has been demonstrated to be much more resistant to photobleaching, acidic pH, and other intracellular environmental effects. To drive the expression of the gene markers we use the *Arabidopsis thaliana* Elongation Factor-1 alpha (EF1a) promoter strongly expressed both in the nodule meristem and in the nodule-invaded cells (1). Thus, we combined the constitutive expression of the EF1a promoter, the citrine fluorescent marker, and two well-known epitope tags to generate a collection of fluorescent organelle marker plant lines that can be used in both live imaging and immune electron microscopy to study the subcellular

localization of new proteins. This plant collection will be useful for immunohistochemical analysis and cellular fractionation detection assays and will be freely available to the international research community, contributing to the utility of community resources currently available for the study of this model legume species. This work is being supported by NSF-2012-934002.

Reference:
Auriac and Timmers (2007). MPMI Vol. 20, No.9; pp 1040-1047

5	Development	Li, W.L.	GmGBP1, a homolog of human ski interacting protein in soybean, regulates flowering stem elongation and heat tolerance

GmGBP1, a homolog of human ski interacting protein in soybean, regulates flowering stem elongation and heat tolerance

Zhao, L.Z.[1], Zhang, YW.Z.[1], Liu, LX.L.[2], and Li, W.L.[1*]. [1]Soybean Research Institute (Chinese Educational Ministry's Key Laboratory of Soybean Biology), Northeast Agricultural University; [2]Soybean Research Institute (Chinese Educational Ministry's Key Laboratory of Soybean Biology), Northeast Agricultural University,. *(wenbinli@yahoo.com)

Soybean is a typical short-day legume crop, and its photoperiodic and gibberellin (GA) responses for the control of flowering are critical to seed yield. GmGBP1 mRNA abundance in leaves was dramatically increased in SDs compared to that in LDs and GmGBP1 exhibited a circadian rhythm in SDs. Ectopic overexpression of GmGBP1 (GmGBP1-ox) in tobaccos caused early flowering by increasing NtCO mRNA levels. GmGBP1-ox Arabidopsis also exhibited earlier flowering and less number of rosette leaves. GmGBP1 mRNA abundance was also increased by GAs. GmGBP1-ox tobacco exhibited increased GA signaling-related phenotypes including flowering and plant height promotion. Furthermore, the hypocotyl elongation, early-flowering and longer internode phenotypes were largely accelerated by GA3 application in the GmGBP1-ox tobacco seedlings. Being consistent, overexpression of GmGBP1 resulted in significantly enhanced GA signaling (evidenced suppressed expression of NtGA20ox) both with and without GA treatments. GmGBP1 had transcriptional activity in C-terminal. GmGBP1 could interact with R2R3 domain of GmGAMYB1 in SKIP domain to take part in gibberellin flowering pathway. Arabidopsis myb33 mutant plants with ectopic overexpression of GmGBP1 showed the same flowering phenotype with wild type. Therefore, GmGBP1 was a positive regulator of both photoperiod and GA-mediated flowering responses. Heat-inducible GmGBP1 also enhanced thermo-tolerance in transgenic GmGBP1-ox tobaccos and Arabidopsis during seed germination and growth. GmGBP1 protein was localized in nucleus. Analyses of a series of 50-deletions of the GmGBP1 promoter suggested that several cis-acting elements, including P-BOX and three HSE elements were necessary to induce gene expression by GA and heat stress in the promoter region.

6	Development	Nelson, M.N.	What does it take to make lupins flower? Molecular and ecophysiological approaches to understanding phenology in Lupinus angustifolius L.

What does it take to make lupins flower? Molecular and ecophysiological approaches to understanding phenology in *Lupinus angustifolius* L.

Nelson, M.N.[1,2*], Pradhan, A.[1], Besharat, N.[1], Jost, R.[1], Erskine, W.[2,3], Ludwig, C.[4], and Berger, J.D.[3,4]. [1]School of Plant Biology, The University of Western Australia; [2]The UWA Institute of Agriculture, The University of Western Australia; [3]Centre for Plant Genetics and Breeding, The University of Western Australia; [4]CSIRO Plant Industry.

*(matthew.nelson@uwa.edu.au)

Narrow-leafed lupin (*Lupinus angustifolius* L.) is a major grain legume in Australia and a regionally important crop in northern Europe. The development of early flowering types of lupin was crucial for the successful adaptation of this grain legume to short-season regions of southern Australia and northern Europe. In Mediterranean-type climatic regions of Australia, early flowering lupin varieties are able to mature before the onset of terminal drought in the late spring / early summer. In northern Europe, early varieties could mature in time to avoid the cold, wet autumn. Most early-flowering varieties rely on a single dominant locus: *Ku*, which removes vernalisation requirement. We are using molecular and ecophysiological approaches to understand how *Ku* functions and to discover currently untapped phenological variation in wild germplasm. In collaboration with the Institute of Plant Genetics (Poznan, Poland), we are characterising a candidate gene for *Ku* using genomic, gene expression and genetic linkage methods. Using controlled environment experiments we are determining how lupin responds to vernalisation, photoperiod and ambient temperature with the goal of developing a full photothermal model for flowering for this species. A multi-environment QTL analysis will identify regions of the genome controlling responses to environmental cues along with linked markers for breeding purposes. We will present current progress towards these goals and discuss how this information can be used by breeders to adapt narrow-leafed lupin to new and changing environments.

7	Development	Yang, Tianquan	Floral asymmetry in the model legume Medicago truncatula

Floral asymmetry in the model legume *Medicago truncatula*

Yang, TIANQUAN.[1*], He, Liangliang.[1], Wang, Ruoruo.[1], Xu, Ronghua.[1], Xia, Yongmei.[1], Cheng, Xiaofei.[2], Mysore, Kirankumar S.[2], Wen, Jiangqi.[2], and Chen, Jianghua.[1]. [1]Key Laboratory of Tropical Plant Resource and Sustainable Use, Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences, 88 Xuefu Road, Kunming 650223, Yunnan, P. R. China; [2]Plant Biology Division, Samuel Roberts Noble Foundation, Ardmore, OK 73401. *(yangtianquan@hotmail.com)

TCP (TB1, CYC and PCFs) genes encode putative transcription factors, which contain a basic helix-loop-helix domain referred to as the TCP domain and play an important role in plant development. During zygomorphic floral development, it has been shown that the CYC-like TCP genes are key regulators recruited independently in several species to control the dorsal-ventral (DV) identity. In papillionoideae, the model legume *Medicago truncatula*, provides a good system to investigate the mechanism in the control of floral asymmetry or the zygomorphic development. We will use reverse genetic approach to characterize the function of TCP gene family.

8	Evolution	Coyne, C.C.	Phylogeography and genetic diversity of the Pisum genus, with inference to pea domestication

Phylogeography and genetic diversity of the Pisum genus, with inference to pea domestication

Smykal, P.S.[1], McGee, R.M.[2], and Coyne, C.C.[2*]. [1]1 Department of Botany, Palacký University in Olomouc, Czech Republic; [2]2 USDA-ARS, WSU, Pullman, USA. *(clarice.coyne@ars.usda.gov)

Tribe *Fabeae* is considered one of the most advanced groups in the legumes, with crown age of 23-16 Mya, in the mid-Miocene. The tribe contains five genera: *Lathyrus*, *Lens*, *Pisum*, *Vicia* and *Vavilovia*. The genus *Pisum* L. has recently been shown to be included in the *Lathyrus/Vicia* complex. Although there is around 98,000 pea accessions world-wide, there are only a fraction are truly wild. We selected the 150 wild pea accessions of *Pisum sativum/elatius* complex, 30 *P. fulvum* and 25 *P. abyssinicum,* with reliable information on origin, supplemented with 85 herbarium specimens. The analysis of chloroplast loci (*trnSG, matK, trnFL, rbcL*) and ITS region was used to reveal the diversity. This resulted in separation of two haplotype groups within *Pisum sativum/elatius* complex, broadly corresponding to *P.*

sativum subsp. elatius and *P. sativum subsp. sativum*. Although most of *P. fulvum* were separated, there were several accessions which were placed within both *Pisum sativum/elatius* haplotype groups, suggesting possible hybridization events. *P. abyssinicum* was positioned outside of the *P. s.* subsp. *sativum* clade, suggesting *abyssinicum* pea probably represents an independent domestication event, derived from *elatius* or *fulvum* ancestry, or more likely be of hybrid origin. This has been supplemented with RBIP analysis of 27 loci. Selected representative subset of 96 samples was further analysed for sequence diversity of 8 nuclear genes. This study provides the framework for both taxonomical species definition, setting up the global *Pisum* germplasm diversity as well as suggesting a model for the domestication of the cultivated species.

9	Evolution	Javadi, F.	Genetic diversity in wild and domesticated Azuki beans

Genetic diversity in wild and domesticated Azuki beans

Javadi, F.[1*], Fukushima, M.[2], and Yamaguchi, H.[3]. [1]Kyushu University, Japan; [2]Osaka Municipal Central Library, Japan; [3]Tokyo University of Agriculture, Japan. *(javadisf@hotmail.com)

The Azuki bean, *Vigna angularis* (Willd.) Ohwi & H. Ohashi var. *angulari*s, is grown for its edible bean in the region of East Asia, Southeast Asia, and the Himalayan highlands, and has recently expanded its traditional cultivation areas. However, knowledge on the level of genetic diversity is very limited in this crop and its wild relatives, *V. angularis* var. *nipponensis* and *V. nakashimae*. Such information would help us to understand the evlotionary process of domesticated species. We analyzed the patterns of nucleotide polymorphism of five nuclear genes in the wild and domesticated Azuki beans, and *V. nakashimae*. The results indicate that four of the five loci surveyed appeared to be evolving primarily under purifying selection, while the remaining locus may have been the subject of positive selection. A phylogenetic analysis of our data revealed that the cultivated Azuki bean was related to at least two genetically distinct wild populations. One group includes *V. nakashimae*, a Korean accession of wild Azuki bean, and the cultivated Azuki bean which are distributed in a wide area from Japan to Southwest China. The second group consists of wild and cultivated Azuki beans which are distributed in the Himalayan highlands and Southwest China. The present data suggests that the Azuki bean may have been domesticated from East Asian populations of wild Azuki, followed by geographical isolation of wild Azuki populations.

10	Evolution	Kang, Y.J.	Genome sequence of mungbean and insights into evolution within Vigna species

Genome sequence of mungbean and insights into evolution within Vigna species

Kang, Y.J.[1*], Kim, S.K.[1], Kim, M.Y.[1], Lestari, P.[1,2], Kim, K.H.[3], Ha, B.K.[4], Jun, T.H.[5], Hwang, W.J.[1], Lee, T.[1], Lee, J.[1], Shim, S.[1], Yoon, M.Y.[1], Jang, Y.E.[1], Han, K.S.[1], Taeprayoon, P.[6], Yoon, N.[1], Somta, P.[6], Tanya, P.[6], Kim, K.S.[1], Gwag, J.G.[7], Moon, J.K.[3], Lee, Y.H.[1], Jackson, S. A.[8], Schafleitner, R.[9], Srinives, P.[6], Varshney, R.K.[10], and Lee, S.H.[1]. [1]Department of Plant Science and Research Institute for Agriculture and Life Sciences, Seoul National University, Seoul 151-921, Korea; [2]Indonesian Center for Agricultural Biotechnology and Genetic Resources Research and Development, IAARD, Jl. Tentara Pelajar 3A Bogor 16111, Indonesia; [3]National Institute of Crop Science, Rural Development Administration, Suwon, 441-770, Korea; [4]Division of Plant Biotechnology, College of Agriculture and Life Science, Chonnam National University, Gwangju 500-757, Korea; [5]Department of Plant Bioscience, College of Natural Resources & Life Science, Pusan National University, Pusan, 627-706, Korea; [6]Department of Agronomy, Faculty of Agriculture at Kamphaeng Saen, Kasetsart University, Kamphaeng Saen Campus, Nakhon Pathom 73140, Thailand; [7]National Agrobiodiversity Center of NAAS, RDA, Suwon 441-707, Korea; [8]Institute for Plant Breeding, Genetics and Genomics, University of Georgia, 111 Riverbend Rd, Athens, GA 30602, USA; [9]Biotechnology/Molecular Breeding,

AVRDC-The World Vegetable Center, 60, Yi-Min Liao, Shanhua, Tainan 74199, Taiwan R.O.C; [10]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Andhra Pradesh, India. *(kangyangjae@gmail.com)

Mungbean (*Vigna radiata*) belongs to the subgenus *Ceratotropis*and is a fast-growing, warm-season legume crop that is primarily cultivated in developing countries of Asia. We constructed a draft genome sequence of mungbean to facilitate genome research into the subgenus *Ceratotropis* andto enable a better understanding of the evolution of leguminous species. The draft genome sequence covers 80% of the estimated genome, of which 50.1% consists of repetitive sequences. In total, 22,427high confidence protein-coding genes were predicted. Based on the *de novo* assembly of additional wild mungbean species, the divergence of what was eventually domesticated and the sampled wild mungbean species appears to have predated domestication. Moreover, the *de novo* assembly of a tetraploid *Vigna* species (*Vigna reflexo-pilosa*) provided genomic evidence of a recent allopolyploid event. To further study speciation, we compared *de novo* RNA-seq assemblies of 22 *Vigna* accessions of 18 species and the protein sets of *Glycine max*, *Lotus japonicus*, *Medicago truncatula*, *Cicer arietinum* and *Cajanus cajan*, by Bayesian Markov chain Monte Carlo method using the loci containing the confident orthologs for all 27 accessions. The present assembly of *V. radiata* will facilitate genome research and accelerate molecular breeding of the subgenus *Ceratotropis.*

11	Evolution	Pauls, K.P.	Comparisons between Bean and Soybean Genomes Lead to Insights into Gene Function and Evolution in Both Species

Comparisons between Bean and Soybean Genomes Lead to Insights into Gene Function and Evolution in Both Species

Pauls, K.P.[1*], Reinprecht, Y.[1], Perry, G.[1], Martin, J.[1], DiNatale, C.[2], Crosby, W.[2], Siddiqua, M.[1], Wright, L.C.[1], Qi, Y.[1], and Smith, T.[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada, N1G 2W1; [2]Department of Biological Sciences, University of Windsor, Windsor, ON, Canada, N9B 3P4. *(ppauls@uoguelp.ca)

Genome comparisons between common bean (*Phaseolus vulgaris* L.) and soybean (*Glycine max* L. Merr) have confirmed that for most genes in common bean, two homologous genes occur in soybean. The DNA sequence correspondence between common bean and soybean, agrees to a large extent with previously reported patterns of shared synteny between these two species and supports conclusions that the soybean genome was duplicated after the establishment of Phaseolus and Glycine from a common progenitor. We used *in silico* analyses to identify the genomic locations of over 100 phenylpropanoid pathway genes in common bean and soybean and examined putative relationships between these genes and genes for seed coat colour and flower colour. A similar approach was used to characterize genes for enzymes in the folate synthesis pathway as well as a gene potentially related to yield in both crops. The high degree of shared synteny between the two species facilitated the identification of gene function and allowed information from a highly characterized crop like soybean to be associated with specific loci and genes in bean.

12	Evolution	Steele, K. P.	Genome Size Estimation in Medicago (Fabaceae): Independent Loss and Gain?

Genome Size Estimation in *Medicago* (Fabaceae): Independent Loss and Gain?

Steele, K. P.[1*], Mandakova, T.[2], Johnson, K.[3], Taylor, R.[3], Steier, J.[3], and Wojciechowski, M. F.[3]. [1]Science and Mathematics Faculty, Arizona State University Polytechnic Mesa, AZ, USA; [2]Central European Institute of Technology (CEITEC), Masaryk University, Brno, Czech Republic; [3]School of Life Sciences, Arizona State University, Tempe, AZ USA. *(kelly.steele@asu.edu)

Genome size in flowering plants has been correlated with various aspects of life history, rarity and geographic

distribution. To consider these and other hypotheses for the genus *Medicago* we obtained genome size estimates for more than 56 species (89 species in the genus) representing all major lineages using standard methods of flow cytometry performed on a FACSCalibur. Two primary internal standards were used, *Glycine max* (Polanka), 2.5 picograms (pg) and *Medicago truncatula* Jemalong, 1.15 pg. Genome size ranged from just under 1.0 to 3.8 pg among diploid species. All five polyploid species have smaller genome sizes than the two diploid species with the largest genome sizes, *M. carstiensis* (3.8 pg) and *M. suffruticosa* (3.5 pg). Chromosome numbers were obtained from these same accessions to confirm identification of morphologically similar 2n=14 versus 2n=16 species and to obtain new counts for early diverging taxa. Genome sizes were mapped onto a phylogeny based on analyses of DNA sequence data of four molecular markers (nuclear rDNA ITS, *GA3oxidase*, *CNGC5* and the plastid *trn*K/*mat*K) to examine patterns of genome size distribution. Genome size has a non-random distribution, with some clades being characterized by smaller genome sizes than others.Two separate derived clades of annual species are characterized by an average genome size smaller than that of their sister groups: one clade that includes *M. polymorpha* has an average genome size of 1.16 pg and another clade that includes *M. truncatula*, has an average genome size of 1.19 pg, supporting the hypothesis of independent loss of genetic material in these two clades.

13	Evolution	Susek, K.	Cyto-molecular tracking of lupin chromosome evolution

Cyto-molecular tracking of lupin chromosome evolution

Susek, K.[1*], Wyrwa, K.[1], Ksiazkiewicz, M.[1], Bielski, W.[1], Lusinska, J.[2], Szczepaniak, A.[1], Rychel, S.[1], Naganowska, B.[1], Hasterok, R.[2], and Wolko, B.[1]. [1]Department of Genomics, Institute of Plant Genetics of the Polish Academy of Sciences, 60-479 Poznan, Poland; [2]Department of Plant Anatomy and Cytology, University of Silesia, Jagiellonska 28, 40-032 Katowice, Poland. *(ksus@igr.poznan.pl)

Chromosomal rearrangements have been demonstrated to have profound effects on diversification rates and speciation in plants. Thus they can be useful cytogenetic landmarks to study karyotype evolution. We have investigated rearrangements at the chromosomal level in the 'Old World' lupin (OWL) species, varying both in their basic chromosome numbers (x=6-9, 13) and chromosome numbers (2n=32-52), with mostly small and uniform metacentric chromosomes. The use of *Lupinus angustifolius* as a reference speciesprovides a unique opportunity to track chromosome rearrangements and understand the mechanisms shaping lupin genomes. Many of fundamental techniques have been initially applied to comparisons, including BAC library screening, interspecific BAC-FISH, DNA marker development, PCR-based genetic mapping and cross-genera genome wide comparative *in silico* sequence analysis. We have obtained markers specific for particular chromosomes of *L. angustifolius*. Using the *L. angustifolius*-derived sets of BACs along with *Medicago truncatula* and *Lotus japonicus* BACs as probes for FISH, we have identified chromosome rearrangements among chosen species. We have also detected in the lupin gene-rich regions conserved microsynteny links to the genome sequences of several other legume species (*M. truncatula*, *L. japonicus*, *Glycine max*, *Phaseolus vulgaris*, *Cajanus cajan* and *Cicer arietinum*). This work has considerable implications for karyotype studies of OWLs. Comprehensive synteny analyses have provided novel evidence of ancient duplications in the species analysed. Furthermore, our study demonstrated that a cyto-molecular approach can effectively reinforce the multidisciplinary phylogenomics.

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14	Evolution	Wong, M.M.L.	A Whole Genome Duplication potentially drove diversification in Fabaceae

A Whole Genome Duplication potentially drove diversification in Fabaceae

Wong, M.M.L.[1,2*], Vaillancourt, R.[3], Freeman, J.S.[3], Hudson, C.J.[3,4], Bakker, F.T.[5], Cannon, C.H.[6], and Wickneswari, R.[1]. [1]School of Environment and Natural Resource Sciences, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, Malaysia; [2]Department of Plant Sciences, University of Saskatchewan, Canada; [3]School of Plant Science, University of Tasmania, Australia; [4]Tasmanian Alkaloids, Australia; [5]Biosystematics Group, Wageningen University, Wageningen, The Netherlands; [6]Department of Biological Science, Texas Tech University, USA. *(melissa.wong@usask.ca)

Legumes (Fabaceae) are globally important crops for food, forage, and nitrogen-fixation. Fabaceae is traditionally split into three subfamilies, Papilionoideae, Mimosoideae and Caesalpinioideae. The Papilionoideae, the best studied subfamily, share a Whole Genome Duplication (WGD), dated at 59 Mya. In this study, we compared species from all three subfamilies, to understand genomic evolution at the family level. First, we constructed sequence-based linkage maps for *Acacia auriculiformis* and *A. mangium* and discovered evidence for a similar WGD event. To further validate this WGD event, we reconstructed the *Medicago truncatula* ancestral genome and investigated the genome evolution of *M. truncatula* and *Acacia* after WGD. Using synonymous substitution rate (Ks) analysis, we confirmed the presence of a WGD event in *Acacia* which corresponds with the timing and structure of the WGD previously discovered in the Papilionoideae. Further Ks analysis in diverse taxa from three subfamilies suggested that this WGD event is shared by all legumes. This is the first study to elucidate underlying mechanisms in the genome formation of Fabaceae and suggests that this WGD event is associated with their initial divergence and potentially driving the rapid diversification in the Fabaceae.

15	Genomics and Genetics	ABDI KETEMA, D.	Mapping QTLs for Days to Flowering, Photoperiod Sensitivity and Ascochyta Blight Reaction in a Chickpea Recombinant Inbred Population

Mapping QTLs for Days to Flowering, Photoperiod Sensitivity and Ascochyta Blight Reaction in a Chickpea Recombinant Inbred Population

ABDI KETEMA, D.*, Amit, D., Warkentin, T.D., and Tar'an, B. Department of Plant Sciences/ Crop Development Centre, University of Saskatchewan, SK, Canada. *(kea530@mail.usask.ca)

Chickpea (*Cicer arietinum* L. 2n= 16), is the second most important food legume in the world. The crop was only recently introduced to western Canada which has a very short growing season for which crop maturation often occurs under environmental conditions that could be too cool and wet. To achieve optimum yield of chickpea, crop duration must closely match the available growing season. Ninety-two Recombinant Inbred Lines (CP-RIL-1) were developed from a cross between ICCV 96029 (desi type, early maturing, highly susceptible to ascochyta blight) and CDC Frontier (kabuli type, late maturing, moderately resistant to ascochyta blight). The RILs were evaluated for their flowering response under long (16 hours light) and short (10 hours light) days in growth chambers. The difference in number of days to flowering under long vs. short days was considered in describing the photoperiod sensitivity of each line. A genetic linkage map consisting of eight linkage groups was developed using 349 SNP and RADs markers. Days to flowering and photoperiod sensitivity were negatively and significantly associated with ascochyta blight resistance. Three QTLs were identified for photoperiod sensitivity on LGs 1, 4 and 5. Four QTLs were identified for days to flowering under indoor conditions on LGs 3, 4 and 5. Twenty-four QTLs distributed over all LGs except LG5 were identified for ascochyta blight resistance. In most cases, genomic regions associated with days to flowering were also associated with ascochyta blight resistance and photoperiod sensitivity.

16	Genomics and Genetics	Agunbiade, TA	Development of Reference Transcriptomes for the Major Field Insect Pests of Cowpea: A Toolbox for Insect Pest Management Approaches in West Africa

Development of Reference Transcriptomes for the Major Field Insect Pests of Cowpea: A Toolbox for Insect Pest Management Approaches in West Africa

Agunbiade, TA.[1*], Sun, W.[1], Coates, BS.[2], Djouaka, R.[3], Tamò, M.[3], Ba, MN.[4], Binso-Dabire, C.[4], Baoua, I.[5], Olds, B.[6], and Pittendrigh, BR.[1]. [1]Department of Entomology, University of Illinois at Urbana-Champaign, USA; [2]Corn Insects and Crop Genetics Research Unit, United States Department of Agriculture, Agricultural Research Service, Ames, Iowa, USA; [3]International Institute of Tropical Agriculture, Cotonou, Benin; [4]Institut de l'Environnement et de Recherches Agricoles, Ouagadougou, Burkina Faso; [5]Institut National de la Recherche Agronomique du Niger, Maradi, Niger; [6]Department of Animal Biology, University of Illinois at Urbana-Champaign, Urbana, Illinois, USA. *(agunbia1@illinois.edu)

Cowpea is a widely cultivated and major nutritional source of protein for many people that live in West Africa. Annual yields and longevity of grain storage is greatly reduced by feeding damage caused by a complex of insect pests that include the pod sucking bugs, *Anoplocnemis curvipes* Fabricius (Hemiptera: Coreidae)and *Clavigralla tomentosicollis* Stål (Hemiptera: Coreidae); as well as phloem-feeding cowpea aphids, *Aphis craccivora* Koch (Hemiptera:Aphididae) and flower thrips, *Megalurothrips sjostedti* Trybom (Thysanoptera: Thripidae). Efforts to control these pests remain a challenge and there is a need to understand the structure and movement of these pest populations in order to facilitate the development of integrated pest management (IPM) strategies. Molecular tools have the potential to help facilitate a better understanding of pest populations. Towards this goal, we used 454 pyrosequencing technology to generate 319,126, 176,262, 320,722 and 227,882 raw reads from *A. curvipes*, *A. craccivora*, *C. tomentosicollis* and *M. sjostedti*, respectively. The reads were *de novo* assembled into 11,687, 7,647, 10,652 and 7,348 transcripts for *A. curvipes*, *A. craccivora*, *C. tomentosicollis* and *M. sjostedti*, respectively. Functional annotation of the resulting transcripts identified genes putatively involved in insecticide resistance, pathogen defense and immunity. Additionally, sequences that matched the primary aphid endosymbiont, *Buchnera aphidicola*, were identified among *A. craccivora* transcripts. Furthermore, 742, 97, 607 and 180 single nucleotide polymorphisms (SNPs) were respectively predicted among *A. curvipes*, *A. craccivora*, *C. tomentosicollis* and *M. sjostedti* transcripts, and will likely be valuable tools for future molecular genetic marker development. These results demonstrate that Roche 454-based transcriptome sequencing could be useful for the development of genomic resources for cowpea pest insects in West Africa.

17	Genomics and Genetics	Ali, M.B.	Development and mapping of SNP markers associated with zt-1 and zt-2 genes controlling zero tannin in faba bean (Vicia faba L.)

Development and mapping of SNP markers associated with zt-1 and zt-2 genes controlling zero tannin in faba bean (Vicia faba L.)

Ali, M.B.[1*], Vandenberg, A.[1], and Bett, K.[1]. [1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK S7N 5A8, Canada. *(mba522@mail.usask.ca)

Faba bean (*Vicia faba* L.) is an inexpensive source of protein for both animals and humans, but the polyphenolics in the seed coat have been associated with reduced nutritional bioavailability at the protein and mineral level. There are two complimentary genes, *zt-1* and *zt-2*, that affect the polyphenolic pathway and the presence of the homozygous recessive form of either will result in what is known as the "zero tannin" phenotype: unpigmented seed coats and white flowers. This is reminiscent of white flower/clear seed coat phenotype in pea where the *A* gene, a bHLH transcription factor, is responsible for the phenotype. This gene is part of the Myb-bHLH-WD40 transcription factor complex that regulates flavonoid biosynthesis. *Zt-1* is likely the WD-40 gene (O'Sullivan, pers.comm.) and we hypothesize that *Zt-2* is a bHLH, like in pea, or a Myb homologue.

We used available sequences of these genes from other legumes to investigate *zt-1* and *zt-2* in faba bean to design sequencing primers to amplify these genes in Snowbird (*zt-1*), Disco (*zt-2*) and high tannin lines (wild type). Sequences will be compared to try to identify SNPs or other indels for which specific marker assays can be developed and tested in segregating populations. These SNP markers will facilitate identification of specific zero tannin genotypes and allow breeders to know which gene is in their crossing parents and to predict whether there will be segregation or not in the offspring.

18	Genomics and Genetics	Araujo, S.S.	Unraveling grain filling mechanism in Phaseolus vulgaris L. under water deficit: transcriptomic and proteomic approaches

Unraveling grain filling mechanism in Phaseolus vulgaris L. under water deficit: transcriptomic and proteomic approaches

Parreira, J.R.[1,2], Almeida, A.M.[1,2], Silvestre, S.[3,4], Paiva, J.A.P.[1,2], Bernardes da Silva, A.B.[3,4], Marques da Silva, J.[3,4], Fevereiro, P.[4,5], and Araujo, S.S.[1,5*]. [1]Instituto de Investigação Cientifica Tropical (IICT), Rua da Junqueira 86, 1300-344 Lisboa, Portugal; [2]Instituto de Biologia Experimental e Tecnológica (IBET), Av. da República (E.A.N.), 2780-157 Oeiras, Portugal; [3]Center for Biodiversity, Functional and Integrative Genomics (BioFIG), Campo Grande, 1749-016 Lisboa, Portugal; [4]Departamento de Biologia Vegetal, Faculdade de Ciências da Universidade e Lisboa, Campo Grande, 1749-016 Lisboa, Portugal; [5]Instituto de Tecnologia Química e Biológica da Universidade Nova de Lisboa (ITQB-UNL), Av. da República (E.A.N.), Apartado 127, 2781-901 Oeiras, Portugal. *(susana.araujo@iict.pt)

Common bean (*Phaseolus vulgaris* L.) is a major staple crop in developing countries in Latin America and Sub-Saharan Africa, where water deficit (WD) is a continuous concern. Grain filling proceeds during the seed maturation phase playing a major role in storage reserve composition thus affecting the yield, the quality and the nutritional value of beans.

Our work aims to unravel the molecular mechanisms associated with grain development and how they are affected and modulated by WD. We are using global scale studies based in Omic approaches to understand their major pathways and regulatory steps. We are comparing two bean genotypes with contrasting performances concerning WD resistance and grain productivity. The genotype SER16 stood out with increased WD resistance, as seen by its better photosynthetic and photochemical performance in comparison with the WD sensitive reference Tio Canela.

Seed samples were collected from SER16 and Tio Canela from two environmental conditions (control vs WD) at four time points of grain development (10, 20, 30 and 40 days after anthesis). These time points reflect the four relevant stages associated with grain development. The kinetics of seed development will be addressed by studying the dynamics in transcript and proteomic profiles in those experimental conditions. Massive analysis of cDNA Ends is being conducted to perform differential analysis of bean transcriptome across studied conditions. For proteomic studies, preliminary 2D gels are being established to pursue further with the differential in-gel electrophoresis (DIGE). Future work will also include gel free based proteomics experiments (LC-MS/MS).

19	Genomics and Genetics	Bhatnagar-Mathur, P.	Drought tolerant transgenic peanut moves closer to reality

Drought tolerant transgenic peanut moves closer to reality

Bhatnagar-Mathur, P.[1*], Vadez, V.[1], and Sharma, K.K.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, AP 502 324, India. *(p.bhatnagar@cgiar.org)

Peanut, is a valuable cash crop for smallholder and resource-poor farmers that occupies the largest portion of Low

Income Food Deficit Countries (LIFDC; FAO, 2008) farming systems, grown in 20.6 million ha, often fitting into underutilized crop niches. Globally, drought contributes to annual losses of over 6.7 million metric tons to the productivity of peanut, resulting in estimated monetarily losses equivalent to over US$520 million. Nevertheless, efforts to breed peanuts for enhanced water use efficiency have been constrained due to the lack of sufficient genotypic variability, thus making it critical to find transgenic solutions for drought tolerance trait in this legume crop. In our efforts to develop a transgenic solution for drought tolerance in peanut using stress-inducible At*DREB1A* transcription factor, over 50 independent transgenic events were developed and screened to ascertain whether changes at the molecular and biochemical level were followed by water productivity differences and transpiration efficiencies (TE). Four events with high TE and desirable root traits were selected for further evaluation of yield under greenhouse and confined field drought conditions over a period of four years across varying vapour pressure deficits (VPDs). A thorough assessment of different traits that possibly lead to better coping with drought was carried out prior to their field-testing. Results will be presented in support of our findings on stress-inducible expression of *DREB1A* in transgenic peanuts, conferring enhanced drought tolerance by contributing to higher yield (18-23%) and harvest index under water-limiting conditions, and no yield penalty under normal irrigated conditions.

20	Genomics and Genetics	Buchwaldt, L.	Resistance in chickpea to Ascochyta rabiei is conferred by genes encoding pathogen recognition and other genes in basic defense pathways

Resistance in chickpea to Ascochyta rabiei is conferred by genes encoding pathogen recognition and other genes in basic defense pathways

Prabhakaran, R.[1], Varshney, R.[2], Gali, K.[1], Sharpe, A.[3], and Buchwaldt, L.[1*]. [1]Agriculture and Agri-Food Canada, 107 Science Place, Saskatoon, SK, S7N 0X2, Canada; [2]ICRISAT, Patancheru, Andhra Pradesh, 502 324, India; [3]National Research Council, 110 Gymnasium Place, Saskatoon, SK, S7N 0W9, Canada. *(Lone.Buchwaldt@agr.gc.ca)

This study examines the molecular basis of resistance to *Ascochyta rabiei* in chickpea. An inter-specific population of RIL derived from *C. arietinum* ICC4958 x *C. reticulatum* PI489777 was used to develop a high-density linkage map consisting of 1328 SNP and SSR markers. Progenies were inoculated separately with two isolates from Canada and one from Syria using a detached leaf-assay. This allowed an accurate record of lesion development over time that was used to calculate the area under the disease progress curve (AUDPC). The parental lines interacted differentially with the isolates as AUDPC were 20.6, 9.3 and 4.4 in ICC4958 compared to 2.0, 3.2 and 9.3 in PI489777. Ten quantitative resistance loci (QRL) explained 5 to 26% of the phenotypic variation. The two parents contributed to resistance at different loci. Each QRL interacted with a single isolate, except one that interacted with two isolates. Since a portion of the SNP markers were designed in exonic sequences a search of GenBank and *Medicago* data bases revealed annotated gene function. A major discovery was a match of SNP markers at six QRL with genes encoding serine/threonine kinase proteins involved in pathogen recognition, innate immune response, programmed cell death and signal transduction. Genes at the remaining QRL were associated with well known basic defense pathways such as thaumatin, chalcone-stilbene, peroxidase and ethylene. Evidence suggest that recognition of *A. rabiei* results in qualitative disease phenotypes seen in some studies, while the quantitative nature of resistance in other studies might be a result of activation of additional networks of basic defense pathways.

21	Genomics and Genetics	Burstin, J.	PeaMUST, a large multidisciplinary project dedicated to pea improvement

PeaMUST, a large multidisciplinary project dedicated to pea improvement

BURSTIN, J.[1*], Pilet-Nayel, M.L.[2], Rameau, C.[3], Thompson, R.[1], Carrouée, B.[4], Rivière, N.[5], Brochot, A.L.[1], and

Chaillet, I.[6]. [1]INRA, UMR1347 Agroecologie, 17 rue de Sully, 21065 Dijon cedex, France; [2]INRA, UMR IGEPP, BP35327, Le Rheu cedex, France; [3]INRA, UMR IJPB, Route de St Cyr, Versailles cedex; [4]UNIP, 11 rue de Monceau - CS 60003 - 75378 PARIS cedex 08; [5]BIOGEMMA, CS90126, 63720 Chappes; [6]ARVALIS, Rue de Noetzlin – Bât. 630, 91405 Orsay cedex. *(judith.burstin@dijon.inra.fr)

Background and Objectives: Legume use in arable rotations provides several significant ecological services that can help to meet the challenge of delivering high-quality food and feed in an economically and environmentally sustainable manner. Nevertheless, grain legumes are underused by European farmers mainly because of yield inconsistency. PeaMUST overall objective is to develop novel pea varieties and optimize plant-symbiotic interactions for seed yield and quality regularity, in the context of pesticide reduction and climate change.

Methodologies: PeaMUST project will take advantage of high-throughput sequencing, genotyping and phenotyping technologies to tackle the multiple-stress challenge. PeaMUST approach will combine different complementary approaches: (i) develop genomic selection programs based on naturally occurring variability and targeting yield stability, (ii) enhance allele mining for durable marker assisted selection (MAS) for resistance through comparative mapping, and (iii) create innovative plant architecture ideotypes by screening mutations and symbiotic biological regulations for improved stress tolerance. PeaMUST will also develop unique tools for gene identification and characterization (high throughput genotyping, association genetics, translational genomic tools, improved TILLING facilities and VIGS platform).

Expected outcomes: PeaMUST will provide new insights into the mechanisms underlying multi-stress tolerance through a combination of genomics, genetics, physiology, and agronomic modelling. PeaMUST approach will allow rapid translation of genomics knowledge to breeding applications by the efficient use of the species natural diversity as well as induced diversity. PeaMUST will deliver adapted germplasm and devise novel breeding programs strategies to better exploit genetic resources that will be assessed for their socio-economic sustainability.

22	Genomics and Genetics	Cannon, EKS	PeanutBase: The Genomic Data Portal for Arachis

PeanutBase: The Genomic Data Portal for Arachis

Cannon, EKS.[1*], Dash, S.[1], Kalberer, S.[2], Weeks, N.[2], Huang, W.[1], Farmer, A.[3], Dickerson, JA.[1], and Cannon, SB.[2]. [1]Iowa State University; [2]USDA-ARS; [3]National Center for Genomic Research. *(ethy@a415software.com)

PeanutBase (http://peanutbase.org) was started in April 2013 at Iowa State University with funding from The Peanut Foundation and in kind contributions from the USDA-ARS. It provides a web portal for genomics, genetics and trait information for peanut. Compared to most crop species, genomic resources for peanut breeders have been in their infancy. PeanutBase will develop and deploy tools for harvesting both existing resources -- genetic maps, genetic and molecular markers, QTL data -- and new reources that are now being developed for peanut: a reference genome, gene models, transcriptomes, proteome and functional gene model annotations. Data curation plays a prominent role in loading and presenting these data. The genomes of the two wild progenitors of cultivated peanut, Arachis duranensis and Arachis ipaensis, have been sequenced and the data is now served from PeanutBase. Transcriptome data from peanut and these two wild species are being mapped to these two diploid genomes and are available via the Genome browser. Genetic maps are being served as interactive CMap graphics in collaboration with the Legume Information System (LIS;http://comparative-legumes.org). QTL data sets have also been collected and are available from PeanutBase.PeanutBase is implemented with Tripal and Chado.

23	Genomics and Genetics	Dastmalchi, M	Soybean chalcone isomerase: evolutionary history of the fold as told by sequence, expression and localization of the gene family

Soybean chalcone isomerase: evolutionary history of the fold as told by sequence, expression and localization of the gene family

Dastmalchi, M.[1,2*], and Dhaubhadel, S.[1,2]. [1]Department of Biology, University of Western Ontario, London, ON, Canada N6A 5B7; [2]Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, London, ON, Canada N5V 4T3. *(mdastmal@uwo.ca)

Soybean produces a diverse array of natural products via the phenylpropanoid pathway important for plant signalling, attraction, protection and development, as well as bearing human health benefits. A branch-point enzyme of the pathway, chalcone isomerase (CHI), catalyzes the reaction producing flavanones, the skeletal backbone for many downstream metabolites, including flavonoids and the legume-specific isoflavonoids. We have identified twelve soybean *CHIs*, including five new members, across ten chromosomes that fall into four subfamilies. The evolutionary history of the family was studied in the context of various *CHIs* and *CHI*-like homologues across divisions in the plant kingdom and beyond. The fold appears to have evolved from catalytically inactive homologues in fungal and protist ancestors, to fatty acid binding-proteins (FAPs) in plants, to sterically restricted folds that gave rise to the chalcone-to-flavanone isomerase activity. We have found four CHIs in soybean with such functionality. The members of the family showed differential temporal and spatial expression, pointing to the potential function of *CHI1A* and *CHI1B1* in isoflavonoid production. Promoter analysis of the *CHIs* driving *GUS* expression in *Arabidopsis* was used to study the minutiae of sub-organ expression patterns. Subcellular localization of the family showed that members with catalytic function localize to the nucleus and cytoplasm, while CHI isoforms closely associated with the FAPs localize to the chloroplast, confirming such function. Study of the soybean *CHI* family, in the post-genome sequencing era has allowed us to comprehensively update our knowledge on the family, its evolutionary history, and differential expression and localization.

24	Genomics and Genetics	Deokar, A	QTL to Candidate Genes: Understanding Photoperiod Sensitivity and Flowering Time in Chickpea

QTL to Candidate Genes: Understanding Photoperiod Sensitivity and Flowering Time in Chickpea

Deokar, A.[1*], Daba, K.[1], and Tar'an, B.[1]. [1]Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada. *(amd749@mail.usask.ca)

Photoperiod insensitivity is one of the important traits for adaptation of chickpea to a short growing season particularly in Western Canada where growing period is often restricted by end of season frost. Identifying QTLs/genes that regulate photoperiod insensitivity and flowering time will help to understand genetic mechanism of photoperiod sensitivity in chickpea as well as to develop candidate gene-based markers for marker-assisted selection (MAS) of photoperiod insensitivity trait. In this research we identified 103 chickpea ortholog of the Arabidopsis genes involved in regulating flowering time pathway. The FLOWERING LOCUS D (*FLD*), CRYPTOCHROME 2 (*CRY2*) and GIGANTEA (*GI*) genes with single nucleotide polymorphism (SNP) between ICCV 96029 (photoperiod insensitive) and CDC Frontier (photoperiod sensitive) were genetically mapped in the inbred population. We identified major QTL regions on LG5 explaining more than 50% phenotypic variation for photoperiod sensitivity in chickpea. The QTL contains a circadian rhythm gene EARLY FLOWERING 3 (*ELF3*) that has been reported to regulate the flowering pathway in Arabidopsis and Rice. The *CaELF3* could be the most likely candidate gene regulating photoperiod sensitivity in chickpea.

25	Genomics and Genetics	Diapari, Marwan	Synteny analysis of markers associated with iron and zinc concentration in pea and chickpea with *Medicago truncatula*

Synteny of Markers Associated with Iron and Zinc Concentrations in Pea and Chickpea with Medicago truncatula

Diapari, MARWAN.[1*], Wong, Melissa.[1], Tar'an, Bunyamin.[1], and Warkentin, Tom.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, S7N 5A8, Canada. *(m.marwan@usask.ca)

Comparative sequence analyses were done between pea and chickpea with *Medicago truncatula* in an effort to identify association between genetic variations and iron and zinc concentrations in seeds of pea and chickpea. Recently, a set of SNP markers associated with iron and zinc concentration in pea and chickpea have been identified. The gene sequences containing these SNP markers were BLASTed against the *Medicago truncatula* genome to predict their orthologous genes associated with seed iron and zinc concentrations in both pea and chickpea. The analysis identifed a set of SNPs from pea and chickpea which were orthologous to the same genomic region in *M. truncatula* suggesting that pea and chickpea shared some syntenic regions responsible for iron and zinc concentration in seeds.

26	Genomics and Genetics	Dickstein, R.	An improved genetic crossing method for Medicago truncatula

An improved genetic crossing method for *Medicago truncatula*

Veerappan, V.[1], Kadel, K.[1], Alexis, N.[1], Scott, A.[1], Kryvoruchko, I.[2], Sinharoy, S.[2], Udvardi, M.[2], and Dickstein, R.[1*]. [1]Department of Biological Sciences, University of North Texas, Denton, TX 76203 USA; [2]Plant Biology Division, The Samuel Roberts Noble Foundation, Ardmore, OK 73401 USA. *(beccad@unt.edu)

Genetic crossing is essential for both forward and reverse genetic approaches to understand the biological functions of genes. For *Medicago truncatula,* various crossing techniques have been described which differ by the methods used to open and dissect the female parent's flower bud to remove immature anthers to prevent self-pollination. Here, we introduce the keel petal incision method for genetic crossing in *M. truncatula*. In this method, the standard petal is temporarily lifted away from the keel petal and a cut is made along the central line of the keel petal from the bottom 1/3rd of the female parent's flower bud to its distal end. Anthers are removed from the flower bud and male donor pollen is deposited on the stigma. After pollination, the keel petal, wing petals and standard petal are repositioned around the pollinated stigma to form a pouch. This pouch prevents the deposited pollen from dislodging from the stigma and keeps the internal floral organs from drying out, without using cling-film or water-containing chambers to maintain a humid environment. In our hands, the keel petal incision protocol shows a marked improvement over existing methods with respect to the ease of crossing and the percentage of successful crosses. Investigators of varying experience have achieved genetic crosses in *M. truncatula* using this method. The protocol showed an overall approximate 80% success rate in the R108, Jemalong A17 and A20 ecotypes, and is expected to work with other ecotypes. We acknowledge support from NSF IOS-1127155.

27	Genomics and Genetics	Guo, Y.	Developing a platform for allele mining in soybean (Glycine max) and its application to functional marker development and genotype identification

Developing a platform for allele mining in soybean (Glycine max) and its application to functional marker

development and genotype identification

Guo, Y.[1*], and Qiu, L.-J.[1]. [1]The National Key Facility for Crop Gene Resources and Genetic Improvement (NFCRI), Institute of Crop Science, Chinese Academy of Agricultural Sciences. *(guoyong@caas.cn)

Development of superior crop varieties was made by accumulation of beneficial alleles from vast plant genetic resources. But a significant portion of these beneficial alleles were not utilized in crop breeding. Functional makers for beneficial alleles could accelerate the usage of these alleles in the field of molecular genetics and molecular breeding. In order to accelerate the usage of alleles and functional markers in soybean, a platform for allele mining, marker development and molecular breeding was developed based on representative accessions and core collections selected from the full soybean collection of China. Using this platform, seven alleles including three low frequency novel alleles of two P450-dependent mono-oxygenases encoding genes *GmF3'H* and *F3'5'H* were identified. A set of gene-tagged markers was developed and verified based on the sequence diversity of all seven alleles. Furthermore, the markers were used to analyze soybean accessions including 170 cultivated soybeans (*G. max*) from a mini core collection and 102 wild soybeans (*G. soja*). For both *F3'H* and *F3'5'H*, the markers selection efficiencies for pubescence color and flower color were determined. The results showed that one *GmF3'H* alleleexplained 92.2% of the variation in tawny andtwo*gmf3'h* alleles explained63.8% of the variation in gray pubescence colors. In addition, two *GmF3'5'H* allelesandone *gmF3'5'h* allele explained 94.0% of the variation in purple and 75.3% in white flowers, respectively. By the combination of the two loci, seed coat color was determined. In total, 90.9% of accessions possessing both the *gmf3'h-b* and *gmf3'5'h* alleles had yellow seed coats.

28	Genomics and Genetics	Gupta, P.	Genetic diversity at EST-SSR markers and its relationship to ODAP content under heat stress in grass pea (Lathyrus sativus L.)

Genetic diversity at EST-SSR markers and its relationship to ODAP content under heat stress in grass pea (Lathyrus sativus L.)

Gupta, P.[1*], Henkrar, F.[2], El Hanafi, S.[2], Barpete, S.[2], Udupa, S.M.[2], Rathore, A.[3], Kumar, S.[2], Mathur, P.[4], and Baum, M.[5]. [1]BIGM, International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat-Office, Morocco; [2]ICARDA, Rabat-Office, Morocco; [3]ICRISAT, Patancheru, India; [4]Bioversity, South Asia office, Delhi, India; [5]ICARDA, Amman office, Jordan. *(p.gupta@cgiar.org)

Grass pea (*Lathyrus sativus* L.) is considered as one of the hardiest crops for adaptation to climate change, combining drought tolerance with waterlogging tolerance. It is a highly valued crop for human food and animal feed and fodder, because of its protein-rich seeds (>30%) and leaves (~17% protein). However, this crop remains underutilized and neglected because of the poorly characterized genetic resources. Here, we characterized 101 accessions of cultivated species along with 17 wild species, each represented by one accession, with 18 EST-SSR markers. A total of 67 alleles were detected with an average of 3.72 alleles per locus and polymorphism information content (PIC) of 0.515. The STRUCTURE analysis indicated evidence for the presence of significant population structure in grass pea. The entire population identified four genetically distinct groups or admixtures within the *L. sativus* and wild species. Group I consisted of 34 accessions including the accession of *L. cicera,* which showed low β-N-Oxalyl-L-α, β-diamino propionic acid (β-ODAP) content. Group II was represented by 19 accessions, which included the remaining 16 wild species along with three cultivated accessions, local landrace, Bang-9 and Bang-11. Group III had 36 accessions of cultivated species with high β-ODAP germplasm, while Group IV consisted of 29 accessions of cultivated species, which had high β-ODAP content under heat and drought stress.

29	Genomics and Genetics	Hamwieh, A.	Mapping QTLs across environments for heat related traits in Chickpea (Cicer arientinum L.)

Mapping QTLs across environments for heat related traits in Chickpea (Cicer arientinum L.)

Mohamed, A.A.[1], Hamwieh, A.[2*], Abdelmula, A.A.[3], and Imtiaz, M.[4]. [1]Hudeiba Research Station - Agricultural Research Corporation (ARC) P. O. Box 31, Eddamer, Sudan; [2]International Centre for Agricultural Research in the Dry Areas (ICARDA), 15 G. Radwanl bn El-Tabib Street, Giza, P.O. Box 2416, Cairo, Egypt; [3]Department of Agronomy, Faculty of Agriculture, University of Khartoum - postal code: 13314, Shambat-Sudan; [4]International Maize and Wheat Improvement Centre (CIMMYT) Pakistan Office, NARC, Park Road, Islamabad 44000, Pakistan. *(a.hamwieh@yahoo.com)

Heat stress particularly at the reproductive stage adversely affects chickpea (*Cicer arietinum* L.) production in many regions of the world including Sudan. To identify quantitative trait loci (QTL) associated with heat tolerance in chickpea under different environments, eighty recombinant inbred lines (RILs) derived from a cross between ILC588 and ILC3279 were evaluated in seven field environments in Sudan. The environments include three locations (Hudeiba, Medani and Shambat), two growing seasons (2011/12 and 2012/13) and two sowing dates (early November and late December). Data were recorded on heat tolerance score (HTS), seven phenological traits and eight yield related traits. One hundred and eight simple sequence repeats (SSR) markers have been used to generate linkage map. A total of 62 SSR markers were mapped spanning 520 cM on seven linkage groups and 46 markers remained unlinked. The quantitative trait loci (QTLs) analysis detected 103 significant QTLs (LOD ≥ 2.0) across 16 traits measured in this study. The highest phenotypic variation (22 %) was explained by the QTLBP (podded branches/plant). The heat tolerance (QTLHTS) was conserved under stressed environments and linked to markers TS-19 and STMS-21 on LG3. Another QTLHTS was linked to markers SCY17, TA72 and NCPGR74 on LG4. The QTLHTS on LG3 and LG4 may contain QTLs with pleiotropic effects. The markers associated with heat tolerance identified in this study should be validated in other backgrounds and could be used in future to improve breeding for heat tolerance.

30	Genomics and Genetics	Ibrahim, Hossam M.	Effectiveness of Breeding Methods for Production of Superior Genotypes and Maintenance of Genetic Variance in Fabe Bean (Vicia faba, L.)

Effectiveness of Breeding Methods for Production of Superior Genotypes and Maintenance of Genetic Variance in Fabe Bean (Vicia faba, L.)

Ibrahim, HOSSAM M.[1*]. [1]Department of Agronomy, Faculty of Agriculture, Alexandria University, Alexandria. Egypt. *(Hossam99_2000@yahoo.com)

The present study was carried out during the period from 2007/ 08 to 2011/2012 at Agricultural Research Station, Faculty of Agriculture, Alexandria University, Alexandria, Egypt. The study aimed at evaluating the effectiveness of pedigree (P), bulk [natural selection, (B)], and mass selection breeding (MS) methods. Two F2 populations, derived from two crosses, were used. Eighteen families derived from each of the three breeding methods in each cross were tested for seed yield (t/ ha), seed yield per plant (g) and its components in F6 generation. A randomized complete block design with three replications was used. Significant differences existed, within F6 families of each cross, for seed yield, seed yield per plant and its components by applying either of the three methods. The widest range in seed yield was obtained by the bulk method. The bulk breeding method produced consistently more superior families in either and over the two crosses with 19, 15 and 14 families for bulk, Pedigree and MS methods, respectively. The genotypic (d2G) and phenotypic (d2Ph), for seed yield, variances estimated from bulk method were the highest compared with the other breeding methods over the two crosses. Heritability estimates, in broad sense, and expected genetic advance from selection for higher seed yield indicated that the bulk method recorded higher values (h2= 0.87-0.93, DG= 0.51- 0.85) compared with the other two methods. Based on the obtained results, it seems that the bulk breeding method was more effective compared to the other two breeding methods, in producing superior genotypes in

seed yield and maintaining genetic variance for further selection and improvement of that character.

31	Genomics and Genetics	Igrejas, G.	Can proteomic markers be used to evaluate genetic diversity in Portuguese populations of sweet chestnut (Castanea sativa Mill.)?

Can proteomic markers be used to evaluate genetic diversity in Portuguese populations of sweet chestnut (Castanea sativa Mill.)?

Freitas, M.[1,2], Ribeiro, M.[1,2], Ferreira-Cardoso, J.[3], Marinho, C.[1,2], and Igrejas, G.[1,2*]. [1]Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro, 5001-801 Vila Real, Portugal; [2]Institute for Biotechnology and Bioengineering, Centre of Genomics and Biotechnology, University of Trás-os-Montes and Alto Douro, 5001-801 Vila Real, Portugal; [3]Centre for Research and Technology of Agro-Environment and Biological Sciences,University of Trás-os-Montes and Alto Douro, 5001-801 Vila Real, Portugal. *(gigrejas@utad.pt)

Sweet chestnut (*Castanea sativa* Mill.) is a widely distributed multipurpose tree species which is of great economic value for its fruit and timber, and its landscaping and environmental attributes.

Storage proteins, present in all seeds, have proved to be useful in evaluating genetic variability in many species. The possibility of using storage proteins as genetic diversity markers in forest species has not been fully explored.

We evaluated whether storage proteins could be used as markers of genetic diversity in *Castanea sativa* Mill. Seed storage proteins of six Portuguese cultivars that are most representative of the Trás-os-Montes region, namely 'Benfeita', 'Côta', 'Judia', 'Lada', 'Longal' and 'Martaínha', were separated by one-dimensional electrophoresis (SDS-PAGE). These cultivars were found to be highly polymorphic for albumins (34 bands) and globulins (24 bands). The presence/absence of bands was used to measure genetic dissimilarity indices and create phylogenetic trees. There was a wide distribution of the storage proteins studied in these cultivars. The 'Benfeita' cultivar was more genetically distant from other cultivars while the 'Lada' and 'Martaínha' cultivars showed the closest relationship.

Two-dimensional electrophoresis, namely isoelectric focusing followed by SDS-PAGE, was used to investigate the full proteomes of Portuguese cultivars of *Castanea sativa* Mill.. Subsequent protein identification by matrix-assisted laser desorption/ionization mass spectrometry (MALDI-TOF MS) highlighted the proteins that were differentially expressed.

The analysis of storage protein proved to be a useful tool to give complementary information to explain the genetic and adaptive diversity within different cultivars of *Castanea sativa*.

32	Genomics and Genetics	Igrejas, G.	SDS-PAGE of storage proteins as a way to discover genetic diversity of garbanzo beans (Cicer arietinum L.)

SDS-PAGE of storage proteins as a way to discover genetic diversity of garbanzo beans (Cicer arietinum L.)

Baptista, A.[1,2], Santos, T.[1,2], Carnide, V.[1,2], and Igrejas, G.[1,2*]. [1]Department of Genetics and Biotechnology, University of Trás-os-Montes and Alto Douro, 5001-801 Vila Real, Portugal; [2]Institute for Biotechnology and Bioengineering, Centre of Genomics and Biotechnology, University of Trás-os-Montes and Alto Douro, 5001-801 Vila Real, Portugal. *(gigrejas@utad.pt)

The garbanzo bean (*Cicer arietinum* L.), also known as the chickpea, belongs to the legume family and is an important crop for human consumption due to its high protein content and nutritional quality. The aim of this work was to study

the genetic diversity of globulins in a collection of 24 garbanzo bean genotypes.

All the genotypes studied were the Kabuli type, except Elmo, Elf and Elite, which are the Desi type. Of the 24 genotypes analysed 11 were of Portuguese origin, 8 of Spanish origin and 5 were from ICARDA. Protein samples were separated by gel electrophoresis in the presence of sodium dodecyl sulphate (SDS-PAGE) and the banding patterns were sketched and analysed in a dendrogram using the program NTSYSpc 2.10a.

Using two methods of extraction, 49 different profiles were obtained. There was a total of 40 bands for the higher molecular weight globulins and 41 bands for the lower molecular weight globulins. Some bands occurred at a high frequency among the different profiles, with rates of occurrence ranging between 75% and 100%.

The electrophoretic profiles were grouped into five clusters. Calculated genetic distances between the various lines ranged between 0 and 0.90. Based on these results we conclude that there is a set of profiles that are repeated either within the same genotype (intravariability) or between genotypes (intervariability). The application of higher resolution techniques to study storage proteins of *Cicer arietinum* L. will make it possible to further distinguish between the known genotypes.

33	Genomics and Genetics	Jain, P.	Differential Expression of Acetohydroxyacid Synthase Genes and Response to Imazamox Herbicide in Chickpea

Differential Expression of Acetohydroxyacid Synthase Genes and Response to Imazamox Herbicide in Chickpea

Jain, P.[1*], and Tar'an, B.[1]. [1]Crop Development Centre, University of Saskatchewan. *(paj445@mail.usask.ca)

Chickpea (*Cicer arietinum* L.) is a relatively new pulse crop introduced to the Canadian Prairies as rotation crop with cereals and oilseed. Its production on Canadian Prairies is challenging due to lack of effective weed management mainly because of poor competition ability of the crop and limited registered herbicide options. Chickpea genotype with resistance to imidazolinone (IMI) herbicides has been identified, but the molecular mechanism is not fully understood. In many plant species acetolactate/acetohydroxyacid synthase (ALS/AHAS; EC 2.2.1.6) the first enzyme to catalyze biosynthesis of branched amino acids has been identified as the target site for IMI herbicides. A point mutation in the AHAS1 gene from chickpea imazamox susceptible genotype CDC Frontier and resistant CDC Cory at C581 to T581 resulting in an amino acid substitution from Ala194 to Val194 (position 205, standardized to Arabidopsis) confers the resistance to imazamox. Quantitative real time PCR, protein structure analysis and enzyme activity assay indicated that the herbicide resistance is not at the transcription level but suggests that the point mutation (A205 to V205) in chickpea AHAS1 gene resulted in alteration of protein folding/activity thereby preventing imazamox herbicides attachment to the enzyme, resulting in herbicide resistance. This study demonstrated the molecular mechanism of chickpea resistance response to imazamox herbicide.

34	Genomics and Genetics	Joshi, T	Soybean Knowledge Base (SoyKB): Bridging the gap between soybean translational genomics and breeding

Soybean Knowledge Base (SoyKB): Bridging the gap between soybean translational genomics and breeding

Joshi, T.[1,2,3*], Chen, S.[1], Zhang, H.[1], Wang, J.[1], Stacey, G.[2,3,4], Nguyen, H.T.[2,3,4], and Xu, D.[1,2,3]. [1]Department of Computer Science, University of Missouri, Columbia; [2]Christopher S. Bond Life Sciences Center; [3]National Center of Soybean Biotechnology; [4]Division of Plant Sciences; University of Missouri, Columbia. *(joshitr@missouri.edu)

Many genome-scale data are available in soybean including genomic sequence, transcriptomics (microarray, RNA-seq), proteomics and metabolomics datasets, together with growing knowledge of soybean in gene, microRNAs,

pathways, and phenotypes. This represents rich and resourceful information which can provide valuable insights, if mined in an innovative and integrative manner and thus, the need for informatics resources to achieve that.

Towards this we have developed Soybean Knowledge Base (SoyKB), a comprehensive all-inclusive web resource for soybean translational genomics and breeding. SoyKB handles the management and integration of soybean genomics and multi-omics data along with gene function annotations, biological pathway and trait information. It has many useful tools including Affymetrix probeID search, gene family search, multiple gene/metabolite analysis, motif analysis tool, protein 3D structure viewer and download/upload capacity for experimental data and annotations. It has a user-friendly web interface together with genome browser and pathway viewer, which display data in an intuitive manner to the soybean researchers, breeders and consumers.

SoyKB has new innovative tools for soybean breeding including a graphical chromosome visualizer targeted towards ease of navigation for breeders. It integrates QTLs, traits, germplasm information along with genomic variation data such as single nucleotide polymorphisms (SNPs) and genome-wide association studies (GWAS) data from multiple genotypes, cultivars and *G.soja*. QTLs for multiple traits can be queried and visualized in the chromosome visualizer simultaneously and overlaid on top of the genes and other molecular markers as well as multi-omics experimental data for meaningful inferences. SoyKB can be publicly accessed at http://soykb.org.

35	Genomics and Genetics	Kamphuis, L.G.	The narrow-leafed lupin genome assembly, transcriptome sequencing of different tissue types and generation of gene-based molecular markers

The narrow-leafed lupin genome assembly, transcriptome sequencing of different tissue types and generation of gene-based molecular markers

Kamphuis, L.G.[1,2*], Hane, J.K.[1], Nelson, M.N.[2,3], Gao, L.-L.[1], Atkins, C.A.[3], and Singh, K.B.[1,2]. [1]CSIRO Plant Industry, Private Bag 5, Wembley, WA 6913, Australia; [2]The UWA Institute of Agriculture, University of Western Australia, Crawley, WA 6009, Australia; [3]The School of Plant Biology, University of Western Australia, Crawley, WA 6009, Australia. *(lars.kamphuis@csiro.au)

Narrow-leafed lupin (NLL) is the main grain legume grown in Australia and forms an important part of sustainable farming systems, reducing the need for nitrogenous fertilizer, providing valuable disease breaks and boosting cereal yields. We have generated a draft genome assembly for the NLL cultivar Tanjil. We have performed tissue-specific transcriptome sequencing for three cultivars with sequenced tissues from roots, stems, leafs, flowers and seeds, which aided the annotation and identification of the gene-rich regions. From this dataset we have identified several groups of genes that are tissue specific. We have adopted high-throughput molecular marker techniques for assaying gene-based SNPs and indels in NLL derived from the transcriptome datasets, which we used to improve the reference genetic map. *In silico* PCR identified SNP and indel markers for each scaffold in the current assembly and the genotyping of markers on the largest scaffolds is underway. Together these resources will significantly improve and accelerate NLL breeding programmes, especially since NLL has only been 'domesticated' for little more than 50 years.

36	Genomics and Genetics	Kaur, P	First Genome Draft of subterranean clover (Trifolium subterraneum L.)

First Genome Draft of subterranean clover (*Trifolium subterraneum L.*)

Kaur, P.[1*], Hideki, H.[2], Appels, R.[3], Erskine, W.[1], Nichols, P.[4], and Isobe, S.[2]. [1]Centre for Plant Genetics and Breeding, The University of Western Australia, 35 Stirling Highway, Crawley, WA 6009, Australia; [2]Kazusa DNA Research

Institute, Kazusa Kamatri 2-6-7, Kisarazu, Chiba, Japan; [3]Murdoch University, 90 South Street, Murdoch, WA 6150, Australia; [4]Department of Agriculture and Food Western Australia, 3 Baron-Hay Court, South Perth, WA 6151, Australia. *(Parwinder.kaur@uwa.edu.au)

Subterranean clover (*Trifolium subterraneum L.)* is the key forage pasture legume species in Australia for ruminant production and is also an ideal reference species for comparative mapping within the Leguminosae. It is a diploid (2n =16), predominantly inbreeding annual species that can be readily hybridised. It also has a wide range of diversity for both qualitative and quantitative agronomic and morphological characters. The diploid level of the subterranean clover genome makes it much simpler to study than the tetraploid genomes of red and white clover. Here we present a ~480-Mb draft whole genome sequence of subterranean clover cultivar Daliak, which represents 86% of the estimated 556.6 Mb subterranean clover genome. We used an Illumina next-generation sequencing platform to generate 277.1 Gb (HiSeq) + 23.6 Gb (MiSeq) of genome sequence, which along with sequences derived from a Roche 454 machine (2.72 Gb) enabled us to assemble a total of 53,781 scaffolds (N50 size of 0.216 Mb; the largest scaffold was 2.2 million base pairs). This reference genome sequence will serve as a genomic resource of subterranean clover and facilitate identification of the genetic basis of agronomically important traits, which are vital for the future genetic improvement of pasture legumes.

37	Genomics and Genetics	Kaur, S	Legume genomics – perspectives, progress and challenges

Legume genomics – perspectives, progress and challenges

Kaur, S.[1*], Hobson, K.[2], Leonforte, A.[1], Materne, M.[1], Paull, J.[3], Slater, T.[1], Forster, J.[1], and Cogan, N.[1]. [1]Department of Environment and Primary Industries, Victoria, Australia; [2]NSW Department of Primary Industries, NSW, Australia; [3]School of Agriculture, Food and Wine, The University of Adelaide, South Australia, Australia.
*(sukhjiwan.kaur@depi.vic.gov.au)

Legume crops have long been considered to be under-resourced species from a genomics perspective. In the last decade, advancements in genomic technology development have changed the whole dynamics of molecular biology research. Significant genomic resources have been delivered even for the less well-studied crops such as cool-season food legumes (lentil, chickpea field pea and faba bean) in order to facilitate the application of markers into breeding programs. Highly-saturated genetic linkage maps have been generated based on SSRs and SNPs and used for the identification of genomic regions involved in key traits for grain legume breeding. A range of key agronomic traits have been quantified in appropriate germplasm, and markers in close linkage to trait-specific genes are now available for breeding programs. However, application and implementation of the latest technologies will still require more time and effort in order to deliver the improved cultivars to growers. Recent genome sequencing efforts will assist in the assessment of genetic diversity as well as candidate gene identification for diagnostic marker delivery through re-sequencing and skim-sequencing approaches.

These approaches will ultimately enable molecular biologists and breeders to target genes underlying key agronomic traits with greater precision and accuracy. Analysis of germplasm collections with new-generation genomic tools will accelerate trait discovery through genomic wide approaches such as association mapping. Ultimately, the availability of cost- and time-efficient sequencing and genotyping technologies in combination with automated phenotyping methods, will increase the utilisation of genomic tools into breeding programs.

38	Genomics and Genetics	Khadke, S.G.	Development of Superior Mutants in Moth Bean (Vigna aconitifolia (Jacq.) Marechal) Through Induced Mutation Breeding

Development of Superior Mutants in Moth Bean (Vigna aconitifolia (Jacq.) Marechal) Through Induced Mutation Breeding

Khadke, S.G.[1*]. [1]Department of Botany, Smt. Kasturbai Walchand College, Sangli-416416. M.S. India. *(shivramkhadke@gmail.com)

A large number of legume species hitherto unexploited possess great potential for contributing to not only protein rich food for humans, but also excellent quality forage for animals. Among such novel legumes the moth bean (*Vigna aconitifolia* (Jacq.) Marechal) is quite notable. Seeds of local variety of moth bean were treated with aqueous solution of chemical mutagens EMS and SA with three concentrations each. The morphological mutants were scored in M2 and M3 generations. The mutants were screened under local conditions for yield performance, besides maturity features. A wide spectrum of viable mutants with varying morphological traits could be observed in M2 generation of moth bean. The various types of viable mutants like the Branched, Tall, Dwarf with erect habit, Early maturing, High yielding, Late maturing, Short pod and bold seeded and Large leaf were obtained in the moth bean.

In the present study it was observed that mutants like branched, high yielding and late maturing consistently maintained superiority in yield and number of pods per plants over control, early maturing mutants exhibits earliness in maturity while the short pod/bold seeded mutant showed higher weight of 100 seeds than the control. The results obtained in the present study was decisively demonstrated the usefulness and the effective potential of the induced mutational approaches in genetic improvement of moth bean for recovering superior mutant plant types having high seed yield, early maturity besides low trypsin inhibitor content.

39	Genomics and Genetics	Khazaei, H.	The Faba bean Genome Sequencing Consortium

The Faba bean Genome Sequencing Consortium

Stoddard, F.L.[1], Khazaei, H.[1*], and Schulman, A.H.[2]. [1]Department of Agricultural Sciences, P O Box 27 (Latokartanonkaari 5), FIN-00014, University of Helsinki, Finland; [2]Institute of Biotechnology, FIN-00014, University of Helsinki, Finland. *(hamid.khazaei@helsinki.fi)

Faba bean (*Vicia faba*) is one of the oldest domesticated crops, native to West Asia. It is an excellent protein source, a staple food in many developing countries including North Africa and Ethiopia, and important for animal feed. It has one of the largest (13 Gbp) diploid genomes among cultivated crops and is an "orphan" due to the limited availability of genomic and genetic information. The African Orphan Crops Consortium (AOCC) has given priority to sequencing this species in 2014-2015 and we are coordinating this initiative. The AOCC has obtained in-kind contributions for this task from industrial partners in the sequencing sector.A reference inbred line will be chosen by the members of the consortium and sequenced at the Beijing Genomics Institute. This line should have agronomic value and at least one disease resistance. Resequencing a set of ~100 accessions will provide information on genetic diversity, shed light on the effects of both natural selection and breeding, and help define targets for future breeding efforts. Effective assembly and characterization of the genome will require a high-density genetic map and “genomic genetic” approaches such as Population Sequencing and Genotyping by Sequencing, and optical mapping to correctly integrate and order the sequenced contigs and their scaffolds of the gene space. The consortium currently comprises 45 scientists from 33 institutions. We hope to provide an umbrella for coordinating the many specific tasks and approaches needed for such a large genome and for bringing benefits for the widest possible community.

40	Genomics and Genetics	Kim, M.Y.	Genome-wide analysis of UV-B induced mutations in soybean (Glycine max (L.) Merr.)

Genome-wide analysis of UV-B induced mutations in soybean (*Glycine max* (L.) Merr.)

Kim, M.Y.[1,2*], Shim, S.R.[1], Yoon, M.Y.[1], Kim, K.D.[1], Jang, H.J.[1], and Lee, S.H.[1,2]. [1]Department of Plant Science and Research Institute of Agriculture and life Sciences, Seoul National University; [2]Plant Genomic and Breeding Research Institute, Seoul National University. *(moonykim@snu.ac.kr)

After treated with or without UV-B, genomics DNAs from these two genotypes, Buseok and Cheonja 3 were isolated. Mapping of 93% short reads in both of buseok with or without UV-B treatment resulted in over 87% of genome coverage with average of 5-fold depth. Non-irradiated Cheonja 3 was also sequenced at similar genome coverage as Buseok but genome sequence mapping coverage of UVB-irradiated Cheonja 3 was mere 72%. This result indicates that 11.2% unmapped reads of irradiated Cheonja 3 have much more DNA variations than allowable mismatches for alignment to reference genome. DNA variation calling of single nucleotide polymorphisms (SNPs) and insertion/deletion (indels) was conducted between UV-B non-irradiated and irradiated genomes of Buseok and Cheonja 3. Under overlapped 74.6 Mb sequence positions among these four genomes, a total of 13,992 and 17,078 SNPs generated by UV-B irradiation were identified in Buseok and Cheonja 3, respectively. The chromosomal distribution of these SNPs suggests that several hotspots for UV-B DNA mutagenesis may exist in soybean genome. Transition of G→A + C→T and T→C + A→G was found to be about twice more abundant than other single nucleotide mutations. The irradiated genomes of Buseok and Cheongja 3 had 392 and 347 mRNA affected by 235 and 238 non-synonymous SNPs, respectively. Additionally, five and seven SNPs that might lead to premature termination were induced by UV-B in Buseok and Cheongja 3, respectively. Gene ontology analysis revealed that non-synonymous SNPs of irradiated Cheonja 3 were distributed among 28 diverse GO terms.

41	Genomics and Genetics	Kisha, T.J.	Genetic Diversity of the Phaseolus acutifolius A. Gray Collection of the USDA National Plant Germplasm System Using Targeted Region Amplified Polymorphism (TRAP) Markers Designed form Genes Associated with Heat and Drought Stress

Genetic Diversity of the *Phaseolus acutifolius* A. Gray Collection of the USDA National Plant Germplasm System Using Targeted Region Amplified Polymorphism (TRAP) Markers Designed form Genes Associated with Heat and Drought Stress

Kisha, T.J.[1*], and Bhardwaj, H.L.[2]. [1]USDA-ARS, Western Regional Plant Introduction Station; [2]Virginia State University. *(theodore.kisha@ars.usda.gov)

Molecular genetic relationships among 222 accessions of the *Phaseolus acutifolius* A. Gray collection were assessed using Targeted Region Amplified Polymorphic (TRAP) markers designed from sequences of genes associated with heat and drought tolerance. Genetic relationships were compared to reactions to drought stress using measurements of variable fluorescence to maximum fluorescence (Fv/Fm). Cluster analysis using NTSys-pc and STRUCTURE found 3 major groups and 8 sub-groups with an average Fst of 0.71, but there was no association of drought tolerance with any group. In fact, some plants separated by seed color within an accession tested as both drought tolerant and susceptible, though genetically similar at all marker loci tested. In other cases, plants separated by seed type clustered apart in different groups. Given the level of diversity among groups, marker production will continue along with the addition of AFLP loci for future association mapping.

42	Genomics and Genetics	LAVAUD, L.C.	Constructing near-isogenic lines by Marker-Assisted-Selection to validate QTL for resistance to Aphanomyces euteiches in pea

Constructing near-isogenic lines by Marker-Assisted-Selection to validate QTL for resistance to

Aphanomyces euteiches in pea

LAVAUD, L.C.[1*], LESNE, L.A.[2], MOUSSART, M.A.[3], BOUTET, B.G.[4], BARANGER, B.A.[5], DELOURME, D.R.[6], and PILET, P.M.L.[7]. [1]clement.lavaud@rennes.inra.fr; [2]angelique.lesne@rennes.inra.fr; [3]Anne.Moussard@rennes.inra.fr; [4]gboutet@rennes.inra.fr; [5]alain.baranger@rennes.inra.fr; [6]regine.delourme@rennes.inra.fr; [7]Marie-Laure.Pilet@rennes.inra.fr. *(clement.lavaud@rennes.inra.fr)

Common root rot of pea, due to *Aphanomyces euteiches,* is one of the most damaging diseases in many countries. The development of resistant varieties is a major objective to manage the disease. Seven main consistent quantitative trait loci (QTL) controlling partial resistance were recently discovered in different genetic pools (Hamon *et al*., 2013). Our aim was to validate the resistance QTL effects in different genetic backgrounds, by creating and evaluating near-isogenic lines (NILs) carrying resistance alleles at individual or combined QTL. Five back-cross assisted selection programs were developed, each consisting in transferring resistance alleles at one to three of the seven main QTL into susceptible pea cultivars. The resulting NILs were phenotyped for resistance to *A. euteiches* in controlled conditions at young plant stage. A total of 157 selfed BC5 or BC6 NILs, carrying no, one, two or three resistance introgressions were obtained in a reference line (Puget, DSP or Baccara), a spring variety (Eden) and a winter variety (Isard). The NILs carrying resistance alleles at QTL *Ae-Ps7.6*, individually or in combination with resistance alleles at other QTL, showed significant reduced disease severity compared to NILs carrying no resistance alleles, especially in the winter variety Isard. QTL effects on resistance in NILs are under validation in field infested nurseries and analyzed regarding fine NIL genomic characterization using high density SNPs. The NILs will be valuable for further identification of genes underlying QTL and of best allele combinations to increase partial resistance.

43	Genomics and Genetics	Lightfoot, D.A.	Two decades of QTL analysis among Forrest, Essex, Hartwig and Flyer RILs and NILs

Two decades of QTL analysis among Forrest, Essex, Hartwig and Flyer RILs and NILs

Lightfoot, D.A.[1*]. [1]SIUC. *(ga4082@siu.edu)

Novel tools underlying the plant response to FRR have been developed for soybean over the past 2 decades. About 18 resistance loci have been identified. To be selected 8-10 loci per cross must be stacked and this is a hard task for plant breeders. The reason for the large number of loci is that the resistance mechanisms that have evolved in plants provide only partial protection. This may be because the plants have to contend with a group of fungi with a wide host range and flexible hemibiotrophic lifestyle. Consequently, full resistances are rare, or absent, among legumes, brassicas, cucurbits and solanaceous plants. SDS is a combination of two disease effects caused by translocated toxins, rotted roots and toxin restricted roots. The leaf effects of toxins have several causal agents with different target proteins. Effects on the roots include variations in infection severity and infection frequency. Breeding for FRR resistance has begun with some exciting new tools for pathogen quantification in roots. GmRLK18-1 (gene model Glyma_18_02680 at 1,071 kbp on chromosome 18 of the genome sequence) has been proven by transgenesis to be an SDS resistance gene. Consequently there is a new time of opportunity for new breeding initiatives targeting SDS.

44	Genomics and Genetics	Lightfoot, D.A.	Why is resistance to soybean cyst nematode so complicated compared to sudden death syndrome?

Why is resistance to soybean cyst nematode so complicated compared to sudden death syndrome?

Lightfoot, D.A.[1*], and Hemmati, N.M.[2]. [1]SIUC; [2]Monsanto. *(ga4082@siu.edu)

Soybean *Glycine max (L.) Merr.* suffers yield losses due to root infestation by *Heterodera glycine I.* (soybean cyst nematode SCN) and *Fusarium virguliforme* (Snyder, Haas, Aoki; sudden death syndrome (SDS)). The major

resistance locus to both was *Rhg1/Rfs2* (chr18; LgG). Analysis of Sanger DNA sequence of BAC-B73P06 (82,157 bp) encompassing *Rfs2/Rhg1* identified 800 SNPs and 57 indels between resistant 'Forrest' and susceptible 'Williams82' and 'Asgrow3244'). The latter shared 12 SNPs and no indels. Polymorphisms were clustered within 59 kbp. There were 5 predicted recombination breakpoints. The third and fourth breakpoints were located before gene 3 and after gene 5 (Glyma18g02680; the RLK at *Rhg1/Rfs2*) which is therefore inferred to be Peking derived DNA within *Rhg1/Rfs2* region. Comparisons of single nucleotide polymorphisms (SNPs) identified in Illumina sequences from 31 semi-domesticated genomes showed 80% of the total SNPs in Forrest were found among the 31 genomes! Annotation and gene prediction showed the BAC gene prediction encoded 9-10 genes . There were 31 SNPs within exons and 137 among introns. Just 11 SNPs caused amino acid changes. There were 5 SNPs in CREs and 14 in promoters. Other researchers suggested a copy number varaition in the 3-5 genes just 5 genes distal to this BAC alters resistance to race 6 of SCN. We have good evidence the SNAP gene and amino acid transporter are involved in resistance. Polymorphisms indicated the regions that were introgressed from Peking had defined limits. Genes at the locus are highly conserved and subject to purifying selection.

45	Genomics and Genetics	Madrid, E	Large-scale transcriptome analysis in faba bean (Vicia faba L.)

Large-scale transcriptome analysis in faba bean (Vicia faba L.)

Ocaña, S.[1], Seoane, P.[2], Bautista, R.[2], Torres, A.M.[3], Claros, M.G.[2], and Madrid, E.[4*]. [1]Área de Mejora y Biotecnología, IFAPA Centro Alameda del Obispo, Apdo 3092, 14080 Córdoba, Spain; [2]Departamento de Biología Molecular y Bioquímica, y Plataforma Andaluza de Bioinformática. Universidad de Málaga, 29071 Málaga, Spain; [3]Área de Mejora y Biotecnología, IFAPA Centro "Alameda del Obispo", Apdo 3092, 14080 Córdoba, Spain; [4]Institute for Sustainable Agriculture, CSIC, Apdo 4084, E-14080 Córdoba, Spain. *(b62mahee@uco.es)

Although faba bean is one of the biggest traded pulse crops, genomic resources are still limited. A comprehensive characterization of the faba bean transcriptome was performed using the Illumina platform. Two faba bean genotypes (Vf29H and Vf136) with differential reaction to *Ascochyta fabae* and 106.397 ESTs found in different public databases were used for *de novo* transcriptome assembly using a work flow with OASES, and CAP3. The resulting unigenes were annotated with Full-LengtherNext. The preliminary analysis of the 120.922 unigenes collection revealed that 20,804 out of the 39,269 were non-redundant transcripts based on orthologue ID. 2,752putative ncRNAs were found. Futhermore, 7,165 unigenes lacking homology could be considered as putative legume-specific genes. Single nucleotide polymorphisms identified through data mining provide a database for genotyping and integration of translational genomics in breeding programmes. In addition, the faba bean and chickpea transcriptome alignment revealed that 81.27% of the faba bean transcripts where present in the chickpea transcriptome despite of using a single faba bean source of tissue.

As the genotypes sequenced show differential reaction to *A. fabae* and the cDNA libraries were constructed using inoculated and non-inoculated leaves, genes with differential expression in both genotypes were characterized. Thus, 348 and 327 transcripts where found to be unique in resistant and susceptible genotypes, respectively. On the other hand, 212 and 282 transcripts were found to be overexpressed in both lines. These transcripts might represent candidate genes associated with the *A. fabae* resistance.

46	Genomics and Genetics	Madrid, E	Candidate gene expression analysis of the genes located in the QTLAR3 in chickpea related with Ascochyta blight resistance

Candidate gene expression analysis of the genes located in the QTLAR3 in chickpea related with Ascochyta blight resistance

Madrid, E.[1*], Gil, J.[2], Barro, F.[1], Millan, T.[2], and Rubio, J.[3]. [1]Institute for Sustainable Agriculture, CSIC, Apdo 4084, E-14080 Córdoba, Spain; [2]Departamento de Genética, Universidad de Córdoba, Campus Rabanales, Edif. C5, 14071 Córdoba, Spain; [3]Área de Mejora y Biotecnología, IFAPA Centro "Alameda del Obispo", Apdo 3092, 14080 Córdoba, Spain. *(b62mahee@uco.es)

Recently, the location of the QTLAR3, related with resistance to pathotype I of *Ascochyta rabiei* in chickpea, has been redefined using an interespecific recombinant inbred line population (ILC72xCr5-10). The location of the QTLAR3 peak was linked to an ethylene insensitive 3-like gene (*Ein3*), explaining 44.3% of the total phenotypic variation for resistance to blight. This genomic region was predicted to be at the Ca2 physical position 32-33 Mb, comprising 42 genes. Candidate genes located in this region include *Ein3*, *Avr9/Cf9* and *Argonaute 4*, directly involved in disease resistance mechanisms (Madrid et al. 2014).

Two parental lines (ILC72 and Cr5-10) were incoculated with PathI and total RNA was extracted in both inoculated and non-inoculated leaves. In an attempt to elucidate the implication of these three genes in blight resistance, the temporal expression patterns at 12, 24 and 48 hour after inoculation (h.a.i.) were investigated doing qPCR. Preliminary analysis revealed transcriptional changes in response to Ascochyta blight for the three genes. Differential transcript accumulation was observed for all the genes in respect with the susceptible genotype. An induction of the expression was observed in ILC72 for both *Ein3* and *Argonaute 4* at 24 h.a.i whereas the susceptible genotype (Cr5-10) did not show differential expression at the different timepoints analyzed. *Avr9/Cf9* showed activation at 12 h.a.i. reaching basal levels at 24 h.a.i. in the resistant genotype.

47	Genomics and Genetics	Marsolais, F.	Genomic analysis of polymorphisms conferrring storage protein deficiency in common bean

Genomic analysis of polymorphisms conferrring storage protein deficiency in common bean

Pandurangan, S.[1,2], Crosby, W.[3], Pauls, K.P.[4], and Marsolais, F.[1,2*]. [1]Department of Biology, University of Western Ontario, London, Ontario, Canada; [2]Genomics and Biotechnology, Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, London, Ontario, Canada; [3]Department of Biological Sciences, University of Windsor, Windsor, Ontario, Canada; [4]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada. *(Frederic.Marsolais@agr.gc.ca)

A series of genetically related lines of common bean (*Phaseolus vulgaris*) integrate a progressive deficiency in major storage proteins, the 7S globulin phaseolin and lectins. To understand the genomic basis for variations in protein profiles previously determined by proteomics, the four genotypes were submitted to short-fragment genome sequencing using an Illumina HiSeq 2000 platform. Reads were aligned to reference sequences from G19833, BAT-93 and OAC-Rex, and a genomic clone of the lectin locus from an arcelin-5 genotype. The results of the analyses identified polymorphisms responsible for the lack of specific storage proteins, as well as those associated with large differences in storage protein expression.

48	Genomics and Genetics	Mishra, N.	Exploiting potential of wild Cicer species for improving chickpea

Exploiting potential of wild Cicer species for improving chickpea

Mishra, N.[1*], Chaturvedi, S.K.[1], Soren, K.R.[1], and Sarker, A.[2]. [1]Indian Institute of Pulses Research, Kanpur 208024 India; [2]International Center for Agricultural Research in Dry Areas, SERC Office, New Delhi 110012, India. *(nlmishra9@gmail.com)

Chickpea (*Cicer arietinum* L.) is one of the most important pulse crops of India covering 9.19 m ha area producing 8.80 m t of the grain. In view of the narrow genetic base of existing chickpea varieties, pre-breeding efforts involving diverse genotypes and closely related species initiated to broaden the genetic base and development of high yielding and efficient plant types through ICARDA collaborations. In present research, two *Cicer* species (C. reticulatum acc. ILWC 21, C. echinospermum acc. ILWC 179 and ILWC 245) were crossed to develop 5 Interspecific crosses (Shubhra x ILWC 21, GNG 469 x ILWC 21, IPC 2008-57 x ILWC 21, IPC 2006-88 x ILWC 179, IPCK 2002-29 x ILWC 245) with a view to broaden the genetic base cultivars. All F1s plants were normal and fertile. The hybridity of F1s was confirmed using SSR markers for crosses involving *C. echinospermum*. Large amount of significant variability for yield attributes viz., primary branches, secondary branches and pods per plant was observed in all 5 F2 populations. However, in F2 crosses involving *C. echinospermum*, 23% single plants showed partial sterility and plants had only 3-5 pods with shriveled seeds. All single plant were grown as progenies in F3 generation and again 15-18% plants in 23 progenies showed partial sterility. Further, on the basis of phenotype large number of single plant selections were made from fertile progenies. 29 selected plants have 112-189 pods per plant and 1.66 seeds per pod. The improvement in yield attributes clearly indicate the potential of wild *Cicer* species for chickpea improvement.

49	Genomics and Genetics	Omar Idrissi, O.I	Assessment of genetic variation of lentil (Lens culinaris Medik) landraces from Morocco

Assessment of genetic variation of lentil (*Lens culinaris* Medik) landraces from Morocco

Omar Idrissi, O.I.[1,2*], Chafika Houasli, .[2], Ellen De Keyser, .[3], Patrick Van Damme, .[1,4], and Jan De Riek, .[3].
[1]Department of Plant Production, Ghent University, Coupure links 653, 9000, Ghent, Belgium; [2]Institut National de la Recherche Agronomique du Maroc (INRA) Centre Régional de Settat, B.P 589 Settat, Morocco; [3]Institute for Agricultural and Fisheries Research (ILVO)-Plant Sciences Unit, Applied genetics and breeding, Caritasstraat 21, 9090, Melle, Belgium; [4]Faculty of Tropical AgriSciences, Czech University of Life Sciences Prague, Prague, Czech Republic. *(o.idrissi@yahoo.fr)

In order to give useful information for more targeted conservation and valorization as well as more efficient use in breeding programs, and in the absence of any previous molecular characterization, we assessed the genetic diversity and population structure of 53 lentil (Lens culinaris Medik) landraces from different Moroccan origins using Short Sequence Repeat (SSR) and Amplified Fragment Length Polymorphism (AFLP) molecular markers. Moderate to high genetic diversity was observed within and between accessions. The statistical analyses performed highlighted different groups with contrasting sizes: a main group containing the largest number of landraces and a few groups with low numbers of landraces. Interestingly, one of the smallest groups only contained landraces from the dry Abda region. While the other small group contained one landrace collected from a small area in Zear region. The latter lentil is known for its excellent seed quality and was previously proposed to obtain the Protected Designation of Origin (PDO) quality mark. Both SSR and AFLP markers allowed to set apart the latter landrace supporting the possibility of attributing a PDO for the benefit of local farmers. The landraces group from the dryland region may share closely related genetic material selected over years for drought and heat stress tolerance that could be used in breeding programs. Two other landraces from the medium Atlas Mountains may have been selected for cold tolerance. Specific adaptation of these landraces to their respective agro-environments and possible evolution into distinct ecotypes may be the reasons of their genetic differentiation compared to other landraces.

50	Genomics and Genetics	O'Rourke, J.A.	Gene Expression Patterns in Soybean Fast Neutron Mutants

Gene Expression Patterns in Soybean Fast Neutron Mutants

O'Rourke, J.A.[1*], Young, N.[2], Bucciarelli, B.[2,3], Roessler, J.[2], Stupar, R.M.[2], and Vance, C.P.[2,3]. [1]Corn Insect Crops Genomics Research Unit, USDA-ARS, Ames, Iowa; [2]Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN; [3]Plant Science Research Unit, USDA-ARS, St. Paul, MN. *(jorourke@iastate.edu)

The soybean (*Glycine max* L. merr) fast neutron mutant population has proven a valuable resource for investigating genomic variation potentially impacting yield and composition. While large-scale structural variations have been well characterized in the population, the impact of these mutations on gene expression has not yet been examined. In this study we use RNA-seq analysis to identify genes exhibiting altered expression patterns in leaves, roots, and seeds of three soybean fast neutron mutant plants as compared to the wild type (WT). These analyses reveal small, well-defined, genomic deletions impact gene expression throughout the genome often resulting in 'hot-spots' of differentially expressed genes unique to individual mutants. Additionally, while phenotypic examination of two mutants identified changes in single traits (trichomes or seed oil composition), our RNA-seq analyses reveals gene expression is altered between mutants and WT plants in all tissues examined. These analyses provide a foundation to investigate the genetics underlying the biologically important processes of trichome development and function, the partitioning of resources for protein and oil biosynthesis, and plant architecture in soybean.

51	Genomics and Genetics	Pérez de la Vega, M.	A genetic map of lentil based on retrotransposon derived genetic markers.

A genetic map of lentil based on retrotransposon derived genetic markers.

Rey, R.[1], García, P.[1], Sáenz de Miera, L.E.[1], and Pérez de la Vega, M.[1*]. [1]Area de Genética, Universidad de León, 24071 León, Spain. *(m.perez.delavega@unileon.es)

Retrotransposons are genetic elements ubiquitous components in the genome of many eukaryotes and particularly abundant in plants. They consist of two subtypes, the long terminal repeat (LTR) and non-LTR retrotransposons. Their copy numbers and genomic locations are plastic, varying in abundance and chromosomal location. The majority of plant LTR retrotransposons belong to either *Copia* or *Gypsy* superfamily.

Several kinds of genetic markers have been developed from retrotransposon sequences. The most frequent ones are derived from LTR sequences, e.g., Sequence Specific Amplification Polymorphism (SSAP) or Retrotransposon Microsatellite Amplified Polymorphism (REMAP), or from the Primer Binding Site (PBS), e.g., iPBS, sequences between close and inverted elements.

Using primers complementary to the PBS, several lentil retrotransposon LTRs were sequenced. From four LTR (2 *Copia*, 1 *Gypsy*, 1 TRIM), a set of non-degenerate primers were designed to obtain SSAP and REMAP markers in lentil. Likewise PBS primers have been used to obtain iPBS markers.

A set of these markers, 175 iPBS, 8 REMAP and 19 SSAP were mapped in 94 lines of a F7 RIL obtained from the cross between *Lens culinaris* ssp. *culinaris* cv. Lupa and the wild ancestor *L. c.* ssp. *orientalis.* The genetic map included other 104 markers (morphological, ISSRs, SSRs, etc.) previously mapped in this segregant population. The whole set of markers generated a map with 14 linkage groups, although uneven in the number of markers included in each of them. The whole map covered 2304 cM. Retrotransposon derived markers (mainly SSAPs) are grouped in several discrete clusters in the map.

52	Genomics and Genetics	Pérez de la Vega, M.	An annotated collection of EST sequences from lentil (Lens culinaris Medik.)

An annotated collection of EST sequences from lentil (*Lens culinaris* Medik.)

García, P.[1], González, A.I.[1], Hoffmeier, K.[2], Krezdorn, N.[2], Polanco, C.[1], Sáenz de Miera, L.E.[1], Vaquero, F.[1], Vences, F.J.[1], Winter, P.[2], and Pérez de la Vega, M.[1*]. [1]Area de Genética, Universidad de León, 24071 León, Spain; [2]GenXPro, Altenhöferallee 3, 60438 Frankfurt am Main, Germany. *(m.perez.delavega@unileon.es)

A collection of approx. 180,000 EST sequences was obtained1 within the LEGRESIST project from lentil polyA RNA by high throughput 454 sequencing. Assembled contigs ranged from approximately 100 bp to more than 2000 bp and included part or all the ORF and the 3'-UTR. Sequences longer than 900 bp were selected to identify putative gene orthologs by BLAST searchs against EST and genomic sequences in databases. The lentil sequences were aligned with available genomic sequences from *M. truncatula, C. arietinum*, *G. max* and EST and TSA sequences from lentil. Generally, each different lentil sequence matched a single ortholog in the diploids *M. truncatula* and *C. arietinum*. To date, 1,000 of these lentil sequences have been identified in relation to sequences from other legume species. In particular sequences related to biotic and abiotic stresses (e.g., PR, dehydins, etc.), development and flowering (e.g., TFL, CONSTANS, FRIGIDA, etc.), transcription factors and kinases were searched. This information can help in lentil breeding by identifying allelic variants. Notably, almost 10% of the sequences are of unknown or uncertain function.

The level of polymorphism in ORFs and the 3'-UTR is low. Currently we are therefore searching for polymorphisms in introns by designing primers in exons from our data base to increase the number of available polymorphism for genetic mapping and breeding. The genic lentil sequences are mapped against the *M. truncatula* genomic sequence to exploit the synteny between these species.

53	Genomics and Genetics	Porch, T.G.	Association mapping analysis of the response to Macrophomina phaseolina in the Andean Diversity Panel

Association mapping analysis of the response to Macrophomina phaseolina in the Andean Diversity Panel

Porch, T.G.[1*], Cichy, K.A.[1], Alameda, M.[2], and Beaver, J.S.[2]. [1]USDA-ARS; [2]University of Puerto Rico. *(timothy.porch@ars.usda.gov)

The Andean Diversity Panel was evaluated for response to inoculation with charcoal rot in a field trial in Isabela, Puerto Rico in 2012. The trial was inoculated with backpack sprayers at flowering and a visual evaluation was conducted three weeks later. There was a broad range of response, with about 20 genotypes out of 392 showing resistant reactions. Association mapping analysis indicated a genomic region on Pv09 associated with resistance.

54	Genomics and Genetics	Rajandran, V	Genetic control of early flowering in lentils

Genetic control of early flowering in lentils

Rajandran, V.[1*], Freeman, J.[1], Hecht, V.[1], and Weller, JL.[1]. [1]School of Biological Sciences, University of Tasmania, Australia. *(vinodanr@utas.edu.au)

Lentils (*Lens culinaris*) are an important legume crop that is cultivated across a broad climatic range. The timing of the transition to the reproductive phase is an important factor in the adaptation of lentils to different growing environments, with the species demonstrating considerable variation in flowering time and responsiveness to photoperiod and temperature. Early flowering is a key agronomic trait for adaptation to short season environments and genetic characterization of early-flowering variants is therefore of interest. However, the genetic control of flowering time in lentils is poorly understood. Although several QTLs for flowering time have been reported, only one major locus, *Sn*, is known.

We previously used a candidate gene approach to show that the lentil *Sn* locus is an ortholog of the circadian clock

gene *Hr* in pea and ELF3 in Arabidopsis. More recently, we performed genetic analysis of flowering under short-day conditions in a second cross between the photoperiod-sensitive cv. Northfield (ILL5588) and an early-flowering Indian landrace ILL2601). This analysis has distinguished two new flowering time QTLs located on lentil linkage group 6.

While the molecular basis for these QTLs is not yet known, comparative mapping with Medicago has enabled the identification of potential candidate genes in both regions. Recent progress on the characterisation of these QTLs and evaluation of candidates will be presented.

55	Genomics and Genetics	Ramsay, L.D.	Progress on the Lentil Draft Genome Assembly

Progress on the Lentil Draft Genome Assembly

Ramsay, L.D.[1*], Sharpe, A.G.[2], Cook, D.R.[3], Penmetsa, R.V.[3], Gujaria-Verma, N.[1], Wong, M.[1], Vandenberg, A.[1], and Bett, K.[1]. [1]University of Saskatchewan, Saskatoon, SK, Canada; [2]National Research Council, Saskatoon, SK, Canada; [3]University of California at Davis, Davis, CA. *(l.ramsay@usask.ca)

Lentil has minimal genomic resources available despite its growing production as a global food crop. Construction of a reference sequence provides a solid basis for further crop improvement through genomics assisted breeding and resequencing of close relatives. A lentil variety from the University of Saskatchewan's Crop Development Center, CDC Redberry, was chosen as a reference for sequencing. 125x shotgun sequencing will be performed using Illumina paired-end sequencing of varying fragment lengths, and mate-pair data from both Illumina and 454 technologies with a range of libraries from 2.7 to 40Kb will be produced. An initial draft of 23x paired-end coverage produced 2.7Gb of scaffolds out of an estimated 4Gb genome with an N50 of 44Kb. Genotyping by sequencing (GBS) was performed on a small panel of cultivars, allowing identification of the L. culinaris RIL populations with the highest degree of genetic diversity. Three of these populations will be chosen for GBS sequencing and further anchoring of scaffolds. The final assembly will be annotated with both RNAseq and computational gene prediction software (MAKER), and selected cultivars of interest will be sequenced at ~30x coverage, with an additional survey of lentil genetic variability done by low-coverage skim sequencing.

56	Genomics and Genetics	RANA, J.C.	Developing trait specific sets of germplasm in selected grain legumes in India

Developing trait specific sets of germplasm in selected grain legumes in India

RANA, J.C.[1*], Sharma, T.R.[2], and Singh, N.[3]. [1]National Bureau of Plant Genetic Resources Regional Station, Phagli, Shimla – 171 004 (HP), India; [2]Plant Biotechnology, CSK Himachal Pradesh Agricultural University, Palampur- 176 061 (HP), India; [3]Department of Food Science and Technology, GNDU, Amritsar-143 005, India. *(ranajc2003@yahoo.com)

The linkage drag caused by positive correlations between desirable and undesirable traits limit the random use of germplasm in plant breeding. Thus, development and identification of traits specific sets of germplasm is a most sought activity in the seed banks to enhance the use of germplasm in conventional and molecular breeding. The Regional Station of National Bureau of Plant Genetic Resources at Shimla has evaluated germplasm of kidney bean (4274 accessions), pea (701), rice bean (458), adzuki bean (116), horse gram (118) and cowpea (228) for agronomic, disease and quality traits. Trait specific sets of germplasm have been developed for plant type, crop maturity, pod and seed size, agronomic superiority in all the crops; resistance to powdery mildew and ascochyta blight in pea, anthracnose and bean common mosaic virus in kidney bean; and content of amlyose, protein, fat, minerals, structural, thermal, rheology and cooking properties of seeds in kidney bean, pea, rice bean and adzuki bean. Specific sets of accessions with multiple trait superiority have also been developed in kidney bean and pea. Germplasm have been

screened in the disease hot-spots and resistance accessions were further confirmed in the laboratory under artificial inoculation for developing sets for resistance to diseases. This paper discuss the nature and magnitude of genetic diversity indentified through multivariate and genetic divergence analysis using phenotypic and molecular data, characteristic features and values of traits specific sets of germplasm. We assume that these sets of germplasm for different traits have great significance to legume breeders.

57	Genomics and Genetics	Roorkiwal, M.	Prediction of breeding values using genome wide markers for yield related traits in chickpea

Prediction of breeding values using genome wide markers for yield related traits in chickpea

Roorkiwal, M.[1*], Rathore, A.[1], Das, R.R.[1], Singh, M.K.[1], Srinivasan, S.[1], Gaur, P.M.[1], Bharadwaj, C.[2], Tripathi, S.[2], Hickey, J.M.[3], Lorenz, A.[4], Jannink, J.L.[5], and Varshney, R.K.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Indian Agricultural Research Institute, Delhi, India; [3]The Roslin Institute, The University of Edinburgh, Midlothian, Scotland, UK; [4]University of Nebraska, Lincoln, USA; [5]Cornell University, Ithaca, USA. *(m.roorkiwal@cgiar.org)

Genomic selection (GS) is a modern breeding approach that predicts breeding value of lines and makes selection prior to phenotyping using genome-wide molecular marker profiling. GS can help to overcome the issues related to long selection cycles by accelerating breeding cycles so that the rate of annual genetic gain can be enhanced. In view of low productivity in chickpea, a collection of 320 elite breeding lines was selected as the “training population”. Training population was phenotyped for four yield and yield related traits at two locations for two seasons under rain-fed and irrigated conditions. Training population was also genotyped using KASPar assays (651) and DArT arrays (15,360). Genome-wide marker profiling data in combination with phenotypic data was used with six statistical methods to predict genomic estimated breeding values (GEBVs) for four yields and yield related traits. Correlation inside training (CIT) for the models tested varied from 0.138 to 0.912. Heat map analysis using genotyping data to understand the relationship within these lines suggested possibility of two different groups. As population structure can influence the accuracy in GS, analysis was re-performed by implementing population structure for calculation of GEBV. Population structure significantly affected the CIT that varied from 0.001 to 0.745 for desi group, and 0.004 to 0.727 for kabuli group. In general, Bayesian based model showed better prediction accuracy. The best prediction accuracy was obtained for 100 seed weight while prediction accuracy was low in case of seed yield.

58	Genomics and Genetics	Saha, Shyamali	Wild Relatives of Lentil: Removing Obstacles to Increased Genetic Gain

Wild Relatives of Lentil: Removing Obstacles to Increased Genetic Gain

Saha, SHYAMALI.[1,2*], Tullu, Abebe .[1,2], , Yuan, H.Y.[1,2], Lulsdorf, M.M.[1,2], Bett, Kirstin.[1,2], and Vandenberg, Albert.[1,2]. [1]Department of Plant Sciences, University of Saskatchewan; [2]Crop Development Centre. *(shyamali.saha@usask.ca)

Crop wild relatives are used in breeding to broaden the narrow genetic base of cultivated crops to expand the range of sources of resistance to biotic and abiotic stresses, to improve quality related traits and to increase yield. For the cultivated lentil (*Lens culinaris*) no crossing barriers are found between cultivated lentil and its closely related sub-species. Obtaining mature hybrid seed from crosses between the cultivated lentil and the secondary or tertiary gene pool species, *L. nigricans, L. ervoides, L. lamottei* or *L. odemensis,* is a biological challenge. A technique was developed for rescuing embryos of 14 day old immature interspecific hybrid seeds. Removal of the integument from developing seeds and culturing the interspecific zygotic embryos in media containing auxin 4-chloroindole-3 acetic acid (4-Cl-IAA) improved hybrid recovery. Embryo rescue success improved to 13- 56 % in interspecific cross combinations involving the different gene pool. Grafting of embryo-rescued lentil shoots onto faba bean root stock was

used to reduce generation time and to overcome limitations imposed by poor rooting of hybrid embryos from interspecific crosses with both primary and secondary gene pool lentil species. Cloned F1 plants were used to maximize F2 seed production to allow subsequent genetic studies of interspecific hybrids.

59	Genomics and Genetics	Sameer kumar, C.V.	A unique hybrid parental line identification system using obcordate leaf shape marker in Pigeonpea

A unique hybrid parental line identification system using obcordate leaf shape marker in Pigeonpea

Sameer kumar, C.V.[1*], Saxena, K.B.[1], Patil, S.B.[1], Vijaykumar, R.[1], Mula, M.G.[1], Saxena, R.K.[1], and Varshney, R.K.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, Hyderabad, India. *(c.sameerkumar@cgiar.org)

Pigeonpea has been ushered in to the group of cultivated crops where heterosis has been commercially exploited through hybrid development. The male sterile parental lines derived through CGMS technology transmuted the crop from often cross pollinated nature to completely cross pollinated. Maintenance of purity by following principles of seed production is a prerequisite in commercial hybrid seed production. To enhance efficacy of hybrid seed production and for easy identification of off types in the parental lines obcordate trait (single gene recessive) has been introgressed in male sterile line. The hybrids derived from crosses involving obcordate leaf A-lines and normal leaf fertility restorers (R-lines) were fully fertile and had normal lanceolate leaves; thus the difference between A-line and hybrids was clear. The use of obcordate leaf as a NEP (naked eye polymorphic) marker in pigeonpea would contribute to preserve parental line purity and confirm hybrid status. Heterotic hybrid combinations are developed by using the female parent with this NEP trait exhibited 30 to 40 per cent superiority in yield over high yielding ruling varieties. Among male sterile (A) lines, ICPA 2204 and ICPA 2203 were the best general combiners and among testers, ICPL 20116 and ICPL 20108 were the best general combiners. Obcordate female parent based hybrids ICPH 4563, ICPH 4567 and ICPH 4564, were the best with positive significant SCA effect and higher mean performance for grain yield, 100-seed mass, number of seeds/pod and resistance to wilt disease.

60	Genomics and Genetics	Sanderson, LA	KnowPulse: a breeder-focused web portal that integrates genetics and genomics of pulse crops with model genomes

KnowPulse: a breeder-focused web portal that integrates genetics and genomics of pulse crops with model genomes

Sanderson, LA.[1*], Vandenberg, A.[1], Tar'an, B.[1], Warkentin, T.[1], and Bett, KE.[1]. [1]Dept. of Plant Sciences, University of Saskatchewan, 51 Campus Dr. Saskatoon, SK, Canada. *(lacey.sanderson@usask.ca)

Integrating phenotypic and genotypic data is critical for the effective use of the vast quantities of genomic data being generated today. To this end, we have developed KnowPulse (http://knowpulse.usask.ca), a web-based resource for use by breeders and geneticists interested in pulse crops. Currently, sequence data resources including legume and model organism NCBI datasets and DFCI gene indices are available at KnowPulse with sequences having detailed page views and links to the original data source. Genotypic data for pea and lentil are now available through an interface that allows for side-by-side comparisons among individuals. Plans for the future include the development of tools to manage phenotypic data and integrate them with genotypic data for use in both the breeding and genetics programs. Also, Knowpulse plans to integrate with other legume databases such as Legume Information System (http://www.comparative-legumes.org) and Cool Season Food Legumes (http://www.coolseasonfoodlegume.org) allowing two-way sharing of data. We expect that these tools would allow breeders to associate marker genotypes with breeding materials, enhance crossing design and improve germplasm development strategies.

61	Genomics and	Santalla, M.	Characterization of QTLs for flowering date in a mapping

	Genetics		population of the legume species Phaseolus vulgaris

Characterization of QTLs for flowering date in a mapping population of the legume species *Phaseolus vulgaris*

Santalla, M.[1*], González, A.M.[1], Cruz, J.J.[1], Godoy, L.[1], Yuste, F.[2], and Lozano, R.[2]. [1]Grupo de Biología de Agrosistemas (BAS). Misión Biológica de Galicia-CSIC. P.O. Box 28. 36080 Pontevedra, Spain; [2]Departamento de Biología y Geología (Genética), Centro de Investigación en Biotecnología Agroalimentaria (BITAL). Universidad de Almería. 04120 Almería, Spain. *(msantalla@mbg.csic.es)

Adaptation to the environment and reproduction are dependent on the date of flowering in the season. Despite the genetic and complexity and quantitative nature of flowering time, many genes regulating this trait has been molecular isolated and functional characterized in the model species *Arabidopsis thaliana,* even some of their homologues have also been identified in other legume species. However, regulatory genes involved in the transition to flowering have not been characterized so far in common bean (*Phaseolus vulgaris* L.). With this aim, we have evaluated the effect of photoperiod on flowering date of the legume species, *Phaseolus vulgaris* and described the genetic architecture of this trait. For this purpose, a mapping population of 185 recombinant inbred lines (RILs) derived from a cross between a temperate and a tropical inbred line was generated and grown under short- and long-day photoperiod conditions. Multi-environment QTL analyses for flowering date and photoperiod sensitivity were conducted; as result additive and additive-by-environment effects were found. In addition, additive-by-additive epistatic effects were detected by means of two-locus QTL analyses. Overall, the results obtained revealed that the genetics of flowering date and photoperiod sensitivity is complex in nature, where both individual additive and epistatic effects are important components of the genetic variance. By using these QTLs in a marker assisted-selection program, it would be possible to select for desirable photoperiod sensitivity alleles leading to better adapted common bean varieties. This work was partially financed by the MINECO (AGL2011-25562), Junta de Andalucía (P10-AGR-06931) and Campus de Excelencia Internacional Agroalimentario-CeiA3. J.J. Cruz and L. Godoy were recipients of fellowships from CONACYT and INIFAP from México and SENESCYT from Ecuador Governments, respectively.

62	Genomics and Genetics	Saxena, R.K.	Fast forward genetic mapping provide candidate genes for resistance to fusarium wilt and sterility mosaic disease resistance in pigeonpea (Cajanus cajan L. Millsp.)

Fast forward genetic mapping provide candidate genes for resistance to fusarium wilt and sterility mosaic disease resistance in pigeonpea (Cajanus cajan L. Millsp.)

Singh, V.K.[1], Khan, A.W.[1], Takagi, H.[2], Saxena, R.K.[1*], Kumar, V.[1], Sharma, M.[1], SameerKumar, C.V.[1], Sinha, P.[1], Chitikineni, A.[1], Patil, S.[1], Ghanta, A.[3], Yamini, K.N.[3], Parupalli, S.[1], Muniswamy, S.[4], Dharmaraj, P.S.[4], Terauchi, R.[2], and Varshney, R.K.[1]. [1]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Iwate Biotechnology Research Center, Kitakami, Iwate, Japan; [3]Agricultural Research Station (ARS)-Tandur, Acharya N G Ranga Agricultural University (ANGRAU), Hyderabad, India; [4]Agricultural Research Station (ARS)-Gulbarga, University of Agricultural Sciences (UAS), Raichur, Karnataka, India. *(r.saxena@cgiar.org)

Fast forward genetic mapping combines with whole genome sequencing (WGS) and bulked segregant analysis (BSA) approach was used to identify the candidate genes for *Fusarium* wilt (FW) and sterility mosaic disease (SMD) resistance in pigeonepa. To map the targeted genomic regions, F7 RILs developed by crossing ICPL 20096 (R) × ICP 332 (S) and segregating for FW and SMD resistance were phenotyped at two different locations in India. Based on the phenotyping, 16 RILs in each category were selected for development of resistant (R-Bulk) and susceptible bulks (S-Bulk). These two bulks along with resistant parent (ICPL 20096) were re-sequenced and generated ~19GB of 250 bp pair-end data with ~15× genome coverage. WGS data generated from R- and S- Bulks were aligned with resistant

parent. As a result a total of 35,877 SNPs with SNP index of ≥3 were identified. Out of 35,877 SNPs only 4,139 (11.54%) SNPs were found homozygous. Based on the SNP index (0 for R-Bulk and 1 for S-Bulk) and SNP substitution effect three significant SNPs including two on CcLG07 and one on CcLG11 affects a total of four candidate genes. Functional annotation of these four genes indicated their role to initiate defence mechanism against fungal and viral diseases.

63	Genomics and Genetics	Schafleitner, R.	Next-Generation Genotyping of Mungbean (Vigna radiata)

Next-Generation Genotyping of Mungbean (Vigna radiata)

Schafleitner, R.[1*], Huang, S.M.[1], Krishnan, B.[1], Chen, H.M.[1], Penmetsa, V.[2], Carrasquilla-Garcia, N.[2], Tung, C.W.[3], Nguyen, T.L.H.[4], and Nair, R.[5]. [1]AVRDC – The World Vegetable Center; [2]University of California, Davis, USA; [3]National Taiwan University; [4]Vietnam Academy of Agricultural Sciences; [5]AVRDC – The World Vegetable Center, south Asia, Hyderabad, India. *(roland.schafleitner@worldveg.org)

Current marker systems for mungbean are insufficient to sustain molecular breeding because of the crop's narrow genetic base. This reduced genetic diversity results in a low marker polymorphism rate. Single nucleotide polymorphism (SNP) markers are abundant in the genome and would provide an appropriate resource for molecular breeding. We have applied restriction site associated DNA (RAD) sequencing and genotyping by sequencing (GBS) methods on mungbean breeding parents and mapping populations to produce a critical number of polymorphic SNP markers for molecular breeding purposes. A first test of RAD sequencing on parental material produced more than 250,000 RAD tags with polymorphism rates among mapping parents ranging around 5%, resulting in a wealth of mappable markers. A GBS approach on population NM94 x KPS2 segregating for resistance to *Mungbean yellow mosaic virus* (genus *Begomovirus*) resulted in about 100,000 sequence tags mapped to the reference genome, with a polymorphism rate of 4%. Mapping of resistance genes against *Mungbean yellow mosaic virus* is ongoing in this population. Our experiments show that RAD sequencing and GBS are efficient tools to produce a large number of polymorphic markers for mungbean, greatly facilitating molecular breeding approaches for this crop.

64	Genomics and Genetics	Sen Gupta, D.	A validated source panel of SSR markers for effective discrimination of lentil species

A validated source panel of SSR markers for effective discrimination of lentil species

Sen Gupta, D.[1*], Cheng, P.[2], Sablok, G.[3], Thavarajah, D.[4], Thavarajah, P.[4], McGee, R.[5], Main, D.[6], Coyne, C.J.[7], Kumar, S.[8], and Baum, M.[9]. [1]Cereal Science Graduate Program, Department of Plant Sciences, NDSU, Fargo, ND 58108, United States; [2]Department of Crop and Soil Sciences, Johnson Hall, WSU, Pullman, WA 99164, United States; [3]Department of Biodiversity and Molecular Ecology, Research and Innovation Centre, Fondazione Edmund Mach, Via E Mach 1, 38010S Michele all'Adige, TN, Italy; [4]School of Food Systems, NDSU, Fargo, ND 58108, United States; [5]Grain Legume Genetics and Physiology Research Unit, Agricultural Research Service, U.S. Department of Agriculture, Johnson Hall, WSU, Pullman, WA 99164, United States; [6]Department of Horticulture, WSU, Pullman, WA 99164, United States; [7]Western Regional Plant Introduction Station, Agriculture Research Service, U.S. Department of Agriculture, WSU, Pullman, WA 99164, United States; [8]BIGM Program, ICARDA, P.O. Box 6299, Rabat-Institute, Rabat, Morocco; [9]BIGM Program, ICARDA, P.O. Box 950764, Amman, Jordan. *(debgpb@gmail.com)

Lentil (*Lens culinaris* Medik.) is a diploid (2n=14) with a genome size of more than 4000 Mbp and is an important cool season food legume grown in the world. The total world production of lentil is 4.56 M tons. Development of highly polymorphic molecular markers is a priority in lentil. In this study, 9513 expressed sequence tags (EST) were systematically downloaded from the National Center for Biotechnology Information database to develop unigene-

based simple sequence repeat (SSR) markers. The ESTs were assembled into 4053 unigenes, and then analyzed to detect 374 SSRs using the microsatellite identification tool, MISA. Among the 374 SSRs, 26 compound SSRs were observed. Primer pairs for these SSRs were designed using Primer3 v1.14. To classify the functional annotation of ESTs, and EST-SSRs, BLASTx searches (E-value, 1x10-5) were performed against the publicly available UniProt (www.uniprot.org) and NCBI (www.ncbi.nlh.nih.gov) databases. Further functional annotation was performed using the PLAZA comparative genomics and GO annotation was slimmed using the Plant GO Slim category. Among the synthesized 312 primers, 219 successfully amplified *Lens* DNA. A diverse panel of twenty-four *Lens* genotypes consisting of *L. culinaris* advanced breeding lines, parents of mapping populations, wild types and genotypes of *L. nigricans, L. culinaris ssp. orientalis, L. lamottei* were tested to identify polymorphic markers. A highly polymorphic set of 57 markers successfully discriminated the test genotypes. This set of polymorphic markers with the functional annotation data could be used as molecular tools to lentil breeding.

65	Genomics and Genetics	Si, P.	Non-target-site mechanism of metribuzin tolerance in induced mutants of narrow-leafed lupin (Lupinus angustifolius L.)

Non-target-site mechanism of metribuzin tolerance in induced mutants of narrow-leafed lupin (Lupinus angustifolius L.)

Si, P.[1*], Pan, G.[2], Yu, Q.[3], and Powles, S.[3]. [1]Centre for Plant Genetics and Breeding, School of Plant Biology, the University of Western Australia, Crawly, 6009, Australia; [2]Department of Agronomy, College of Agriculture and Biotechnology, Zhejiang University, Hangzhou, 310029, China; [3]Australian Herbicide Resistance Initiative (AHRI), School of Plant Biology, the University of Western Australia, Crawly, 6009, Australia. *(ping.si@uwa.edu.au)

Weed management has been a predominant agronomic issue ever since farming started. Herbicide tolerant crops have proven to be one of the most effective tools to manage weeds in field crops. Metribuzin is an important herbicide for the control of weeds in narrow-leafed lupin (*Lupinus angustifolius* L.) and metribuzin tolerant varieties have been grown. Metribuzin tolerance mechanism in narrow-leafed lupin was investigated by comparing two induced mutants (Tanjil-AZ-33 and Tanjil-AZ-55) of higher metribuzin tolerance with the susceptible wild type in sequencing of the target-site gene, leaf photosynthetic rate and P450 monooxygenase inhibitors. Sequencing of the highly conserved region of the chloroplast *psb*A gene (target site) revealed that the sequences of the wild type and the mutants were identical and therefore metribuzin tolerance is not target site based. The leaf photosynthetic rate of the two tolerant mutants was initially inhibited after metribuzin treatment, but recovered within 2.5 days whereas that of the susceptible plants remained inhibited over 6 days. The photosynthetic measurements confirmed the target site chloroplast was susceptible and the tolerance mechanism is non-target site based. Inheritance of the tolerance gene was controlled by nuclear, not maternal. Investigation with known cytochrome P450 monooxygenase inhibitors (omethoate, malathion and phorate) showed that tolerance could be reversed in both mutants, indicating the tolerance mechanism in two tolerant mutants may involve cytochrome P450 enzymes. In conclusion, metribuzin tolerance mechanism in lupin mutants is non-target site based, likely involving P450 mediated metribuzin metabolism.

66	Genomics and Genetics	Slater, SMH	An integrated breeding technology for accelerating generation advancement and trait introgression into dry bean (Phaseolus vulgaris).

An integrated breeding technology for accelerating generation advancement and trait introgression into dry bean (Phaseolus vulgaris).

Slater, SMH.[1*], Bett, KE.[1], Lulsdorf, MM.[1], and Warkentin, TD.[1]. [1]Crop Development Centre. *(smhslater@gmail.com)

Removing the late maturation phase of seed development and minimizing the juvenile phase decreases the lifecycle

of a dry bean plant. The use of embryo culture and growth environments which trigger flowering achieves these dual goals. When these two methodologies are combined with marker assisted selection, disease resistance traits can be rapidly integrated into elite dry bean germplasm. Conditions allowing rapid initial growth followed by environmental stressors which increased the triggers for flowering minimized the juvenile phase. These environmental stressors included minimizing space by growing the plants in root trainers containing 15:1 perlite: Sunshine mix#3 and a complete hydroponic solution, high light intensity with a low red to far-red ratio, moderate temperature conditions, and a shortened photoperiod. Embryos excised at 18-22 days after pollination were cultured in sterile perlite and a complete liquid medium. During excision, half a cotyledon was removed for genomic DNA extraction and genotyping for Co-1 and SU91 markers. By using all three methodologies, the generation time was decreased to 75 days and the space requirement to achieve this drop from 90 ft2 to 30 ft2. The integration of anthracnose and common bacterial blight resistance into the elite breeding line 1190m-13 took 1.5 years versus 2-2.5 years by traditional methods.

67	Genomics and Genetics	Slater, SMH	Hardseededness in dry bean – effect of genotype, environment andmaturity.

Hardseededness in dry bean – effect of genotype, environment andmaturity.

Slater, SMH.[1*], Bett, KE.[1], Lulsdorf, MM.[1], and Warkentin, TD.[1]. [1]Crop Development Centre. *(smhslater@gmail.com)

Hardseededness, a type of seed coat imposed dormancy, can be a problem in dry beans which have not been after-ripened. These preliminary experiments were to establish dormancy rates in dry bean produced under field and greenhouse environments. Harvesting pods at the late maturation stage, physiological maturity, and desiccation stage of seed development, we evaluated the seeds for percent germination and hardseededness. Three conclusions were made. (1) Under greenhouse environments, harvesting during desiccation stage appears to increase hardseededness. (2) In breeding line 1190m-13, harvesting during late maturation stage appears to increase non-hard seed rated dormancy. (3) Hardseededness is associated with genotype, although field grown material tends to have a greater proportion of hardseededness than greenhouse grown material. Generally, minimizing hardseededness requires harvest greenhouse material at physiological maturity and field material after it has entered the desiccation phase of seed development.

68	Genomics and Genetics	Smitchger, J.A.	SSR AA122 is Linked to the Classical Morphological Mutation am2 in Pisum sativum

SSR AA122 is Linked to the Classical Morphological Mutation am2 in Pisum sativum

Smitchger, J.A.[1*], May, D.B.[1], and Weeden, N.F.[1]. [1]Montana State University. *(jasmitchger@yahoo.com)

In *Pisum sativum* (Ps) two classical mutations change vacuolar pH, causing anthocyanins to remain in their clear, leuco form and resulting in a seed disorder and white flower phenotype. Both mutations act in a recessive fashion and have been designated *am1* and *am2*. The locus *am1* is located on Linkage Group (LG) I near Mendel's cotyledon color locus I. The *am2* gene has not previously been mapped on the pea linkage map. Similar phenotypes have been observed in *Arabidopsis thaliana* and *Petunia spp.* conditioned by the genes GLA3 and AN1, respectively, but both Ps GLA3, mapped on LG II, and Ps AN1, mapped on LG VII, assorted independently from *am2*. We therefore investigated several crosses segregating for *am2* using previously mapped SSR markers. We found linkage between *am2* and SSR AA122, previously found to be on LG IV (Loridon et al 2005). Few morphological markers have been mapped to this region of the linkage map, explaining why *am2* has not been previously located and indicating that this mutation may be useful in future mapping studies. The underlying role of *am1* and *am2* in controlling vacuolar pH remains unexplained and appears to involve different genes than in *Petunia* and *Arabidopsis*.

69	Genomics and	Smykal, P.	Establishment of wild pea Pisum fulvum chromosome

	Genetics		segment substitution lines in cultivated P. sativum genetic background, as a tool to study domestication and to broaden genetic diversity.

Establishment of wild pea Pisum fulvum chromosome segment substitution lines in cultivated P. sativum genetic background, as a tool to study domestication and to broaden genetic diversity.

Smykal, P.[1*]. [1]Department of Botany, Palacký University in Olomouc, Czech Republic. *(petr.smykal@upol.cz)

Plant evolution under domestication has altered numerous traits, including self-pollination which reinforced fertility barriers between wild and cultivated populations, facilitating fixation of the desired genotype. Domestication bottleneck has resulted in high degree of relatedness, leading to narrower genetic base of cultivated germplasm, prone to pests and diseases. The study of genetic diversity showed that although wide diversity is captured among cultivated pea, wild material provides yet broader diversity. The chromosome segment substitution lines containing genomic segments of wild pea (*Pisum fulvum* WL2140) in the cultivated pea (*P. sativum subsp. sativum* WL1238/cv. Terno) genetic background were developed. Twenty eight microsatellite and 44 gene-specific markers at 2 to 82 cM spacing, were used to make initial molecular characterization of 105 lines. The heterozygozity was detected in 533 (8%), *Pisum sativum* parent was present in 4552 (69%) and introgressed segments of *P. fulvum* in 1551 (23%). There were 5 to 14 segments per line, with mean of 9.6. These lines were described for 14 traits (including branching, height, nodes, pod and seed numbers). Establishment of such permanent introgression library will allow phenotypic characterization of unlimited number of target traits, which, coupled together with higher density markers, will provide means for QTL and gene identification and subsequent incorporation in desired genotypes. In parallel the series of lines is being established with *Pisum sativum* subsp. *elatius* parent. This work was supported by ME10062 project and current research received funding from the European Community's Seventh Framework Programme (FP7/ 2007-2013) under the grant agreement n°FP7-613551, LEGATO project.

70	Genomics and Genetics	Srinivasan, S	A major QTL identified for vernalization response in chickpea

A major QTL identified for vernalization response in chickpea

Srinivasan, S.[1*], Gaur, PM.[1], Kamatam, S.[1], Thudi, M.[1], and Varshney, RK.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru-502 324, India. *(s.srinivasan@cgiar.org)

Wild species can be utilized as potential source to transfer new genes/alleles into domesticated chickpea. Wild chickpea species induce early flowering when exposed to low temperatures (vernalization). Genetics of vernalization was studied in an interspecific F10 recombinant inbred line (RIL) population [ICC 4958 (*Cicer arietinum*) x PI 489777 (*Cicer reticulatum*)] for two consecutive years (2009-10 and 2010-11) under field conditions. After vernalization (at 4°C) for one month, the seedlings of RILs were transplanted in the field along with control treatment (without vernalization). Flowering time difference between vernalization and control treatments was considered as vernalization response. A linkage map available from the public sources for the above population has been used for QTL analysis. A major QTL contributing 55% of phenotypic variation for vernalization response trait was identified on linkage group (LG) 3 at LOD score of 29. The simple sequence repeat (SSR) markers TA64 and CaM1515 were flanking the QTL which spans a distance of 22 cM. Further, integration of six Bacterial Artificial Chromosome (BAC)-end sequence derived SSRs (CaM0717, CaM2086, CaM1760, CaM1364, CaM1122, and CaM0886) present in the major QTL region, on to physical map can eventually help in isolation of vernalization genes. Among 84 flowering related genes present in this region, Ca_06280 related to MADS box genes, was reported to play important role in vernalization in cereals. Understanding the genetic control of vernalization response in chickpea will greatly help in exploitation of wild *Cicer* species in chickpea improvement.

71	Genomics and Genetics	Sudheesh S	SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (Pisum sativum L.)

SNP marker discovery, linkage map construction and identification of QTLs for enhanced salinity tolerance in field pea (Pisum sativum L.)

Leonforte, A.[1,2], Sudheesh, S.[3,4*], Cogan, N.[3], Salisbury, P.[2,3], Nicolas, M.[2], Forster, J.[3,4], and Kaur, S.[3]. [1]Department of Environment and Primary Industries, Biosciences Research Division, Grains Innovation Park, PMB 260, Horsham, Victoria 3401, Australia; [2]Melbourne School of Land and Environment, University of Melbourne, Parkville, Victoria 3010, Australia; [3]Department of Environment and Primary Industries, Biosciences Research Division, AgriBio, the Centre for AgriBioscience, 5 Ring Road, Bundoora, Victoria 3083, Australia; [4]La Trobe University, Bundoora, Victoria 3086, Australia. *(shimna.sudheesh@depi.vic.gov.au)

Field pea is a self-pollinating, diploid, cool-season legume food crop. Production is constrained by multiple biotic and abiotic stress factors including salinity that reduce growth and yield. Recent advances in genomics have permitted development of low-cost high-throughput genotyping systems, allowing construction of saturated genetic maps for identification of quantitative trait loci (QTLs) associated with traits of interest, such as saline stress tolerance.

Marker discovery was performed based on transcriptome sequencing of a sub-set of field pea cultivars. A total of 36,188 variant nucleotide positions were detected through *in silico* analysis, of which 768 were selected for genotyping across a recombinant inbred line (RIL) population derived by crossing single genotypes of the varieties Kaspa and Parafield. A total of 410 SNPs and 48 SSRs were successfully mapped to the genetic map in order to obtain an evenly distributed genome-wide coverage (cumulative length of 1916 cM with an average interval of 4.2 cM). Parents and RIL progeny were screened at the seedling growth stage for symptoms of salinity stress, imposed by watering with a 18 dsm-1 saline solution. Phenotypic variation for salinity induced symptoms was normally distributed and increased with severity over time. QTLs for salinity were identified on LGs 1 and 2 explaining 30% of the phenotypic variance, with flanking SNP markers suitable for selection of resistant cultivars.

The SNP assays and associated genetic linkage maps developed in this study will facilitate the identification of salt resistance cultivars, candidate gene identification and development of diagnostic tools for marker-assisted selection (MAS).

72	Genomics and Genetics	Sudheesh, S.	Transcriptome atlas of field pea (Pisum sativum L.)

Transcriptome atlas of field pea (Pisum sativum L.)

Sudheesh, S.[1,2*], Lombardi, M.[1], Kennedy, P.[3], Cogan, N.[1], Forster, J.[1,2], and Kaur, S.[1]. [1]Department of Environment and Primary Industries, Biosciences Research Division, AgriBio, The Centre for AgriBioscience, 5 Ring Road, Bundoora, Victoria 3083, Australia; [2]La Trobe University, Bundoora, Victoria 3086, Australia; [3]Department of Environment and Primary Industries, Biosciences Research Division, Grains Innovation Park, PMB 260, Horsham, Victoria 3401, Australia. *(shimna.sudheesh@depi.vic.gov.au)

Field pea *(Pisum sativum* L.*)* is a cool-season grain legume that is cultivated worldwide for both human consumption and stockfeed. Recent advances in next generation sequencing (NGS) and genomics technologies now provide unprecedented opportunities to develop enriched genomic resources in understudied crops such as field pea. The objective of this study was to develop a transcriptome atlas of field pea to examine differences in the genic content of three pea varieties that differ in seed and plant morphological characteristics. Transcriptome sequencing was performed on different tissues (seedling, leaf, stipule, stem, tendril, flower, stamen, pistil, immature pod, immature

seed, root, root tip and nodule) from three field pea genotypes - Kaspa, Parafield and ATC1836. Tissue samples were collected at various growth stages and a total of 33 cDNA libraries were sequenced using Illumina HiSeq 2000 and MiSeq. A total of 0.2 billion paired-end reads were *de novo* assembled using Trinity assembler that yielded 182,724 contigs with average contig size of 538 bp and N50 698 bp. All contigs were further filtered on the basis of known gene annotations to obtain transcriptome reference of field pea. The paired end reads from each genotype were aligned to the reference using Bowtie 2 to identify specific gene sets from each of the three field pea genotypes. Sub-sets of genes common between all three genotypes as well as uniquely expressed in each genotype have been identified. This study provided the most comprehensive assembled and annotated transcriptomic suite of the field pea that is available for functional, structural and comparative genomics research.

73	Genomics and Genetics	Thudi, M	CaTILL: A resource for novel alleles for chickpea (Cicer arietinum) improvement

CaTILL: A resource for novel alleles for chickpea (Cicer arietinum) improvement

Thudi, M.[1*], Gaur, PM.[1], Samineni, S.[1], Ganeshram, S.[2], Niranjan, V.[3], Ramaswamy, G.[3], and Varshney, RK.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Tamil Nadu Agricultural University (TNAU), Coimbatore, India; [3]Genotypic Technology Pvt. Ltd., Bangalore, India. *(t.mahendar@cgiar.org)

TILLING-by-sequencing (TBS) is a powerful approach for identification of novel alleles/mutations in candidate genes. In order to identify novel alleles in candidate genes, a TILLING population referred as "*Ca*TILL", comprising of 3,164 M3 lines was developed by treating ICC 4958, a chickpea (*Cicer arietinum*) genotype with 0.2% ethyl methane sulfonate (EMS). A set of 23 key candidate genes, involved in abiotic (drought and salinity), biotic (*Ascochyta* blight) stresses, flowering, symbiosis, nodulation and plant development were selected for allele mining using TBS approach. Of 78.62 GB sequence data generated by sequencing 80 barcode indexed Illumina libraries, 89.58 % of reads (on an average) were mapped to 23 candidate gene reference sequences. In total, 91 novel alleles/mutations were identified in 23 genes, of which 53 were C>T transitions and 38 were G>A transitions. The number of mutations identified per gene ranged from 1 (*Late1*) to 12 (*Dmi*2). Three mutations (one each in *Nac3*, *Ca220909* and *Ahc* genes) were predicted to generate pre-mature stop codons, 40 mutations were mis-sense, 29 mutations were same-sense and 19 mutations were in introns. The mutation density in the population varied from one in 151.9 Kb (*Ahc* gene) to one in 3.9 Mb (*Prodh* gene) and the overall mutation density was one mutation per 708 Kb or ~1042 mutations per genome. M4 lines suitable for mechanical harvesting, early flowering, abaxial pods, large seed size (45.78 gm 100-seed weight) and superior lines for several other agronomically important traits were identified.

74	Genomics and Genetics	Thudi, M	Fine mapping of a "QTL-hotspot" for drought tolerance in chickpea (Cicer arietinum L.)

Fine mapping of a "QTL-hotspot" for drought tolerance in chickpea (Cicer arietinum L.)

Jaganathan, D.[1,2], Kale, S.[1], Thudi, M.[1*], Ruperao, P.[3], Kavi Kishore, PB.[2], Gaur, PM.[1], Mohan Katta, AVSK.[1], Nguyen, HT.[4], Batley, J.[3], Edwards, D.[3,5], Sutton, T.[6], and Varshney, RK.[1]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Department of Genetics, Osmania University, Hyderabad, India; [3]University of Queensland, Brisbane, QLD, Australia; [4]University of Missouri, Columbia, USA; [5]Australian Centre for Plant Functional Genomics, University of Queensland, Brisbane, QLD, Australia; [6]Australian Centre for Plant Functional Genomics, University of Adelaide, SA, Australia. *(t.mahendar@cgiar.org)

To understand the genetic complexity and mechanism of drought tolerance in chickpea, a genomic region (~35 cM) harboring QTL for drought tolerance traits was identified on linkage group 04 (CaLG04) using a linkage mapping

based approach. To enhance marker density in this region, two approaches were adopted: (i) genotyping-by-sequencing (GBS) and (ii) re sequencing at low coverage referred to as Skim sequencing. The GBS approach, with 5X and 0.2X coverage on parental lines and 232 RILs, respectively, provided 828 single nucleotide polymorphism (SNP) markers. A total of 49 SNPs were integrated in the "*QTL-hotspot*" region that narrowed the QTL interval from 35cM to 14 cM (~7 Mb on the physical map). The Skim sequencing approach, with 7-8X and 0.72X coverage on parental lines and 232 RILs respectively, identified 53,175 high quality SNPs utilized to construct a bin map with 1,610 recombination bins. QTL analysis using the bin map and precise phenotyping data split the ~7 Mb QTL into four regions: (i) 13.16-13.23 Mb region harboring 8 candidate genes and QTL for 5 drought tolerance traits; (ii) 13.39-13.54 Mb region harboring 11 candidate genes and QTL for 4 drought tolerance traits (iii) 14.15-14.27 Mb region harboring 11 candidate genes and QTL for pod number (POD) (iv) 14.99-15.08 Mb region harboring 9 candidate genes and QTL for POD. In addition to an approach that will enable further fine mapping of the QTL regions identified, candidate genes ware being characterized for potential to improve drought tolerance in chickpea.

75	Genomics and Genetics	Tikle, A.N.	Stability of male sterility and fertility restoration in pigeonpea(Cajanus cajan (L.) Millsp.) under different regimes of temperature and locations

Stability of male sterility and fertility restoration in pigeonpea(Cajanus cajan (L.) Millsp.) under different regimes of temperature and locations

Tikle, A.N.[1*], Choudhary, Sunil.[2,3], Tamesh, Uttamchand.[2,3], Yadava, H.S.[4], and Saxena, K.B.[5]. [1]R.A.K.College of Agriculture Sehore (Madhya Pradesh) India; [2]R.A.K.College of Agriculture, Sehore (M.P.) India; [3]International Crops Research Institute for the Semi Arid Tropics,Patancheru; [4]Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior; [5]International Crops Research Institute for the Semi Arid Tropics, Patancheru. *(antiklepb@gmail.com)

For effective utilization of a male-sterility system in hybrid breeding, it is important that the expression of both the male-sterility and its fertility restoration are stable over years and locations. Pigeonpea (*Cajanus cajan* (L.) Millsp.) is unique among legumes as its floral morphology allows both self as well as insect-aided cross-pollination and their extents vary from place to place. The study was carried out to investigate stability of male sterility in nine CMS lines under different temperature regimes (11.3-28.60C in December to 22.6-37.80C in March) and fertility restoration in ten CMS based pigeonpea hybrids in three locations of India (South India 17º53'N, 78º27'E, 545.0 MSL, North India; 23º17'N, 85º19'E, 625.0 MSL and Central India 23º12'N, 77º05'E, 498.8 MSL). The results revealed significant variability for pollen fertility and sterility among the hybrids and CMS lines. All the hybrids except ICPH 3494 and ICPH 3491 exhibited high (>80 %) pollen fertility across the locations. Hybrids ICPH 2671, ICPH 2740 and ICPH 3933 had 100% male fertile plants across the locations. All the CMS lines had complete male sterile plants across the different dates of sowing. CMS lines BRG 1A, Hy3C A, BRG 3A and TTB 7A exhibited 100 % pollen sterility in different dates of sowing. The pooled analysis revealed significant genotype × environmental interactions for pollen fertility and sterility. The GGE biplot of hybrids showed that hybrids ICPH 2671, ICPH 2740, ICPH 3933 and ICPH 3461 were stable for fertility restoration with an exception of ICPA 2047 and ICPA 2051.

76	Genomics and Genetics	Toker, C.	Induction and inheritance for Resistance to Herbicide in Cicer reticulatum Ladiz.

Induction and inheritance for Resistance to Herbicide in Cicer reticulatum Ladiz.

Toker, C.[1*], Ceylan, F.O.[1], Ikten, C.[1], and Uzun, B.[1]. [1]Akdeniz University, Faculty of Agriculture, TR 07070. *(toker@akdeniz.edu.tr)

One of the most effective ways to struggle with weeds in agricultural lands is improved for resistance to herbicide in crop species. In order to improve herbicide resistance in chickpea (*Cicer arietinum* L.) via conventional breeding

methods, nine accessions of the cultivated chickpeas, one accession of *C. bijugum* K.H. Rech. and two accessions of *C. reticulatum* Ladiz. were irradiated with gamma rays. One mutant was isolated as highly resistant for imidazolinone. The present study was therefore undertaken to set forth gene(s) conferring IMI resistance in *Cicer reticulatum*. A mutant of *C. reticulatum* was crossed with a susceptible line of the cultivated chickpea. The parents, F1, F2 and backcross plants were assessed in greenhouse and field experiments, and phenotyped as resistant (absent any damage of the herbicide) and susceptible (shoot tips of seedlings were wilted after five days and then plants were started to dry after 10 days) plants after application of IMI herbicide. All the F1 plants were found as susceptible, whereas F2 and backcross plants segregated as resistance and susceptible. Segregation in F2 and backcrossing fitted well with the 3 : 1 and 1 : 1 ratios, respectively. IMI-resistance in *C. reticulatum* was governed by a recessive single gene that designed as '*hrhr*'. Heterosis and some transgressive segregants were noticed in F1 and F2, respectively. IMI-resistance can be easily transferred from in *C. reticulatum* to the cultivated chickpea due to a monogenic recessive trait.

77	Genomics and Genetics	Trujillo, D.I.	Genomic characterization of the LEED..PEEDs, a gene family unique to Medicago species

Genomic characterization of the LEED..PEEDs, a gene family unique to Medicago species

Trujillo, D.I.[1*], Silverstein, K.A.T.[1], and Young, N.D.[1]. *(truji033@umn.edu)

The LEED..PEED (LP) gene family in *Medicago truncatula* (A17) is composed of 13 genes coding small putatively secreted peptides with a conserved domain of negatively charged residues. This family is not present in the genomes of *Glycine max*, *Lotus japonicus* or *Cicer arietinum*. LP genes were not detected in a *Trifolium pratense* draft genome or *Pisum sativum* nodule transcriptome, which were sequenced *de novo* in this study, suggesting that the LP gene family arose within the past 25 million years. *M. truncatula* accession HM056 has 13 LP genes with high similarity to those in A17, while *M. tricycla* (R108) and *M. sativa* each have 11 and 10 LP gene copies, respectively. In *M. truncatula* A17, twelve LP genes are located on chromosome 7 within a 93 Kb window, while one LP gene copy is located on chromosome 4. A phylogenetic analysis of the gene family is consistent with most gene duplications occurring prior to *Medicago* speciation events, mainly through local tandem duplications. Synteny comparisons between R108 and A17 confirm that gene order is conserved between the two species, though a further duplication occurred in A17 after speciation. In *M. truncatula* A17, all 13 LPs are exclusively expressed in nodules, and absent from other plant tissues, including roots, leaves, flowers, seeds, seed shells, and pods (RNA-seq data from Young et al. 2011). The recent expansion of LP genes in *Medicago* species and their timing and location of expression suggest a novel function in nodulation, possibly as an aftermath of the evolution of bacteroid terminal differentiation or potentially associated with rhizobial-host specificity, and merits further research.

78	Genomics and Genetics	Varshney, R.K.	Identification and validation of heat stress responsive genes in chickpea (Cicer arietinum L.)

Identification and validation of heat stress responsive genes in chickpea (Cicer arietinum L.)

Kudapa, H.[1], Agarwal, G.[1], Doddamani, D.[1], Kumar, V.[1], Khan, A.W.[1], Chitikineni, A.[1], Katta, K.[1], Gaur, P.M.[1], and Krishnamurthy, L.[1]. *(r.k.varshney@cgiar.org)

Heat stress/high temperatures during flowering and pod development is increasingly becoming a major constraint in chickpea production. Heat tolerant varieties are needed for improving chickpea yields in warm season environments and late sown conditions. With an objective of identifying genes and/or markers associated with heat tolerance for accelerated development of heat tolerant chickpea varieties RNA-Seq based transcriptome analysis was performed. Vegetative (leaves and roots) and reproductive (leaves, roots and flowers) tissues of six contrasting heat responsive

(tolerant - ICCV 92944, ICC 1356, ICC 15614 and sensitive - ICC 5912, ICC 4567, ICC 10685) genotypes were selected for the study. A total of ~504 million reads were generated and alignment of these reads against the comprehensive chickpea transcriptome assembly (CaTA v2) resulted in covering of 44,185 out of 46,369 transcript assembly contigs. A total of 6,799 genes including 1,172 novel genes were significantly differentially expressed with a log2 fold change of ≥2 between tolerant and sensitive genotypes. A set of 56 differentially expressed genes belonging to abiotic stress family proteins was selected for further validation using quantitative real time PCR. Furthermore, >22,456 single nucleotide polymorphisms (SNPs)/INDELs were identified between lines that are the parental genotypes of two mapping populations (ICC15614 × ICC 4567 and ICC 1356 × ICC 4567). Novel genes along with the marker resources identified in this study should help breeders in developing heat tolerant chickpea lines in efficient manner.

79	Genomics and Genetics	Varshney, R.K.	Identification of internal housekeeping genes for studying gene expression in pigeonpea by quantitative real-time PCR

Identification of internal housekeeping genes for studying gene expression in pigeonpea by quantitative real-time PCR

Sinha, P.[1], Saxena, R.K.[1], Singh, V.K.[1], Suryanarayana, V.[1], Krishnamurthy, L.[1], and Varshney, R.K.[1*]. [1]International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India. *(r.k.varshney@cgiar.org)

Gene expression analysis usingquantitative real-time PCR(qRT-PCR) is a very sensitive technique which completely depends on stable performance of reference genes used in the study. A number of housekeeping genes have been used in various expression studies however, they found to be varying under different stress conditions. To identify the suitable housekeeping genes in pigeonpea for expression analysis under different abiotic stress conditions (drought, heat and salinity) we have compared relative expression variations of 10 commonly used housekeeping genes (EF1α, UBQ10, GAPDH, 18srRNA, 25srRNA, TUB6, ACT1, IF4α, UBC and HSP90) on various tissues (root, stem and leaves) of Asha (ICPL 87119). Based on analysis of drought stress conditions IF4α followed by TUB6 and HSP90 were identified as most stable reference genes. For heat stress conditions EF1α, UBC and HSP90 were found most stable reference genes. Similarly, for salinity stress conditions, GAPDH followed by UBC and ACT1 were identified as the most stable reference genes. Stable and most unstable genes identified in the study were validated to estimate the expression level of candidate gene in pigeonpea (*Cc_cds_33874*) for drought tolerance and result obtained confirm the ranking of the reference genes identified in the study.

80	Genomics and Genetics	Varshney, RK	Selection of appropriate genomic selection model in an unstructured germplasm set of peanut (Arachis hypogaea L.)

Selection of appropriate genomic selection model in an unstructured germplasm set of peanut (Arachis hypogaea L.)

Pandey, MK.[1], Rathore, A.[1], Das, RR.[1], Khera, P.[1], Upadhyaya, HD.[1], Jannink, J-L.[2], Hickey, JM.[3], and Varshney, RK.[1*]. [1]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad, India; [2]Cornell University, Ithaca, USA; [3]The Roslin Institute, The University of Edinburgh, Midlothian, Scotland, UK. *(r.k.varshney@cgiar.org)

Prediction of genomic values with better accuracy is a key to success in genomic selection (GS) breeding. With an objective to deploy GS in peanut breeding, we evaluated six GS models in an unstructured germplasm set containing 184 individuals. In this context, multiseason phenotyping data for three important agronomic traits (days to flower,

seed weight and pod yield) and genotyping data with 2356 DArT markers were generated on this germplasm set. Phenotypic analysis revealed lowest coefficient of variation (CV), genetic variance (GV), genotypic coefficient of variation (GCV) for days to flower followed by seed weight and pod yield. In contrast, the heritability was highest in days to flower (78.85%) than seed weight (75.46%) and pod yield (62.53%). Upon analysing phenotypic together with genotypic data with six GS models, cross-validation values were found to be higher for days to flower followed by seed weight and pod yield across all the models. Of the six GS models used, Ridge Regression-BLUP and Bayesian LASSO performed better than Random Forest Regression, Kinship GAUSS, BayesCπ and BayesB. Thus, Ridge Regression-BLUP and Bayesian LASSO may be the choice for further GS analysis in peanut as these two models performed better for high (days to flower and seed weight) as well as moderate (pod yield) heritable traits. Further analysis is continue on this germplasm set and detailed results will be presented in the conference.

81	Genomics and Genetics	Vaz Patto, M.C.	Take a walk on the bean side: The Portuguese genetic diversity

Take a walk on the bean side: The Portuguese genetic diversity

Leitão, S.T.[1], Tomás, D.[1], Dinis, M.[1], Šatović, Z.[2], Veloso, M.M.[3], and Vaz Patto, M.C.[1*]. [1]Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa (ITQB-UNL), Avenida da República, 2780-157 Oeiras, Portugal; [2]Faculty of Agriculture, Department of Seed Science and Technology, University of Zagreb, Svetosimunska 25, 10000 Zagreb, Croatia; [3]Instituto Nacional de Investigação Agrária e Veterinária (INIAV), Avenida da República, Quinta do Marquês, 2780-157 Oeiras, Portugal. *(cpatto@itqb.unl.pt)

Common bean (*Phaseolus vulgaris* L.) has a history of more than five centuries of cultivation in Portugal. Diverse landraces are still widely grown at farmers' fields, commonly in intercropping systems, for example with maize *(Zea mays* L.). Portuguese bean landraces, well adapted to local environmental conditions and to quality farmers' preferences, may represent important sources of interesting traits, such as biotic and abiotic stresses resistance and high organoleptic and nutritional quality for food, not yet fully explored on breeding programs.

In order to study the genetic diversity of the Portuguese common bean germplasm, 135 representative landraces, selected based on their geographical origin from the INIAV national common bean collection (PRT005), were analyzed using 23 microsatellite markers.

Using ten individuals per landrace, several genetic parameters were estimated, namely allelic diversity and richness, gene diversity, polymorphic information content (PIC) and proportion-of-shared-alleles distance. Phylogenetic clustering, analysis of molecular variance (AMOVA) and of population structure were also performed.

With this study we characterized the genetic diversity of Portuguese common bean germplasm to better explore this valuable high quality and resistant underused resource. The breeding of common bean varieties with these improved traits will better meet consumers´ and farmers' present expectations and needs, supporting the development of a more sustainable agriculture.

82	Genomics and Genetics	Wen, J.	Generation and Application of Medicago truncatula Tnt1 Mutants

Generation and Application of Medicago truncatula Tnt1 Mutants

Wen, J.[1*], Cheng, X.[1], Mysore, K.S.[1], Ratet, P.[2], and Udvardi, M.[1]. [1]The Samuel R. Noble Foundation, 2510 Sam Noble Parkway, Ardmore, OK 73401, USA; [2]Institut des Sciences du Vegetal, CNRS, Avenue de la Terrasse 91198, Gif sur Yvette Cedex, France. *(jwen@noble.org)

Medicago truncatula is a model legume species for genetics, genomics, and functional genomics studies. As a model legume, it has been utilized for research in many areas, including plant physiology, nutrition, metabolism, growth and development, and plant-microbial and plant-environmental interactions. To better facilitate characterization of gene functions in *M. truncatula* and other legume species, we have generated more than 21,000 *Tnt1* retrotransposon insertion lines over the last 10 years, encompassing approximately 500,000 insertions in the genome of *M. truncatula*, at The Noble Foundation. To make maximal utilization of the mutants, two reverse genetics platforms have been established: one is the searchable web-based database (http://medicago-mutant.noble.org/mutant/), which currently contains more than 120,000 *Tnt1*-flanking sequence tags (FSTs) mapped to pseudo-chromosomes and we expect to have more than 200,000 FSTs available by the end of 2014; the other is the PCR-based reverse screening, which provides screening service for genes-of-interest in genomic DNA pools of insertion lines. Over the past six years, more than 900 genes have been screened by the PCR approach. One or more *Tnt1* insertions have been successfully identified in 85% of these genes, ranging from ~0.5 to 22 kb with genomic or cDNA sequences. So far, we have distributed more than 4600 *Tnt1* lines to scientists in 24 countries.

83	Genomics and Genetics	Wolko, B.	Lupinus angustifolius gene copy number quantification

***Lupinus angustifolius* gene copy number quantification**

Szczepaniak, A.[1], Wyrwa, K.[1], Podkowinski, J.[2], Ksiazkiewicz, M.[1], Wolko, B.[1*], and Naganowska, B.[1]. [1]Department of Genomics, Institute of Plant Genetics of the Polish Academy of Sciences, Strzeszynska 34,60- 479 Poznan, Poland; [2]Department of Molecular and Systems Biology, Institute of Bioorganic Chemistry Polish Academy of Sciences, Noskowskiego 12/14, 61-704 Poznan, Poland. *(bwol@igr.poznan.pl)

Copy number variation (CNV) has gained considerable pertinence for trackingmolecular bases of phenotypic diversity and plant genome evolution. The underlying methodology however is not fully reliable. Here we report several methods to detect the CNV of eleven genes playing crucial roles in nitrogen fixation and fatty acid synthesis in *Lupinus angustifolius* (narrow-leafed lupin), a reference species for genomic studies within the genus *Lupinus*. First, we measured the copy number of analyzed genes using quantitative Real-Time PCR (qPCR). This method is popular but has two major shortcomings: as qPCR requires normalization to either to a reference or to a standard curve, it provides only a relative quantification. Furthermore, variations in amplificationefficiency may affect the reliability of the results. To overcome these drawbacks, highthroughput Droplet Digital PCR (ddPCR) was performed. The ddPCR system provided more precise results than real-time PCR. Finally, to confirm data obtained from qPCR and ddPCR, we used BAC clones from the *L. angustifolius* nuclear genome library, carrying analysed genes as probes in fluorescent *in situ* hybridization (FISH) experiments. Particular gene copies were localized in metaphase chromosomes by BAC-FISH and mapped in appropriate linkage groups by BAC-based genetic markers. Gene CNV as a common form of genome natural diversity has enormous potential for model organism research, evolutionary biology, and crop science. In the present study we compare three methods for the detection of CNV and show that ddPCR is the method of choice.The authors acknowledge financial support from the Polish National Science Centre (NN301 391939).

84	Genomics and Genetics	YANG, SY	Faba bean genomic study and its future application

Faba bean genomic study and its future application

YANG, SY.[1*], PAULL, JG.[1], McMurry, L.[2], MAO, D.[2], Oldach, K.[2], and Wilkinson, M.[1]. [1]The University of Adelaide, Australia; [2]South Australian Research and Development Institute. *(shi.yang@adelaide.edu.au)

Faba bean *(Vicia faba)*originated in the Middle East and is an important food and feed crop in China, Mediterranean and African countries. There is around 3.2 million hectares of faba bean grown with over 4.7 million tonnes produced in 2012(FAO stat). The production of faba bean in Australia has increased significantly from 82,000 hectares in 1995 to nearly 180,000 hectares in 2012 (ABARES). Genomic studies have been conducted to develop SSR and SNP markers for genetic mapping and diversity studies for faba bean. There have been rapid developments in genome sequencing technologies recently, however, genomic study of faba bean by next generation sequencing is limited. While over 40 plant whole genomes were sequenced by 2013, whole genome sequencing of faba bean has not yet occurred due to the lack of resources and its large genome. Faba bean (2n=12) genome is approximately 13.4Gb, the largest genome in the grain legume family. The rapid development of sequencing technologies provide opportunities for the whole genome faba bean to be sequenced. The availability of sequence information will enable the discovery of genes and molecular markers associated with diverse traits, and the wealth information combined with advanced genotyping methods permits the application of genome wide association studies to establish the link between genetic variation and agronomic traits. The identification of genes and molecular markers underlying traits will help accelerate the breeding process and lead to improved varieties with yield and quality, tolerance to unfavourable environmental conditions and resistance to diseases.

85	Genomics and Genetics	Yuan, H. Y.	Developing a genomic in situ hybridization protocol for genomic studies of lentil

Developing a genomic *in situ* hybridization protocol for genomic studies of lentil

Yuan, H. Y.[1*], Wong, M.[1], Vandenberg, A.[1], and Bett, K.[1]. [1]Crop Development Centre, University of Saskatchewan, Saskatoon, SK. *(haiying.yuan@usask.ca)

In situ hybridization (ISH) techniques allow specific nucleic acid sequences to be detected in morphologically preserved chromosomes, cells or tissue sections. In combination with immunocytochemistry, ISH can relate microscopic information to gene activity at the DNA, mRNA, and protein level. Genomic *in situ* hybridization (GISH), which uses total genomic DNA of one of the parents as the probe, permits identification and characterization of genomes and chromosomes in hybrid plants and recombinant inbred lines. This is a useful tool for the detection of chromatin transfer or introgression, especially between distantly or even closely related species. We report a GISH protocol that we developed recently for lentil genomic study using a metaphase chromosome spread. Procedures on metaphase chromosome spread, conditions for hybridization and post-hybridization wash are discussed.

86	Genomics and Genetics	Yuan, H. Y.	Pubescence, can it be used to differentiate L. tomentosus from L. orientalis?

Pubescence, can it be used to differentiate *L. tomentosus* from *L. orientalis*?

Yuan, H. Y.[1*], Saha, S.[1], Tullu, A.[1], Bett, K.[1], and Vandenberg, A.[1]. [1]Crop Development Centre, University of Saskatchewan, Saskatoon, SK. *(haiying.yuan@usask.ca)

Wild *Lens* species are an important genetic resource for broadening the genetic base of lentil breeding. Better understanding of genetic relationships among the wild species through the development of intra-specific and inter-specific genetic maps will accelerate the potential for understanding and managing introgression. Development of good mapping populations is a key resource. *L. orientalis* is considered the closest wild progenitor of the cultivated lentil, while *L. tomentosus* was proposed as a separate species in the late 1990s. Both species share similar morphological characters. Our recent program on developing intra-specific populations of *L. orientalis* and *L. tomentosus* required us to screen the accessions from both species using the morphological characters and next generation sequencing technology (GBS). Here we report our results with detailed microscopy information on leaf and

pod pubescence, which allows us to clear some of the confusion (or misclassification) existing in the current *L. orientalis* and *L. tomentosus* germplasm collections.

87	Genomics and Genetics	Zou, X.	Genome-wide SNP and InDel discovery and transcriptional profiling of CBB resistance in common bean

Genome-wide SNP and InDel discovery and transcriptional profiling of CBB resistance in common bean

Zou, X.[1*], Shi, C.[2], Austin, R.[1], Merico, D.[3], Munholland, S.[4], Marsolais, F.[1], Navabi, A.[2,5], Crosby, W.[4], Pauls, K.[5], Yu, K.[2], and Cui, Y.[1]. [1]Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, London, Ontario, Canada; [2]Greenhouse and Processing Crops Research Centre, Agriculture and Agri-Food Canada, Harrow, Ontario, Canada; [3]The Centre for Applied Genomics, The Hospital for Sick Children, Toronto, Ontario, Canada; [4]Department of Biological Sciences, University of Windsor, Windsor, Ontario, Canada; [5]Department of Plant Agriculture, University of Guelph, Guelph, Ontario, Canada. *(xiaolu.zou@agr.gc.ca)

Next generation sequencing and microarray technique have empowered researchers to approach SNPs (single nucleotide polymorphisms) and InDels (Insertions/Deletions) discovery and gene expression analysis on a genomic scale. In this report, a total of 43,698 putative SNPs and 1,267 putative InDels were discovered through deep sequencing of reduced representation libraries constructed from 36 common bean genotypes grown in Canada. Of the SNPs, 43,504 were bi-allelic and 194 were tri-allelic, and the InDels comprised 574 insertions and 693 deletions. With the aid of the recent release of the first chromosome-scale version of *Phaseolus vulgaris*, 24,907 bi-allelic SNPs, 79 tri-allelic SNPs, 315 insertions, and 377 deletions were located in 8,758, 77, 273, and 364 genes, respectively. Meanwhile, a total of 113 putative SNPs were randomly chosen for validation using high-resolution melt analysis. Of the 113 candidate SNPs, 105 (92.9 %) contained the predicted SNPs. Besides, a common bean whole genome microarray was used to evaluate global gene expression on CBB (common bacterial blight) resistant and susceptible lines challenged by bacterial *Xap* (*Xanthomonas axonopodis* pv. *Phaseoli*). The expression levels of 1103 genes were significantly altered with 688 up-regulated and 415 down-regulated in CBB resistant plants over susceptible plants challenged by *Xap*. Among these genes, the transcription levels of 32 genes involved in stress response were up- (22 genes) or down-regulated (10 genes). Moreover, the expression levels of 62 genes encoding transcription factors were up- (34 genes) or down-regulated (28 genes) by *Xap*.

88	Nitrogen Fixation and Symbiosis	ARRIGHI, J.F.	Aeschynomene evenia, a model plant for studying the molecular genetics of the Nod-independent rhizobium-legume symbiosis

Aeschynomene evenia, a model plant for studying the molecular genetics of the Nod-independent rhizobium-legume symbiosis

ARRIGHI, J.F.[1*], CHAINTREUIL, C.[1], CARTIEAUX, F.[1], BROWN, S.C.[2], RODIER-GOUD, M.[3], BENA, G.[1], and GIRAUD, E.[1]. [1]IRD, Laboratoire des Symbioses Tropicales et Méditerranéennes, UMR IRD/SupAgro/INRA/UM2/CIRAD, Campus International de Baillarguet, TA A-82/J, 34398 Montpellier Cedex 5, France; [2]CNRS, IBiSA imagerie Gif, Institut des Sciences du Végétal, UPR 2355, 23/24, avenue de la Terrasse, 91198 Gif-sur-Yvette, France; [3]CIRAD, Laboratoire de Cytogénétique Moléculaire, UMR AGAP, TA-A 108/03, 34398 Montpellier Cedex 5, France. *(jean-francois.arrighi@ird.fr)

Research on the nitrogen-fixing symbiosis has been mainly focused on two model legumes, *Medicago truncatula* and *Lotus japonicus*, which use a sophisticated infection process involving infection thread formation. However, in 25% of the legumes, the bacterial entry occurs more simply in an intercellular fashion. Among them, some *Aeschynomene* species are nodulated by *Bradyrhizobium* that do not produce Nod factors.

To advance in our knowledge of this unique Nod-independent symbiosis, we performed a molecular phylogeny for the genus *Aeschynomene* that evidenced the Nod-independent infection process arose in a single lineage. Exploration of the genetic species diversity within this lineage enabled the identification of *A. evenia* as an ideal species to constitute a *bona fide* model legume. *A. evenia* is a short-perennial and autogamous species, with a diploid and relatively small genome (2n=20; 430 Mb/1C). A manual hybridization procedure has been set up allowing directed crosses. It is efficiently transformed by *Agrobacterium rhizogenes*, allowing functional gene analysis. Species delimitation from the closely related but polyploid *A. indica* and characterization of the intraspecific diversity in *A. evenia* facilitated the choice of the most appropriate lines to be used as the reference line and as the polymorphic mapping parent for forward genetics. Thanks to the advantageous characteristics of *A. evenia*, it should be relatively straightforward to unravel the molecular determinants of the Nod-independent process. This should shed new light on the evolution of rhizobium-legume symbiosis and could have important agronomic implications.

89	Nitrogen Fixation and Symbiosis	Gisiora, J. K.	Investigating the Development of M. truncatula Symbiosome Membrane Using ENOD16 and Vacuolar H+-ATPase

Investigating the Development of *M. truncatula* Symbiosome Membrane Using ENOD16 and Vacuolar H^+-ATPase

Gisiora, J. K.[1*], Catalano, C. M.[2,3], Mendiola, J.[2], and Sherrier, D. J.[2,3]. [1]Department of Biological Sciences, University of Delaware, Newark DE, 19716, USA; [2]Department of Plant and Soil Sciences, University of Delaware, Newark DE, 19717, USA; [3]Delaware Biotechnology Institute, Newark DE, 19711, USA. *(jmogire@udel.edu)

The objective of this project is to study the development of the symbiosome membrane in nitrogen-fixing root nodules. *Medicago truncatula* is a model legume that forms an endosymbiotic relationship with the nitrogen-fixing bacterium, *Sinorhizobium meliloti*. In the absence of sufficient nitrogen, significant gene expression changes between the plant and bacteria results in the reprogramming of root hair tip growth and cortical cell divisions forming a nodule primordium. The bacteria encompassed within curled root hairs, grow, divide and infect the cortical cells via infection threads. Through endocytosis, bacteria are release from these infection threads gaining a plant-derived outer membrane called the symbiosome membrane. Little is known about the biogenesis and differentiation of the symbiosome membrane. We are currently generating a collection of plasmids encoding different organelle markers and proteins to serve as tools that will enable us to understand: (1) the localization of symbiosome-specific proteins; and (2) the development of the symbiosome membrane. Using confocal and transmitted electron microscopy, we will investigate the localization of early nodulin 16 protein (ENOD16) and Vacuolar H+-ATPase in the symbiosome membrane as well as other regions of the cell. Preliminary proteomic studies have identified ENOD 16 and Vacuolar H+-ATPase protein as components of the symbiosome membrane. We expect to see ENOD16 protein localized in the symbiosome membrane early during its development and Vacuolar H+-ATPase later in development.

90	Nitrogen Fixation and Symbiosis	Maalouf, F.	Rhizobium nodulation of an Ethyl methanesulfonate (EMS) mutagenized faba bean population

Rhizobium nodulation of an Ethyl methanesulfonate (EMS) mutagenized faba bean population

Maalouf, F.[1*], Bakro, F.[2], Hamwieh, A.[2], and Mouslemanie, N.[1]. [1]Dept. of Botany, Faculty of Science, University of Aleppo; [2]International Center for Agriculture Research in the Dry Areas (ICARDA), 15 G Ibn Tabib, Giza, Cairo Egypt. *(F.maalouf@cgiar.org)

Biological nitrogen fixation in faba bean is an important and essential phenomenon to enrich soil fertility. The purpose of this study was to evaluate the genetic variation of rhizobium nodulation in an EMS faba bean mutagenesis. A total of 548 mutant lines (M3 generation) derived from BPL710 were evaluated for rhizobium nodulation under insect proof

cages in 2011-2012 cropping season at ICARDA station (Tel Hadya- Syria). The experimental design used was alpha design with two replications and with repetitive parental check BPL710. The rhizobium nodules were scored from 0 (no nodulation) to 5 (high nodulation density). Results showed significant variation among the mutant lines: 28% of the M3 population did not differ from the control in terms nodulation whereas 16% of mutant lines showed higher nodulation and 38% lower nodulation than the check. The line ML486 showed super nodulation (3.58±0.09) and the line ML337 very low nodulation (0.02±0.09) in comparison to the check (2.56±0.09).

91	Nitrogen Fixation and Symbiosis	Molla, M.M	Response of chickpea varieties to Rhizobium inoculation under different agro-ecological zones of Ethiopia.

Response of chickpea varieties to Rhizobium inoculation under different agro-ecological zones of Ethiopia.

Molla, M.M.[1,2*], Walelign, W.W.[2], Rosalind, R.B.[1], Fran, F.W.[3], and Bunyamin, T.[1]. [1]Dept. of Plant Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8; [2]Dept. of Plant Sciences, Hawassa University College of agriculture, Awassa, Ethiopia; [3]Dept. of Soil Sciences, University of Saskatchewan, Saskatoon, Saskatchewan, Canada S7N 5A8. *(mam043@mail.usask.ca)

Low yield of chickpea in Ethiopia is mainly attributed to the lack of improved technology packages. There is a potential to increase chickpea production in the area through the use of Rhizobum. Five chickpea varieties; Natoli, Habru, Ejere, Worku and local land race were tested at three locations over two years (2011 and 2012) in Ethiopia to evaluate their response to inoculation under different agro-ecology. Combined analysis across locations and year indicated that there were highly significant ($p<0.001$) variety effects on yield, branch number, and pod number. Effects of variety on maturity, 100 seed weight, grain yield and harvest index depended on the year and location. Effect of inoculation treatment was not significant for most of the traits. Failure to observe significant N fixation due to inoculation could be resulted from a number of factors including the presence of native rhizobial strains which resulted in high competition, high temperature at planting and nodulation stage, and ineffective inoculant. On the other hand, there were significant variations among varieties for N uptake. Differences in the amount of N removed from the soil among varieties (25-51kg/ha) indicated that there is advantage of using high N fixers over low N fixers. The results of this research demonstrated that early and best performing varieties with preferred marketable seed size and color like Habru and Ejere can be used in the cropping system for improving soil fertility while producing reasonable yield in the rotation system.

92	Nitrogen Fixation and Symbiosis	TROMAS, A	Lotus japonicus AMP1 and HAR1 act synergistically to regulate root architecture

Lotus japonicus AMP1 and HAR1 act synergistically to regulate root architecture

TROMAS, A.[1*], Kim, C.S.[2], Held, M.[3], Suzaki, T.[4], Sato, S.[5], Tabata, S.[5], Kawaguchi, M.[4], and Szczyglowski, K.[1,2]. [1]Agriculture and Agri-Food Canada, Southern Crop Protection and Food Research Centre, London, ON, N5V4T3, Canada; [2]University of Western Ontario, Department of Biology, London, ON, N6A5B7, Canada; [3]University of Minnesota, Department of Biochemistry, Saint Paul, MN 55108, USA; [4]National Institute for Basic Biology, Division of Symbiotic Systems, Aichi 444-8585, Japan; [5]Kazusa DNA Research Institute, Kisarazu, Chiba 292-0812, Japan. *(alexandre.tromas@gmail.com)

Deleterious mutations in the *L. japonicus HYPERNODULATION ABERRANT ROOT FORMATION 1* (*HAR1*) locus lead to hypernodulation and hypermycorrhization phenotypes but also restrict root length and significantly increase root branching of un-inoculated *har1-1* mutant plants. *HAR1* is a central regulator of symbiotic and non-symbiotic root development in *L. japonicus*. A search for genetic suppressors of the *har1-1* phenotype lead to the identification of a root branching hypermorph, called *L. japonicus cluster root-like1* (*crl1*; so named for its superficial resemblance to

genuine cluster roots). Instead of wild-type root architecture, *crl1* forms one large cluster of short rootlets with limited growth capacity. Genetic analyses have shown that the *crl1* root phenotype is determined by two independently segregating recessive mutations, *har1-1* and *Ljamp1-1*. We show that the *L. japonicas AMP1* gene encodes a predicted homologue of the *Arabidopsis* ALTERED MERISTEM PROGRAM 1 protein. As in *Arabidopsis*, the *Ljamp1-1* mutation has a pleiotropic effect on *L. japonicus* as reflected by increased cotyledon number, low fertility and short and highly branched shoots and roots. Thus, root architecture seems to be regulated by a synergistic action between *HAR1* and *LjAMP1* and the simultaneous impairment of these two genes results in reduced apical dominance. Although the *Ljamp1* single mutant root phenotype resembles *har1-1,* the *Ljamp1* mutation does not affect the symbiotic properties of *L. japonicus* Gifu, which isunlike an allelic *Ljamp1* mutation in *L. japonicus* MG20 (Suzaki et al., 2013). We are currently testing the root architecture and nodulation phenotype of two new Gifu null *amp1* mutants.

93	Nitrogen Fixation and Symbiosis	Wang, J.	Towards dissecting the genetic basis of peanut nodulation

Towards dissecting the genetic basis of peanut nodulation

Wang, J.[1,2*], Tan, L.[1], Liu, F.[1], Lopez, Y.[1], and Gallo, M.[3]. [1]Agronomy Department, University of Florida, Gainesville, FL 32611; [2]Plant Molecular and Cellular Biology, Genetics Institute, University of Florida, Gainesville, FL 32611; [3]College of Tropical Agriculture and Human Resources, University of Hawai'i at Mānoa, Honolulu, HI 96822. *(wangjp@ufl.edu)

Peanut rhizobia enter the peanut root primarily through a crack at the sites of lateral root emergence and spread intercellularly in root cortical cells, which does not resemble the infection processes in other model legume species. Understanding the molecular mechanisms of peanut nodulation will reveal novel insights into nodule organogenesis. The objectives of this study are 1) to isolate peanut native rhizobia strains with high nitrogen fixation function and 2) to genetically map the genes controlling the peanut nodulation for the genetic basis studies. Single colonies from peanut nodules were sampled for 16S rDNA sequencing. Seven different rhizobia strains belonging to two different genera, Bradyrhizobium and Paenibacillus were identified. All of the seven strains are Gram-staining positive, and can infect different peanut types and form functional nodules but with varied nodule number and nitrogen fixation rate. To map the genes controlling peanut nodulation, two non-nodulating peanut mutants were cross-pollinated with their nodulating near isogenic peanut lines to generate two F2 segregating populations, respectively. The segregating ratio of nodulating : non-nodulating of the two populations were 9:7 and 3:1, respectively. Genotyping of the two pairs of near isogenic lines revealed their genome identity of 93.6% and 84.6%, respectively. Two markers on chromosome B07 and B06 can explain 20% of phenotypic variance of one F2 population and 9% phenotypic variance of the other F2 population, respectively. Dissecting the genetic basis of peanut nodulation and symbiosis through crack entry infection is critical specifically for developing crop cultivars wtih highly efficient symbiosis.

94	Nitrogen Fixation and Symbiosis	Wijesinghe, M.A.K.	Commercial Arbuscular Mycorrhizal (AM) Inoculants Change the Diversity of AM Communities Associated with Roots and Rhizosphere of Field Pea

Commercial Arbuscular Mycorrhizal (AM) Inoculants Change the Diversity of AM Communities Associated with Roots and Rhizosphere of Field Pea

Wijesinghe, M.A.K.[1*], Germida, J.J.[1], and Walley, F.L.[1]. [1]Department of Soil Science, University of Saskatchewan, Sk, S7N 5A8. *(maw397@mail.usask.ca)

Arbuscular mycorrhizal fungi (AMF) are ubiquitous and crucial for enhancing plant growth and sustaining ecosystem functions. Hence, AMF inoculation is becoming a common technology in agriculture and land reclamation industries, and more recently AMF inoculants have been introduced in western Canada for commercial field crop production.

Field pea is an important pulse crop, and Canada is the world leader in field pea production. Previous research showed that AMF inoculation can improve field pea production and change AMF communities colonizing in field pea roots. However, application rate of commercial inoculant has to be optimized to maximize the yields and reduce the impact on important ecological aspects such as AMF diversity associated with the crop. A growth chamber experiment was conducted to study the impact of different rates of commercial AMF inoculant (*Glomus irregulare*) on field pea growth, nutrient uptake, yield parameters, and AMF communities associated with the roots and rhizosphere of field pea grown in three different soils.

Although soil type had a significant effect on the pea growth and nutrient uptake, the only significant effect detected due to AMF inoculation was root weight. However, pyrosequencing data revealed that commercial AMF inoculation altered the AMF communities associated with rhizosphere and roots of pea. Our results indicate that care has to be taken when selecting commercial mycorrhizal inoculants in improving plant growth.

95	Nitrogen Fixation and Symbiosis	Woo, S.L.	Effects of microbe-legume interactions on agricultural production

Effects of microbe-legume interactions on agricultural production

Woo, S.L.[1,2*], Varlese, R.[1], Vinale, F.[2], Ruocco, M.[2], Lombardi, N.[3], Marra, R.[1], Lanzuise, S.[3], Manganiello, G.[1], Pascale, A.[1], and Lorito, M.[1,2]. [1]University of Naples "Federico II", Dept. Agriculture, Via Università 100, 80055 Portici (NA), Italy; [2]National Research Council–Institute for Plant Protection (CNR-IPP), Via Università 133, 80055 Portici (NA), Italy; [3]University of Naples "Federico II", Dept. Agriculture; Via Università 100, 80055 Portici (NA), Italy. *(woo@unina.it)

The multitude of interactions that occur between soil microbiota and the plant may have a positive as well as a negative impact on agricultural production. Soil microorganism beneficial effects on plants include disease control, growth promotion, enhanced resistance to abiotic stresses, increased nutrient assimilation. The analysis of the entire microbial diversity in the soil is very complex, because efficient characterization methods have thus far been optimized mainly for bacteria, and much less for fungi. In this work, we used a combination of classical plating, New Generation Sequencing and bioinformatics methods to study the microbiome of soil samples collected from fields in crop rotations with different legumes and wheat. The aim was to identify a correlation between the identity and relative abundance of the microbial species present, and observed effects of crop rotations on agronomic parameters, including yield. Interestingly, the use of various selective substrates indicated that, at least for the bacterial component, Colony Forming Unit counts were highest in soils where legumes were grown alone, with lowest CFU levels obtained from no crop (fallow) or wheat alone samples. The importance of the fungal component was also studied by augmenting highly active *Trichoderma* strains used commercially for biological control and seed treatments. The effects on seed germination, plant growth and nutrient assimilation were determined. Understanding the qualitative and quantitative changes of the soil microbiome associated with legume-cereal rotations may allow an increase in the positive outcome of this important agronomic practise, and may provide an opportunity for developing new biofertilizers.

96	Seeds and Nutrition	Adhikari, E.	Genetic and Environmental Effect on Mineral Nutrient Accumulation in Pea

Genetic and Environmental Effect on Mineral Nutrient Accumulation in Pea

Adhikari, E.[1*], Grusak, M. A.[2,3,4,5], and McPhee, K. E.[6]. [1]Plant Sciences Graduate Program, Department of Plant Sciences, North Dakota State University, Fargo ND 58108; [2]Children's Nutrition Research Center; [3]Department of Pediatrics, Baylor College of Medicine; [4]Delta Obesity Prevention Research Unit, Little Rock, AR; [5]USDA-ARS Office of Scientific Quality Review, Beltsville, MD; [6]Department of Plant Sciences, North Dakota State University, Fargo ND

58108. *(elina.adhikari@my.ndsu.edu)

Pea (*Pisum sativum* L.) is a cool season food legume, rich in carbohydrate, protein, vitamins, fiber, amino acids, and mineral nutrient. Genetic control of sensitivity to the environment is a very important consideration for mineral nutrient accumulation in pea. Analysis from regional variety trials in North Dakota and Montana for four successive years will allow the quantification of Ca, Cu, Fe, K, Mg, Mn, P, Se and Zn concentrations in seed and subsequent characterization of genetic, environmental and genotype × environmental interaction effects on mineral nutrient accumulation. Mineral nutrients concentration in the seed was quantified using inductively coupled plasma-mass spectrometer and PROC_GLM (SAS version 9.3) was used to analyze the ecomometric data.Preliminary findings showed that the, genotype x environment effect does not have a significant role play in mineral nutrient accumulation, suggesting, one or a few locations of testing will be adequate for determining genetic potential of mineral nutrient accumulation in pea. The average mean mineral nutrient concentration for different breeding lines of pea at six locations of North Dakota in 2013 was observed to have Ca = 0.70 mg/g Dry weight (DW), Cu = 6.34 µg/g DW, Fe = 55.69 µg/g DW, K = 8.84 mg/g DW, Mg = 1.33 mg/g DW, Mn = 14.23 µg/g DW, P = 3.90 Mg/g DW, Zn = 35.92 µg/g DW.

97	Seeds and Nutrition	Adhikari, E.	Compositional Mineral Nutrient Variation in Lentil

Compositional Mineral Nutrient Variation in Lentil

Adhikari, E.[1*], Grusak, M. A.[2,3,4,5], and McPhee, K. E.[6]. [1]Plant Sciences Graduate Program, Department of Plant Sciences, North Dakota State University, Fargo, ND 58108; [2]Children's Nutrition Research Center; [3]Department of Pediatrics, Baylor College of Medicine; [4]Delta Obesity Prevention Research Unit, Little Rock, AR; [5]USDA-ARS Office of Scientific Quality Review, Beltsville, MD; [6]Department of Plant Sciences, North Dakota State University, Fargo, ND 58108. *(elina.adhikari@my.ndsu.edu)

Mineral nutrient composition in lentil (*Lens culinaris* Medikus subsp *culinaris*) seed varies with genotype, environment and soil conditions in which it is grown. This cool season food legume is rich in dietary protein, amino acids, vitamins, fiber and different mineral nutrients. Mineral nutrient (Ca, Cu, Fe, K, Mg, Mn, P, Se and Zn) concentration in the seed was quantified using inductively coupled plasma-mass spectrometry. Characterization of the effect of genetic, environmental and genotype×environmental interaction in mineral nutrient accumulation at different locations was done using PROC_GLM (SAS version 9.3). Preliminary findings from 4 successive years of regional variety trials showed that, higher soil nutrient content was the key determinant of mineral nutrient accumulation in the seed. Variety showed a significant (P<0.05) effect for average means mineral nutrient accumulation across 12 locations of North Dakota and Montana. The average mean mineral nutrient concentration in 2013 small green lentil breeding lines at three locations of North Dakota was found to be Ca = 0.64 mg/g DW, Cu = 7.18µg/g DW, Fe =70. 37µg/g DW, K =8.21 mg/g DW, Mg = 1.05 mg/g DW, Mn = 15.86 µg/g DW, P = 3.75 mg/g DW, and Zn = 39.73 µg/g DW. Therefore the understanding of genetic potential, environmental effect and the interaction of these two factors in seed mineral nutrient accumulation is very crucial for selection and breeding of a nutrient-dense lentil seed.

98	Seeds and Nutrition	Bangar, P	Increasing iron concentration and bioavailability in field pea

Increasing iron concentration and bioavailability in field pea

Bangar, P.[1*], Diapari, M.[1], Stonehouse, R.[1], Bett, K.E.[1], Whiting, S.[2], Glahn, R.P.[3], and Warkentin, T.D.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8; [2]Department of Pharmacy and Nutrition, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8; [3]USDA-ARS, Cornell University, Ithaca, NY, USA. *(parm.bangar@usask.ca)

This research aims to increase iron concentration and iron bioavailability in field pea seeds. To increase iron concentration, QTL analysis for iron concentration will be conducted in three recombinant inbred line (RIL) populations

(PR-02, PR-07 and PR-15), and arising markers will be validated in a fourth RIL (PR-10). To address increased iron bioavailability, carotenoid and phytate-phosphorus concentrations will be considered. Iron absorption from foods increases with supplementation of carotenoids. In previous research in our group, green cotyledon pea cultivars (16-21µg g-1) were richer in total carotenoids than yellow cotyledon cultivars (7-12 µg g-1), and low phytate phosphorus pea varieties displayed greater iron bioavailability than normal phytate varieties. Hence, iron bioavailability will be compared in two pea populations segregating for cotyledon color and phytate phosphorus concentration using the Caco-2 cell culture model.

99	Seeds and Nutrition	Boux, G.B.	Effects of Pre-milling Treatments of Yellow Peas on Spaghetti Quality

Effects of Pre-milling Treatments of Yellow Peas on Spaghetti Quality

Boux, G.B.[1*]. [1]Cigi. *(gboux@cigi.ca)

Whole yellow pea flour when blended with durum semolina can be successfully used to produce high quality nutritionally enhanced pasta. It has been suggested that pre-treatment of peas prior to milling can improve the nutritional and functional quality of the pea flour. It is not known however, if pre-treatment of the peas prior to milling will effect the end quality characteristics of pasta. Whole yellow peas were pre-treated using dry heat by roasting at 120^0 C for 20 minutes and by infrared/micronization processing. Untreated whole and dehulled peas and roasted and micronized peas were milled into flour using a Buhler lab roller mill and blended using a ratio of 30/70 pea flour to durum semolina. Blended flours were extruded into spaghetti using a Namad lab scale single screw extruder and dried at 85^0 C. Pasta quality was assessed by measuring dried pasta colour, optimal cooking time and cooking loss. Firmness of cooked pasta was also determined using a TA-XT2 texture analyzer. Significantly higher ($p \leq 0.05$) L* and lower a* values were found for spaghetti made with micronized and roasted pea flours compared to the spaghetti made from whole and split pea flours. Micronized pea flour pasta was significantly less firm compared to spaghetti made from dehulled, roasted and whole pea flours. Overall, cooking time and cooking loss were not affected by the addition of pea flour, regardless of the pre-treatment. Spaghetti made from micronized peas had the most comparable quality to conventional 100% durum semolina spaghetti.

100	Seeds and Nutrition	Cichy, K.A.	Genome Wide Association Mapping of Cooking Time in Andean Dry Beans

Genome Wide Association Mapping of Cooking Time in Andean Dry Beans

Cichy, K.A.[1,2*], Salat, Y.[2], and Katuuramu, D.[2]. [1]USDA-ARS, East Lansing, MI; [2]Plant, Soil, and Microbial Sciences Department, Michigan State University. *(karen.cichy@ars.usda.gov)

Dry beans (*Phaseolus vulgaris* L) are a nutrient dense, low cost food and an excellent value for consumers. Consumption, however, is often limited by the long cooking times necessary to make beans edible. This is true in developing countries where cooking fuel is sometimes scarce and in developed countries where consumers don't want to invest time in cooking. Understanding the genetic variability for cooking time in beans would help efficiently breed fast cooking bean varieties. The objective of this study was to evaluate the cooking time and conduct genome wide association mapping on a panel of 250 Andean bean lines which are part of the Andean Diversity Panel (ADP). This germplasm is from diverse market classes and seed types important in major bean growing and consuming regions of Africa and the Americas. The lines were grown in 2012 and 2013 at the Montcalm Research Farm in Entrican, Michigan. The cooking time of each entry was determined using a Mattson cooker. The optimum cooking time was recorded as the time it takes for 80% of the plungers to pierce the seeds. The ADP was genotyped with the BARCBean6K_3 SNP array. Cooking times ranged from 17 to 90 min. Association mapping was conducted with

Tassel 4.0 and revealed significant marker trait associations on chromosomes Pv02 and Pv05.

101	Seeds and Nutrition	Dhaubhadel, S.	Seed coat RNAseq analysis of two Pinto bean cultivars that differ in post-harvest seed coat darkening

Seed coat RNAseq analysis of two Pinto bean cultivars that differ in post-harvest seed coat darkening

Dhaubhadel, S.[1,2*], Austin, R.[1], Marsolais, F.[1,2], Mainali, H.R.[2], Poormohammadvalibehnami, S.[2], Pajak, A.[1], and Chen, L.[1]. [1]Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON, Canada N5V 4T3; [2]Department of Biology, University of Western Ontario, London, ON, Canada N6A 5B7. *(sangeeta.dhaubhadel@agr.gc.ca)

Post-harvest seed coat darkening in pinto bean is an undesirable trait resulting in a loss in the economic value of the crop. During the storage of the bean, seed coat color changes from bright white to pale white or dark. The extent of darkening varies between the cultivars and the storage condition. The main objective of this research is to identify and characterize gene (s) controlling the post-harvest seed coat darkening in pinto bean. A comparative gene expression analysis was conducted in two pinto bean cultivars: CDC Pintium (regular darkening, rd) and 1533-15 (slow darkening, sd). Total RNA was isolated from the seed coat tissues of both cultivars and RNA-seq performed using 4 biological replicates per cultivar on an Illumina HiSeq. This yielded over 295 million 100 bp paired-end reads, with an average of 18 million read-pairs per replicate. Reads were mapped to representative transcripts of the *Phaseolus vulgaris* genome (Phytozome release V1.0, "Primary Transcript Only" file) using BWA (base quality >30; mapping quality >20). Read counts for each transcript were then assessed for differential expression between cultivars using the R package DESeq. Genes such as phenylpropanoid genes, transporters, and those involved in regulation or modification were found differentially expressed between CDC-Pintium and 1533-15.

102	Seeds and Nutrition	Diederichsen, A.	Seed characteristics in cultivated Cicer arietinum and wild Cicer species preserved by Plant Gene Resources of Canada

Seed characteristics in cultivated *Cicer arietinum* and wild *Cicer* species preserved by Plant Gene Resources of Canada

Diederichsen, A.[1*], Kessler, D.[1], and Sander, T.[1]. [1]Plant Gene Resources of Canada (PGRC), Agriculture and Agri-Food Canada (AAFC), 107 Science Place, Saskatoon, SK, S7N0X2. *(axel.diederichsen@agr.gc.ca)

Crop wild relatives have recently gained more attention by researchers and plant breeders as a source of genetic diversity for increasing resilience in cultivated plants. For cultivated chickpea (*Cicer arietinum* L.), the primary genepool includes the cultivated species and the species *C. reticulatum* Ladiz., which therefore is sometimes also considered a subspecies of *C. arietinum*. The secondary genepool contains *C. echinospermum* P.H. Davis and the tertiary genepool has the remaining 7 annual and 35 perennial species of the genus *Cicer*. The Canadian genebank, Plant Gene Resources of Canada (PGRC), maintains collections of 8 annual and 10 perennial *Cicer* species, which have been characterized for morphological features relevant for species identification. Of particular interest are seed characteristics, as the genetic effects on seed characteristics are of great relevance when using wild *Cicer* species in crossings with *C. arietinum*. In cultivated *C. arietinum*, the 1000 seed weight in 495 accessions at PGRC ranged from 95 g to 483 g. In the 8 annual species it ranged from 15.3 g to 226.6 g. In the perennial species it ranged from 17.0 g to 120.7 g. Some wild *Cicer* taxa produced seeds that were comparable in size to seeds of the small seeded cultivated types of *Cicer arietinum*. Although most wild species shatter the seeds spontaneously, some differences in this character were also observed. While many wild legumes have bitter seeds, this was not found in the *Cicer* species at PGRC. These findings suggest that that seeds of the wild *Cicer* species may be attractive to wild animals but may also have attracted attention by early human seed gatherers.

103	Seeds and Nutrition	Emmrich, P.M.F.	Lifting the curse of the grass pea

Lifting the curse of the grass pea

Emmrich, P.M.F.[1*], Wang, T.L.[1], and Martin, C.[2]. [1]John Innes Centre, Norwich Research Park, NR4 7UH, United Kingdom; [2]John Innes Centre - Department of Metabolic Biology, Norwich Research Park, NR4 7UH, United Kingdom. *(peter.emmrich@jic.ac.uk)

Highly tolerant to drought as well as flooding, rich in protein and able to able to grow with virtually no inputs, the grass pea (*Lathyrus sativus*) is an excellent food source for low-income countries. In times of weather extremes it is often the last crop standing and sustains people and livestock through times of famine. But with this blessing comes a curse: grass peas produce a toxin (β-N-oxalyl-L-2,3-diaminopropionic acid; β-L-ODAP) that can cause permanent paralysis of the legs in people suffering from malnourishment. This often strikes the poorest in society, many of whom have to rely solely on grass pea in times of famine. Relatively little research attention has been focused on this crop and even the function of the toxin in the plant remains highly controversial. The levels of the toxin in the seed appear to be very sensitive to the environment and all attempts to produce a reliably toxin-free variety by breeding using natural variation have been unsuccessful.

We are performing a large-scale screen of EMS-mutagenised seedlings for toxin-free mutants of grass pea, in order to unlock the potential of this life-saving crop. Identifying complete knockout mutants of β-L-ODAP-synthesis will allow us to study the role of the toxin in the plant. More importantly, they will provide a resource for plant breeders to develop toxin-free cultivars that can be safely consumed by humans and livestock. This development could directly benefit millions of people facing malnutrition, extreme poverty and a changing climate.

104	Seeds and Nutrition	GAAD, D.	Morphological and Biometrical characterization of seeds of some Algerians lentil accessions: Quantitative and Qualitative characters.

Morphological and Biometrical characterization of seeds of some Algerians lentil accessions: Quantitative and Qualitative characters.

GAAD, D.[1,2*], Laouar, M.[1], and Abdelguerfi, A.[1]. [1]National School of Agriculture-El Harrach-Algeria; [2]National Research Center for Biotechnology-Constantine-Algeria. *(gaad_djouher@yahoo.fr)

Abstract. The preliminaries characterization of a collection of thirty two Algerians accessions of lentil (*Lens culinaris* M.) were done before sown. Seed thickness (STH), Seed diameter (SDM), thickness/diameter ratio (T/D) and Weight of 100 seeds (WHS), are a quantitative traits measured. Altitude and Rainfall of location of origin of accessions are considered as a supplement variables.Also, qualitative characters: Grain form (GFR), Ground color of seed testa (GCT), Pattern of testa (PAT), Cotyledons color (COC), were considered.

From the result of Principal Component Analysis (PCA), axis 1 explains 65.08% of the variance in the qualitative character and it showed a strange negative correlation with seed diameter (DMT), Weight of 100 seeds (PCG) and altitude (ALT).Whereas, it was positively and significantly correlated with thickness/diameter ratio (E/D) variable. The second component, accounting for 23.58 % of the total variation, was correlated positively with seed thickness (EPS). Hierarchical discriminate analysis revealed major differences between accessions from different regions. Three major regional groups were apparent: 1) a Western group characterized by accessions of the *Macrosperma* type, 2) a more Northern group of the *Microsperma* type and 3) A mixture group gathered all regions and the two types.

Regarding qualitative traits, the application of Multiple Correspondence Analyses (MCA) showed that seeds with globular form (*Microsperma*) are two types: 1) Brown or green tasta with yellow cotyledons and 2) Brown tasta with

orange cotyledons. In addition, seeds with flat form (*Macrosperma*) are divided into two types:1) Brown, Beige or Green tasta with yellow cotyledons, 2) Brown tasta with dotted seed coat pattern and orange cotyledons.

105	Seeds and Nutrition	Gaikwad, N. B.	Trypsin inhibitor, Polyphenol and Lectin content in Soybean (Glycine max (L.) Merrill)

Trypsin inhibitor, Polyphenol and Lectin content in Soybean (*Glycine max* (L.) Merrill)

Gaikwad, N. B.[1*], and Sawant, R. S.[1]. [1]Department of Botany, Shivaji University, Kolhapur -416 004, Maharashtra, India. *(nbgaikwadsu@gmail.com)

Soybean seeds are considered as a good source of protein and oil, but presence of anti nutritional factors in soybean exerts a negative impact on the nutritional quality of soybean. Considering the nutritional importance of soybean, sixty soybean genotypes were analyzed for trypsin inhibitor, polyphenol and lectin content. The trypsin inhibitor content ranged from 310.69 TIU/min/g seed powder to 1083.33 TIU/min/g seed powder. The polyphenol content ranged from 6.9 mg/g to 10.7 mg/g of seed powder. Lectin activity was determined by hemagglutination assay using erythrocytes which showed a range of specific activity from 3.67 to 86.95. The results obtained certainly demonstrated the great variation in the anti nutrient content in soybean genotypes. The soybean genotypes with low anti nutrient content are highly significant nutritionally.

106	Seeds and Nutrition	Grusak, M. A.	Plant genotype, location, and their interaction effects on the concentrations of selected minerals in seed of kabuli chickpea breeding lines and cultivars examined in the US Pacific Northwest.

Plant genotype, location, and their interaction effects on the concentrations of selected minerals in seed of kabuli chickpea breeding lines and cultivars examined in the US Pacific Northwest.

Grusak, M. A.[1*], and Vandemark, G. J.[2]. [1]USDA-ARS Children's Nutrition Research Center, Houston ,TX 77030; [2]USDA-ARS Grain Legume Genetics and Physiology Research Unit, Pullman, WA 99163. *(mike.grusak@ars.usda.gov)

Dietary mineral deficiencies contribute to a wide range of human health issues. Developing pulse crops with elevated seed concentrations of minerals can contribute to alleviating the effects of these maladies. The objectives of this study were to examine variance components that affect the concentration of minerals in chickpea seeds and to identify chickpea genotypes with high concentrations of selected minerals. The concentrations of 14 different minerals (B, Ca, Co, Cu, Fe, K, Mg, Mn, Mo, Na, Ni, P, S, and Zn) were determined from seed samples of 18 kabuli chickpea breeding lines and four cultivars grown at three locations in WA and ID over two years (2010 - 2011). Significant genotype, location, and their interaction effects were observed for all 14 minerals. Many significant correlations were observed between pairs of minerals. For example, the concentration of magnesium (Mg) had a positive and significant correlation with the concentration of several other minerals including Ca, Fe and P. The concentration of potassium (K), a nutrient of concern for cardiovascular health, had a significant negative correlation with concentrations of Ca, Fe, and Mg. The greatest positive correlation (0.58) was between concentrations of K and P. Breeding lines and cultivars were identified with high seed concentrations of several minerals. These results have allowed us to identify promising genotypes for use in developing nutritionally improved chickpea cultivars.

107	Seeds and Nutrition	Hu, J.	L-DOPA (L-3,4-dihydroxy phenylalanine) concentration variation in the leaf and flower tissues of six faba bean lines

L-DOPA (L-3,4-dihydroxy phenylalanine) concentration variation in the leaf and flower tissues of six faba

bean lines

Hu, J.[1*], Kwon, S. J.[1], Park, J. J.[2], Landry, E. J.[3], Mattinson, D. S.[4], and Gang, D. R.[2]. [1]USDA-ARS Western Regional Plant Introduction Station, 59 Johnson Hall, Washington State University, Pullman, WA 99164, USA; [2]Institute of Biological Chemistry, Washington State University, Pullman, WA 99164, USA; [3]Department of Crop and Soil Sciences, Washington State University, Pullman, WA 99164, USA; [4]Department of Horticulture, Washington State University, Pullman, WA 99164, USA. *(jinguo.hu@ars.usda.gov)

L-DOPA (L-3,4-dihydroxy phenylalanine) is the major ingredient of several prescription drugs used to treat Parkinson's disease (PD), the second most common neurodegenerative disorder. PD is characterized by the loss of muscle control, which causes trembling of the limbs, head as well as impaired balance. L-DOPA can cross the blood-brain barrier, where it is converted to dopamine, a monoamine neurotransmitter. We investigated the variation of L-DOPA concentration in the leaf and flower tissues of six faba bean accessions with common and rare flower colors in two consecutive years, using an ACQUITY UPLC in line with a Synapt G2 HDMS quadrupole time-of-flight mass spectrometer. Our study revealed a high level of variation in L-DOPA concentration for leaf and flower tissues among six faba bean lines studied in two consecutive years. The average L-DOPA concentration based on dry weight (DW) in flowers ranged from 27.8 to 63.5 mg/g and 18.2 to 48.7 mg/g for leaf tissues. There was no significant correlation between L-DOPA concentrations in flowers and leaves. The crimson flower line had the highest L-DOPA concentration (63.5 and 64.3 mg/g) in flowers for both years. The brown flower line had high average L-DOPA concentrations for flowers (55.7 mg/g) and leaves (48.7 mg/g) across both years compared to the other lines tested. It seems that the brown flower line is the most promising genetic resource for developing a functional food crop, as a potential natural remedy for improving the quality of life for the estimated seven to ten million PD patients worldwide.

108	Seeds and Nutrition	Joshi, J.	Analysis of candidate enzymes for the biosynthesis of S-methylcysteine in seed of common bean (Phaseolus vulgaris)

Analysis of candidate enzymes for the biosynthesis of S-methylcysteine in seed of common bean (Phaseolus vulgaris)

Joshi, J.[1,2*], Pandurangan, S.[1,2], and Marsolais, F.[1,2]. [1]Department of Biology, University of Western Ontario, London, ON, Canada; [2]Genomics and Biotechnology, Southern Crop Protection and Food Research Centre, Agriculture and Agri-Food Canada, 1391 Sandford Street, London, ON, Canada. *(jjoshi7@uwo.ca)

Common bean (*Phaseolus vulgaris)* provides 22% of the total protein requirement worldwide. While high level of protein, fibre and minerals has defined the importance of common bean in the human diet, sub-optimal protein quality due to low levels of essential sulphur amino acids, Met and Cys, requires a dedicated scientific approach for improvement. Seeds accumulate high levels of the non-protein sulphur amino acid, *S*-methylcysteine (SMC), which cannot substitute for Met or Cys in the diet. Information on SMC biosynthesis could help formulate a strategy to improve Met and Cys levels. Comparative transcriptome analysis of *P. vulgaris* with *Vigna mungo*, which accumulates g-Glu-Met rather than g-Glu-*S*-methylcysteine, helped to build a candidate gene approach for the SMC biosynthetic pathway. Among β-substituted alanine synthase (BSAS) family members, *BSAS3;1*,encoding a b-cyanoalanine synthase, had 10-fold higher expression in *P. vulgaris*. A *BSAS3;1* cDNA was cloned from *P. vulgaris* and an N-terminal His-tagged protein, lacking a predicted chloroplast transit peptide, was produced in *Escherichia coli*. Purified BSAS3;1 was highly active as a b-cyanoalanine synthase, using cyanide and Cys as substrates. The enzyme catalyzed a similar thiol exchange reaction with methanethiol and Cys as substrates, forming SMC. The rate of the two reactions was similar. The enzyme had a higher affinity for cyanide than methanethiol. However, the apparent *Km* value for methanethiol was in the low mM range. This work identifies BSAS3;1 as a putative candidate enzyme for the

formation of SMC in seeds of common bean.

109	Seeds and Nutrition	Jaillais, B.	Phenotyping of internal structure of seeds of legume crops by imaging and chemometrics

Phenotyping of internal structure of seeds of legume crops by imaging and chemometrics

Jaillais, B.[1*], Bertrand, D.[2], Magnin-Robert, J.B.[3], and Duc, G.[4]. [1]INRA, Nantes, France; [2]data_frame, Nantes, France; [3]INRA, Dijon, France; [4]INRA, DIjon, France. *(benoit.jaillais@nantes.inra.fr)

Improvement of phenotyping in legume breeding is a major challenge to increase yield or to imagine novel food uses. The analysis of large genetic resources collections requires for developing fast, cheap and reliable screening tools and related data processing.

Artificial vision with several lighting of different wavelengths seems to be a good alternative to characterize seeds of genetic resources collections. This technique consists in the acquisition of a set of spectral images on a unique sample. The aim of this work is to develop a new methodology of seeds phenotyping, which can be applied to different legume species.

To achieve this goal, we have used multispectral imaging and chemometrics for evaluating the phenotypic variability of the internal structure of faba bean and lupin seeds. For each cultivar, 10 seeds were cross-sectioned at half-length and a multispectral image (spatial size of 10 mm * 9 mm) of this section was acquired. The images gave many relevant pieces of information about the variability of some criteria related to internal texture, shape parameters and color. Some spectral signatures were assigned to tissues and exploited to label histological areas in seeds. PCA analysis of these images highlighted that some cultivars a low intra-genotype variability, and that the inter-genotypic variability was higher than intra genotype for shape of seeds.

110	Seeds and Nutrition	Kang, B.K.	The Effect of sprouting temperatures on Growth characteristics, Protein content and Antioxidant activity of Pea(Pisum sativum L.) sprouts

The Effect of sprouting temperatures on Growth characteristics, Protein content and Antioxidant activity of Pea (*Pisum sativum* L.) sprouts

Kang, B.K.[1*], Kim, H.Y.[1], Choi, M.S.[1], Koo, S.C.[1], Lee, Y.H.[1], Kim, H.T.[1], Yun, H.T.[1], and Baek, I.Y.[1]. [1]Department of Functional Crop, NICS, RDA, 20, Jeompiljaero, Miryang, 627-803, Korea. *(hellobk01@hotmail.com)

Pea, *Pisum sativum* L, is an important legume crop grown throughout the world. Here we show characteristics of pea sprouts and optimum germplasms for a sprout material. Peas were germinated at 20°C, 23°C and 25°C during 7 days. We investigated characteristics of Pea sprouts and analyzed protein, antioxidant compounds and activities.

It was a 5 day that Hypocotyl length was adequate to use as a food because the average length was close to 8cm that is known as the most preferable length of soybean sprouts. The range of whole length, hypocotyl length, thickness and yield rate of sprouts germinated at 20°C, 23°C and 25°C on 5day was 10.4∼20.8㎝, 4.4∼12.1㎝, 1.22∼1.53㎜, 329∼677%, respectively. PI269803 and PI343300 had high yield rate at 23°C on 5day.

The range of protein at 20°C, 23°C and 25°C on 5 day was 22.8~36.2%. PI269803 had the highest protein content among 5 germplasms. Protein contents are not significantly different among three temperatures except PI343283 and PI343307.

Total polyphenol content(㎎ GA eq/g), DPPH and ABTS radical scavenging activity(㎎ Trolox eq/100g sample) of

PI269803 at 23°Con 5 day were 257, 146, 96 repectively and the values at 23°C were higher than at 20°C and 25°C. Three values at 23°C of PI343300 were also higher than at 20°C and 25°C.

Yield rate and Antioxdidant activities of pea sprouts germinated at 23°C on 5 day were higher than at 20°C and 25°C. Especially, PI269803 and PI343300 were promising to use them for pea sprouts because of high yield rate and high Antioxidant activities.

111	Seeds and Nutrition	Kim, S.U.	Variation of lignan content for sesame seed across origin and growing environments

Variation of lignan content for sesame seed across origin and growing environments

Kim, S.U.[1*], Oh, K.W.[1], Lee, M.H.[1], Lee, B.K.[1], Hwang, C.D.[1], Pae, S.B.[1], Jung, C.S.[1], Kim, M.S.[1], and Baek, I.Y.[1]. [1]RDA NICS, 20th, Jeompiljaero, Miryang, Gyeongnam, 627-803, Rep. of Korea. *(sesameup@korea.kr)

Sesame lignan, including sesamin and sesamolin has been reported to exhibit an antioxidant, antihypertensive and anticancerous activities. The objective of this study were to analyze the lignan variation of 143 sesame accessions from core collection in Korea and to test the effects of growing years and locations on lignan and lipid content of Korea sesame elite lines.

143 core sesame accessions in Korea had broad variation of lignan content from 2.33 to 12.17㎎/g with an average 8.18㎎/g. Among tested sesame accessions, the IT184615 had the highest lignan content of as 12.17㎎/g. So this accession will be a good genetic resource for developing a high lignan sesame variety. The sesamin and sesamolin content for sesame accessions had significant difference across origin and seed coat color.

Twenty two sesame elite lines were cultivated in three locations. The analysis of variance showed that the variation of lignan and lipid content was significantly different across elite lines, locations and their interaction.

Thirty four sesame elite lines were cultivated for three consecutive years. The analysis of variance showed that the variation of lignan and lipid content was significantly different across elite lines, years and their interaction.Therefore, it is important to use sesame accessions having high lignan content. Besides we need to study about environmental condition related with accumulation of lignan.

112	Seeds and Nutrition	Kundu, Shudhangshu	Optimizing zinc analysis of seeds of wild lentil species

Optimizing zinc analysis of seeds of wild lentil species

Kundu, SHUDHANGSHU.[1*], and Vandenberg, Albert.[1]. [1]Department of Plant Sciences/Crop Development Centre, University of Saskatchewan. *(ssk637@mail.usask.ca)

Lentils (*Lens culinaris* Medik. ssp. *culinaris)* are a source of protein, fiber, vitamins, antioxidants and both mesonutrients (K, Ca, P, Mg and Na) and micronutrients (Fe, Zn, Cu, and Mn). Lentil is a good source of dietary Zn, which plays has a major role for normal growth, development, and activity of various enzyme systems in plants and animals. An overall goal in cultivated lentil breeding is expansion of available genetic variability using wild crop relatives. Seeds of wild lentil species are much smaller than those of the cultivated species, and are relatively difficult to produce in large quantities because the plants are small and have dehiscent pods. Flame atomic absorption spectrometry (F-AAS) is often used for micronutrient analysis because it combines fast analysis time and relative simplicity with cheap analytical performance. Our objective was to determine the minimum number of seeds required to achieve the minimum acceptable experimental error in F-AAS determination when using whole seed digestion as an alternative to the use of ground seed samples. Seed samples of one accession from each lentil species in the

genus *Lens* were evaluated in experiments to determine Zn concentration by F-AAS. Overall, results show that a sample of 20 seeds is sufficient for reliable determination of Zn concentration for F-AAS.

113	Seeds and Nutrition	Liu, X.	Iron bioavailability in low phytate pea

Iron bioavailability in low phytate pea

Liu, X.[1*], Glahn, R.[2], Bett, K.[1], and Warkentin, T.D.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan; [2]USDA-ARS, Cornell University, Ithaca, NY, USA. *(xil044@mail.usask.ca)

Field pea (*Pisum sativum* L.) seeds have high nutritional value but also contain anti-nutritional factors such as phytate or polyphenols which can inhibit the absorption and utilization of iron. To increase the iron nutritional value of field pea seeds, two low phytate lines (1-150-81 and 1-2347-144) containing higher inorganic phosphorus concentration (IN-P) and lower phytate-phosphorus concentration (PA-P) than the normal phytate varieties were developed from CDC Bronco in previous research. This research used the *in vitro* digestion/Caco-2 cell culture bioassay to determine the effect of genotype and environment on iron bioavailability in low and normal phytate pea varieties, the effect of seed coats on iron bioavailability in varieties differing in seed coat pigmentation, and the inheritance of iron bioavailability in field pea by evaluating RILs differing in phytate concentration. Iron concentration did not differ significantly between normal and low phytate varieties. Iron bioavailability (FEBIO) of the two low-phytate lines was 1.4 to 1.9 times higher than that of the three normal phytate varieties, although environment played a significant role. Pea varieties with pigmented seed coats contained 7 times lower FEBIO than varieties with non-pigmented seed coat. The removal of the seed coat increased the FEBIO in peas with pigmented seed coat by 5 to 6 times. FEBIO followed a bimodal frequency distribution in the PR-15 RIL population, characteristic of single gene control, and was highly correlated with PA-P.

114	Seeds and Nutrition	Loader T.	Effect of Yellow Pea Flour Protein Content on End-Quality of Spaghetti

Effect of Yellow Pea Flour Protein Content on End-Quality of Spaghetti

Loader, T.[1*], Maskus, H.[1], and Bourre, L.[1]. [1]Canadian International Grains Institute. *(tloader@cigi.ca)

North American consumers have been demanding more protein in their diets to promote weight loss and satiety. With increasing rates of obesity and chronic disease it is necessary to optimize formulations for health-promoting products containing protein-rich ingredients like pulses such as yellow peas. By roller milling peas, the production of pea flour streams with low (21%), med (24%), and high (26%) protein levels were achieved. Partial replacement of durum semolina for yellow pea flour (YPF) in spaghetti can increase consumer intakes of protein but may affect sensory attributes and cooking quality of spaghetti. The objective of this work was to enhance the protein content of YPF and assess the effect of pea protein content on durum/pea spaghetti quality properties. Spaghetti was processed following a low temperature-long time drying method of 50°C for 16.5 hours. Colour, texture, and cooking quality of spaghetti were analyzed. Results demonstrated significant differences ($p<0.05$) in colour of spaghetti as affected by pea protein content, where high protein YPF spaghetti had increased redness (9.6) and yellowness (54.8) values compared to low protein YPF spaghetti redness (7.3) and yellowness (51.1). Med protein YPF spaghetti was also significantly more yellow than low protein YPF spaghetti ($p<0.05$). No significant differences in brightness, texture, or cooking quality ($p\geq0.05$) were observed among the three spaghetti formulations indicating that YPF with high protein content can be utilized in spaghetti to improve nutritional value without compromising quality.

115	Seeds and Nutrition	Lu, JL	Starch morphology and compositions correlate with protein contents in field peas

Starch morphology and compositions correlate with protein contents in field peas

Lu, JL.[1*], Hou, HW.[1], and Bing, DJ.[2]. [1]Lethbridge Research Centre, AAFC, Lethbridge, Alberta T1J4B1, Canada; [2]Lacombe Research Centre, AAFC, Lacombe, Alberta T4L 1W1, Canada. *(luj@agr.gc.ca)

Field pea (*Pisum sativum* L.) is the largest pulse crop in Canada. With an annual acreage of approx. 4 million acres and an annual production of almost 3 million tons, Canada is the largest field pea producer and exporter in the world. To develop Canadian pea cultivars with special or unique characteristics for functional food applications, a long-term breeding program has been established to improve pea protein content in AAFC-Lacombe. In this study, 64 pea germplasm and breeding lines were investigated for their protein content, starch morphology and compositions. Field peas normally contain approx. 23% protein. Some pea lines developed in our breeding program or pea germplasm show over 30% protein, in which MI3391 and P0538-60 have 34.9% and 33.3%, respectively. There are significant differences on starch granule morphology, starch and amylose contents between common field peas and high protein peas. Scanning electron microscopy (SEM) revealed that starch granules of common field peas show an oblong or kidney shape, but high protein peas have small starch granules with irregular polygonal shapes. There is a negative correlation between protein and starch contents in field peas. Common field peas have approx. 44-48% total starch contents, but MI3391 and P0538-60 have 27.2% and 29.2%, respectively. In contrast, the high protein peas have significantly high amylose contents. Common field peas have approx. 50% amylose in starch granules, but high protein pea lines P0538-7 and P0540-9 have 89.2% and 87.6%, respectively.

116	Seeds and Nutrition	Mahla Mirali, M.M.	Polyphenols in whole seeds and seed coats of lentil market classes.

Polyphenols in whole seeds and seed coats of lentil market classes.

Mahla Mirali, M.M.[1*], Albert Vandenberg, A.V.[1], and Randy W. Purves, R.W.P.[1,2]. [1]Plant Sciences Department, University of Saskatchewan, Saskatoon, SK S7N 5A8; [2]ACRD, National Research Council of Canada, Saskatoon, SK S7N 4K9. *(mam194@mail.usask.ca)

Polyphenols are a large group of secondary metabolites in plant tissues that are characterized by the presence of an -OH group and an aromatic ring. These metabolites are associated with health benefits in human nutrition, for example, anti-oxidant, anti-tumour, and anti-heart disease properties. Lentils (*Lens culinaris* Medik.) are a good source of polyphenols as well as proteins, carbohydrates, dietary fiber, minerals, and vitamins. Most polyphenols in lentils are in the seed coat, which can have a range of patterns and colours including green, tan, gray, brown, and black. The seed coat colour and pattern determine the market class and value of lentils in specific end use markets around the world. Whole seeds and hull samples of lentil seeds with 5 different base colours were compared to determine the specific polyphenol profile of anthocyanidins, flavan-3-ols, flavones, flavonols, hydroxybenzoic acids, proanthocyanidins and stilbenes. Experiments were conducted using HPLC with UV detection coupled to a triple quadrupole mass spectrometer equipped with an electrospray ionization interface. The results showed that genotypes with black seed coats had the highest content of flavones and flavonols in while the green seed coat genotypes were rich in the flavan-3-ols. Furthermore, the results for the whole seed and seed coat samples were correlated showing that using the whole seeds as a direct food or the seed coats as an ingredient in processed foods could be a good source of dietary polyphenols. Knowing the specific phenotypic polyphenol profile of each lentil market class, and associating these with the genetic basis for the profile, will allow breeders to efficiently design genetic improvement strategies for the nutritional profile of lentils.

117	Seeds and Nutrition	Nayyar, H	Heat stress impairs reproductive function, sucrose metabolism and severely reduces seed yield in Chickpea and Lentil genotypes

Heat stress impairs reproductive function, sucrose metabolism and severely reduces seed yield in Chickpea and Lentil genotypes

Nayyar, H.[1*], Gaur, P.[2], Siddique, K.H.M.[3], Singh, S.[4], Kumar, S.[5], Kaushal, N.[6], and Bhandari, K.[6]. [1]Panjab University, Botany Department, Chandigarh; [2]International Crops Research Institute for Semi-Arid Tropics, Hyderabad, India; [3]The UWA Institute of Agriculture, The University of Western Australia, Crawley WA 6009, Australia; [4]Panjab Agricultural University, Ludhiana 141001, India; [5]International Center for Agricultural Research in the Dry Areas , Morocco; [6]Department of Botany, Panjab University, Chandigarh 160 014, India. *(harshnayyar@hotmail.com)

The global mean surface air temperature has increased by 0.5°C during the 20th century and is expected to rise a further 1.5–4.5°C this century. This steady elevation of temperature, especially in tropical and sub-tropical regions, is proving detrimental for the growth and yield of crops, leading to significant loss of yield potential. Cool-season food legumes Chickpea and Lentil have been found to be highly sensitive to temperatures higher than 32/20oC (day/night), especially during reproductive stages, which result in abortion of flowers and pods as well as poorly-developed seeds. These legumes are likely to face increasing spells of heat stress at the time of flowering and podding stages as a result of change in cropping patterns and expansion of their cultivation to warmer environments. Our group focus on the developmental and physiological mechanisms associated with reproductive failures in chickpea and lentil, which have not been established so far. Our approach involves screening the germplasm for contrasting heat sensitivity, followed by investigation at various organisational levels to establish the reasons associated with heat tolerance/sensitivity. Our tests include photosynthetic stability, carbon assimilation in leaves, sucrose synthesis and its utilization in leaves and anthers, leaf water status, stomatal conductance. The flowers are assessed for the functioning of pollen grains on the basis of some tests on pollen viability, pollen germination, fertilization events, stigma receptivity and ovule viability. The plants are also being grown in growth chambers at varying day/night temperatures to assess their sensitivity to various high temperature situations. Our findings have revealed sucrose metabolism in leaves and anthers as a vital mechanism governing the reproductive function. Information on these aspects would be presented.

118	Seeds and Nutrition	Pastor-Corrales, M.A.	Establishment of the Andean Diversity Panel and its implementation in screening for key dry edible bean production: constraints and nutrition traits for Sub-Saharan Africa

Establishment of the Andean Diversity Panel and its implementation in screening for key dry edible bean production: constraints and nutrition traits for Sub-Saharan Africa

Porch, T.[1], Cichy, K.[2], Grusak, M.A.[3], Pastor-Corrales, M.A.[4*], Miklas, P.[5], and Fourie, D.[6]. [1]USDA-ARS, Mayaguez, Puerto Rico; [2]USDA-ARS, East Lansing, Michigan, USA; [3]USDA-ARS, Houston, Texas, USA; [4]USDA-ARS, Beltsville, Maryland, USA; [5]USDA-ARS, Prosser, Washington, USA; [6]ARC-Grain Crops Institute, Potchefstroom, South Africa. *(talo.pastor-corrales@ars.usda.gov)

Large-seeded dry edible beans (*Phaseolus vulgaris* L.) are preferred by consumers in the markets of sub-Saharan Africa. These large-seeded beans derive from the Andean gene pool. With the goal of genetic improvement of large-seeded beans for Sub-Saharan Africa in mind, we sought to assemble and characterize a panel of Andean accessions for disease resistance, drought tolerance, low fertility tolerance, biological nitrogen fixation capacity, seed nutrient density, and cooking duration. The Andean Diversity Panel (ADP) consists of more than 400 accessions primarily from Africa and the Americas. The ADP has been grown under field conditions in South Africa, Mozambique, Tanzania, Uganda, Zambia, Haiti, Honduras, Puerto Rico, and the United States to screen for various phenotypic traits. Lines with superior performance under various biotic, especially disease, and abiotic stress conditions have been identified and are being utilized in breeding programs. The ADP has also been genotyped with 5398 SNPs (Illumina Infinium

BeanChip). Association mapping that revealed QTL for different traits. This work is supported by the Norman Borlaug Commemorative Research Initiative between USAID Feed-the-Future and USDA-ARS, and benefits from partnership with the ARC-Grain Crops Institute.

119	Seeds and Nutrition	Singh, Renu	To exploit genotype x environment interactions (G x E) for developing mung bean with increased micronutrients

To exploit genotype x environment interactions (G x E) for developing mung bean with increased micronutrients

Singh, RENU.[1,2*], Sjaak van Heusden, A. W.[1], Kumar, R.[3], and Visser, R.G.F.[1]. [1]Laboratory of Plant Breeding, Plant Research International (PRI), Wageningen University, The Netherlands; [2]Department of Biotechnology and Molecular Biology, CCS Haryana Agricultural University, Hisar, Haryana, India; [3]Department of Plant Breeding, College of Agriculture, CCS Haryana Agricultural University, Hisar, Haryana, India. *(renuboora@gmail.com)

One of the benefits of mung bean is its nutritional properties. Of the seven essential micronutrients, especially iron and zinc play a vital role in human and animal health. Breeding for varieties with a potential high concentration of micronutrients should be complemented with studies of environmental effects on the accumulation of micronutrients in seeds. GxE interactions were studied for plant height, number of pods and branches per plant, seed yield, iron and zinc seed content. Our major emphasis was to see the effect of iron and zinc supplementation on seed micronutrient content and other agronomic traits. Therefore, to study different compositions of the soil, six artificial conditions with different levels of micronutrients were created. Soil supplemented with ZnSO4 or with ZnSO4 and 0.5% FeSO4 was beneficial for agronomic traits but not favourable for iron and zinc content of seeds. The main effects and interactions were statistically significant different. Three stability parameters (Mean, bi and S2di) were calculated. No genotypes were found where the seed yield was not influenced by changes in environmental conditions.

120	Seeds and Nutrition	Smykal, P.	Structural, genetical and chemical analysis of the seed coat role in establishment of dormancy of the pea seed

Structural, genetical and chemical analysis of the seed coat role in establishment of dormancy of the pea seed

Smykal, P.[1*], Soukup, A.[2], Saldanha, H.[3], and Bednář, P.[3]. [1]1 Department of Botany, Palacký University in Olomouc, Czech Republic; [2]2 Department of Experimental Plant Biology, Charles University, Prague, Czech Republic; [3]3 Regional Centre of Advanced Technologies and Materials, Department of Analytical Chemistry, Palacký University in Olomouc, Czech Republic. *(petr.smykal@upol.cz)

Timing of seed germination is one of the key steps in plant life. It determines when plants begin growth in natural or agricultural ecosystems. In the wild, many seeds exhibit dormancy. In contrast, crops germinate as soon as they are imbibed usually at planting time. Moreover, legume seed imbibition has a crucial role in cooking ability. Physical dormancy involves the development of a water-impermeable seed coat. The objective of our study is to identify genetic, structural a chemical basis of seed dormancy by comparative analysis of wild and domesticated pea genotypes. We have tested seed imbibition and germination, resulting in range from 100 to 40% dormancy in wild, while primitive landraces display 50 to 0%. This set was analysed for seed coat content of metabolites using the up-to-date analytical methods for direct surface analysis and several differential compounds were found. Combination of untargeted MALDI - ion mobility - high resolution tandem mass spectrometric analysis with principal component allowed segregation of dormant from non-dormant samples. Among the signals several polyphenolics compounds were detected. Elucidation of the structure of markers and evaluation of their relations is in progress. The seeds were also anatomically and histologically analysed, revealing differences in testa structure. Contrasting wild x cultivated

genotypes is used to generate mapping populations for candidate and interval mapping of respective gene(s) together with aforementioned anatomical and chemical analyses. This research is funded by Grant Agency of Czech Republic, 14-11782S project and Operational Program Research and Development for Innovations (CZ.1.05/2.1.00/03.0058).

121	Seeds and Nutrition	Thompson, R.D.	LEGumes for the Agriculture of TOmorrow (LEGATO project)

LEGumes for the Agriculture of TOmorrow (LEGATO project)

Thompson, R.D.[1*], Duc, G.[1], Annichiarico, P.[2], Rubiales, D.[3], Salon, C.[1], Vaz Patto, C.[4], Jensen, E. S.[5], and Belcher, S.[6,7]. [1]INRA, UMR1347 Agroécologie, DIJON, FRANCE; [2]CRA, LODI, ITALY; [3]CSIC ISA CORDOBA SPAIN; [4]ITQB LISBON PORTUGAL; [5]SLU ALNARP SWEDEN; [6]PGRO Research, PETERBOROUGH, UK; [7]ON BEHALF OF THE EU-KBBE LEGATO PROJECT CONSORTIUM. *(thompson@dijon.inra.fr)

The four year FP7 European project LEGATO (Legumes for the Agriculture of Tomorrow) is aimed at improving the competitiveness of legumes in European agriculture. Grain legumes represent less than 2% of cultivated arable land in Europe, which relies heavily on imported plant protein sources. The project brings together 17 research institutions and 10 companies or professional associations from 12 European states to focus on breeding and management methods for the principal grain legumes or pulses grown in Europe, the pea and faba bean. Among the actions proposed will be the use of advanced breeding methods taking advantage of recent genomics data, exploitation of genetic resource collections, techniques of high-throughput phenotyping including non-destructive root imaging, legume-based cropping systems including intercropping, and exploration of new food products incorporating legume flours. Project Web site: http://www.legato-fp7.eu/

122	Seeds and Nutrition	Timmerman-Vaughan, G.M.	Candidate gene based association mapping of allelic polymorphisms associated with variation in seed starch chain length distribution

Candidate gene based association mapping of allelic polymorphisms associated with variation in seed starch chain length distribution

Carpenter, M.A.[1], Cooper, R.[2], Frew, T.J.[1], Butler, R.[1], Murray, S.R.[1], Moya, L.[1], Coyne, C.J.[3], and Timmerman-Vaughan, G.M.[1*]. [1]New Zealand Institute for Plant and Food Research, PO Box 4704, Christchurch New Zealand; [2]New Zealand Institute for Plant and Food Research, 120 Mt Albert Rd, Mt Albert, Auckland New Zealand; [3]USDA-ARS, Washington State University, Pullman, Washington, USA. *(gail.timmerman-vaughan@plantandfood.co.nz)

A candidate gene association mapping approach was taken to understand how allelic variation in 25 sucrose or starch metabolism pathway genes and *R* locus affect the variation in pea seed amylopectin chain length distribution (CLD); a structural attribute related to starch functional properties. Using 97 single seed derived USDA-ARS Plant Introduction (PI) lines that were grown in two replicated trials, starch CLD variation was quantified by fluorophore-assisted carbohydrate electrophoresis. The lines consisted of both round (*R*_, n = 86) and wrinkled seeded types (*rr*, n = 11). In addition, polymorphisms were identified in alignments of partial sequences of the 25 candidate genes by resequencing PCR products. Association mapping was conducted using the mixed linear model (MLM) implemented using TASSEL software with population structure and kinship accounted for using a Q matrix (k = 4, four subpopulations, estimated using STRUCTURE software) and a K (kinship) matrix (the MLM + Q + K model). Q-values were used to determine significant associations that met or exceeded a false discovery rate (FDR) criterion of $\alpha \leq 0.05$. With the 97 lines, *R* locus accounted for most of the variation in CLD (81% and 87% from the trials). Allelic variation in ADP glucose pyrophosphorylase S2 subunit, UDP glucose pyrophosphorylase and phosphoglucan water dikinase were also associated with CLD variation in starch from both trials, and an additional four genes from one trial

only. Using the subset of 86 round lines, association was identified with allelic variation in five of the candidate genes.

123	Seeds and Nutrition	Vasconcelos, M.W.	Development and characterization of a white lupin-enriched symbiotic yogurt

Development and characterization of a white lupin-enriched symbiotic yogurt

Ribeiro, C.[1], Gullón, P.[1], Vasconcelos, M.W.[1*], and Gomes, A.M.[1]. [1]CBQF- Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa/Porto, Rua Dr. António Bernardino Almeida, 4200-072 Porto, Portugal. *(mvasconcelos@porto.ucp.pt)

Pulses have the potential to be used as prebiotic agents due to their specific nutritional qualities, in particular, the presence of raffinose family oligosaccharides (RFOs), which can promote the growth of probiotic bacteria, and when incorporated into a suitable food matrix can contribute to human health. The main objective of this work was to describe the formulation and characterization of a symbiotic yogurt enriched with white lupin (prebiotic) and *Bifidobacterium animalis* Bb12 (probiotic). Pasteurized milk supplemented with milk powder (8,6%) for protein concentration standardization purposes was enriched with lupin at 4%, homogenized and sterilized prior to inoculation with 0.2% (w/v) starter culture of ultra-frozen concentrates: *Streptococcus thermophilus* and *Lactobacillus delbrueckii* subsp. *bulgaricus*. After fermentation the yogurt was supplemented with 2% *B. animalis* Bb12 and analysis was conducted at 0, 3, 5, 7, 14, 21 and 28 days of refrigerated storage (4ºC). Sensorial analysis, microbial viability and product acidification analysis were conducted.

The probiotic strain *B. animalis* Bb12 remained viable throughout storage in the yogurt with and without lupin, at the desired levels of 107-109 cfu/g. Also, a slight pH decrease was observed. Regarding sensorial analysis, 11 untrained panelists compared the yogurts with and without lupin. The yogurt with lupin presented a similar visual appearance and odor to the yogurt without lupin, but showed different texture, flavor and mouth feel.

The bifidogenic property of white lupin prebiotic oligosaccharides validates the utilization of pulses in the development of a novel symbiotic food product such as the yogurt developed in this work.

124	Seeds and Nutrition	Vasconcelos, M.W.	Potential of white lupins (Lupinus albus L.) to promote the growth of Bifidobacterium and Lactobacillus strains

Potential of white lupins (Lupinus albus L.) to promote the growth of Bifidobacterium and Lactobacillus strains

Ribeiro, C.[1], Gullón, P.[1], Gullón, B.[1], Sousa, S.[1], Vasconcelos, M.W.[1*], and Gomes, A.M.[1]. [1]CBQF - Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa/Porto, Rua Dr. António Bernardino Almeida, 4200-072 Porto, Portugal. *(mvasconcelos@porto.ucp.pt)

White lupins are grain legumes with good nutritional quality and have the potential of being good sources of prebiotic components for the growth of probiotics. Here we assessed the capacity of lupin flour to support the growth of seven probiotic strains: *Lactobacillus acidophilus* LAFTI L10 and Ki, *Lactobacillus casei* ssp. *paracasei* LAFTI L26, *Lactobacillus rhamnosus* R11, *Bifidobacterium animalis* subsp. *lactis* Bb12 and Bo, and *Bifidobacterium breve*.

To this end, a basal culture medium (Man Rogosa Sharpe (MRS) without glucose) was supplemented with different percentages of lupin flour (2, 4 and 6%) and the growth, acidification and metabolic profiles of the probiotics were observed. Each inoculated medium was homogenized, incubated at 37 ◦C for 48 hours and sampled at different time-points for their physicochemical and microbiological evaluation.

MRS with lupin flour at different percentages, predominantly at 6% (w/v), supported the growth of all microorganisms

above 108 cfu/g, except *L. acidophilus* L10. Growth in MRS with 6% lupin flour was similar to that obtained in MRS with glucose, and was accompanied by a decrease in medium pH and an increase in organic acids' concentration, predominantly lactic and acetic acids. In conclusion, the preliminary results obtained herein showed that pulses, in particular white lupins, may be used to improve the formulation of probiotic-enriched foods from both a nutritional and a bacterial growth enhancement perspectives. This opens doors to innovation in the development of symbiotic foods utilizing pulses as nutrient sources for probiotics, and in the positive marketing for alternative uses for pulses.

125	Seeds and Nutrition	Wang, N.	Effect of variety and crude protein content on quality of gluten-free pasta prepared from lentil flour by high temperature extrusion

Effect of variety and crude protein content on quality of gluten-free pasta prepared from lentil flour by high temperature extrusion

Wang, N.[1*], Maximiuk, L.[1], and Santos, J.[1]. [1]Grain Research Laboratory, Canadian Grain Commission, Winnipeg, MB R3C 3G8, Canada. *(ning.wang@grainscanada.gc.ca)

High temperature extrusion process is commonly used to produce a wide variety of cereal-based foods. Pasta/noodles made from pulse starch and flour by this process have also been reported. However, little information is available on how factors other than processing variables affect the pulse pasta quality. Therefore, the objective of this work was to investigate the effect of variety and crude protein content on quality characteristics of pasta made from lentil flour by high temperature extrusion. Eight lentil varieties, each with two levels of protein content, were selected for this study. Crude protein content overall ranged from 260.1 to 317.6 g kg-1 DM. Quality characteristics of lentil pasta were evaluated according to published methods. Analysis of variance showed that variety and crude protein content had a significant effect on cooking time, cooking loss, firmness and stickiness of lentil pasta. Color was significantly affected by variety. Protein content was negatively correlated with cooking time ($r=-0.498$, $p<0.01$) and firmness of cooked pasta ($r=-0.779$, $p<0.001$), but positively correlated with cooking loss ($r=0.351$, $p<0.05$) and stickiness ($r=0.702$, $p<0.001$). Lentil pasta had acceptable flavor, and exhibited shorter cooking time and less firm texture after cooking as compared to commercial wheat-based pasta. Lentil pasta also had superior nutritive value in terms of protein and lysine content since lentils contained twice the level of protein as wheat, and about 2.5 times the lysine level. Because lentil contains no gluten, lentil pasta would be nutritional and functional alternatives to wheat-based pasta for consumers who cannot tolerate wheat gluten.

126	Seeds and Nutrition	Warkentin, T.D.	Towards biofortification of pea

Towards biofortification of pea

Warkentin, T.D.[1*], Shunmugam, A.S.K.[1], Liu, X.[1], Delgerjav, T.[1], Rehman, A.U.[1], Kaliyaperumal, A.[1], Bangar, P.[1], Arganosa, G.C.[1], Raboy, V.[2], Glahn, R.[3], Bett, K.E.[1], and Tar'an, B.[1]. [1]University of Saskatchewan; [2]USDA-ARS, Aberdeen, ID; [3]USDA-ARS, Cornell University. *(tom.warkentin@usask.ca)

Field pea seeds, like those of other pulse crops, are rich in protein, slowly digestible carbohydrates, and fiber. To further enhance nutritional value, biofortification efforts are underway. Phytate is often considered an antinutrient in crop seeds; although it is the major storage form of phosphorus, it is relatively indigestible by humans and chelates minerals including iron. Field pea lines were identified with a 60% reduction in phytate-phosphorus concentration in seeds, while the inorganic (available) phosphorus concentration increased by a similar amount. These lines were relatively sound agronomically, but with a 15% yield penalty compared to their progenitor, and breeding efforts are in progress to overcome this deficit. A single recessive gene controls the low phytate trait and it is being mapped on the pea genome. Iron bioavailability of seed of the low phytate lines was 30-100% greater than those of their progenitor

depending on their location of production. Green cotyledon field pea lines had approximately 2-fold greater concentration of total carotenoids than yellow cotyledon lines. Experiments are in progress to assess potential additive effects of carotenoid and phytate concentration on iron bioavailability.

127	Seeds and Nutrition	Wiesinger, J.A.	The Nutritive Value of Fast Cooking Dry Beans (Phaseolus vulgaris L)

The Nutritive Value of Fast Cooking Dry Beans (Phaseolus vulgaris L)

Wiesinger, J.A.[1*], Hooper, S.[2], Salat, Y.A.[1], and Cichy, K.A.[1]. [1]United States Department of Agriculture - Agricultural Research Service (ARS), Sugarbeet and Bean Research Unit, Michigan State University; [2]Department of Food Science and Human Nutrition, Michigan State University, East Lansing, MI, 48824. *(wiesinge@anr.msu.edu)

Dry beans (*Phaseolus vulgaris* L) are a nutrient dense food rich in protein and micronutrients. To make these nutrients available to humans, dry beans must first undergo a thermal transformation. Cooking with hot water is the most commonly employed method used by households, which serves to enhance dry bean digestibility by solubilizing the fibrous seed coat and catalyzing the gelatinization of starch granules. Despite its high nutrient density, long cooking times limit the purchase and consumption of dry beans worldwide. This is especially true for the nations of East Africa where wood is a major source of cooking fuel and is often expensive or scarce. The research presented in this study evaluates the cooking time, storage potential and nutritive value of several Andean fast cooking bean lines from diverse market classes in major bean growing and bean consuming regions of Africa and the Americas. The goal of this research is to test the hypothesis that reducing the cooking time of dry beans does not comprise the nutrient density or availability. This study examines the relationship between changes in dry bean cooking time and nutrition by comparing the concentrations of protein, starch, resistant starch and trace minerals in faster, normal and slower cooking genotypes within 4 different market classes (yellow, cranberry, red mottled, light red kidney). Cooking time and nutritive value was also examined in these same genotypes after a year of storage. Initial findings suggest faster cooking genotypes have less nutrient loss compared to slower cooking genotypes, especially for protein and iron.

128	Seeds and Nutrition	Yang, A.	Sensory Attributes of Soymilk and Tofu from Soybean Varieties Lacking Lipoxygenases

Sensory Attributes of Soymilk and Tofu from Soybean Varieties Lacking Lipoxygenases

Smyth, H.[1], James, A.T.[2], and Yang, A.[2*]. [1]QAAFI, University of Queensland, St Lucia, Qld 4072, Australia; [2]CSIRO Plant Industry, St Lucia Qld 4067 Australia. *(aijun.yang@csiro.au)

The production and use of soybeans for human consumption has been increasing rapidly due to its high nutritional value and potential health benefits. Utilisation of soybean seeds as food materials, however, has sometimes been limited because of their beany flavour. Consumers associate this undesirable flavour with off-flavours, which results from oxidation of unsaturated lipids by lipoxygenases (LOXs). Soybeans are known to be the richest source of LOX. The removal of all or some of the LOXs present in soybeans through breeding has produced soybean lines lacking LOXs. Our preliminary work showed that soymilk and tofu produced from soybeans lacking all three major lipoxygenases (Lox1-3) were preferred by the taste panel compared with controls which had all three major LOXs. Lox1-3 products also had low levels of hexanal on day 1 and day 8 during refrigerated storage. In a separate study we compared soybean genotypes developed in Australia which lacked LOX1 and 2 (Lox1-2), Lox1-3 and a control. The rancid/grassy odour was rated the lowest by the taste panel in Lox1-3 products, followed by Lox1-2 with the control products given the highest rancid odour rating. The sweetness note was rated significantly higher in the Lox1-2 and Lox1-3 products than the controls. Conversely, bitterness was rated higher in the control tofu and soymilk. These results demonstrated that soybean varieties lacking Lox1-2 or all three major isomers can produce soy foods with less

rancid and more sweet aroma and therefore are likely more acceptable to the consumers.

129	Abiotic Stress	Abbad Andaloussi, F.	Promote proven technologies for wheat – legume rotation systems under changing climate in Morocco

Promote proven technologies for wheat – legume rotation systems under changing climate in Morocco

Abbad Andaloussi, F.[1*], Moussadek, R.[1], Lhaloui, S.[2], Hamal, A.[3], Ramdani, A.[3], Benchekroun Krimi, S.[2], El Bouhsini, M.[4], Souihka, A.[1], and Hamida, H.[1]. [1]INRA Rabat, Morocco; [2]INRA, Settat, Morocco; [3]INRA, Meknès, Morocco; [4]ICARDA, Rabat, Morocco. *(abbadandaloussi@yahoo.fr)

Trials of cereals and food legumes have been installed in pilot sites at different farmer's fields. These are three conservation agriculture trials. At INRA experimental station, the experiment has been conducted with the purpose to optimize seeding rates and nitrogen quantity for No tillage system. At farmer's level, two plots, of one hectare each, were conducted to compare the no-till and the conventional tillage systems. Two IPM platform were also installed at two farmer's fields. Chemical treatments were also conducted among farmer's plots to provide practical and cost-effective control of recurring pest problems. These treatments concerned the control of botrytis on faba bean, chemical weed control, especially against bromus associated with wheat and monocots and dicots associated with food legumes. Other trials were established to demonstrate chemical control of foliar diseases in wheat and control of broomrape associated with faba bean. Activities of the various tests were performed with the effective participation of farmers. These sites were supervised by a multidisciplinary team of researchers from INRA who regularly monitored the experiments. In this context, field schools were organized during crop growth period on: - Weeds control, especially bromes associated with wheat and broadleaf weeds in fields of food legumes;- Treatment of foliar diseases and pests of wheat and grain legumes. Field days were also held before harvesting in order to inform farmers on crop losses and the possibilities to minimize them. A participatory selection session was also organized of new varieties and elite lines from INRA/ICARDA joint breeding program.

130	Abiotic Stress	Abd El-Rahman, R.	Identification of genetic variability for tolerance to metribuzin in faba bean

Identification of genetic variability for tolerance to metribuzin in faba bean

Abd El-Rahman, R.[1*], and Maalouf, F.[2]. [1]Agricultural Research Center (ARC)-Egypt; [2]International Center for Agricultural Research in the Dry Areas, Cairo office 15 G Ibn Tabib (ICARDA). *(rehab3mm@yahoo.com)

Weeding is a costly common practice. Herbicides are not safe due to faba bean sensitivity. This study was to evaluate 250 faba bean lines to post emergence treatment with metribuzin. The trial was conducted at ARC Egypt, Sids station using an augmented design with two checks (ILB1814 and Misr2). Each plot is divided in three sub-plots for two different spray treatments (T1 and T2) and one control (C). T1 was sprayed one time 45 days after sowing (DAS) with 259 g a.i. ha-1 of metribuzin using 370 litres of water, while T2 was sprayed twice with the same previous dose at 45 and 60 DAS respectively. Herbicide tolerance score HTS (1-5 scale) was collected 3 and 5-weeks after herbicide treatment, where 1 = highly tolerant, 2 = tolerant (slight inhibition of growth with minor burning of leaves in some leaves), 3 = moderately tolerant (clear difference on plant appearance comparing with C, with necrosis in lower leaves and less than 25% death of the plants), 4 = sensitive (no further development of new leaves with severe burning of leaves with more death between 25% and 75% of the plants), and 5 = highly sensitive (complete burning of leaves leading to more than 75% mortality of the plants). Thirty genotypes were highly tolerant to T1 while only four genotypes were highly tolerant to T1 and moderately tolerant to T2. 23 genotypes initially with HTC (2 to 5) recuperated their performance after five weeks of treatment 1 while none of them was recuperated after treatment with T2.

131	Abiotic Stress	Bueckert, R.A.	Controlled heat stress on pod and seed components in pea – ovule and pollination failure

Controlled heat stress on pod and seed components in pea – ovule and pollination failure

Bueckert, R.A.[1*], Lindsay, D.[1], and Peru, J.[1]. [1]Department of Plant Sciences, University of Saskatchewan. *(rosalind.bueckert@usask.ca)

Heat stress during reduces pea yield via lower seed numbers and smaller sized seed. Flower, ovule and seed abortion cause lower seed numbers. Our goal was to determine the relative sensitivity of the yield components within pods (ovules per ovary, seeds per pod, pod and seed weight) on the first four flowering nodes to a short 3-day period of heat stress. Genotypes were grown under control conditions (24°C/18°C day/night) and half were transferred to 32°C/18°C when flowers opened in the first flowering node (node 1). In the warm regime the maximum temperature reached >30°C for at least 6 hours for each of three days. The pod weight, seeds per pod, aborted seed and failed ovules on plants were counted three weeks later on flowering nodes 1 to 4. Genotypes and nodes varied in components. In a node, the distal (younger) flower was more likely to abort than the proximal (older) flower. Heat reduced pod weight and seed weight. As younger nodes formed, pod weight, seed weight and seed number per pod decreased. The number of failed ovule fertilizations and aborted seeds each increased from 2 at node 1 to > 4.5 at node 4. The percentage of failed funiculi (unfertilized ovules) increased from 27 to 73% at node 4. The percentage of set peas that shrivelled was not changed (about 10 due to the short duration of the stress. Implications of these patterns will be discussed with relevance to screening for heat tolerance in pea genotypes.

132	Abiotic Stress	Coyne, C.J.	Screening chickpea for cold tolerance under controlled conditions

Screening chickpea for cold tolerance under controlled conditions

Coyne, C.J.[1*], McGee, R.J.[2], Piaskowski, J.L.[3], Abbo, S.[4], Vandemark, G.[2], and Zhang, H.[5]. [1]Plant Germplasm Introduction and Testing Unit, USDA-ARS, Pullman, WA; [2]Grain Legume Genetics and Physiology, USDA-ARS, Pullman, WA; [3]Department of Crop & Soil Sciences, Washington State University, Pullman, WA; [4]Faculty of Agriculture, Hebrew University of Jerusalem, Rehovot, Israel; [5]Department Soil and Crop Sciences, Texas A&M University, College Station, TX. *(clarice.coyne@ars.usda.gov)

Throughout the temperate regions, chickpea is spring planted due to its lack cold hardiness alleles to survive in freezing temperatures. Two major disadvantages of spring planted chickpeas are limited grain yield and insufficient crop residue for soil cover. Additionally, shifting climatic patterns are projected to result in longer, wetter springs that delay planting and hotter, drier summers resulting in heat stress during flowering and pod set. The development of a fall-planted winter chickpea could improve yields by increasing the length of the growing season, providing additional protection from cool temperatures during seed set in the early spring and helping escape late season drought. The wild progenitor of domesticated chickpea, *Cicer reticulatum*, carries alleles for winter hardiness. Therefore, we have developed a screening procedure using controlled freeze conditions that are able to differentiate RILs of a population segregating for winter hardiness. Two-week old seedlings of parents, *C. arietinum* (cultivated chickpea) and *C. reticulatum,* of the RIL population and 14 RILs with the highest and lowest cold tolerance from field studies were acclimated for four weeks, followed by step-down freezing for 16 hours at -3 °C and one hour at -5 °C, -7 °C, -9 °C, -11 °C, -13 °C and -15 °C, repeated twice. It was found that the two-step down temperatures to -5 °C was sufficient to clearly differentiate cold tolerant vs. cold susceptible lines. This procedure may be useful for future breeding of winter hardy cultivars as well as for further experiments to identify candidate genes conferring cold tolerance.

133	Abiotic Stress	Fevereiro, P.	Physiological responses toward water deficit of a M. truncatula homozigoustransgenic line expressing the oat

			Adc gene

Physiological responses toward water deficit of a M. truncatula homozigoustransgenic line expressing the oat Adc gene

Duque, A.S.[1], López-Gómez, M.[2], Kráčmarová, J.[1], Araújo, S.S.[1,3], Lluch, C.[2], and Fevereiro, P.[1,4*]. [1]Instituto de Tecnologia Quimica e Biologica (ITQB), Apt. 127, 2780-901, Oeiras, Portugal; [2]Departamento de Fisiología Vegetal, Facultad de Ciencias, Universidad de Granada, 18071, Granada, Spain; [3]Instituto de Investigação Científica e Tropical, Av. Universidade Técnica, 300-477 Lisboa, Portugal; [4]Departamento de Biologia Vegetal, Faculdade de Ciências Universidade de Lisboa Campo Grande, 1749-016 Lisboa, Portugal. *(psalema@itqb.unl.pt)

In this work the physiological responses to water deficit of an homozygous transgenic *Medicago truncatula* line (L-108) expressing the *Avena sativa* arginine descarboxylase encoding gene *(Adc)* under the p35s constitutive promoter were compared to those of wild type plants. The arginine decarboxylase is considered a key enzyme of the polyamine biosynthetic pathway and these transgenic plants contain higher level of putrescine and spermidine. Polyamines have been implicated in the regulation of many physiological processes and a variety of stress responses in plants, including water deficit stress conditions.

The transgenic plants show greater ability to avoid tissue dehydratation when compared to the non-transgenic plants by maintaining the same leaf water status as the ones under the well watered conditions. Moreover, higher stomatal conductance (gs), transpiration rate (E) and photosynthetic rate (A) under water deficit conditions were observed in the transgenic L-108 line. The physiological data showed that transgenic *M. truncatula* plants are able to tolerate water deprivation better than wild type plants, however, under well water situation there is no benefit from the constitutive expression of the oat *Adc* gene.

134	Abiotic Stress	Ghanem, M.E.	Assessment of water-saving traits in terminal drought adaptation of contrasting lentil genotypes

Assessment of water-saving traits in terminal drought adaptation of contrasting lentil genotypes

Ghanem, M.E.[1*], Gupta, P.[1], Kumar, S.[1], Kumar, J.[2], Kholova, J.[3], and Vadez, V.[3]. [1]International Center for Agricultural Research in the Dry Areas (ICARDA-Morocco); [2]Indian Institute of Pulses Research, Kanpur, India; [3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT-India). *(m.ghanem@cgiar.org)

Lentil (*Lens culinaris* Medikus subsp. *culinaris),* is an important cool-season food legume crop of South Asia, North America, West Asia and North Africa (WANA), and Australia (Erskine et al. 2011). In areas where lentil is grown, crop often encounters terminal moisture stress, thus leading to forced maturity and lower yield. Although many studies have addressed the effects of drought on lentil yield, only a few have considered the response to many key yield-related traits such as the sensitivity of transpiration rate (TR) to vapour pressure deficit (VPD) - a function of air temperature and relative humidity or to the fraction of transpirable soil water (FTSW) threshold. In lentil, no reports are available to document such influences. The objective of this study was to assess the response to these two physiological processes of 17 genotypes of lentil (9 drought tolerant and 8 sensitive) characterized in previous field trials and contrasting in yield under drought and heat stress. The study revealed (i) a large genetic variability in those responses; and (ii) compensation mechanisms between leaf areas and transpiration sensitivities to VPD together with differential acclimation strategies of these sensitivities with respect to drought scenarios. These findings open the way to implementing breeding strategies based on traits influencing plant water budget and that can improve lentil yields under different drought scenarios.

135	Abiotic Stress	H. Mobini, S.	Shortening generation time in faba bean (Vicia faba) by application of cytokinin and cold stress

Shortening generation time in faba bean (*Vicia faba*) by application of cytokinin and cold stress

H. Mobini, S.[1*], M. Lulsdorf, M.[1], D. Warkentin, T.[1], and Vandenberg, A.[1]. [1]Crop Development Centre, University of Saskatchewan, 51 Campus Drive Saskatoon, SK S7N 5A8 Canada. *(s.mobini@usask.ca)

For quicker development of recombinant inbred lines for genetic resource development of faba bean, shortening the interval between flowering and seed set is required. Faba bean plants produce abundant flowers, but most of them fail to grow into pods or abort during later development. Exogenously applied cytokinin has a positive effect on pod set in other legumes. We examined the mode and time of exogenous cytokinin application in racemes of two Canadian faba bean cultivars (FB9-4, CDC Snowdrop). Plants were maintained in controlled environmental conditions with a 20 h day length, 21/16oC day/night temperature and 500 µmol.m-2.s-1 light intensity. Application of the cytokinin 6-benzylaminopurine (BAP) at 10-4 and 10-5 M on racemes at 0, 4, 8, and 12 d after flowering (DAF) affected pollen germination and pod set. Application of 10-5 M BAP at 4 DAF doubled seed set at nodes #10-12 compared to the control. Cold stress (2 d at 10/8oC day/night) induced earlier seed set at lower nodes (node #7-9 vs. #19-20 for control). All plants started flowering at 30 d after seeding, however pod development began earlier (15 vs. 50 DAF) and pollen germination percentage was improved in plants exposed to cold (53% vs. 22% at 7 DAF). Since faba bean is a cold tolerant species, exposing the plants to cold at the time of flower initiation could be beneficial for enhancing early seed set and yield in controlled environments. Testing the combination of BAP application and cold stress treatments will be the next step in improving seed set in faba bean.

136	Abiotic Stress	He Yu Hua, H.Y.H	Early maturity innovation studying on Faba bean

Early maturity innovation studying on Faba bean

He Yu Hua, H.Y.H.[1,2,3,4*]. [1]Bao Shiying; [2]Wang Liping; [3]Lv Meiyuan; [4]Yang Feng. *(trbio@163.com)

With outcrossing method, and make use of early maturity faba bean germplasms to construct the mixed population. The genetic background is expanded as a result above breeding program, new varieties are improved significantly in maturity, quality of fresh seeds and ability of avoiding insects. Take the new variety - 'Yundou 7' for example to detail above three aspects:

Early maturity: the whole maturity is 100days in cool season. Early maturity is important on fresh seeds/pod market, especially in China.

Quality: big seeds and thin seed coat. 3-4 seeds per pod and the tannin less 0.66%.

Ability of avoiding insects, disease and drought: compare with other varieties, 'Yundou 7' is earlier, it has been harvested for fresh seeds/pods before rust spots, leaf miner or aphids burst.

The study of maturity innovation (early maturity) on faba bean is a response for Chinese market. 'Yundou 7' has been grown 70,000 hectare at past three years, the grow area is 38.2% of total faba bean area, production of fresh pods are 14,655 kilo gram each hectare, increased 22%.

137	Abiotic Stress	Huang, S	Characterizing the cross of CDC Sage and CDC Centennial field pea for heat resistance through flowering duration

Characterizing the cross of CDC Sage and CDC Centennial field pea for heat resistance through flowering duration

Huang, S.[1*]. [1]U OF S, Department of Plant Science. *(shh068@mail.usask.ca)

Field pea as a cool season legume crop is extremely sensitive to high day temperature especially during flowering. The amount of seed per plant decreases drastically when temperatures exceed 30°C for 1 to 3 days during flowering. To date, we have generated a RIL population PR-11, from the cross of heat susceptible cultivar CDC Sage and heat resistant cultivar CDC Centennnial, which has variation in flowering date and flowering duration. Our first goal was to characterize the physiological mechanisms associated with heat-induced yield production and identify physiological traits in PR-11 for drought escape through early flowering, and drought avoidance through prolonged flower duration in order to fit a warming climate. Our second and ultimate objective was to identify quantitative loci associated with these desirable traits for heat stress tolerance. So far, we have collected phenotypic data for flower date and duration, pod and seed number per plant, and seed weight of members of PR-11 grown in summer 2013. The statistical analysis of these data and QTL mapping will be done soon.

138	Abiotic Stress	Jiang, Y	Heat stress on pollen development and seed-set in pea

Heat stress on pollen development and seed-set in pea

Jiang, Y.[1*], and Bueckert, R.[1]. [1]Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, Saskatchewan, Canada S7N 5A8. *(yunfei.jiang@usask.ca)

Heat stress is one of the main environmental stresses affecting yield of pea under the semi-arid agricultural conditions in Saskatchewan. Experiments have been conducted under environmentally controlled conditions to evaluate heat stress on pollen development and seed-filling in selected cultivars from the Pea Association Mapping Panel.

Our first objective was to determine the critical daytime temperature above which pollen viability and pollen tube germination of pea starts to fail. Preliminary results showed that heat stress reduced pollen viability in cv. CDC Golden and cv. CDC Sage. Our second objective was to evaluate the effect of high night temperature during reproductive growth, especially heat effects on pollen development and seed-set. A synchrotron-based X-ray imaging technique was also used to produce 2-D images of different stages of flower development in cv. CDC Golden and cv. CDC Sage. Cultivar differences in flower, fruit and ovule abortion in response to heat, and the X-ray images of pea flower development will be presented.

139	Abiotic Stress	Jitendra, K.	Phenotyping for heat tolerance under field conditions in lentil

Phenotyping for heat tolerance under field conditions in lentil

Jitendra, K.[1*], Srivastava, E.[1], Kant, R.[1], Chaturvedi, S.K.[1], Sarker, A.[2], Kumar, S.[3], and Singh, N.P.[1]. [1]Indian Institute of Pulses Research, Kanpur, India; [2]International Center for Agricultural Research in the Dry Areas (ICARDA), South Asia & China Regional Program, New Delhi, India; [3]ICARDA, Rabat-Instituts, Rabat 10112, Morocco. *(jitendra73@gmail.com)

Rising temperature has emerged as a major challenge and it has been predicted that heat stress will have more adverse effects on vulnerability of agricultural crops under climate change. In order to identify heat tolerant germplasm in lentil, phenotyping for heat tolerance under field conditions was taken up at IIPR, Kanpur during 2012 and 2013 in collaboration with ICARDA. 334 accessions were sown on 15 January 2012 under late sown conditions to expose plants to high temperature during the reproductive phase. The maximum day temperature during the reproductive phase (March 15 to April 30, 2012) varied between 30.6 and 43ºC. To avoid possible drought effects, sufficient moisture in soil was maintained by applying regular irrigation. 176 accessions flowered and matured before the onset of heat stress and were excluded for further experimentation. Among the remaining 158 accessions, 62 with no flowers were considered highly sensitive to heat stress while the remaining 96 accessions whose flowering coincided

with the heat stress were subjected to observations on number of filled and unfilled pods, grain yield, and the development of pods and seeds on terminal branches at maximum day temperature (37 to 43ºC) at flowering stage. During 2013, only 158 accessions were re-evaluated following the same procedure. Significant variability was observed for these traits in both the years. Three genotypes (IG4258, FLIP2009-55L, IG2507) were considered heat tolerant based on maximum number of filled pods on terminal branches at >37ºC. These genotypes can be used as potential donor for use in lentil breeding program.

140	Abiotic Stress	Jogloy, S.	Nutrient uptakes and their contributions to yield in peanut genotypes with different levels of terminal drought resistance

Nutrient uptakes and their contributions to yield in peanut genotypes

with different levels of terminal drought resistance

Htoon, W.[1], Jogloy, S.[1,2*], Vorasoot, N.[1], Toomsan, B.[1], Kaewpradit, W.[1], Puppala, N.[3], and Patanothai, A.[1]. [1]Department of Plant Science and Agricultural Resources, Faculty of Agriculture, Khon Kaen University, Muang, Khon Kaen 40002, Thailand; [2]Peanut and Jerusalem Artichoke Improvement for Functional Food Research Group, Khon Kaen University; [3]New Mexico State University, Agricultural Science Center, Clovis, New Mexico 88101, USA. *(sanun@kku.ac.th)

Different peanut yield under terminal drought might be due to the different nutrient uptakes and efficiencies among peanut genotypes. Nutrient uptake and efficiency were presumed to be drought resistant traits, and they might involve drought tolerance mechanisms. The aims of this study, therefore, were to characterize the effect of terminal drought on the nutrient uptakes and to investigate the genotypic variability and their interactions to terminal drought for nutrient uptakes and efficiencies. Field experiments were conducted at the Field Crop Research Station of Khon Kaen University, Khon Kaen, Thailand during October 2010 to January 2011 and October 2011 to January 2012. Six peanut genotypes were tested under well-watered and terminal drought conditions. Data were recorded for uptakes and efficiencies of N, P, K, Ca, Mg, biomass (BM) and pod yields (PY). Terminal drought significantly reduced the nutrient uptakes in both years, and peanut genotypes considerably differed with respect to nutrient uptakes at well-watered and terminal drought conditions. ICGV 98324 and ICGV 98348 were the best genotypes for the nutrients uptakes and efficiencies. Tainan 9 and Tifton 8 had low nutrient uptakes under both conditions. ICGV 98308 and Tifton 8 had medium uptake efficiencies whereas Tainan 9 was the lowest. Significant correlations between nutrient uptakes and BM and PY were mostly observed under well-watered and drought conditions. Drought tolerant peanut genotypes could maintain high nutrient uptakes and efficiencies across water regimes, and consequently, these traits can also be used as efficient tools for selection of peanut genotypes with terminal drought tolerance.

141	Abiotic Stress	Kaur, Jagmeet	Identification of genetic variability for water logging and salinity tolerance in pigeonpea

Identification of genetic variability for water logging and salinity tolerance in pigeonpea

Grover, Pooja.[1], Kaur, JAGMEET.[1*], Singh, Inderjit.[1], Kaur, Jasdeep.[1], Choudhary, O.P.[2], Hingane, A.[3], Saxena, K.B.[3], and Singh, Sarvjeet.[1]. [1]Department of Plant Breeding & Genetics, Punjab Agricultural University, Ludhiana, India; [2]Department of Soil Science, Punjab Agricultural University, Ludhiana, India; [3]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, India. *(jagskaur@gmail.com)

Pigeonpea (*Cajanus cajan* L. Millsp.) an important legume crop is grown in many parts of Indian subcontinent. It encounters major abiotic stresses like water logging and salinity which affect the crop productivity adversely. In the present study, a set of 120 pigeonpea genotypes, acquired from diverse sources, was screened for water logging and

salinity tolerance *in vitro* (168 hrs submergence in normal water and 30mM NaCl solution) and *in vivo* (5 days incubation in ponds containing normal water and 30mM NaCl solution) conditions. Analysis of variance revealed significant differences among the genotypes for traits like germination, seedling length, dry weight and vigor index studied under *in vitro* conditions. Genotypes AL1843, PAU881 and ICPL 332 were found promising in water logged treatment whereas genotypes ICP 8859, SGBS 6 and ICPL 20237 showed promising results in salinity treatment under *in vitro* conditions. The germination, seedling length, dry weight and vigor indices under *in vitro* conditions exhibited lower values under saline conditions than in water logged conditions. Genotypes exhibiting higher vigor index also showed higher seedling length, dry weight and germination under both the conditions. On the basis of photosynthetic efficiency and survival rate under *in vivo* conditions, genotypes viz., ICPA 2039, BS 8 and AL1849 were found to be promising candidates for water logged conditions, while genotypes viz., AH-06-7, H-2000-14 and H-02-28 were found promising under saline conditions.

142	Abiotic Stress	Maalouf, F.	Development of photoperiod insensitive faba bean breeding lines with tolerance to heat stress

Development of photoperiod insensitive faba bean breeding lines with tolerance to heat stress

Maalouf, F.[1*], Khalifa, G.[2], Sefera, T.[3], and Abou khater, L.[4]. [1]International Center for Agricultural research in Dry Areas (ICARDA), 15 Ibn Tabib, Giza Cairo; [2]Agricultural Research Corporations (ARC), Hudaiba, Sudan; [3]Ethiopian Institutes for Agricultural Research (EIAR), Addis Ababa, Ethiopia,; [4]International Center for Agricultural research in Dry Areas (ICARDA), Terbol Lebanon. *(F.maalouf@cgiar.org)

Faba bean is grown under a wide range of agro-ecological conditions with temperatures as low as -15oC and as high as 37oC. Due to climate change and subsequent temperature increases, the crop is frequently exposed to higher temperature causing heat damage. A set of 200 populations representing different geographical regions were evaluated at ICARDA station (Terbol -Lebanon) for four consecutive years (2008-2011) during summer season (maximum temperatures from June till September varied from 36 to 40o C and normal cool winter season (minimum temperatures from -12 to -5 oC). Recurrent selection technique was applied to identify single plants adapted to temperature above 35oC during flowering and pod set. The selection criteria were number of filled pods and grain yield at maturity at this temperature. The breeding lines were subjected to contrasting photoperiods with opposite long-days gradient to develop germplasm adapted to different latitudes. 470 single plant progenies derived from 70 original populations were retested in an augmented design with repetitive checks in summer 2012 in Terbol-Lebanon. The lines were scored from 1 (100% of plants had pods) to 9 (aborted flowers and pods). Days to flowering varied from 45 to 60 DAS (days after sowing), and days to maturity from 119 to 130 DAS. 88 lines scored less than 3 with early flowering were multiplied and tested in 2013 and 2014 in Sudan where heat stress at the test site is predominant (maximum temperature above 35 o C in winter season). 26 of them were tested in Kulumnsa Research station (Ethiopia). Results indicated that 7 genotypes selected in Terbol were heat tolerant under Sudanese conditions, while 19 lines were adapted to Ethiopian highlands (average temperature 17o C) with yield varying from 3 to 7 tons/ha.

143	Abiotic Stress	Maharjan, K.L.	Farmers' Decision in Land Allocation for Spring Season Crops: A Case Study in the Tarai Region of Nepal

Farmers' Decision in Land Allocation for Spring Season Crops: A Case Study in the Tarai Region of Nepal

Maharjan, K.L.[1*], Khanal, N.P.[1], Sapkota, A.[2], Sharma, J.N>.[3], Joshi, K.D.[4], Haarris, D.[4], and Witcombe, J.R.[4]. [1]Hiroshima University, Japan; [2]Forum for Rural Welfare and Agricultural Reform for Development (FORWARD Nepal); [3]Local Initiative for Biodiversity Research and Development (LI-BIRD), Nepal; [4]Center for Arid Zone Studies, University of Wales, UK. *(mkeshav@hiroshima-u.ac.jp)

Sustainable intensification of rice-wheat system through legume integration is the recommended strategy for enhancing food security in Indogangetic plain; however, it has not been achieved in many cases. This paper explores the climatic, demographic, economic and institutional variables explaining variability in spring season cropped area. The data for the study were collected from 640 households spreading across the eight tarai districts of Nepal in 2010. The major crops grown in the spring season are mungbean, maize and *Chaite* (spring season) rice, and farmers allocate difference proportion of their land for these crops. So, these three crop specific regressions were simultaneously modeled through Multivariate Tobit model with the assumption that households' allocate their lands considering the potential benefit they could get from these crops in the spring reason. Results show that rainfall has positive impact on maize and rice whereas it is negative for mungbean. Similarly, this study reveals that male headed households allocate larger proportion of their lands for each of these crops than female headed households. This might be due to higher risk bearing capacity of male headed households because growing spring season crops subjects to more risks from various factors such as free grazing. Moreover, households with higher operational holdings grow mungbean, and maize in larger area but it is just opposite in case of rice.

144	Abiotic Stress	Meier, K.	Investigating the genetics of improved metribuzin herbicide tolerance in lentil

Investigating the genetics of improved metribuzin herbicide tolerance in lentil

Meier, K.[1*], McMurray, L.[2], Willenborg, C.[1], and Vandenberg, A.[1]. [1]University of Saskatchewan, Saskatoon, Saskatchewan, Canada; [2]2The University of Adelaide, Glen Osmond, South Australia, Australia.
*(ksm645@mail.usask.ca)

Worldwide, lentil (*Lens culinaris* Medik.) is an important pulse crop. Canada is now the leading exporting country for lentil, with Saskatchewan alone exporting more than 1.8 MMT. Lentil crops are poor competitors with both grass and broad-leaved weeds, resulting in up to 84% yield loss in western Canada.Due to the increasing frequency of imidazolinone (Group 2) resistance in weed populations, an increase in metribuzin use is expected in western Canada. Metribuzin is a Group 5 broad-spectrum herbicide that can cause extensive damage to lentil under certain environmental conditions. Lentil germplasm was screened for improved resistance, and tolerant genotypes were identified in both Saskatchewan and Australia. The purpose of this study was to characterize the mode of inheritance of resistance to metribuzin in lentil for Canadian genotypes. Two breeding lines with improved metribuzin tolerance were identified from screening trials and were crossed with a highly susceptible line, with each other, and with regular breeding lines. In spring of 2013, F2 populations derived from these crosses, along with the parental and susceptible lines, were sown in 1m2 microplots (50 seeds/plot) in the field. Metribuzin was applied at 3x (618 g a.i./ha) at the 3-5 node stage. Initial screening showed that the metribuzin tolerant parents and F2 populations had higher survival rates 25% compared the 14% survival rate of the susceptible parents. The MB tolerant parents had higher average harvest index (28%) than susceptible parents (15%). The F3 progeny of surviving F2 plants will be re-screened and assessed next field season along with the same crosses grown in the contra-season in New Zealand to further investigate the pattern of genetic inheritance of metribuzin tolerance in lentil. Parental sources of metribuzin tolerance in lentil are also being assessed in dose response studies, conducted in controlled environments, to confirm tolerance.

145	Abiotic Stress	Nath, Rajib	Comparative study on seedling performance due to imposed drought in lentil

Comparative study on seedling performance due to imposed drought in lentil

NATH, R.[1*], KUMAR, S.[2], TAMANG, S.[1], DE, DILIP KUMAR.[1], SARKAR, N.[1], LEGO, N.[1], GUNRI, S.KR.[1], BISWAS, T.[1], and SARKER, A.[3]. [1]BIDHAN CHANDRA KRISHI VISWAVIDYALAYA, MOHANPUR, INDIA; [2]INTERNATIONAL CENTER FOR AGRICULTURAL RESEARCH IN THE DRY AREAS (ICARDA) RABAT OFFICE, MOROCCO;

[3]ICARDA-SOUTH ASIA &CHINA REGIONAL PROGRAM, NEW DELHI, INDIA. *(rajibbckv@yahoo.com)

Drought adversely affects many physiological processes and has emerged as a major abiotic constraint to lentil productivity. Polyethylene glycol (PEG, Molecular weight 6000) solution of pre-standardised strength of (-) 0.3 MPa was used to impose drought stress for 10 days after germination in 56 lentil genotypes. The experiment was carried out in three replications along with untreated control on slanted glass plate wrapped with moist germination paper in the laboratory. Our results indicate that PEG treatment reduced morphological (length, fresh weight and dry weight of root, shoot and leaves) and biochemical (Proline and chlorophyll a and b contents) parameters in all genotypes. However, in some genotypes, the root length was significantly higher under PEG treatment than the control. Significantly higher total seedling length (length of root + shoot) was rendered either by higher length of both root and shoot or only by root length but rarely by shoot length. Genotypes that produced significantly higher root dry weight invariably had higher shoot dry weight also. Eight genotypes viz., RLG147, HPCL649, ILL10231, NDL11-1, ILL10220, ILL10971, KLS143, and KLS314 showed significantly higher seedling dry weight under PEG treatment and grouped as putative drought tolerant. Proline content was also higher in these genotypes as compared to susceptible ones. Genotypic and phenotypic coefficients of variation, heritability in broad sense and genetic gain compared to grand mean revealed additive genetic control of root length, root fresh weight, and leaf fresh and dry weights. Total dry weight showed significant positive association with root characters. Path analysis revealed that the positive direct effects of root fresh weight, root dry weight and shoot dry weight on total dry weight was the cause of significant correlation among them. Genotypes with lower mean for seedling traits under PEG treatment also had lower relative reduction under PEG treatment and such genotypes were DL10-1, DL10-3 and ILL10232 in case of root length and PL101, KLS314, and DL10-3 in case of shoot length.

146	Abiotic Stress	Omar Idrissi, O.I	Genetic variation of root and shoot traits at early stage in a lentil (Lens culinaris Medik) recombinant inbred lines population under drought: towards QTL mapping

Genetic variation of root and shoot traits at early stage in a lentil (*Lens culinaris* Medik) recombinant inbred lines (RILs) population under drought: towards Quantitative Trait Loci (QTL) mapping

Omar Idrissi, O.I.[1,2*], Chafika Houasli, .[2], Ellen De Keyser, .[3], Patrick Van Damme, .[1,4], and Jan De Riek, .[3].
[1]Department of Plant Production, Ghent University, Coupure links 653, 9000, Ghent, Belgium; [2]Institut National de la Recherche Agronomique du Maroc (INRA) Centre Régional de Settat, B.P 589 Settat, Morocco; [3]Institute for Agricultural and Fisheries Research (ILVO)-Plant Sciences Unit, Applied genetics and breeding, Caritasstraat 21, 9090, Melle, Belgium; [4]Faculty of Tropical AgriSciences, Czech University of Life Sciences Prague, Prague, Czech Republic. *(o.idrissi@yahoo.fr)

Well-developed roots and vigorous shoots at early-seedling stage are important for drought tolerance in lentil (Lens culinaris Medik). 135 RILs derived from a cross between two contrasting parents ILL6002 and ILL5888 (obtained from JF Muehlbauer, Washington State University) is under phenotyping and genotyping in order to assess the genetic control behind root and shoot traits at early growth stage. The phenotyping was carried out in a plastic pot experiment under well-watered and progressive drought-stressed treatments. ILL6002 is a vigorous line with a well developed root system showing drought tolerance, while ILL5888 has a less developed root system and vegetative biomass showing drought sensitivity. The analysis of variance shows significant differences between the RILs for all the studied traits. Significant correlations with drought tolerance were observed for dry root weight (0,616), root surface area (0,516), lateral root number (0,476), root-shoot ratio (0,377) and chlorophyll content (0,452) and dry shoot weight (0,282). The frequency distributions of dry root weight, lateral root number, taproot length, mean taproot diameter, root surface area, dry shoot weight, shoot length at 12 and 22 days after sowing, seedling vigour, chlorophyll content, root-shoot

ratio and drought score in the RILs were quantitative, continuous and normally distributed. Thus, suggesting polygenic control of these traits involving probably many QTLs of variable effects. The existing genetic map is being saturated by Amplified Fragment Length Polymorphism and microsatellite markers in order to enhance the resolution of QTL mapping.

147	Abiotic Stress	Rachaputi, R.C.N.	Genotype and environment interaction for resource use efficiency of chickpea (Cicer arietinum L) grown under water limited environments in subtropical Australia

Genotype and environment interaction for resource use efficiency of chickpea (*Cicer arietinum* L) grown under water limited environments in subtropical Australia

Rachaputi, R.C.N.[1*], Cox, H.[2], Seymour, N.[2], and Fletcher, S.[2]. [1]Queensland Alliance for Agriculture and Food Innovation, The University of Queensland, Australia; [2]Department of Agriculture, Fisheries and Forestry, Queensland, Australia. *(rao.rachaputi@uq.edu.au)

Chickpea production in the northern cropping region in eastern Australia is constrained by low rainfall, frost, soils with low plant available water capacity and sub-soil salinity. Conservation farming practices such as zero-tillage, soil cover, and deep planting have contributed to improving yield of chickpea to some extent. However, optimising water and nutrient use and N-fixation efficiency can further enhance productivity of rain fed chickpea in a sustainable manner. The study investigates effects of three row spacing and plant density combinations on resource-use efficiency of three selected chickpea genotypes grown in two diverse production environments. The two test sites located in the Darling Downs region of Queensland represented major chickpea production environments with contrasting seasonal conditions, with one site receiving adequate rainfall but two severe frosts during flowering while the other site experiencing severe and prolonged drought from flowering to harvest.

While plant density effects were not significant, narrow row spacing treatments significantly out yielded wide row spacing in both production environments. There was a significant interaction between site x genotype x row spacing for major productivity parameters such as yield, shoot dry matter, total intercepted radiation, water use efficiency and total N up take. The N-fixation capacity was also significantly affected by site and row spacing treatments. Resource capture models were used to explain the basis of yield variation due to genotypes and spatial arrangement of plants in the two contrasting growing environments. The study also used APSIM chickpea model in conjunction with the 123 years of climate data and site-specific soil properties for the two sites to generate long term yield scenarios and assess the value of narrow row spacing as a means of improving average chickpea yield in production environments characterised by high climate variability.

148	Abiotic Stress	Singh, Sarvjeet	Identification of genetic variability for tolerance to Imazethapyr and Metribuzin in lentil (Lens culinaris)

Identification of genetic variability for tolerance to Imazethapyr and Metribuzin in lentil (Lens culinaris)

Singh, SARVJEET.[1*], Rajendran, K.[2], Sharma, S.R.[1], Gill, R.K.[1], Agrawal, Navneet.[1], Grover, Pooja.[1], Kapoor, Karan.[1], and Kumar, Shiv.[2]. [1]Punjab Agricultural University (PAU), Ludhiana-141004, India; [2]International Center for Agricultural Research in the Dry Areas, Rabat-Office, Morocco. *(sarvjeetm@rediffmail.com)

Lentil (*Lens culinaris*), an important cool-season legume crop in several South Asian, Sub-Saharan, and Mediterranean countries, encounters problems of weeds due to initial slow growth and poor canopy. Currently, pre-emergence herbicides application is in practice as post-emergence herbicides are not safe due to sensitivity of lentil. In present study, 190 germplasm accessions were screened to identify sources of tolerance to post-emergence herbicides, imazethapyr (amino acid synthesis inhibitor) and metribuzin (photosynthesis inhibitor). The genotypes

were planted in paired rows of 2m length spaced at 25cm with two replications at PAU, Ludhiana, India. The crop was sprayed 50 days after sowing with 75 g a.i. of imazethapyr and 175 g a.i. of metribuzin using 375 litres of water ha-1. Effect of herbicides on weeds was recorded 2-weeks after spray. Visual scoring for herbicide tolerance in lentil genotypes was done on a scale of 1 (highly tolerant) to 5 (highly sensitive). The results revealed that both imazethapyr and metribuzin were able to control the major broad-leaf weed *Oenothera drumundii*. Imazethapyr was found more effective in controlling *Cyperus rotundus* than metribuzin. The sensitive genotypes developed chlorotic and necrotic symptoms on lower leaves followed by premature senescence of leaves and finally complete death of plants. Initially, the growth of plants was suppressed but tolerant genotypes recovered and showed secondary growth after 25-30 days of spray. The preliminary results showed that genotypes EC28514, DPL15, LL1366, LL1376, LL1384 and LL1385 were tolerant to imazethapyr, whereas genotypes EC78477, EC267544, LL1376 and LL1384 showed tolerance against metribuzin.

149	Abiotic Stress	Singh, Sarvjeet	Identification of sources of post-emergence herbicide tolerance in chickpea and lentil

Identification of sources of post-emergence herbicide tolerance in chickpea and lentil

Singh, SARVJEET.[1*], Singh, Inderjit.[1], Gaur, P.M.[2], Grover, Pooja.[1], Singh, G.[1], Agarwal, Navneet.[1], Gill, R.K.[1], Sharma, S.R.[1], and Kumar, Shiv.[3]. [1]Department of Plant Breeding & Genetics, Punjab Agricultural University, Ludhiana, India; [2]International Crops Research Institute for the Semi-Arid Tropics, Patancheru, AP, India; [3]International Center for Agricultural Research in the Dry Areas, Rabat-Office, Morocco. *(sarvjeetm@rediffmail.com)

Chickpea (*Cicer arietinum* L.) and lentil (*Lens culinaris* L.), important cool-season legume crops, are known to be sensitive to post-emergence herbicides. Control of weeds through pre-emergence herbicides is less effective and manual weeding is expensive, thus the present study was aimed at identifying sources of tolerance to post-emergence herbicides. In chickpea, 1251 lines including reference set, released cultivars, advance breeding lines, interspecific derivatives and accessions of wild *Cicer* species were screened against imazethapyr (amino acid synthesis inhibitor). Of these, 575 lines were also screened against metribuzin (photosynthesis inhibitor) and 376 lines against carfentrazone-ethyl. In lentil, 190 germplasm lines were screened against imazethapyr and metribuzin. Large genetic variability was observed in both chickpea and lentil for tolerance to different post-emergence herbicides based on visual scoring. In general, chickpea and lentil genotypes were found more sensitive to metribuzin than imazethapyr. Most of the chickpea genotypes including wild *Cicer* species were found sensitive to carfentrazone-ethyl, but later showed a recovery after 15-20 days of spray. In chickpea, a number of genotypes tolerant to imazethapyr (ICC 637, ICC 1398, ICC 17109, ICCV 04303, ICCV 95334, GLW68, GLW12039, GLW12040, GL10061, GLK10093), metribuzin (ICC 11378, ICC 14595, GL22044, GL28127), and carfentrazone-ethyl (GL12011, GLK10101, BG3028) were identified. Similarly in lentil, the genotypes EC28514, DPL15, LL1366, LL1376, LL1384 and LL1385 were tolerant to imazethapyr, whereas genotypes EC78477, EC267544, LL1376 and LL1384 showed tolerance against metribuzin. These genotypes can be used for developing herbicide tolerant cultivars and for carrying out genetic and physiological studies on herbicide tolerance in chickpea and lentil.

150	Abiotic Stress	Souter, J.R.	Ureide Accumulation and Abiotic Stress Resistance in a Population of Common Bean, Tepary Bean, and Interspecific Hybrids

Ureide Accumulation and Abiotic Stress Resistance in a Population of Common Bean, Tepary Bean, and Interspecific Hybrids

Souter, J.R.[1*], Bett, K.E.[2], Porch, T.G.[3], and Todd, C.D.[1]. [1]Department of Biology, University of Saskatchewan;

[2]Department of Plant Sciences, University of Saskatchewan; [3]USDA-ARS, Mayaguez. *(jrs293@mail.usask.ca)

Introducing stress tolerance in *Phaseolus vulgaris* (common bean) is necessary to increase production in areas where bean has limited growth due to environmental constraints. A relative which shows higher abiotic stress tolerance, *Phaseolus acutifolius* (tepary bean), has been used to develop interspecific hybrids with the intention of transferring genes for improving stress tolerance to common bean. A comparison of abiotic stress resistance during conditions of chilling and drought between tepary bean, common bean and interspecific hybrids will be presented. Ureide accumulation in this population will also be discussed. Ureides are the product of nitrogen fixation in tropical legumes and ureide concentration has been used as a tool to assess rates of nitrogen fixation. Ureides are also generated during purine remobilization and may serve as scavengers of reactive oxygen species during abiotic stress. The merit of using ureide quantification as a tool to measure abiotic stress resistance in bean species will be debated.

151	Abiotic Stress	Vasconcelos, M.W.	Iron partitioning at an early growth stage impacts iron deficiency responses in soybean plants (Glycine max L.)

Iron partitioning at an early growth stage impacts iron deficiency responses in soybean plants (Glycine max L.)

Santos, C.S.[1], Rorix, Mariana.[1], Carvalho, S.M.P.[1,2], and Vasconcelos, M.W.[3*]. [1]Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Rua Dr António Bernardino de Almeida, s/n, 4200-072 Porto, Portugal; [2]Department of Plant Sciences, Horticultural Supply Chains Group, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands; [3]Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Rua Dr António Bernardino de Almeida, s/n, 4200-072 Porto, Portugall. *(mvasconcelos@porto.ucp.pt)

Fe deficiency chlorosis (IDC) symptoms include leaf yellowing, stunted growth and drastic yield losses. Plants have been divided in 'Fe-efficient', if they resist to IDC and 'Fe-inefficient' if they do not, but the reasons for a contrasting efficiency remain illusive. The main objective of this work was to understand if the ability to partition Fe could be related to IDC efficiency in plants and to investigate the expression of Fe uptake and storage related genes. Fe-efficiency was associated with reduced chlorosis, but the reductase activity was low under Fe-deficiency for both accessions. The removal of the unifoliate leaves reduced IDC symptoms, inducing higher SPAD values, increased shoot to root ratio and increased leaf area. The expression of Fe-uptake related genes *FRO2*-like*, IRT1*-likeand *Ferritin*-like, was always high in the efficient unifoliate leaves under Fe-deficiency, thus suggesting that this organ is highly sensitive to Fe stress. The inefficient plants had higher levels of expression, particularly in the shoots. Fe concentration was analysed in different tissues and the Fe-supplied efficient plants with unifoliate leaves were able to translocate the Fe and distribute it in a balanced way throughout all aboveground plant organs, whereas the inefficient plants tended to accumulate more Fe in the roots. This suggests that Fe remobilization could be linked to the efficiency trait. This work provides new insight into the importance of mineral from different plant organs at an early growth stage, its relation with the expression of known Fe-related genes, and its influence in the efficiency trait for Fe uptake metabolism.

152	Abiotic Stress	Vasconcelos, M.W.	Evaluation of new iron (III)-chelates on mineral nutrition of soybean (Glycine max L.)

Evaluation of new iron (III)-chelates on mineral nutrition of soybean (Glycine max L.)

Santos, C.S.[1], Carvalho, S.M.[1,2], Rangel, A.O.S.S.[1], Rangel, M.[3], and Vasconcelos, M.W.[1*]. [1]CBQF– Centro de Biotecnologia e Química Fina – Laboratório Associado, Escola Superior de Biotecnologia, Universidade Católica Portuguesa, Rua Dr António Bernardino de Almeida, 4200-072 Porto, Portugal; [2]Department of Plant Sciences,

Horticultural Supply Chains Group, Wageningen University, Droevendaalsesteeg 1, 6708 PB Wageningen, The Netherlands; [3]REQUIMTE, Instituto de Ciências Biomédicas de Abel Salazar, Universidade do Porto, 4099-003 Porto, Portugal. *(mvasconcelos@porto.ucp.pt)

Iron Deficiency Chlorosis (IDC) is a serious environmental problem affecting the growth of several crops in the world. Legume grains, such as soybean (*Glycine max* L.), are particularly susceptible to IDC and several strategies have been attempted to prevent and correct iron (Fe) deficiency in plants, but these are usually costly and non-sustainable. Soil application of synthetic Fe(III)-chelates remain the most practical measure for avoiding IDC and the search for alternative and more effective chelators should be considered. Chelators of the 3-hydroxy-4-pyridinone (3,4-HPO) type are nontoxic ligands with high affinity for iron and are utilized in biomedical applications. To the best of our knowledge, these chelators have not yet been used to provide Fe complexes to plants. Herein, we analysed the applicability of (3,4)-HPO Fe complexes as novel IDC correctors and compared them to the commercial fertilizer Fe(III)EDDHA. Plants treated with the (3,4)-HPO Fe complexes were significantly greener and healthier, with 12% higher chlorophyll content and a 21% increase in total leaf area. The activity of the ferric chelate reductase of plants treated with the (3,4)-HPO Fe complexes had a 40% reduction, possibly indicating that the stress caused by the absence of Fe was alleviated. Total Fe content was measured using ICP-OES and whilst plants with (3,4)-HPO iron complexes accumulated about 187 µM, plants treated with the commercial chelator accumulated 124 µM. These results point to use of (3,4)-HPO Fe chelates as promising Fe fertilizers, and research is being conducted to understand how these products interfere with plant Fe metabolism.

153	Abiotic Stress	von Wettberg, EJ	Microenvironmental variation in natural habitats of wild chickpea

Microenvironmental variation in natural habitats of wild chickpea

von Wettberg, EJ.[1*], Yilmaz, MA.[2], Berger, J.[3], Greenspan, A.[4], Reynaldo, Y.[1], Cafferata, B.[1], Rose, J.[1], Temel, H.[2], Bukun, B.[2], Aydogan, A.[5], Kahraman, A.[6], Penmetsa, RV.[4], and Cook, DR.[4]. [1]Florida International University, USA; [2]Dichle University, Turkey; [3]CSIRO, Australia; [4]UC Davis, USA; [5]Central Research Institute for Field Crops, Turkey; [6]Harran University, Turkey. *(eric.vonwettberg@fiu.edu)

Natural habitats are complex and variable. We have examined microsite variation in natural populations of chickpea's annual relatives *Cicer reticulatum* and its sister species *C. echinospermum* to understand the extent of within and between site variation in temperature, moisture, and abiotic characteristics. We have measured 18 aspects of soil chemistry, as well as temperatures and relative humidity in the soil. Variation among sites is considerable. All quantified aspects of soil chemistry as well as temperature and moisture differ among the habitats of the two *Cicer* species compatible with chickpea. There is also substantial variation within sites with soil composition, water availability and thermal regimes varying within sites. Fine-scale characterization of microsite variation will allow us to better understand patterns of local adaptation in wild chickpea, and facilitate the utilization of systematically collected new germplasm from these sites in breeding for complex and variable agricultural conditions in cultivated chickpea.

154	Abiotic Stress	Yadava, H.S.	Genetic enhancement for biotic and abiotic stress resistance in chickpea: Achievements and perspectives in Madhya Pradesh, India

Genetic enhancement for biotic and abiotic stress resistance in chickpea: Achievements and perspectives in Madhya Pradesh, India

Yadava, H.S.[1*], Tikle, A.N.[2], Jain, Sudhanshu.[1], and Shrivastava, S.C.[1]. [1]Rajmata Vijayaraje Scindia Krishi Vishwa Vidyalaya, Gwalior, M.P., India; [2]R.A.K.College of Agriculture, Sehore (M.P.) India. *(hsyadava.rvskvv@gmail.com)

Madhya Pradesh state known as a chickpea bowl of India is the largest producer of chickpea (*Cicer arietinum*) contributing about 27.82% to global chickpea basket from 24.64% world's chickpea area. In the year 2011-12, chickpea production in this state was 3.29 million tons from an area of 3.04 million hectares, in spite of major area falling under rainfed farming and harsh climates. Average yield potential of this crop in the state is 1081kg/ha which is higher than global (941kg/ha) and national (Indian) productivity (912kg/ha). Chickpea improvement in Madhya Pradesh State started in 1950s with aims to assemble promising land races and selection for high yield. Consequently, a number varieties like Indore 22, Pink 2, A1-8, Ujjain 21, Ujjain 24, Gwalior2, JG 1, JG 5, JG 62 and JG 221in the past. The state has privilege to contribute the super sensitive and globally acceptable susceptible check JG 62 and stable resistant donor JG 315 and JG 74 against *Fusarium oxyporum* f.sp. *ciceri*. Genetic enhancement for reduction in maturity from 135 days to below 100 days (JG 11, RVG 203 and RVG 202), durable resistance to *Fusarium* wilt, large seed size have been made in *desi* chickpea by doubling the yield potential (> 2.0 t/ha) in newly bred varieties - JG16, JG 130, JAKI9218, JG6 and RVG201. However, dry root rot caused by *Rhizoctonia bataticola* and collar rot by *Sclerotium rolfsii* coupled with moisture deficits are the major yield reducers. AMMI analysis showed stable tolerance in JG11, JSC 49, Phule G00108, Pusa256, BGD 72 and JG 6 for drought, JSC 49, PhuleG 108, JG130 and WCG 2000-14 for temperature fluctuations; JG 9, JG 130 , JG 6 for dry root rot and moderate collar rot resistance in GNG 1077, JG16 and JSC 3. Genetic amelioration in chickpea is a need for early maturity, better seed size, consumer quality .

155	Abiotic Stress	Yoon, M.Y.	Whole transcriptome analysis of soybean in response to UV-B irradiation using RNA-seq.

Whole transcriptome analysis of soybean in response to UV-B irradiation using RNA-seq.

Yoon, M.Y.[1*], Shim, S.R.[1], Kim, M.Y.[1,2], Kim, K.D.[1], Lee, Y.H.[1], and Lee, S.H.[1,2]. [1]Department of Plant Science and Research Institute of Agriculture and life Sciences, Seoul National University; [2]Plant Genomic and Breeding Research Institute, Seoul National University. *(minyoungyoon1013@gmail.com)

Due to depletion of the stratospheric ozone layer throughout most of this century, increased UV-B radiation has affected seriously to plant growth and development as one of nature mutagens. We surveyed differential expressed genes (DEGs) under UV-B irradiation in UV-B tolerant Buseok compared to UV-B sensitive Cheongja 3 through RNA seq analysis using six RNA samples of Buseok and Cheongja 3 with 0.5 hr and 6 hr UV-B irradiation or without irradiation. After excluding 1003 DEGs due to genetic background difference of two genotypes, a total of 872 DEGs ortholgous to UV-related Arabidopsis genes were identified. BINGO analysis of the DEGs by 0.5 hr UV-B irradiation showed overrepresentation in signalling and cell morphogenesis. Genes related with apoptosis and immune response were overrepresented in 6 hr irradiated Buseok. In addition, KEGG pathway database was used to identify mTOR signalling and phosphatidylinositol signalling pathways. Based on GO and KEGG results, specific focus was given to a serial of genes involved in UV-B defence signalling, besides photomorphogensis and oxidation reduction-related genes. Several genes playing a role in phosphatidylinositol signalling, such as diacylglycerol kinase, phosphatidylinositol-4-phosphate 5-kinase family protein, were highly expressed in UV-B tolerant Buseok by 0.5 hr irradiation. Mitogen-activated protein kinase (MAPK) 19 and 20 were highly expressed in Buseok under 6 hr irradiation. Furthermore, 51 nucleotide binding site – leucine rich repeats (NBS-LRRs) genes were up-regulated in Buseok under 0.5 hr irradiation.

156	Abiotic Stress	Youssef, C.	Cell elongation instead cell number becomes the predominant factor influencing genotypic differences in Medicago truncatula hypocotyl length under abiotic stress

Cell elongation instead cell number becomes the predominant factor influencing genotypic differences in Medicago truncatula hypocotyl length under abiotic stress

Youssef, C.[1*], Aubry, C.[2], Beucher, D.[1], Juchaux, M.[3], and Teulat, B.[1]. [1]AGROCAMPUS OUEST, UMR 1345 IRHS équipe BGL, SFR 149 QUASAV, 16 Boulevard Lavoisier 49045 Angers, France; [2]Université d'Angers, UMR 1345 IRHS équipe BGL, SFR QUASAV, 2 Boulevard Lavoisier 49045 Angers, France; [3]Plateau technique IMAC-SFR 149 QUASAV, INRA 42 rue Georges Morel 49070 Beaucouzé, France. *(chvan.youssef@agrocampus-ouest.fr)

Hypocotyl pre-emergence growth is a crucial stage for stand establishment. In *Medicago truncatula*, we showed that hypocotyl growth in darkness is only due to cell elongation, suggesting that seed cell number can determine genetic potential for hypocotyl length in optimal growth conditions(1). The present study revealed a high genetic variability of seed cell number of hypocotyl epidermis among 16 genotypes belonging to the core collection of the species. Furthermore, cell number was stable for seeds harvested from different productions, suggesting that this trait is under strong genetic control. Hypocotyl growth analysis under various conditions corroborated that cell number was the major determinant of genotypic hypocotyl length variation under optimal conditions. In contrast, cell elongation appeared to be the major or the only determinant of this variation under low temperature and water stress, respectively. Next, QTL mapping, using a population of 101 recombinant inbred lines, pointed out distinct genome regions controlling cell number and maximal cell length reached at low temperature, on LG2 and LG7, and on LG1 and LG8, respectively. QTL co-location analysis revealed the genome regions involved in maximal hypocotyl length variation at low temperature that are specifically associated with either cell number (LG2) or cell elongation (LG1, LG8). This study provides new insights into the genetic bases of hypocotyl pre-emergence growth and provided the framework to carry out molecular analysis of genotypic differences in hypocotyl cell elongation. In this objective, a proteome analysis is in progress.

157	Abiotic Stress	Yuliasti, YL	Response Of Mungbean Mutant Lines To Drought Stress And Genetic Relationships Using SSR Markers

Response Of Mungbean Mutant Lines To Drought Stress And Genetic Relationships Using SSR Markers

Yuliasti, YL.[1*]. [1]Center for Application Isotopes Radiation - National Nuclear Energy Agency Indonesia. *(upikyuliasti@yahoo.com)

Development of mungbean cultivars tolerance to drought through mutation breeding approach will enable us to anticipate climate change effect. The objective of this research was to evaluate yield mungbean mutant lines tolerance to drought and to analyze the genetic diversity and relationship among mutant lines using SSR markers. The study was conducted in the experimental farm of BATAN at Muneng, East Java during the dry season of 2012. The experiment was laid out in a randomized block design five mutant lines with two varieties as control, four replicationn and two environments consisted of two irrigation system: optimal irrigation at least three times: at planting, flowering and during pod filling and Sub-optimal irrigation, that is two times at planting and flowering. Cluster analysis was performed to construct dendrogram using Unweighted Pair Group Method with Arithmetic Mean (UPGMA) based on Euclidean distance of genotypes. The results showed that mutant lines, PsJ30, PsJ31, PsJ32 produced grain yields 1.17, 1.01, 1.04 ton/ha, were significantly higher compare the parent Gelatik and Perkutut as control check (0.85 and 0.871 ton/ha). Based on the sensitivity index PSJ31 had sensitivity index (0.47) tolerant to drought compare parent and nasional varity not tolerant (0.96 & 1.1). These mutant are candidates for new varieties high yield tolerant to drought. Of the 20 SSR markers used in clustering analysis, 9 SSR markers (MB SS R033; satt137; MB SS R008; MB SS R203; MB SS R013; MB SS R021; MB SS R016 and MB SS R136) successfully distinguished mungbean mutant lines.

158	Biotic Stress	Adhikari, K.N.	Breeding and genetic studies of rust (Uromyces viciae-fabae) resistance in faba bean (Vicia faba L.) in Australia

Breeding and genetic studies of rust (Uromyces viciae-fabae) resistance in faba bean (Vicia faba L.) in

Australia

Adhikari, K.N.[1*], Sadeque, A.[1], and Trethowan, R.[1]. [1]The University of Sydney, IA Watson Grains Research Centre, Narrabri, NSW 2390 Australia. *(kedar.adhikari@sydney.edu.au)

Faba bean is one of the oldest grain legumes grown in many countries for both human consumption and animal feed. Rust, caused by *Uromyces viciae-fabae*, is a serious disease of faba beans in sub-tropical agricultural region in Australia. Despite being a major disease, limited information is available on the genetic basis of the rust resistance. Experiments were conducted to assess the variation of rust resistance in the germplasm and study the genetic basis of resistance. Various lines available in the germplasm were screened against rust and the resistant lines identified. Crosses were made between the best resistant germplasm and agronomically suitable parents. Their progenies were advanced and screened against rust under disease pressure. Many lines showed a higher level of resistance than shown by current cultivars. The level of resistance displayed by new lines is high enough to grow reliable crop without any fungicide protection.

To understand the genetics of rust resistance, two F2 and F3 populations derived from different sources of resistance were tested at seedling stage in a glasshouse. Three distinct infection types, hypersensitive, intermediate and susceptible were found in the progeny. In F3 progeny test, however, no homozygous family with intermediate type was found indicating some heterozygotes displayed intermediate type of reaction and this infection type could not be attributed to any independent genes. Segregation of progenies was in consistent with one gene segregation with incomplete dominance. Further studies are needed to confirm whether the same or a different gene for resistance is involved in these populations.

159	Biotic Stress	Armstrong-Cho, C.	The root of the problem: Aphanomyces and Fusarium in Saskatchewan pea and lentil fields.

The root of the problem: *Aphanomyces* and *Fusarium* in Saskatchewan pea and lentil fields.

Armstrong-Cho, C.[1*], Tetreault, M.[1], Chatterton, S.[2], and Banniza, S.[1]. [1]Crop Development Centre, University of Saskatchewan; [2]AAFC Lethbridge Research Centre. *(cheryl.cho@usask.ca)

In recent years, unusually wet spring conditions in Saskatchewan have led to widespread outbreaks of root rot in pea and lentil fields. Unfortunately once symptoms are noted above ground, the roots are already degraded, making it difficult to determine the primary cause. Pea and lentil plants with root rot symptoms were collected from 27 fields in 10 regions of Saskatchewan. Root flora were isolated on PDA and root tissue was examined microscopically for the presence of *Aphanomyces* oospores. A variety of *Fusarium* species, primarily *F. avenaceum*, *F. redolens*, *F. oxysporum* and *F. solani*, were isolated from diseased roots and 75% of root samples contained *Aphanomyces* oospores. Pathogen identification was confirmed by multiplex PCR for *Fusarium* spp. and by real-time PCR for *Aphanomyces*. To observe early stages of root infection, a growth chamber experiment was set up using soil from fields with high incidence of root rot. The soil samples originated from a pea field in the northern, grey soil zone, and from a lentil field in the southern, brown soil zone of the province. Peas were seeded into the field soils and after emergence, normal and saturated moisture treatments were established. Sterilized field soil was used for control treatments at both moisture levels. Marked stunting and reduced root biomass were observed under saturated conditions for both the sterile and non-sterile soils. Roots were examined microscopically for *Aphanomyces* oospores and plated 2 and 3 weeks after seeding. These observations indicated that *Aphanomyces* was the primary pathogen, followed thereafter by *Fusarium* colonization.

160	Biotic Stress	Arwin, AW	BREEDING SOYBEAN SUPER EARLY MATURITY USING INDUCE MUTATION TECHNIQUE FOR HIGH YIELD,

			RESISTANCE TO LEAF RUST and SPOT DISEASE FOR ANTICIPATION CLIMATE CHANGE

BREEDING SOYBEAN SUPER EARLY MATURITY USING INDUCE MUTATION TECHNIQUE FOR HIGH YIELD, RESISTANCE TO LEAF RUST and SPOT DISEASE FOR ANTICIPATION CLIMATE CHANGE

Arwin, AW.[1*]. [1]Center for Application Isotopes and Radiation - National Nuclear Energy Agency Indonesia. *(arwin@batan.go.id)

In Indonesia, soybean is important food after rice. Soybean is important source of vegetable protein because protein content ranged between 36-41%, as alternative compliance needs of protein society in addition to proteins derived from animal. Soybean production in Indonesia insufficient for domestic demand, so that needs must imported to sufficient. Because it is necessary to have new varieties super early maturity, high yield and resistant to pests and major diseases, to support the increase in soybean production in Indonesia. As a parent was used *Tidar* variety, irradiated with a dose of 0.2 kGy by gamma rays then planted as M.1 plant. The M.1 plants harvested as M.2 seeds and planted entirety. In this generation the selection M.2 for early maturity, high yield and resistant to rust and leaf spot diseases. Selection was continued until generation M.5 and M.6 until the plant is stable and is not segregated. From the selection until generation M.6 and preliminary and advanced yield trials mutant lines obtained 5 super early maturity soybean mutant lines seed are: 2- Psj, 4-Psj, 81-Psj, 88-Psj and Q-298. Further adaptation trials conducted 16 locations some place in Indonesia with parent control *Tidar* variety and 2 control national varieties *Grobogan* and *Burangrang*. Of all the tests obtained 2 promising mutant lines that the Q-298 and 4-PSJ and now have been released as national varieties in Indonesia, which was a super early maturity varieties with namely *Gamasugen 1* and *Gamasugen 2*.

161	Biotic Stress	Bazghaleh, N.	Effects of H2 oxidizing bacteria on plant growth and inhibition of fungal pathogens

Effects of H2 oxidizing bacteria on plant growth and inhibition of fungal pathogens

Abdellatif, L.[1], Hamel, C.[1,2], Bazghaleh, N.[1,2*], Yang, C.[1,3], Vujanovic, V.[4], and Gan, Y.[1,3]. [1]Semiarid Prairie Agricultural Research Centre, Swift Current, SK, Canada S9H 3X2; [2]Department of Soil Science, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8; [3]Department of Plant Sciences, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8; [4]Department of Food and Bioproduct Sciences, University of Saskatchewan, Saskatoon, SK, Canada S7N 5A8. *(navid.bazghaleh@agr.gc.ca)

Hydrogen gas, a by-product generated during the process of nodulation in pulse plants, can promote the activity of H2 oxidizing bacteria and enhance plant growth. However, it is unknown whether the positive effect of pulses on H2 oxidizing bacteria may be responsible for much of the beneficial effects of pulse-based cropping systems. The objective of our study is to characterize the beneficial properties of certain H2 oxidizing rhizobacteria (PGPRH2-ox) strains isolated from the rhizosphere soil of red lentil. Molecular and cultural methods were combined with greenhouse assays. The PGPRH2-ox isolates were identified as *Variovorax, Rhodococcus, Mycobacterium, Acinetobacter* and *Curtobacterium* using Sanger sequencing analysis of 16S DNA. The rhizobacterial PGPRH2-ox candidates were screened for antagonistic activity against fungal pathogens. We found that almost all the isolates evaluated in the laboratory study were able to inhibit the fungal pathogens *Fusarium sp*. Eight of the isolates suppressed the growth of *Rhizoctonia sp*. and five isolates suppressed the growth of *Pythium sp.* In the greenhouse study, seven isolates were shown to promote the biomass of the shoot and roots of lentil and wheat, and five isolates could be considered to be potential biocontrol and plant-growth-promoting agents. We conclude that the certain strains of H2 oxidizing rhizobacteria associated with the pulse crops can be used to improve plant growth and inhibit fungal plant pathogens.

162	Biotic Stress	Caudillo Ruiz, K. B.	Seed yield quantity, quality and seed infection caused by Stemphylium blight in lentil.

Seed yield quantity, quality and seed infection caused by Stemphylium blight in lentil.

Caudillo Ruiz, K. B.[1*], and Banniza, S.[1]. [1]Crop Development Centre / Dept. of Plant Sciences, University of Saskatchewan. *(kic200@mail.usask.ca)

Canada is the leading lentil exporter in the world. Production has increased from 342,800 t in 1991 to 1,531,900 t in 2011. In 2012, Saskatchewan produced 1,802,757 t, which represented 96% of Canada's total lentil production. Biotic stress caused by fungal diseases like Stemphylium blight can have negative effects on lentil seed harvests. The objective of this project is to assess the effect of Stemphylium blight on seed yield quantity, quality, and seed infection. A field experiment with a randomized complete block design was established in the spring of 2013 at the University of Saskatchewan. Four replicate plots with plants of cv. 'CDC Robin' were inoculated with 1 ´ 103 spores mL-1 ofisolate 'SB19' at four growth stages (seedling, early-flower, mid-flower, podding), and un-inoculated control plots. Low tunnels were established and successfully created conducive infection conditions while limiting external inoculum. Seed yield in covered plots was only negatively affected compared to the uninoculated control plots when infection occurred at the early-flower stage. Seed yield did not differ among plots inoculated at various growth stages. Seed quality was negatively affected by inoculations. Compared to uninoculated control plots, thousand seed weight was significantly lower in plots inoculated at mid-flower, followed by early-flower and pod inoculation. Seed infection was significantly higher after mid-flower infection compare to control plots. In conclusion, infection at early to mid-flower appears to have a negative impact in lentil seed yield and/or quality. Further field trials will be conducted to confirm these results.

163	Biotic Stress	Chatterton, S.	Fusarium species composition and root rot incidence in Alberta pea fields in 2013

Fusarium species composition and root rot incidence in Alberta pea fields in 2013

Chatterton, S.[1*], Bowness, R.[2], Harding, M.W.[3], Hall, L. M.[4], and Olson, M.[5]. [1]Lethbridge Research Centre, Agriculture and Agri-Food Canada, Lethbridge, AB, Canada; [2]Lacombe Research Centre, Alberta Agriculture and Rural Development (AARD), Lacombe, AB, Canada; [3]Crop Diversification Centre South, AARD, Brooks, AB, Canada; [4]Department of Plant, Food and Nutrition Science, University of Alberta, Edmonton, AB, Canada; [5]AARD, Stony Plain, AB, Canada. *(syama.chatterton@agr.gc.ca)

Field pea is the largest acreage pulse crop in Alberta, recently approaching 1 million acres across the province. Late season root rot of field pea, causing wilting and death of mature plants, is threatening sustainable pea production in some fields. Experienced growers, with a long history of pea production, have reported severe stand and yield losses. To assess the prevalence and severity of root rot in Alberta, pea fields were surveyed in July 2013 for above- and below-ground symptoms of root rot. Roots were dug up at each of 10 sampling sites/field, washed and assigned a visual rating for disease severity (1=healthy up to 7=dead). Root rot symptoms were found in 143 of the 145 fields surveyed with a mean incidence and severity index of 86% and 3.0, respectively. Diseased roots were surface sterilized and plated onto PDA. *Fusarium* spp. were predominantly isolated from roots, and a portion of isolates were identified using morphological and molecular techniques. Composition of *Fusarium* spp. was also determined using DNA, extracted from root samples, in multiplex PCR assays with species-specific primers targeting common Fusarium pathogens. Results indicated that *F. avenaceum, F. solani, F. redolens* and *F. oxysporum* were primarily associated with root rot symptoms. Validation of pathogenicity on pea seedlings for these isolates is currently ongoing. The high incidence and severity of root rots reported in this survey substantiates the concern that Alberta producers have expressed in recent years, and indicates that further investigations into causal agents and control strategies are

warranted.

164	Biotic Stress	Chatterton, S.	Pathogen populations associated with root rot of field pea in western Canada

Pathogen populations associated with root rot of field pea in western Canada

Chatterton, S.[1*], Foroud, N. A.[1], Gossen, B. D.[2], and McLaren, D. L.[3]. [1]Lethbridge Research Centre, Agriculture and Agri-Food Canada (AAFC), Lethbridge, AB, Canada; [2]Saskatoon Research Centre, AAFC, Saskatoon, SK, Canada; [3]Brandon Research Centre, AAFC, Brandon, MB, Canada. *(syama.chatterton@agr.gc.ca)

Root rot of field peas can be a major constraint to production as producers experience severe stand and yield loss. Root rots can be caused by a complex of pathogens, including *Fusarium* spp., *Rhizoctonia solani*, and *Pythium* spp. To compare pathogen populations in healthy and diseased patches of affected fields, three pea fields in each of Alberta, Saskatchewan and Manitoba were chosen for surveying and in-depth sampling in 2013. Fields surveyed in all three provinces showed significant patches of root rot. In Saskatchewan and Manitoba, roots collected from areas within fields that appeared healthy based on above-ground symptoms often showed moderate root rot symptoms. In Alberta, patches with healthy roots were found in two out of the three fields surveyed. *F. avenaceum*, *F. solani*, *F. redolens* and *F. oxysporum* were the primary pathogens detected in preliminary screening of pea root DNA using multiplex PCR with primers for common *Fusarium* pathogens. There were significant differences in proportions of *Fusarium* species detected in roots from diseased and healthy patches from Alberta field samples, but not from Manitoba and Saskatchewan samples. Greenhouse bioassays using field soils confirmed results from Alberta samples; peas grown in soils collected from healthy patches did not develop root rot symptoms, whereas peas grown in full-strength and diluted soils from diseased areas developed severe root rot. Future studies will be aimed at developing a dual-indexed sequencing strategy using the Illimuna Miseq platform for a thorough analysis of fungal communities associated with pea root rot in western Canada.

165	Biotic Stress	Conner, R.L.	Reactions of dry bean cultivars from western Canada to root rot.

Reactions of dry bean cultivars from western Canada to root rot.

Conner, R.L.[1*], Hou, A.[1], Balasubramanian, P.[2], McLaren, D.L.[3], Henriquez, M.A.[3], Chang, K.F.[4], and McRae, K.B.[5]. [1]Agriculture and Agri-Food Canada (AAFC), Morden Research Station, Morden, Manitoba, Canada; [2]AAFC Lethbridge Research Centre, Lethbridge, Alberta, Canada; [3]AAFC Brandon Research Centre, Brandon, Manitoba, Canada; [4]Alberta Agriculture and Rural Development, Crop Diversification Centre-North, Edmonton, Alberta, Canada; [5](formerly) AAFC Atlantic Food & Horticulture Research Centre. Kentville, Nova Scotia, Canada. *(robert.conner@agr.gc.ca)

Root rot is an important disease of dry beans (*Phaseolus vulgaris*) that is caused by a complex of root pathogens. Cultural and fungicidal controls are available to reduce the adverse impact of this disease on seedling emergence, plant growth and yield, but none of these practices are highly effective. The development of disease resistant dry bean cultivars is considered to be an important component of an integrated management system for root rot control. A five-year field study was conducted to identify potential sources of resistance to seedling blight and root rot in dry bean cultivars that are widely grown in western Canada. A total of 37 dry bean cultivars, representing all the bean classes grown in the region, were tested against the root rot pathogens *Rhizoctonia solani*, *Fusarium solani*, *F. redolens* and *F. acuminatum*. Partial root rot resistance was detected in the navy bean cultivar Navigator and the black bean cultivars Black Violet and CDC Jet. The greatest root rot resistance occurred in the cranberry bean cultivars Etna and Cran 09. Reductions in root rot severity were not consistently associated with greater seedling emergence, which

indicates that resistance to seedling blight and root rot may be independent traits. Inoculation with *R. solani* had the most adverse effect on seedling emergence, while infection by *F. solani* f. sp. *phaseoli* resulted in the most severe root rot ratings.

166	Biotic Stress	Durkin, J.M.H.	A change in the Colletotrichumtruncatum population signals a need for new resistance in lentil

A change in the Colletotrichumtruncatum population signals a need for new resistance in lentil

Durkin, J.M.H.[1*], Bissett, J.[2], Song, R.[1], Pahlavani, H.[3], Mooney, B.[1], and Buchwaldt, L.[1]. [1]Agriculture and Agri-Food Canada (AAFC), Saskatoon Research Centre, Saskatoon, SK, S7N 0X2, Canada; [2]AAFC, Eastern Cereal and Oilseed Research Centre, Ottawa, ON K1A 0C6, Canada; [3]Gorgan University of Agricultural Sciences and Natural Resources, Golestan, PO 386, Iran. *(jonathan.durkin@agr.gc.ca)

Canada is one of only a few countries where the fungal pathogen *Colletotrichum truncatum* causes serious yield loss in lentil. Ten years ago it was determined that the pathogen population consisted of two races, Ct0 and Ct1, at about equal frequency. This survey was based on inoculation of 50 isolates onto differential lentil lines including Indianhead which is resistant to Ct1 but susceptible to Ct0. Here we report a DNA probe to distinguish the two races and a recent survey of the *C. truncatum* population. Differentiation of fungal species is often based on polymorphisms in the Internal Transcribed Spacer (ITS) and Intergenic Spacer (IGS) regions of ribosomal DNA. Sequencing of these regions from Ct0 and Ct1 isolates showed a useful length polymorphism in IGS containing a 39 nucleotide repeat. Forward (GAGATAAGTAAAGACGGAGATAAA) and reverse (TAGGCGCCAAGGTAGAAAGT) primers were designed specifically for PCR-amplification of this region. The new 39F/R DNA probe amplified consistently 7 or 9 repeats in Ct1 isolates and 2, 4, 5, 6, 8 or 12 repeats in Ct0 isolates. The amplicons were separated using gel electrophoresis and bands visualized by Gelred staining. A survey in 2012 of 208 *C. truncatum* isolates from 74 commercial lentil fields showed that race Ct0 now constitute 95% of the pathogen population. This finding has important consequence for lentil breeding as the current varieties have Ct1 resistance. Fortunately, new sources of Ct0 resistance have been identified and will be needed to reduce the current reliance on fungicide treatment in western Canada.

167	Biotic Stress	Hassan, F.	Development of Insect and Fungi Resistant Transgenic Pea (Pisum sativum L.)

Development of Insect and Fungi Resistant Transgenic Pea (Pisum sativum L.)

Alemayehu, T.N.[1], Jacobsen, H.J.[1], and Hassan, F.[1*]. [1]Leibniz University Hannover; Institute of Plant Genetics, Section of Plant Biotechnology Herrenhäuser str. 2, 30419 Hannover, Germany. *(hassan@lgm.uni-hannover.de)

Pea (*Pisum sativum* L.) is economically important grain legume as food and feed cultivated worldwide. However, its production and storage is constrained by different species of insect and fungi pests. Thus, development of insect and fungi resistant variety is one of the main goals of breeding and improvement efforts in many producing countries. In this regards, genetic transformation can complement the conventional breeding strategy through widening access to resistance genes beyond the species gene pool.

In this study, transgenic pea plants developed through *Agrobacterium*-mediated transformation using a construct harboring *cry1Ac* gene for insect resistance and *chit* gene for fungi resistance together with *bar* gene for herbicide resistance were characterized using molecular and functional analysis. The result of molecular analysis showed the integration of the transgene construct in the analyzed clones. Further molecular analysis of the filial generations (T5 and T7 for *cry1Ac* and *chit*, respectively) from the transgenic clones showed the stable inherence of the introduced transgene to the next generations. RT-PCR analysis, immunostrip assay and western blots have indicated the expression of the *cry1Ac* and *chit* genes. The leaf paint functional analysis with herbicide solution also showed a clear

difference between transgenic and non-transgenic control plants. The herbicide treated leaves of non-transgenic control plants showed necrosis after 5-7 days of herbicide application while the herbicide treated leaves of transgenic plants showed no sign of necrosis. Gene stacking by conventional crossing was used to combine *cry1Ac* and *chit* genes in one plant to have enhanced resistance for insect and fungi.

168	Biotic Stress	Henriquez, M.A.	Fusarium species from soybean in Manitoba

Fusarium species from soybean in Manitoba

Henriquez, M.A.[1*], McLaren, D.L.[1], Conner, R.L.[2], Balasubramanian, P.M.[3], Chang, K.F.[4], Hwang, S.F.[4], Strelkov, S.E.[5], and Gossen, B.D.[6]. [1]Agriculture and Agri-Food Canada (AAFC), Brandon Research Centre; [2]Agriculture and Agri-Food Canada (AAFC), Morden Research Centre; [3]Agriculture and Agri-Food Canada (AAFC), Lethbridge Research Centre; [4]Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada; [5]University of Alberta, Edmonton, Alberta, Canada; [6]Agriculture and Agri-Food Canada (AAFC), Saskatoon Research Centre. *(MariaAntonia.Henriquez@agr.gc.ca)

Fusarium root rot is a serious disease of soybean in Canada for which successful control has been elusive. In western Canada, little information exists on the occurrence, distribution and pathogenicity of *Fusarium* spp. on soybean. Commercial soybean crops from the major production areas in Manitoba were evaluated to assess root rot diseases during 2012 and 2013. An in-depth study on root rot pathogen identification on commercial soybean from the major production areas in Manitoba was conducted during 2012. Pathogen species were identified based on their morphological characteristics. Species identity was confirmed by sequencing the translation elongation factor 1 alpha (EF1-α) gene, the internal transcribed spacer (ITS) region and the nuclear ribosomal intergenic spacer (IGS). A set of *Fusarium* spp. collected from the diseased soybean roots were screened for pathogenicity on the variety TH32004R2Y. An important finding in this research was the identification of *Fusarium graminearum* causing root rot and wilt in soybean plants. These results stress the need to acquire more information on root rot pathogens in Manitoba soybean crops and cross-pathogenicity studies in order to screen for host resistance and design effective control measures.

169	Biotic Stress	Hou, A.	Combining resistance to common bacterial blight, anthracnose and bean common mosaic virus in drybean

Combining resistance to common bacterial blight, anthracnose and bean common mosaic virus in drybean

Boersma, J.G.[1], Conner, R.L.[1], Balasubramanian, P.M.[2], Navabi, A.[3,4], Yu, K.[3], and Hou, A.[1*]. [1]Agriculture and Agri-Food Canada Cereal Research Centre Morden; [2]Agriculture and Agri-Food Canada Lethbridge Research Centre; [3]Agriculture and Agri-Food Canada Harrow Research Centre; [4]University of Guelph. *(anfu.hou@agr.gc.ca)

Anthracnose, caused by *Colletotrichum lindemuthianum*, and common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *phaseoli*, are major seed-borne diseases impacting dry bean production in Canada. Control of the diseases relies largely on chemical applications because cultivars with multiple disease resistance are unavailable. OAC Rex is a late-maturing navy bean (*Phaseolus vulgaris*) cultivar which possesses molecular markers SU91 and PVctt001 for CBB resistance originating from *Phaseolus accutifolius*. In an effort to transfer the CBB resistance to western Canada adapted dry bean cultivars and pyramid resistance to multiple diseases, molecular marker-assisted backcrossing involving OAC Rex as the CBB resistance donor parent was carried out by a national team. Breeding populations were screened in CBB field disease nurseries across two provinces, and in growth chambers for resistance to anthracnose and bean common mosaic virus. Navy bean lines adapted to western Canada with moderate resistance to CBB and good resistance to anthracnose and bean common mosaic virus (BCMV) were

produced. Pinto and black bean lines resistant to CBB and BCMV were also developed.

170	Biotic Stress	Jendoubi, W.	Development of chickpea near-isogenic lines for Fusarium wilt race 0

Development of chickpea near-isogenic lines for Fusarium wilt race 0

Jendoubi, W.[1*], Bouhadida, M.[1], Rubio, J.[2], Millan, T.[3], Gil, J.[3], Kharrat, M.[4], and Madrid, E.[5]. [1]University of Carthage, Field Crop Laboratory, National Institute for Agricultural Research of Tunisia (INRAT), rue Hédi Karray, 2080 – Tunisia; [2]Área de Mejora y Biotecnología, IFAPA Centro "Alameda del Obispo", Apdo 3092, 14080 Córdoba, Spain; [3]Departamento de Genética, Univ. of Córdoba, Campus Rabanales, Edif. C5, 14071 Córdoba, Spain; [4]Intenational Center for Agricultural Research in the Dry Areas (ICARDA), Rabat Office, Av. Mohamed Belarbi Alaoui, P.O. Box 6299, Rabat-Instituts, Rabat, Morocco; [5]Institute for Sustainable Agriculture, CSIC, 4084, E-14080 Córdoba, Spain. *(war44da@yahoo.fr)

Pairs of chickpea near-isogenic lines (NILs) with resistance/susceptibility to *Fusarium oxysporum* f. sp. *ciceris* (Foc) race 0 have been developed using three different intraspecific recombinant inbred line (RIL) populations: CA2156 × JG62 (susceptible × resistant), ILC3279 x JG62 (susceptible × resistant) and JG62 x ILC72 (resistant × susceptible). NILs were obtained by searching residual heterozygosity in advanced RILs using the sequence tagged microsatellite sequence (STMS) markers TR59 and TS35, closely linked to the first gene of resistance (*Foc01/foc01*) on linkage group (LG) 5 of the chickpea map (Cobos et al. 2005). The progeny of heterozygous plants was genotyped and homozygous descendents (*aa* and *bb*) for both molecular markers were selected from each RIL. In order to contrast genotypic and phenotypic results, the progenies were evaluated for disease reaction to Foc race 0 under controled conditions. The preliminary results confirmed the coincidence between the genotypes obtained with the molecular markers and the phenotype evaluation. Taking advantage of the complete sequence chickpea genome, the genomic region involved in resistance has been localized around the marker TS43. Seven candidate genes have been selected to be genotyped in segregant populations in order to develop diagnostic markers to be used in breeding programs for Foc race 0.

171	Biotic Stress	Jha, A.B.	Identification of quantitative trait loci for mycosphaerella blight resistance in pea using an interspecific cross population

Identification of quantitative trait loci for mycosphaerella blight resistance in pea using an interspecific cross population

Jha, A.B.[1*], Tar'an, B.[1], Banniza, S.[1], and Warkentin, T.D.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada. *(ambuj.jha@usask.ca)

To identify quantitative trait loci (QTLs) associated with mycosphaerella blight resistance, recombinant inbred lines (RILs, PR-19) were generated from a cross between the moderately resistant *Pisum fulvum* accession P651 and the susceptible field pea cultivar Alfetta (*P. sativum*). PR-19 RILs were genotyped using a 1536 single nucleotide polymorphisms (SNPs) Illumina Golden Gate assay (iMAP project; http://knowpulse2.usask.ca/portal/) and phenotyped under field conditions in 2013 at Saskatoon. Out of 1536 SNP markers tested, 940 were polymorphic. Mycosphaerella blight scores of PR-19 ranged from 1.6 to 5.5 at late flowering and 3.5 to 9.0 at physiological maturity on a 0-9 scale. Disease scores were positively correlated with lodging scores ($P < 0.001$) and negatively correlated with days to flower, plant height and days to maturity ($P < 0.001$). Two QTLs, QTL MB-1 (locus PsC26916p194) and QTL MB-2 (locus PsC18299p388) were identified for mycosphaerella blight. These loci explained 20% and 14% of the total phenotypic variation, respectively. In addition, 3 QTLs each were identified for plant height, days to flower and days to maturity, and 1 QTL for lodging. Mycosphaerella blight evaluation of PR-19 seedlings under greenhouse

conditions is in progress to potentially identify additional QTLs. PR-19 RILs will be evaluated again for mycosphaerella blight resistance and other traits under field conditions in 2014 at two locations to strengthen previously identified QTLs or identify new QTL(s). Identified QTLs will be used for development of KASP markers for marker assisted breeding.

172	Biotic Stress	Jimenez-Lopez, J.C.	Lupin (Lupinus angustigolius L.) beta-conglutins as new bioactive seed proteins with fungal growth inhibitory activity

Lupin (Lupinus angustigolius L.) beta-conglutins as new bioactive seed proteins with fungal growth inhibitory activity

Jimenez-Lopez, J.C.[1*], Melser, S.[2], Foley, R.C.[2], Thatcher, L.F.[2], Anderson, J.P.[1,2], Atkins, C.A.[3], and Singh, K.B.[1,2]. [1]The UWA Institute of Agriculture, The University of Western Australia, 35 Stirling Highway, Crawley, Perth 6009 WA, Australia; [2]Molecular Plant Pathology and Crop Genomics, Centre for Environment and Life Sciences (CELS), CSIRO Plant Industry, 147 Underwood Avenue, Floreat, Perth 6014 WA, Australia; [3]School of Plant Biology, The University of Western Australia, 35 Stirling Highway, Crawley, Perth 6009 WA, Australia. *(jose.jimenez-lopez@uwa.edu.au)

Lupin is an emerging crop worldwide due to its wide range of agricultural and health benefits, and as an important source of protein for humans and animals. The identification of proteins playing a crucial role in the molecular mechanisms of plant disease resistance against pathogens has become a subject of increasing importance. In this study, we investigated the fungal growth inhibitory activity of *Lupinus angustifolius* (L.) or narrow-leafed lupin (NLL) seed proteins from the beta-conglutin family (b1, b2, b3, b4, and b6). Constructs were made with the coding sequence fused to the 6xHis-tag, over-expressed in *E. coli* and purified by affinity chromatography using Ni2+-resin packed columns, obtaining proteins of >95% purity. *In vitro* assays to determine antifungal activity and the concentration required for a 50% inhibition of fungal growth (IC50) were performed using four fungal species, namely *Rhizoctonia solani*, *Fusarium oxysporum*, *Alternaria brassicicola*, and *Sclerotinia sclerotiorum*.

All peptides tested showed fungal growth inhibitory activity against the four fungal species. The strongest antifungal activities were shown by b1, b2 and b6, since the growth inhibitory effect continued after 30 days of *in vitro* fungal cultures. In addition, b3 and b4 displayed lower level of antifungal effect.

Results of fungal growth inhibitory effects of recombinant beta-conglutins presented in this study indicate the potential role of a major class of lupin seed proteins in defence against fungal pathogens.

173	Biotic Stress	Jorge A. Acosta-Gallegos, J.A.A.G.	Pathogenic races of Fusarium oxysporum f. sp. ciceris attacking chickpeas at the Bajío region in Central Mexico

Pathogenic races of Fusarium oxysporum f. sp. ciceris attacking chickpeas at the Bajío region in Central Mexico

Brenda Z. Guerrero-Aguilar, B.Z.G.A.[1], Jorge A. Acosta-Gallegos, J.A.A.G.[1*], Pedro Ortega-Murrieta, P.O.M.[2], and Mario M. Gonzalez-Chavira, M.M.G.C.[1]. [1]INIFAP-CEBAJ. Km 6.5 Carretera Celaya-San Miguel Allende Celaya, Guanajuato, México. C.P. 38110; [2]INIFAP-CECH Blvd. Pascual Encinas Félix #21, Col. La Manga, Hermosillo, Sonora, México, 83200. *(jacostagal@gmail.com)

In the Bajío region of Central México, desi chickpeas are grown under residual moisture while improved kabuli cultivars are grown under limited irrigation during the fall-winter season. In this region, the crop is often damaged by *Fusarium oxysporum* f. sp. *ciceris* (FOC). The aim was to identify the prevalent races of FOC by using specific RAPD and SCAR primers and inoculation on a set of eight differential cultivars, and to identify resistant genotypes against local FOC races. Forty-eight isolates from the southern part of Guanajuato were tested with 13 primers that identify

races 0, 1A, 1B/C, 2, 3, 4, 5 and 6 of FOC. Among the 48 isolates three races were identified: 0, 1B/C, and 6. Races 0 and 1B/C that induce wilting were found in higher frequency, whereas race 6 that induces yellowing was restricted in distribution. Representatives of these three races plus an isolate of race 5 were inoculated by the immersion method on the eight differential cultivars (JG.62, Sanford, P2245, CRIL-1-53, CRIL-1-94, CRIL-1-17, CRIL-1-36, and WR-315) and on 29 diverse kabuli and desi genotypes. Results with the differential set were consistent with those from the primers. From the differential set, genotypes CRIL 1-36, WR 315, and CRIL 1-17 were resistant. None of the diverse genotypes was resistant to all four races; six were resistant to race 1B/C, 15 to race 0 and one to race 5; some were resistant to two races. Resistant genotypes can be used as parents to pyramid different resistance genes.

174	Biotic Stress	Jorge A. Acosta-Gallegos, J.A.A.G.	Resistance to Ascochyta rabiei is needed to expand the window frame for chickpea sowing in Central Mexico

Resistance to Ascochyta rabiei is needed to expand the window frame for chickpea sowing in Central Mexico

Jorge A. Acosta-Gallegos, J.A.A.G.[1*], Brenda Z. Guerrero-Aguilar, B.Z.G.A.[1], Yanet JImenez-Hernandez, Y.J.H.[1], Gustavo Fierros-Leyva, G.F.L.[2], Pedro Ortega-Murrieta, P.O.M.[2], and Victor Valenzuela-Herrera, V.V.H.[3]. [1]CEBAJ-INIFAP, Km 6.5 Carretera Celaya a San Miguel de Allende, C.P. 38110, Celaya, Guanajuato, Mexico; [2]CECH-INIFAP, Blvd. Pascual Encinas Felix # 21, Col. La Manga, C.P. 83200, Hermosillo, Sonora, Mexico; [3]CEVACU-INIFAP, Km 17.5 Carretera Culiacan - El Dorado, CP 80000, Culiacan, Sinaloa, Mexico. *(jacostagal@gmail.com)

At the Bajio region of Central Mexico the demand for immature chickpea pods, that are consumed roasted, vapor cooked or green, has grown. Farmers have consecutive plantings from August to February, but early sown chickpea sometimes is damaged by *Ascochyta rabiei*. In the local breeding program, we are attempting two-generations per year. In 2012 several trials were sown out of the regular season, in early and late May, trials included lines, families and sources of root-rot resistance. Ascochyta blight damaged plants in the early-planted trials and the seed of most genotypes was infected. Late-planted trials did not yield, except some of the root-rot resistant sources that were resistant to Ascochyta blight: Ghipsaphyla belaia (Ethiopia), URSS 05-01, ICC 12960, Flipper and Jimbour; last two from Australia Two isolates were made from infected plants and inoculum prepared to test for resistance upon 25 Kabuli genotypes under controlled conditions; all resulted susceptible. During 2013 around 300 families, the differential set for *A. rabiei* and CDC Frontier were sown in May. After the start of the rainy season, all families were lost to a severe attack by *A. rabiei* in July, only CDC Frontier was resistant and the differential Dwelly was tolerant. Results indicate that the local pathotype of *A. rabiei* is highly virulent, similar to pathotype 2 described in India by Grewal (1981) and to pathotype II described by Chen *et al*. (2004) in the USA. Earlier planting in 2014, i.e. February escaped the presence of Ascochyta blight, thus two generation per year are feasible. Resistant genotypes will be used in crosses.

175	Biotic Stress	Kahlon, J. G.	Efficacy of transgenic disease resistant peas against Fusarium root rot (F.solani and F. avenaceum) and Mycosphaerella blight (M. pinodes) in field.

Efficacy of transgenic disease resistant peas against Fusarium root rot (*F.solani* and *F. avenaceum*) and Mycosphaerella blight (*M. pinodes*) in field.

Kahlon, J. G.[1*], Chatterton, S.[2], Strydhorst, S.M.[3], Bing, D.J.[4], Bowness, R.[5], Olson, M.[6], Hassan, F.[7], Jacobsen, H.J.[7], and Hall, L.M.[1]. [1]Dep. of Agric., Food, and Nutritional Sci., Univ. of Alberta, Edmonton, AB; [2]Agriculture and Agri-Food Canada, Lethbridge AB; [3]Alberta Agriculture and Rural Development, Barrhead AB; [4]Agriculture and Agri-Food Canada, Lacombe, AB; [5]Alberta Agriculture and Rural Development Lacombe AB; [6]Alberta Agriculture and Rural Development Stony Plain, AB; [7]Department of Plant Biotech., Institute of Plant Genetics, Hannover, Germany. *(jagroop@ualberta.ca)

In field pea, Fusarium root rot complex and Mycosphaerella blight (*M. pinodes*) are major production-limiting factors in Alberta. Conventional breeding techniques have had limited success at producing resistant varieties but approaches using genetic modification may hold promise. European pea cultivars were genetically transformed with genes encoding for four pathogenesis-related proteins: 1, 3-β glucanase; polygalacturonase inhibiting proteins (PGIPs); anti-microbial small molecules (stilbene synthase) and endochitinase. In summer 2013, two separate field trials were established to test lines transformed with single or stacked genes, compared to German parental and Canadian lines, for resistance to Fusarium root rot and Mycosphaerella blight. Significant differences in disease ratings, % emergence, seed numbers, seed weight (g/plot) and biomass (g/plot) in the presence of disease were observed among transgenic lines in both trials. Differences between promoters, single and stacked genes and transformation events, suggest that efficacy could be optimized. Strict biosafety procedures were maintained throughout the project to ensure safety of the industry, under the auspices of the Canadian Food Inspection Agency (CFIA). Results from this research will provide the Canadian pulse industry and CFIA with information necessary to make a decision on whether or not to consider disease resistant GM pea.

176	Biotic Stress	Kumari, S.G.	Screening and selection of faba bean (Vicia faba L.) germplasm for resistance to Faba bean necrotic yellows virus

Screening and selection of faba bean (Vicia faba L.) germplasm for resistance to Faba bean necrotic yellows virus

Kumari, S.G.[1*], Ekzayez, A.[1], van Leur, J.[2], Maalouf, F.[3], and Najar, A.[4]. [1]International Centre for Agricultural Research in Dry Areas (ICARDA), Tunis, Tunisia; [2]NSW Department of Primary Industries, Tamworth Agricultural Institute, NSW, Australia; [3]ICARDA, Cairo, Egypt; [4]INRAT, Tunis, Tunisia. *(s.kumari@cgiar.org)

Faba bean necrotic yellows virus (FBNYV, genus *Nanovirus*, family *Nanoviridae*) causes a serious disease to several food and fodder legumes. The main symptoms in response to FBNYV infection are leaf yellowing, plant stunting, reddening, and thickening of the leaves and reduction in pod setting. FBNYV is persistently transmitted by various aphid species, and most efficiently by *Acyrthosiphon pisum* and *Aphis craccivora.* FBNYV epidemics have been reported in several countries in West Asia and North Africa. Virus disease management can be achieved through a combination of several approaches; but genetic resistance offers the most economic control option in the longer term. Around 1000 faba bean accessions with a wide genetic background were evaluated during the last decade for their reaction to FBNYV using artificial inoculation with the pea aphid *A. pisum* under field conditions. Differences in resistance were measured by (i) incidence and severity of infection, (ii) virus concentration based on the intensity of reaction by the tissue-blot immunoassay (TBIA), and (iii) yield per plant. Single plants characterized by mild or no symptoms, no or little virus content and good yield were identified. No complete resistance has been found, however five new breeding lines with resistance to FBNYV developed by the pedigree method through the last five growing seasons under heavy infestation by the virus. Three of them were selected from accessions ILB265 (Spain), ILB397 (Tunisia) and ILB895 (China), and two from improved inbred lines BPL423, BPL5277 derived from ILB266 (Spain) and ILB426 (Sudan), respectively. This is the first report on FBNYV resistance in faba bean. In addition, these lines were resistant to Syrian and Tunisian isolates of FBNYV. Inheritance studies will be initiated to study if there are different resistance genes involved that function through different resistance mechanisms.

177	Biotic Stress	Le May, C.	Role of legume host species successions on Aphanomyces euteiches population structure

Role of legume host species successions on Aphanomyces euteiches population structure

Quillévéré-Hamard, A.[1], Pilet-Nayel, M-L.[1], Onfroy, C.[1,2], Moussart, A.[1,2], Andrivon, D.[1], Baranger, A.[1], and Le May,

C.[1,3*]. [1]INRA, UMR1349 IGEPP, Domaine de la Motte, 35653 Le Rheu, France; [2]UNIP-CETIOM, 11 rue de Monceau, CS 60003, F-75378 Paris, France; [3]AGROCAMPUS Ouest, UMR1349 IGEPP, 65 rue de Saint Brieuc, 35042 Rennes, France. *(lemay@agrocampus-ouest.fr)

Aphanomyces euteiches is an oomycete pathogen that causes devastating root rot in many pea-growing countries. This homothallic pathogen is also reported to infect other legume species. As sexual recombination and intraspecific genetic flow remains low, a possible role of legume host plants in the pathogen population structure is expected. Our aim was to evaluate the role of various legume species, cultivated either as single crops or in rotations, on the structuration of pea-infecting *A. euteiches* populations. A collection of *A. euteiches* isolates from pea infested fields with various legumes in their rotation history was genotyped using SSR markers and evaluated for pathogenicity on legume hosts. Isolates from fields including alfalfa, faba bean or vetch in their crop history presented specific molecular and pathogenicity patterns compared to isolates from fields including only pea in their legume crop history. A methodology simulating accelerated single-crop cycles of pea, faba bean and vetch was developed in controlled conditions, to evaluate the filter effect of legume species on a mixture of two co-inoculated French *A. euteiches* isolates showing contrasted structure patterns and originating from fields with different legume cropping histories. Five crop cycles of two weeks were conducted, using infected roots from the previous cycle as inoculum at each cycle. Molecular characterization of strains isolated after the fifth cycle showed that faba bean and vetch filtered one of the two isolates inoculated. These results, under confirmation in biological replicates, suggest that diversifying legumes species in crop rotations would limit pressure of *A. euteiches* populations selected by pea.

178	Biotic Stress	McLaren, D.L.	Fusarium species isolated from dry bean and field pea in Manitoba: Identification, pathogenicity and prognosis.

***Fusarium* species isolated from dry bean and field pea in Manitoba: Identification, pathogenicity and prognosis.**

McLaren, D.L.[1*], Henriquez, M.A.[1], Conner, R.L.[2], Balasubramanian, P.M.[3], Chang, K.F.[4], Hwang, S.F.[4], Strelkov, S.E.[5], and Gossen, B.D.[6]. [1]Agriculture and Agri-Food Canada, Brandon, Manitoba, Canada; [2]Agriculture and Agri-Food Canada, Morden, Manitoba, Canada; [3]Agriculture and Agri-Food Canada, Lethbridge, Alberta, Canada; [4]Alberta Agriculture and Rural Development, Edmonton, Alberta, Canada; [5]University of Alberta, Edmonton, Alberta, Canada; [6]Agriculture and Agri-Food Canada, Saskatoon, Saskatchewan, Canada. *(debra.mclaren@agr.gc.ca)

Fusarium root rot is a serious disease of dry bean and field pea in Canada and can cause significant yield reductions due to poor plant stands and weakened root systems. In Manitoba, little information exists on the identification or pathogenicity of *Fusarium* spp. that occur on field pea and dry bean. Over a 10-year period, commercial pea and bean crops from the major production areas in Manitoba were evaluated to determine the prevalence and incidence of root rot diseases. In 2011, an in-depth study on root rot pathogen identification from three commercial crops each of field pea and dry bean located in the major production areas in Manitoba was conducted. Fungal species isolated from root rot lesions were identified based on their morphological characteristics, with species identity confirmed by DNA sequencing. *Fusarium* spp. collected from the diseased pea and bean roots were screened for pathogenicity on the cultivars Admiral and Envoy, respectively. Important findings in this research were the identification of *Fusarium cuneirostrum* causing root rot in dry bean plants in Canada, and the identification of *Fusarium graminearum,* commonly associated with Fusarium Head Blight in cereals, as a root rot pathogen of dry bean. These results stress the need for further research on the root rot pathogens in Manitoba field pea and dry bean crops and the importance of cross-pathogenicity studies in order to develop effective disease management strategies.

179	Biotic Stress	Miklas, P.N.	Characterizing quantitative resistance to halo bacterial blight in common bean population Rojo/CAL 143

Characterizing quantitative resistance to halo bacterial blight in common bean population Rojo/CAL 143

Trapp, J.[1], Miklas, P.N.[1*], and Fourie, D.[2]. [1]USDA-ARS, Prosser, WA USA; [2]ARC-Grain Crops Institute, Potchefstroom. *(phil.miklas@ars.usda)

Halo bacterial blight (Pseudomonas syringae pv. phaseolicola) is a serious seed borne disease problem for common bean (Phaseolus vulgaris L.) produced in wet-cool regions. The disease is commonly found in bean production regions in East and South Africa. Genetic resistance within the host is the best control method. Major R genes with resistance to specific pathogen races have been characterized, but only quantitative resistance exists for genetic control of the most prevalent Psp race 6. This study investigated the quantitative halo blight resistance observed in red mottled bean CAL 143. Five pathogen races 1, 6, 7, and 8 were used to evaluate reaction to halo blight in Rojo/CAL 143 population consisting of 140 F5:7 RILs. The RILs were assayed for 5,398 SNP markers on an Illumina Infinium BeadChip. JoinMap software was used to construct the linkage map and Qgene was used to conduct the QTL analysis. One major QTL conditioning resistance to race 6 was observed. The QTL occurred on chromosome Pv04 within a large cluster of R genes including the new Pse-6 gene which conditions qualitative resistance to races 1, 5, 7, and 9. This newly discovered QTL will be tagged with markers to facilitate development of bean cultivars with better resistance to the most problematic Psp race 6.

180	Biotic Stress	Nyandoro, R.	Evaluation of soybean variety resistance to fusarium in the management of root rot of soybean in southern Alberta, Canada.

Evaluation of soybean variety resistance to fusarium in the management of root rot of soybean in southern Alberta, Canada.

Nyandoro, R.[1*], Chang, K.F.[2], Hwang, S.F.[2], Strelkov, S.E.[1], Turnbull, G.D.[2], Howard, R.J.[3], and Harding, M.W.[3]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; [2]Crop Diversification Centre North, Alberta Agriculture and Rural Development (AARD), Edmonton, AB T5Y 6H3, Canada; [3]Crop Development Centre South, Alberta Agriculture and Rural Development (AARD), Brooks, AB T1R 1E6, Canada. *(nyandoro@ualberta.ca)

Root rot of soybean (*Glycine max)* is a potentially devastating disease that can reduce yields significantly. Although fungicidal seed dressings and improved agronomic practices reduce the disease, crop losses still occur. Genetic resistance to root rot could complement fungicides in the management of the disease. Ten glyphosate-ready soybean varieties (NSC Portage, 900Y61, 900Y71, 900Y81, 90M01, TH29002RR, TH27005RR, TH32004R2Y, LS003RR, and LS005RR) were evaluated for tolerance to *Fusariun avenaceum.*. Two non-glyphosate-ready cultivars (OAC Prudence and Tundra) also were evaluated in a greenhouse experiment. The experiments were seeded in a randomized complete block design with cultivars as the treatments. The varieties 90M01, 900Y81, 900Y61 and TH29002RR had significantly ($P \leq 0.05$) higher emergence rates (62%, 59%, 59%, and 59%, respectively) compared with the others under field conditions. In the greenhouse, significantly higher crop emergence rates ($P \leq 0.05$) were observed on the varieties NSC Portage, Tundra, LS005R (94, 93, 93, and 91%, respectively) while variety 900Y71 had the lowest emergence. Grain yields were significantly ($P \leq 0.05$) higher in varieties 900Y81, 900Y61, TH32004R, while TH29002R had the lowest grain yield at 2.14 t/ha. Severe seedling stunting occurred on the varieties 900Y81 and NSC Portage with seedling heights of 39 and 40 mm, while the tallest seedlings were of the variety Tundra (61mm). In the greenhouse, seed dry mass was significantly higher ($P \leq 0.05$) on 900Y61, LS003RR, 900Y81 and OAC Prudence. The variety 900Y71 was the most affected by root rot with a disease severity of 2.05 on a scale of 0-4.

181	Biotic Stress	Ortega, P.F.	Blanoro: a new kabuli chickpea cultivar resistant to Fusarium oxysporum f. sp. ciceris

Blanoro: a new kabuli chickpea cultivar resistant to Fusarium oxysporum f. sp. ciceris

Ortega, P.F.[1*], Fierros, G.A.[2], Padilla, I.[3], Gutiérres, E.[4], Castillo, N.[3], Acosta, J.A.[5], and Velarde, S.[6]. [1]INIFAP-CECH. Blvd. Pascual Encinas Félix #21, Col. La Manga, Hermosillo, Sonora, México, 83200; [2]INIFAP-CECH; [3]INIFAP-CENEB; [4]INIFAP-CETODS; [5]INIFAP-CEBAJ; [6]INIFAP-CEVACU. *(ortegampedro@gmail.com)

'Blanoro' is a kabuli chickpea cultivar developed by the Breeding Program of INIFAP, Mexico. Blanoro is adapted to winter sowing in the coastal areas of the Northwest and the central Bajio regions of Mexico, under irrigated conditions. Blanoro was developed from a three-way cross (L-4924 x Blanco Lechoso) x 'Blanco Sinaloa 92'. Early generations were bulk advanced and individual plants were selected in the F5 generation on the basis of resistance to *Fusarium oxysporum* f. sp. *ciceris (FOC)*. Blanoro was included in yield trials in the Northwest region from 2005 to 2010 and in 28 trials during 2011 to 2013 at sites in the states Sonora, Sinaloa, Baja California Sur and Guanajuato. The plant has a semierect growth habit; primary branches are semierect and average three per plant. Leaves are pinnate (22 mm long 16 mm wide) with medium green color and have white flowers. The pods are large (30 mm long, 15 mm wide), have medium green color and the seeds are large (68 g per 100 seeds) with angular shape and light beige color. Blanoro has a medium time to flowering and maturity (47 and 125 d after sowing, respectively). Blanoro outyielded the dominant cultivar Blanco Sinaloa 92 with an average yield of 2,694 kg·ha-1 across sites and seasons, while the yield of Blanco Sinaloa 92 was 2,401 kg·ha-1. Blanoro exhibits resistance to FOC race 5. Seed of Blanoro is maintained at Campo Experimental Costa de Hermosillo, Sonora and samples for research can be requested to the main author.

182	Biotic Stress	Pasche, J.S.	Comparison of Fusarium solani and F. avenaceum Inoculation Methods in Dry Pea

Comparison of *Fusarium solani* and *F. avenaceum* Inoculation Methods in Dry Pea

Jennifer Odom[1], Kevin McPhee[2], Lyndon Porter[3] and Julie S. Pasche[1]. Dept. of Plant Pathology[1], and Plant Sciences[2], North Dakota State University, Fargo, ND Vegetable and Forage Crops Research Unit; USDA-ARS, Prosser, WA[3]

Greenhouse inoculation methods that reliably and efficiently predict the field reaction of a breeding line to a pathogen are invaluable in the development of disease resistant cultivars. The development or identification of effective screening methods can be particularly challenging where a root rotting pathogen complex is concerned. In addition to *Fusarium solani* f. sp. *pisi*, *F. avenaceum* has been determined to be a major pathogen in the pea root rot complex in North Dakota and other major production areas in the US and Canada. Greenhouse inoculation methods have been evaluated for *F. solani* in peas and related pulse crops, however, little information exists to determine if these methods accurately identify resistance to *F. avenaceum*. Additionally, research comparing inoculation methods for *Fusarium* root rot has not been performed in peas. The goal of the research reported here is to provide researchers and breeders with tools to accelerate the development of root rot resistant pea cultivars. Three inoculation methods; inoculum layer, spore suspension, and seed soak, were evaluated under greenhouse conditions across 10 cultivars and three isolates each of *F. solani* and *F. avenaceum*. Preliminary results indicate differences in root rot severity across cultivars, among isolates within *Fusarium* spp., between *F. solani* and *F. avenaceum,* and across all three methods. Results are similar to previous research conducted on the same cultivars using the seed soak method. These results also confirm the importance of isolate and method selection on the identification of resistance.

183	Biotic Stress	Podder, R.	Transfer of Stemphylium Blight Resistance from Lens ervoides to the Cultivated Lentil

Transfer of Stemphylium Blight Resistance from Lens ervoides to the Cultivated Lentil

Podder, R.[1*], Banniza, S.[1], and Vandenberg, A.[1]. [1]Dept. of Plant Sciences, Univ. of Saskatchewan.

*(rap039@mail.usask.ca)

Cultivated lentil (*Lens culinaris* Medik.) suffers yield loss when affected by stemphylium blight (SB), caused by *Stemphylium botryosum* Wallr. Identification of sources of SB resistance and knowledge of inheritance of SB resistance is important for developing resistant cultivars. Two recombinant inbred line (RIL) populations (LR-26 with 123 lines and LR-59 with 46 lines) from crosses between SB resistant parent *L. culinaris* cv. 'Eston' with *Lens ervoides* IG 72815 and L-01-827, respectively, were evaluated for SB resistance in a greenhouse at the University of Saskatchewan and under field conditions at the Pulses Research Centre (PRC), Ishurdi, Bangladesh. Compared to 'Eston', 60% and 68% of the LR-26 RILs and LR 59 RILs, respectively were resistant to SB under natural disease pressure in Bangladesh. Transgressive segregants had significantly improved SB resistance compared to both parents in the LR-26 population. The distribution of disease severity scores for all RILs indicated involvement of more than one major or minor gene for SB resistance in these interspecific populations. The RILs with consistent resistant reactions should prove useful for future crop improvement. Combining SB resistance from two *Lens* species should provide a baseline for future marker assisted breeding strategies using SB resistance genes from wild species of lentil.

184	Biotic Stress	Powell, T.K.	Bacterial auxin production facilitates resource conversion and carbon acquisition by the phyllosphere epiphyte Pantoea agglomerans on Phaseolus vulgaris leaves.

Bacterial auxin production facilitates resource conversion and carbon acquisition by the phyllosphere epiphyte *Pantoea agglomerans* on *Phaseolus vulgaris* leaves.

Powell, T.K.[1*], and Lindow, S.E.[2]. [1]United States Agency for International Development; [2]University of California, Berkeley. *(tpowell@usaid.gov)

The bacterial leaf epiphyte *Pantoea agglomerans* 299R synthesizes indole-3-acetic acid (IAA), an important plant hormone. IAA production was previously shown to confer a significant fitness advantage to *Pa*299R cells inoculated onto common bean (*Phaseolus vulgaris*) leaves, but the mechanism by which bacterial IAA exerted this effect was unknown. Here, we investigate the hypothesis that bacterial IAA production enhances availability of plant sugars, thereby relieving carbon limitation of bacterial growth on the leaf surface. To test this hypothesis, we inoculated bacteria harboring sucrose- and fructose-inducible reporter genes onto bean leaves, and compared reporter induction between wild-type *Pa*299R, its IAA- mutant *Pa*MX149, and *Pa*MX149 co-inoculated with exogenous NAA. In the presence of either exogenous or endogenous auxin, *P. agglomerans* sensed significantly less sucrose, but sensed a transient increase in fructose availability. In *in vitro* assays, *Pa*299R initiated growth more rapidly and at lower nutrient concentrations when using glucose or fructose as a sole carbon source, compared to sucrose. Together, these observations implicate plant cell-wall invertase as a putative plant target for IAA-mediated carbon acquisition by bacteria. They also suggest that IAA biosynthesis may function in a resource conversion strategy: by converting plant-derived sucrose into more readily accessible monosaccharides, bacteria may enhance carbon acquisition and maximize fitness in an oligotrophic, environmentally dynamic phyllosphere. By mediating such host-microbe interactions in the phyllosphere, bacterial IAA influences foliar population dynamics on common bean -- with potential implications for plant health and productivity.

185	Biotic Stress	Rodda, M.S.	Establishment of screening methods and identification of resistant sources for stemphylium blight in lentil

Establishment of screening methods and identification of resistant sources for stemphylium blight in lentil

Kant, P.[1], Rodda, M.S.[1*], Slater, A.T.[1], and Materne, M.[1]. [1]Department of Environment and Primary Industries, Victoria, Australia. *(matthew.rodda@depi.vic.gov.au)

Stemphylium botryosum is a necrophytic fungus that causes stemphylium blight in lentil, a disease of worldwide distribution and economic importance in major lentil growing regions. Yield loss of infected crops has been reported up to 88% in Bangladesh. Stemphylium blight has been sporadically reported in Australia and is considered to be a potential threat to the lentil industry. The disease mostly appears during the reproductive phase and prominent symptoms are leaf chlorosis and browning, which can lead to defoliation in extreme cases and significant yield loss.

In this study, methods were developed for screening lentil cultivars and breeding lines for resistance to stemphylium blight. Two alternative screening methods were developed, a whole plant and a cut-twig method. The whole plant method utilised four to five week old plants, whilst for the cut-twig method, tests were carried out on branches excised from eight week old plants. Plants or branches were sprayed with spore suspension inoculum and incubated at 23-25°C, >90% humidity for 48 h and then periodic moist conditions until disease scoring two weeks after inoculation.

This is the first study that reports evaluation of lentil germplasm against Australian isolates of *S. botryosum*. Screening of Australian lentil varieties and breeding germplasm found disease reactions between susceptible and moderately resistant. These methods were subsequently used to screen landraces for new sources of resistance. Four landraces were identified with resistance to *S. botryosum* and will be crossed with elite Australian lentil lines.

186	Biotic Stress	Rodda, M.S.	Resistance to botrytis grey mould in Australian lentil breeding germplasm

Resistance to botrytis grey mould in Australian lentil breeding germplasm

Rodda, M.S.[1*], Davidson, J.A.[2], McMurray, L.[2], and Li, H.B.[1]. [1]Department of Environment and Primary Industries, Horsham, Victoria, Australia; [2]South Australian Research and Development Institute, GPO Box 397, Adelaide, South Australia. *(matthew.rodda@depi.vic.gov.au)

Botrytis grey mould (BGM) is one of two main diseases affecting Australian lentils. It is a difficult disease to breed resistance against because of the complex nature of resistance mechanisms and the difficulty inducing epidemics artificially. The 2013 growing season in southern Australia was favourable for lentil production but there was also a high incidence and severity of BGM. Regular in-crop rainfall provided optimum conditions conducive to disease, enabling collection of high quality data at four locations on the BGM resistance of breeding germplasm.

In replicated yield trials (predominately F3 or F4-derived lines), disease severity was scored on an ordinal scale based on proportion of the plot area affected (8 m2 plots). High correlations for disease severity were observed between sites and there were strong genetic effects in rankings of breeding lines and pedigree groups. Resistance of lines was assessed based on average and maximum disease scores observed. Of lines in year 3 yield testing (n=146), 37% demonstrated resistance to BGM under high disease pressure and maintained their relative yield rankings (rated resistant or moderately resistant). Conversely, 27% of lines were susceptible or moderately susceptible and yielded poorly. The variety PBA Bolt (bred for drier, shorter season environments) performed poorly under high BGM pressure and conveyed susceptibility to much of its progeny. Resistance mechanisms to BGM need further study, but appear to include resistance to vegetative lodging and a suppression of pathogen spread in the plant that is not well understood.

187	Biotic Stress	Rubiales, D.	Legume breeding for broomrape resistance

Legume breeding for broomrape resistance

Rubiales, D.[1*], Fernandez-Aparicio, M.[1], and Fondevilla, S.[1]. [1]Institute for Sustainable Agriculture, CSIC. *(diego.rubiales@ias.csic.es)

Legume cultivation is hampered in Mediterranean regions by the occurrence of of the parasitic weed *Orobanche*

crenata(broomrape). Breeding for resistance is possible, but is hampered by the lack of sufficient levels of resistance, the complexity of its inheritance and the unreliability of available screening methods. Still, progress have been made in pea and faba bean accumulating the available quantitative resistance by breeding, allowing the release of resistant cultivars. Some resistance have also been identified in lentil, grasspea,commonvetch and chickpea, as well as in their wild relatives.

QTLs for resistance have been identified in faba bean and pea but were are still far for being able of using them effectively in MAS. Not only further saturation of the maps is needed, but also a more refined phenotyping and integration of information obtained from QTL analysis with gene and protein expression analysis. Also, sequence information obtained from other parasitic weeds will help in understanding parasite virulence and host resistance mechanisms.

188	Biotic Stress	Saraf, M	SUPPRESSION OF CHARCOAL ROT DISEASE BY TRICHODERMA spp.IN GLYCINE MAX

SUPPRESSION OF CHARCOAL ROT DISEASE BY TRICHODERMA spp.IN GLYCINE MAX

Saraf, M.[1*], and Thakkar, A.[2]. [1]Gujarat University ,Ahmedabad,India; [2]Gujarat University, Ahmedabad,India. *(sarafmeenu@gmail.com)

Plant disease cause manifold loses in yield and productivity. The objectives of this work were to study the action of *Trichoderma* spp. against the *Macrophomina phaseolina* , causing charcoal rot in *Glycine max*. The selected potent isolate was tested: (i) fungal-pathogen co-cultivation, (ii) anti- pathogen enzymes and metabolites (iii) volatile metabolites Six isolates of *Trichoderma* were isolated from rhizospheric soil . MBAAT was characterized and screened *in vitro* for their biocontrol and PGP traits like phosphate solubilization (121.51 µg/ml), production of IAA (30.12µg/ml), ammonia (24.63 µM/ml), siderophore (29.31mM/ml) and enzymes like chitinase (6.18 U/ml), β-1,3 glucanase (4.93 U/ml) ,cellulase (7.28 U/ml).*Trichoderma citrinoviride* (MBAAT) was able to antagonize two fungal phytopathogens *M. phaseolina* and *S. sclerotiorum* showing 96.36% and 97.45% inhibition. Identification and profiling of Volatile metabolites produced by strain indicated two compounds that were identified as 3-methylbutanal and 2-methyl, 2-butane using GC-MS. The influence of the isolate MBAAT on the disease development was assessed using *Glycine max* as host. The seeds were coated with MBAAT and then inoculated with conidia suspensions of *Macrophomina*. Disease severity and index was evaluated by counting typical lesions of charcoal rot caused by pathogen. The treatments were compared to commercial preparation of *Trichoderma* on all biometric parameters. *T. citrinoviride* effectively controlled the phytopathogens by the volatile metabolites produced.

189	Biotic Stress	Saraf, M	Multifaceted beneficial microbes in rhizosphere to combat phytopathogens in Cicer arietinum.

Multifaceted beneficial microbes in rhizosphere to combat phytopathogens in Cicer arietinum.

Saraf, M.[1*], and Pandya, U.[1]. [1]Gujarat University,Ahmedabad,India. *(sarafmeenu@gmail.com)

The rhizobacteria play an intrinsic role in enhancing the plant growth by an array of activities leading to biofertilization and biocontrol. Present study was carried out to assess the diversity of bacteria from vermicompost amended sites of Gujarat and potential isolates were screened for their biocontrol attributes against soil borne pathogens such *M. phaseolina*, *F. oxysporum* and *R.solani.* Among the 27 isolates, MBCU4 ,a gram positive, endospore forming bacteria was identified as *Bacillus subtilis*. It showed the presence of chitinase, β 1, 3 glucanase, cellulase and HCN production. *B. subtilis* further studied against charcoal rot disease in chickpea plant. Inoculation of seeds with *M. phaseolina* showed maximum 85% of disease incidence. Maximum suppression of percent disease incidence (PDI) was recorded 29%. Maximum increaseof root length (83.25%), shoot length (95.43%), fresh weight (89.49%), dry

weight (125.71%), chlorophyll content (83.52%) and number of pods (69.58%) were recorded in comparison to uninoculated control. It was found that extracellular chitinase was produced from *Bacillus subtilis* which was purified by ammonium sulfate followed by DEAE sepharose CL-6B column chromatography. The purified enzyme was having the molecular weight 31kDa and its activity in the gel was determined by clear zone on zymogram. The enzyme is most active at pH 6.0 and temperature 50 0C. The purified chitinase exhibited high degree of antifungal activity particularly against plant pathogens *M. phaseolina* (69.0%) and *R.solani* (52.0%)

190	Biotic Stress	Simons, K.J.	Seed to Seedling Transmission of Colletotrichum lindemuthianum Under Greenhouse Conditions

Seed to Seedling Transmission of *Colletotrichum lindemuthianum* Under Greenhouse Conditions

Halvorson, J.M.[1], Simons, K.J.[1*], Lamppa, R.S.[1], and Pasche, J.S.[1]. [1]Department of Plant Pathology, North Dakota State University; Fargo, ND 58108. *(Kristin.Simons@ndsu.edu)

Colletotrichum lindemuthianum, the causal agent of dry bean anthracnose, has been shown to reside in infected seeds at varying levels which serve as an important inoculum source for plant infection. These infections can lead to further disease spread under favorable environmental conditions. In previous research, the level of disease symptoms in the seeds was related to the level of seed to seedling transmission, ranging from 85% in severely diseased seeds to 15% in symptomless seed. However, these studies focused primarily on disease development, and no research has been performed to detail the movement of the pathogen within stem tissue. In research reported here, greenhouse trials were performed to determine differences in seed to seedling pathogen movement from seed with infection levels varying from healthy to severe. Data evaluations included seed germination, plant emergence, and fungal quantification using growth on solid nutrient media and real-time PCR assays. In preliminary results, seed germination and plant emergence decreased with increasing seed symptom severity. The real-time quantitative PCR assay developed for *C. lindemuthianum* in infected tissue was more sensitive than previous methods of pathogen detection. No product was amplified from 17 *Colletotrichum* species and 12 other fungal and bacterial dry bean pathogens using this PCR assay. The real-time PCR assay successfully quantified *C. lindemuthianum* in seed with and without symptoms and seed to seedling transmission of the pathogen within the stem tissue grown from all levels of seed infection.

191	Biotic Stress	Sivachandra Kumar, NT	Seed-to-seedling transmission of Ascochyta pisi in field pea

Seed-to-seedling transmission of Ascochyta pisi in field pea

Sivachandra Kumar, NT.[1*], and Banniza, S.[1]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, Saskatoon S7N 5A8, Saskatchewan, Canada. *(nis286@mail.usask.ca)

Ascochyta blight is one of the major diseases of field pea in Saskatchewan. This disease of field pea can be caused by four pathogens of the same anamorphic genus, hence is collectively known as the Ascochyta blight complex. The pathogens causing Ascochyta blight are *Didymella pinodes*, *Ascochyta pisi*, *Phoma medicaginis var. pinodella, Phoma koolunga. Didymella pinodes* is considered to be the most common pathogen in the prairies, but for the past 10 years *A. pisi* has been recovered at higher levels than *D. pinodes* on pea seeds harvested from fields in south and south-western cropping areas of Saskatchewan. Field trials were conducted in 2012 and 2013 at two locations where low natural inoculum was expected, to determine the seed-to-seedling transmission rate of *A. pisi* using 'CDC Patrick'. Commercial seed samples with 14.5% and 0.5% *A. pisi* infection were sourced and mixed to obtain seed lots with *A. pisi* infection levels of 0.5, 5, 10 and 14.5% that were seeded into plots arranged in a randomized complete block design. Seed infection levels were confirmed through seed testing after mixing the seed lots. Seedling emergence was

assessed and disease severity was rated every two weeks. Seed yields and seed infection levels with *A. pisi* were assessed after harvest. Data from both years and locations were pooled for analysis, considering seed infection a fixed factor, and location, year and block as random factors. Results revealed a significant effect of *A. pisi* seed infection on emergence of seedlings ($P < 0.05$). Seed infection levels of 10 and 14.5% resulted in reduced emergence compared to 0.5% seed infection, but the level of seed infection at planting did not have any significant impact on *A. pisi* disease severity, seed infection at harvest or seed yield.

192	Biotic Stress	Tenuta, M.	Results of the Manitoba soybean cyst nematode Survey

Results of the Manitoba soybean cyst nematode Survey

Tenuta, M.[1*], Madani, M.[1], and Lange, D.[2]. [1]Department of Soil Science, University of Manitoba; [2]Manitoba Agriculture, Food and Rural Development. *(mario.tenuta@umanitoba.ca)

We report the findings of a survey conducted in 2012/2013 of soybean fields for the soybean cyst nematode (*Heterodera glycines*) in Manitoba. In total, 48 fields were sampled with fields prone to infestation selected. Fields were sectioned into areas that could be responsible for pest introduction. In total, 282 composite soil samples were analyzed from 48 fields. Overall, 37 of the samples from 22 fields had nematode cysts. Sixty cysts were recovered. Most cysts were heavily damaged but 26 were sufficient for examination. Of these, 23 had circumfenestrate vulval cone structures. Three cysts had bifenestrate vulval cone structures characteristic of the genus *Heterodera*. Not all the cysts contained nematodes either as juveniles or eggs. Most were empty except for 15 circumfenestrate and one bifenestrate cysts. These 16 cysts were then followed up with molecular analyses by ITS sequencing, three SCN species-specific PCR approaches (Ou et al. 1993, Subbotin et al. 2001, Madani et al. 2013), and in one case, by 28s rDNA gene sequencing. ITS sequencing was possible for 14 of the circumfenestrate cysts. These best matched the sequence database for the cyst nematode, *Cactodera*. Only one of the bifenestrate cysts yielded DNA for analysis and its identification was ambiguous between *H, glycines* and *Cactodera*. *Cactodera* is not a pest of soybean or other crop plants in Manitoba. These cyst nematodes are likely naturally present, living on weeds and grasses in the sampled fields. The findings of the current study mean *H. glycines* has still not been detected in Manitoba.

193	Biotic Stress	Tenuta, M.	The stem nematode (Ditylenchus weischeri) on grain pea and creeping thistle in the Canadian Prairie Provinces

The stem nematode (Ditylenchus weischeri) on grain pea and creeping thistle in the Canadian Prairie Provinces

Tenuta, M.[1*], Madani, M.[1], Hajihassani, A.[1], Briar, S.[1], and Subbotin, S.[2]. [1]Department of Soil Science, University of Manitoba; [2]Plant Pest Diagnostic Centre, California Department of Food and Agriculture.
*(mario.tenuta@umanitoba.ca)

The stem nematode (*Ditylenchus dipsaci*) was first described as a parasite of creeping thistle (*Cirsium arvense*) in the Canadian Prairies in 1979. Recently, *Ditylenchus* on creeping thistle in Russia was shown to be *D. weischeri*, which is not a pest. We examined if *D. weischeri* and not *D. dipsaci* is present in yellow pea (*Pisum sativum*) grain samples in 2009 and 2010 and from creeping thistle in Saskatchewan, Alberta and Manitoba. Grower samples from 538 pea fields were received. Two-percent of samples were *Ditylenchus* positive. Numbers ranged from 4-1500 nematodes kg-1 and related to presence of creeping thistle seeds. Positive samples occurred in 2009 but not 2010. The nematode was morphologically dissimilar to *D. dipsaci*. Creeping thistles were collected from pea fields in the Provinces. All from Saskatchewan and Manitoba were infested with *Ditylenchus*. ITS-rRNA regions were amplified using two primer sets. A fragment of *hsp90* was also obtained with U831 and L1110 primers. PCR-ITS products were subjected to RFLP using *Bsh*1236I, *Hinf*I, *Msp*I, *Rsa*I and *Taq*I. The results match those published for *D. weischeri*. The results indicate

the stem nematode found in yellow pea grain is *D. weischeri* and that creeping thistle seeds in grain its source. Host screening studies conducted in greenhouse showed *D. weischeri* to also be distince from *D. dipsaci* in crop-host preference. *D. weischeri* preferred creeping thistle whereas *D. dipsaci* preferred garlic and then yellow pea.

194	Biotic Stress	Thompson, J.P.	Potential of wild chickpea species for improving the resistance of chickpea to root-lesion nematodes

Potential of wild chickpea species for improving the resistance of chickpea to root-lesion nematodes

Thompson, J.P.[1*], Reen, R.A.[2], and Kelly, A.[2]. [1]Centre for Crop Health, University of Southern Queensland, Toowoomba, Australia; [2]Agri-Sciences Queensland, Dept Agriculture, Fisheries and Food,Toowoomba, Australia. *(john.thompson@daff.qld.gov.au)

The root-lesion nematode species *Pratylenchus thornei* and *P. neglectus* are hosted by both wheat and chickpea diminishing the benefits of rotating these crops. Intolerant wheat and chickpea cultivars can lose ~70% and ~20% grain yield respectively in heavily infested fields in Australia and other countries.

The nematodes pass though several life cycles during crop growth with the exponential rate of population increase dependent on the quantitative resistance/susceptibility of the crop cultivar and environmental conditions of soil temperature and moisture. Losses could be substantially reduced if wheat and chickpea cultivars with high levels of resistance to these nematodes were available to growers.

Culivated chickpea (*Cicer arietinum*) began as a crop in the Middle East some 10,000 years ago when selected by neolithic farmers from its wild progenitor *C. reticulatum.* There have been four genetic bottlenecks in the development of modern chickpea cultivars and there may be considerable untapped genetic potential in wild chickpea relatives that could be used for chickpea improvement.

In a number of glasshouse experiments, we assessed resistance to both *P. thornei* and *P. neglectus* of accessions of chickpea (both desi and kabuli genotypes), and the wild species *C. reticulatum, C. echinospermum* and *C. bijugum*.

On average, *C. echinospermum* and *C. bijugum* were more resistant to *P. thornei,* and *C. reticulatum* and *C. echinspermum* were more resistant to *P. neglectus* than *C. arietinum* accessions. Assessing larger new collections of these wild related species would be desirable to ascertain their full potential to provide effective resistance genes to root-lesion nematodes for chickpea breeding.

195	Biotic Stress	Vaz Patto, M.C.	Chickling pea (Lathyrus cicera L.) resistance to rust and powdery mildew under QTLs scrutiny

Chickling pea (Lathyrus cicera L.) resistance to rust and powdery mildew under QTLs scrutiny

Almeida, N.F.[1], Alves, M.L.[1], Leitão, S.T.[1], Rubiales, D.[2], and Vaz Patto, M.C.[1*]. [1]Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa, Av. da República, 2780-157 Oeiras, Portugal; [2]Institute for Sustainable Agriculture, CSIC, Apdo. 4084, E-14080 Córdoba, Spain. *(cpatto@itqb.unl.pt)

Chickling pea (*Lathyrus cicera*) is a feed and fodder crop, with great adaptability to inauspicious environments (drought, flood and salinity), high protein content and resistance to serious diseases, being an alternative to marginal soils and cropping systems diversification.

Partial resistance to rust and powdery mildew has been described in this species, but its genetic control is still not elucidated, hampering its use on resistance breeding. In order to unveil this genetic control, a QTL analysis was performed using a RILs population, segregating for rust and powdery mildew resistance. 108 F5 RILs

(BGE008277xBGE023542) were evaluated for rust (*Uromyces pisi*) and powdery mildew (*Erysiphe pisi*) disease severity under controlled conditions, in three independent experiments.

Significant differences for rust and powdery mildew resistance were detected between genotypes, experiments and also for GxE interaction. QTL mapping was therefore performed separately per experiment. Broad-sense hereditability/ experiment had a maximum value of 78% and 84% for rust and powdery mildew resistance respectively. Using the developed RIL linkage map with a total of 258 markers (SNP, SSR, ITAP), covering 757.11cM in 8 major and 3 minor linkages groups, one common QTL for rust and powdery mildew resistance was detected. This QTL region explained respectively, 15.5 and 16.7 % of the genetic variance observed. In addition, a second non-overlapping QTL was detected for powdery mildew, explaining 23.6 % of the observed genetic variance. These QTLs represent valuable candidate regions for further characterization and development of markers linked to disease resistance in *L. cicera*

196	Biotic Stress	Vijayan, P.	Evaluating secondary effects of strobilurin fungicides on cool season pulse crops in Canada.

Evaluating secondary effects of strobilurin fungicides on cool season pulse crops in Canada.

Vijayan, P.[1*], Riches, L.[2], McDonald, M.R.[2], and Banniza, S.[1]. [1]Department of Plant Sciences, University of Saskatchewan, Saskatoon, Canada; [2]Department of Plant Agriculture, University of Guelph, Guelph, Canada. *(p.vijayan@usask.ca)

Strobilurins are broad-spectrum fungicides that act by inhibiting the fungal respiratory quinol oxidize enzyme. Some strobilurins (Eg. kresoxim-methyl) also induce changes in the hormonal balance in certain crop plants, delay leaf senescence and alleviate drought stress effects. Howeover, delayed leaf senescence has been shown to delay desiccation of the crop and cause potential harvesting problems. However, while some studies have confirmed significant secondary physiological effects of strobilurin fungicides in soybean and wheat in the field, others have failed to find any such effects consistently.

Since no reliable data is available on the physiological effects of strobilurins on cool season legume crops grown in Canada, a systematic evaluation of these fungicides was initiated in 2013 as part of a 3-year experiment. We investigated the effects of the popular strobilurin fungicides Headline® (Pyroclostrobin) and Quadris® (Azoxystrobin) on physiological, growth, disease and yield parameters of the cool season legume crops lentil, chickpea and pea in greenhouse experiments in Saskatoon, as well as field experiments in Saskatoon and Guelph, Ontario, Canada. A non-strobilurin fungicide Bravo® (Clorothalonil) was used as an additional control in field experiments to account for the effects of disease. Preliminary results indicated that the strobilurin fungicides were effective in controlling fungal diseases, and affected the pre harvest moisture content of a pea variety in the field and its yield in the greenhouse. No other significant effects on physiological, developmental or stress tolerance related parameters of the crops were observed in the greenouse or in the field.

197	Biotic Stress	Warale, R. R.	Phylogeny and pathogenicity of *Colletotrichum / Glomerella* species associated with anthracnose on leguminous hosts

Phylogeny and pathogenicity of *Colletotrichum* / *Glomerella* species associated with anthracnose on leguminous hosts.

R.R. Warale and S. Banniza. *Crop Development Centre, Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada*.

A multilocus phylogenetic analysis was conducted to study genetic diversity using isolates of *Glomerella truncate from lentil*, *Colletotrichum truncatum* from Lima bean (epitype), soybean and scentless chamomile, and other closely

related *Colletotrichum* species. Isolates of *G. truncata* formed a single cluster separating them from all other closely related *Colletotrichum* species including the epitype of *C. truncatum* and *C. truncatum* from other hosts. A host range study of *G. truncata*, *C. truncatum*, *C. lindemuthianum*, *C. truncatum* (epitype)*, C. destructivum, C. higginsianum, C. dematium* and *C. linicola* was undertaken on lentil, field pea, chickpea, fababean, soybean, common bean, lima bean, alfalfa, red clover, *Medicago truncatula, Brassica chinensis* and *Arabidopsis thaliana under controlled conditions*. Noticeable differences in host range and disease severity were recorded. *Glomerella truncata* was pathogenic on lentil, field pea and fababean. *Colletotrichum linicola* and *C. higginsianum* had an overlapping host range with *G. truncata*, infecting lentil and field pea, but *C. linicola* was also pathogenic on chickpea, faba bean and *M. sativa*, and *C. higginsianum* on *B. chinensis* and *A. thaliana*. *Colletotrichum destructivum* was pathogenic on pea, soybean and *M. sativa* but not on lentil. The epitype of *C. truncatum* was pathogenic on field pea, soybean, common bean, red clover and *M. sativa,* and the epitype of *C. dematium* on soybean. All isolates caused disease on *M. truncatula* and, except for the isolates of *G. truncata*, on soybean as well.

198	Biotic Stress	Weeden, N.F.	A genetic analysis of the tolerance to Fusarium root rot in pea land races of the 'Afghanistan' type

A genetic analysis of the tolerance to Fusarium root rot in pea land races of the 'Afghanistan' type

Weeden, N.F.[1*], and Porter, L.D.[2]. [1]Dept. Plant Sciences and Plant Pathology, Montana State University; [2]USDA-ARS, VFCRU, Prosser, WA. *(nweeden@montana.edu)

The 'Afghanistan' pea type, a common set of landraces with a unique genetic fingerprint, has been shown to be highly tolerant to root rot caused by *Fusarium solani* f. sp. *pisi*. In a recombinant inbred population derived from a cross between an Afghanistan landrace and a highly susceptible commercial type we identified four QTL, two on linkage group (LG) II, one on LG IV and one on LG VII. By investigating several other crosses and three isogenic pairs of lines we were able to demonstrate that the QTL on the upper arm of LG II was identical to a basic-helix-loop-helix transcription factor, better known as Mendel's clear testa factor, that is required for a functional phenylpropanoid pathway. Investigations of other populations derived from Afghanistan by white-flowered commercial types indicate that the presence of a functional phenylpropanoid pathway is the primary factor determining tolerance to Fusarium root rot, accounting for up to 70% of the variance in this trait.

199	Biotic Stress	Yang, Chao, Y.C.	Hydrogen oxidizing bacteria identified from Lentil field show the effects on plant growth

Hydrogen oxidizing bacteria identified from Lentil field show the effects on plant growth

Yang, Chao, Y.C.[1,2*], Hamel, Chantal, H.C.[2], Gan, Yantai, G.Y.[2], Warkentin, Tom, W.T.[1], and Abdellatif, Lobna, A.L.[2]. [1]Department of Plant Sciences, University of Saskatchewan; [2]Semiarid Prairie Agricultural Research Centre, Agriculture & Agri-Food Canada. *(chy995@mail.usask.ca)

Some H2-oxidizing bacteria associated with N2-fixing soybean grown under a sub-humid climate were shown to possess plant growth promoting effects, such as promote host plant root elongation and shoot biomass, but whether these bacteria would associate with other pulse crops was not reported. In this study, 24 H2-oxidizing bacteria were isolated from the rhizosphere of 14 lentil (*Lens culinaris*) cultivars growing in semiarid Saskatchewan, by using selective-medium based culture, and their hydrogen uptake capabilities were tested by Qubit Open Flow Gas Exchange System. Significant H2 uptake capability of 13 positive H2-oxidizing bacteria was quantified. Greenhouse assays proved that these lentil associated H2-oxidizing bacteria have potential plant growth promoting capabilities, as both inoculated durum wheat and lentil plants showed higher above ground height and leave numbers than the control.

200	Biotic Stress	Zhang X	Evaluating new biological and chemical controls for soybean cyst nematode in dry bean

Evaluating new biological and chemical controls for soybean cyst nematode in dry bean

Zhang, X.[1*], and Gillard, C.L.[1]. [1]Department of Plant Agriculture, University of Guelph, Guelph, ON, Canada. *(xzhang16@uoguelph.ca)

Soybean cyst nematode (*Heterodera glycines* Ichinohe; SCN) is the most serious yield-limiting parasite of soybean (*Glycine max* L.) which causes millions of dollars loss in the world annually. As the alternate host of SCN, dry bean (*Phaseolus vulgaris* L.) is under increasing threat from SCN. Resistance genes are a key control measure to SCN in soybean but there is limited research on genetic controls to SCN in dry bean. Thus biological and chemical controls may play a role to manage this pest in dry bean production. Studies were conducted to evaluate biological controls (*Pasteuria* spp. and *Bacillus firmus*) as seed treatments and the insecticide spirotetramat as a foliar treatment in tolerant and susceptible dry bean market classes. This work may provide producers with new options to control SCN in dry bean production.

201	Biotic Stress	Zhou, Q.X.	Molecular identification of Fusarium species from soybean in Alberta

Molecular identification of Fusarium species from soybean in Alberta

Zhou, Q.X.[1*], Chang, K.F.[1], Nyandoro, R.[2], Hwang, S.F.[1], and Strelkov, S.E.[2]. [1]Crop Diversification Centre North, Alberta Agriculture and Rural Development; [2]Department of Agricultural, Food and Nutritional Science, University of Alberta. *(qixing.zhou@gov.ab.ca)

Soybean (*Glycine max* (L.) Merr) has great potential as an alternative crop to canola in southern Alberta farming systems. The crop is susceptible to root rot, however, which usually results in the occurrence of dead or dying soybean plants in mid-to-late summer. A total of 164 isolates identified as *Fusarium* spp. were recovered from diseased soybean root samples collected from central and southern Alberta from 2011to 2013. Mycelia of each *Fusarium* isolate were harvested for DNA extraction, PCR amplification with *Fusarium* species-specific primer sets and sequencing. A total of 40 isolates were identified as *F. avenaceum*, 16 isolates as *F. oxysporum*, 13 isolates as *F. culmorum*, seven as *F. equiseti*, two as *F. graminearum*, and one as *F. proliferatum*. No product could be amplified from any of remaining isolates. The elongation factor 1-α (EF-1α) was also sequenced for each *Fusarium* isolate. The EF-1α sequence of each isolate was aligned by means of the BLASTn algorithm on the NCBI website to identify species based on a 99-100% sequence identity threshold. A total of 36 isolates were identified as *F. acuminatum*, 18 as *F. avenaceum*, 18 as *F. equiseti*, 15 as *F. culmorum*, 14 as *F. oxysporum*, eight as *F. redolens*, five as *F. torulosum*, three as *F. tricinctum* and one as *F. proliferatum*. The EF-1α sequences of the other 45 isolates were not obtained.

202	Crop management	Ahmed, S.	Effects of supplementary irrigation on Fusarium wilt epidemics and yield of lentil in northern Syria

Effects of supplementary irrigation on Fusarium wilt epidemics and yield of lentil in northern Syria

Ahmed, S.[1*], Karrou, M.[2], and Shiv, A. Kumar.[2]. [1]ICARDA/Addis Ababa, Ethiopia; [2]ICARDA/Rabat, Morocco. *(s.a.kemal@cgiar.org)

Lentil (*Lens culinaris*) is a major legume crop in Syria where its productivity is low mainly due to Fusarium wilt (*Fusarium oxysporum* f.sp. *lentis*) and drought. Although Fusarium wilt resistant cultivars are being introduced for wide production in Syria, recurrent drought pre-disposes the cultivars for high *Fusarium* infections and increased disease epidemics. Farmers apply supplementary irrigation to overcome terminal drought and hence increase yield in food legumes like lentil. However, the role of supplementary irrigation in affecting Fusarium wilt development is not

investigated. This study was conducted for two cropping seasons (2011-2012) in highly infested soil at Tel Hadya, ICARDA research station, northern Syria. Six genotypes with wide range Fusarium wilt reactions were evaluated under rainfed and supplementary irrigation regimes. The experimental design was a split plot where irrigated and rainfed plots were assigned as main plots and genotypes as sub plots. Disease incidence, biomass and seed yields were recorded. The results showed that supplementary irrigation significantly reduced disease incidence in 2011/12 cropping season and increased biomass and seeds yields in both seasons. Moreover, lentil genotypes showed significant differences in their reactions Fusarium wilt, seed yield and biomass yields in 2010/11 cropping season. No significant lentil genotype by supplementary irrigation interactions were observed for the three parameters evaluated indicating the absence of crossover interactions. From this study, we can conclude that if irrigation water is available, providing 1-2 additional irrigations to high yielding and moderately wilt resistant variety, seed and biomass yields can increased under Mediterranean type environment.

203	Crop management	Ali, Omar	Advances of Lentil Research and Development in Bangladesh

Advances of Lentil Research and Development in Bangladesh

Omar, A.[1*], Sarker, A.[2], Kumar, S.[3], Matiur, R.[4], Erskine, W.[5], and Al Imran, M.[5]. [1]Bangladesh Agricultural Research Institute, Gazipur, Bangladesh; [2]International Centre for Agricultural Research in the Dry Areas (ICARDA), New Delhi, India; [3]International Centre for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco; [4]International Rice Research Institute, Dhaka, Bangladesh; [5]Centre for Plant Genetics and Breeding ,The University of Western Australia. *(omaraliprc@gmail.com)

Lentil ranks second in area and production but first in consumer's preference among the pulses in Bangladesh. Area under lentil area started declining in nineties due to expansion of boro rice. Later, development and introduction of short duration (110-120 days) high yielding varieties by BARI in collaboration with ICARDA have helped regain the lentil area in Bangladesh. There is further scope for introduction of lentil in rice- rice system with inclusion of extra-early lentil varieties (<90 days) along with improved production technologies. One such technology is lentil relay planting in standing rice crop, which, in our multi-year experiments, showed 64% yield advantage over the normal sown crop due to maximum use of residual soil moisture and prolonged crop growth period. Relay cropping also reduces cost of cultivation, thus ensures more return to lentil growers. National and international efforts on lentil have developed the capacity of NARS partners including scientists, extension workers, NGOs and lentil growers. As a result, 92% area of lentil is covered by improved technologies resulting in higher production. The present production and yield of lentil are 210000 MT and 1.27 t/ha compared to 157000 MT and 0.75 t/ha in the nineties. Farmers are also giving priority to lentil production due to higher and stable market price. Recently, boro rice area is decreasing due to draw down of ground water, high cost of production and low price and gradually lentil is gaining its area. This has multi-dimensional impact on livelihood and nutritional security of the people of Bangladesh.

204	Crop management	Antanasovic, S	Economically important characteristics of a wild population of Pisum sativum subsp. elatius from Pčinja in southeast Serbia

Economically important characteristics of a wild population of *Pisum sativum* subsp. *elatius* from Pčinja in southeast Serbia

Antanasovic, S.[1*], Mikic, A.[2], Zlatkovic, B.[3], Krstic, D.[1], Eric, P.[1], and Cupina, B.[1]. [1]University of Novi Sad, Faculty of Agriculture, Trg D. Obradovica 8, 21000 Novi Sad, Serbia; [2]Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia; [3]University of Niš, Faculty of Sciences and Mathematics, Višegradska 33, 18 000 Niš, Serbia. *(antanasovic.svetlana@polj.uns.ac.rs)

The upper flow of the river Pčinja, located some 400 km south of the Serbian capital Belgrade and on the very border between modern Serbia and FYROM, is regarded as the richest in the country, with more 1,000 plant species catalogued. Many of them are both almost extinct crops local farmers still grow, such as landraces of maize (*Zea mays* L.), faba bean (*Vicia faba* L.) or chickpea (*Cicer arietinum* L.), as well as diverse and numerous crop wild relatives. Of a particular interest was a re-discovery of a population of *Pisum sativum* L. subsp. *elatius* (Steven ex M. Bieb.) Asch. & Graebn. on the slopes of the Mount Kozjak in 2009. Two and three years later, several joint expeditions by the teams from the Universities of Novi Sad and Niš and the Institute of Field and Vegetable Crops resulted in a large amount of collected *in situ* data and plant material for various *ex situ* research. The morphological and chemical analysis of the plant material collected *in situ* showed a high potential for both forage (8 t ha-1) and grain (4.5 t ha-1) yields, as well as for forage and grain quality, with average crude protein content of 201 g kg-1 in forage and 343 g kg-1 in grain dry matter. The population also had prominent winter hardiness in both *in situ* and *ex situ* conditions, surviving and absolute minimum of more than -20 °C at 5 cm above ground.

205	Crop management	Bandara, M.S.	Impact of the plant growth regulators Prohexadione Calcium, Chlormequat Chloride and Tranexapac Ethyl on growth, maturation and seed yield of the Kabuli-type chickpea cultivars CDC Frontier and CDC Orion in southern Alberta

Impact of the plant growth regulators Prohexadione Calcium, Chlormequat Chloride and Tranexapac Ethyl on growth, maturation and seed yield of the Kabuli-type chickpea cultivars CDC Frontier and CDC Orion in southern Alberta

Bandara, M.S.[1*], Kruger, A.[1], Lokuruge, P.[2], Howard, R.[1], Harms, T.[1], and Harding, M.[1]. [1]Alberta Agriculture and Rural Development; [2]University of Saskatchewan. *(manjula.bandara@gov.ab.ca)

Production of high quality chickpea is challenged by conditions that favour continued growth and flowering, and production of green seed. In 2012, a field study examined the effect of three plant growth regulators [PGRs; prohexadione calcium (PC; 750 and 1500 mg L-1), chlormequat chloride (CCC; 4000 and 6000 mg L-1), and trinexapac ethyl (TE; 1000 and 2000 mg L-1)] on growth, maturation, 1000-seed weight (TSW), and total (TSY) and marketable (MSY) seed yields of CDC Frontier and CDC Orion Kabuli chickpeas. PGRs were applied 21 days after seedling emergence (21 DASE), 20 days after flowering (20 DAF), and 30 days after flowering (30 DAF) at Brooks and Bow Island under rain-fed and irrigated conditions. Only PC and TE significantly arrested growth, but this effect diminished over time. PGRs had no significant effect on either numbers of main stem nodes or pod-bearing branches plant-1. PGRs had no significant effect on maturation or TSY, except PC at 1500 mg L-1, which delayed maturation under irrigation and reduced TSY by 7.1% under rain-fed conditions at Bow Island. PGRs had no significant effect on TSW, but at Bow Island (irrigated), PC at 20 DAF increased TSW and TE at 2000 mg L-1at 30 DAF reduced TSW compared to controls. CCC had no significant impact on TSW, TSY or MSY. TE significantly reduced MSY at all three sites. PC reduced MSY only at Brooks (rain-fed). These results suggest that application of PGRs is not a reliable option to restrict excessive growth or improve yield in chickpeas.

206	Crop management	Bandara, M.S.	Major phenological and physiological traits to be considered in developing soybean genotypes for southern Alberta growing conditions

Major phenological and physiological traits to be considered in developing soybean genotypes for southern Alberta growing conditions

Bandara, M.S.[1*], Kruger, A.[1], and Harms, T.[1]. [1]Alberta Agriculture and Rural Development.

*(manjula.bandara@gov.ab.ca)

Soybean [*Glycine max* (L.)] is a potential grain legume crop for irrigated production in southern Alberta, but genotypes with desirable traits, including high-yielding (>4 t ha-1 or > 60 bu/ac) capability, are required for it to be economically viable. Studies at Bow Island and Brooks in 2012 and 2013 examined the impact of overhead irrigation on crop phenology and relationships between flowering date, crop maturity, seed yields and ambient temperature (measured as corn heat units = CHU). In 2012 and 2013 at Bow Island, 18 and 25 soybean genotypes, respectively, were evaluated for crop growth, maturity and seed yields under rain-fed and supplementary irrigation production regimes. Crop response to irrigation was genotype- and growing-year-dependent. In 2012, on average, irrigation delayed crop maturity by 13 days, produced taller plants, and increased seed yield by about 77%, mean seed weight by about 5%, number of pods plant-1 by 15%, and number of seeds plant-1 by about 5%. In 2013, irrigation delayed maturity by 4 days, without affecting plant height, and increased seed yield by 9% and mean seed weight by about 17%, as compared to rain-fed crops. In 2013, a separate study was conducted using 17 soybean genotypes grown under irrigation at Brooks and Bow Island. Seed yield increased linearly in relation to length of the post-flowering period and number of heat units received after flowering. In summary, genotypes with early flowering and maturing between115-120 days under 2300-2350 CHU are required for economically viable soybean production under irrigation in southern Alberta.

207	Crop management	Beshir, H.M.	Improving snap bean production under low input production systems

Improving snap bean production under low input production systems

Beshir, H.M.[1*], Tar'an, B.[2], Bueckert, R.A.[2], and Tesfaye, B.[3]. [1]PhD Student in Plant Science, University of Saskatchewan; [2]Associate professor, University of Saskatchewan, Canada; [3]Associate Professor, Hawassa University, Ethiopia. *(muzeyenyesuf2003@yahoo.com)

In Ethiopia, snap bean (Phaseolus vulgaris L.) is one of the economically most important vegetable crops grown for both export and local markets. Information on effective Rhizobium strain and snap bean production is lacking in Ethiopia. The study was conducted for two years (2011 and 2012) during the main rainy seasons at three sites in Ethiopia (Debre Zeit, Hawassa and Ziway) with the objective to evaluate the response of eight snap bean genotypes to low input production system using Rhizobium inoculation under rain fed conditions. Two of the tested varieties were developed by Melkassa Agricultural Research Center of Ethiopia. The remaining are introduced commercial varieties normally used for production under irrigated conditions. The varieties were combined with three sources of nitrogen including Rhizobium inoculation. This experiment was also conducted under irrigation for one season in 2012. Nodulation and yield parameters were taken during flowering and harvesting periods respectively. There were significant differences across locations and among varieties for nodulation parameters. The results further indicated that Rhizobium inoculation and straight applied nitrogen improves the total yield of snap bean pod by about 17.7% and 42%, respectively, as compared to no N application under rain fed conditions. However, there was no significant effect of Rhizobium inoculation on yield and quality under irrigation conditions.

208	Crop management	Chaturvedi, S.K.	Tailoring chickpea cultivars for amenability to mechanical harvesting and increasing farm income

Tailoring chickpea cultivars for amenability to mechanical harvesting and increasing farm income

Chaturvedi, S.K.[1*], and Gaur, P.M.[2]. [1]Indian Institute of Pulses Research (IIPR), Kanpur 208 024, India; [2]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru 502 324, AP, India. *(sushilk.chaturvedi@gmail.com)

Chickpea is the most important pulse crop of India and Indian share is about 68% in the global chickpea production. There is a growing demand for machine harvestable chickpea varieties in India due to increasing labor costs. Tall and erect plant types are suited to machine harvesting and ensure higher solar light interception in the plant canopy and help in enhancing photosynthesis. Such plant types also help in reducing humidity inside the canopy which in turn minimizes the incidence of foliar diseases. A large number of tall and erect (broom shaped) elite breeding lines were developed and selected lines were evaluated along with two check varieties (HC 5 - tall and erect and DCP 92-3 - dwarf) over two years. The genotypes IPC 2006-11, IPC 2008-83, IPC 2011-28, IPC 2011-85 and IPC 2011-113 with tall (>70 cm) and erect growth habit were found promising as these genotypes exhibited lodging tolerance and higher yield. The major influence on plant architecture was of branch angle and podding behaviour. Branch angle of 80-850 was found appropriate for machine harvesting under irrigated conditions, whereas branch angle of 600 was adequate under rainfed conditions. It was found that the plant height of about 70 cm leaving 30-35 cm portion from the base of the plants without pods was sufficient for machine harvesting. Tall and erect genotypes showed lower incidence of foliar diseases. These results indicate feasibility of developing chickpea cultivars amenable to machine harvesting and having high yield potential and tolerance to foliar diseases.

209	Crop management	Daoui, K.	Effect of phosphate-solubilizing rhizobia on the growth and phosphorus uptake by Vicia faba

Effect of phosphate-solubilizing rhizobia on the growth and phosphorus uptake by *Vicia faba*

Maghraoui, T.[1,2], Bechtaoui, N.[1], Galiana, A.[3], Wahbi, S.[2,4], Duponnois, R.[2], Hafidi, M.[4], Daoui, K.[5*], de Lajudie, R.[2], and Oufdou, K.[1]. [1]Laboratory of Biology and Biotechnology of Microorganisms, Faculty of Sciences Semlalia, Cadi Ayyad University, PO Box 2390, Marrakech, MOROCCO; [2]IRD, CIRAD, LSTM, Campus de Baillarguet TA A82/J 34398 Montpellier, FRANCE; [3]2IRD, CIRAD, LSTM, Campus de Baillarguet TA A82/J 34398 Montpellier, FRANCE; [4]Laboratory of Ecology and Environment (CNRST, URAC32), Faculty of Sciences Semlalia, Cadi Ayyad University, PO Box 2390, Marrakech, MOROCCO; [5]National Institute for Agricultural Research. Centre Régional de la Recherche Agronomique de Meknès B.P. 547 (VN) Meknès Maroc. *(daoui_khalid@yahoo.fr)

Grain legumes such as Faba bean (*Vicia faba* L.) are important crops as they are valuable sources of proteins, play a vital role in the sustainability of ecosystems and improve soil health by fixing atmospheric nitrogen. Rhizobial strains, beneficial N2-fixing symbiotic partners of legumes, were reported to solubilize both organic and inorganic complex phosphates. This study is carried out to evaluate and compare the effect of rhizobial strains nodulating *V. faba* plants in Marrakech-Haouz region and able to solubilize rock phosphate, on growth and phosphorus uptake by Moroccan varieties of faba bean plants. Greenhouse experiments were undertaken including comparison of rhizobia inoculated plants cultivated with rock phosphate as sole P source (amendment) against non-inoculated plants growing on (soluble) KH2PO4 as sole P source (P-fertilized plants). Results show that inoculating plants with rock phosphate-solubilizing rhizobia may compensate the phosphorus-deficient conditions. This effect was amplified in the Aguadulce variety compared to Defes variety, and different depending on the inoculated strain and the symbiotic combination. Furthermore, in some symbiotic combinations, rhizobia strains made phosphorus available to the plant at significant increased concentrations and sometimes not significantly different to those registered for the P-fertilized plants.

210	Crop management	Douglas, C.A.	Evaluation of physiological diversity and yield potential of mungbean, Vigna radiata (L.) Wilczek in Australian production environments

Evaluation of physiological diversity and yield potential of mungbean, *Vigna radiata* (L.) Wilczek in Australian production environments

Douglas, C.A.[1*], Ryan, M.J.[1], Martin, W.D.[1], and Bellingham, T.[1]. [1]Department of Agriculture Fisheries and Forestry,

Queensland, Australia. *(col.douglas@daff.qld.gov.au)

Mungbean (*Vigna radiata* (L.) Wilczek) is established as the main summer rotation in tropical and sub-tropical cereal-based farming systems of north eastern Australia where growers appreciate the short duration, flexible sowing window as well as rotational benefits in soil health, soil nutrition and enhanced weed control options.

Australia's mungbean industry was founded in the late 1960's and has grown through public sector research tightly linked to industry and market requirements with commercial partner the Australian Mungbean Association (AMA). Coordinated germplasm introduction, breeding and the development of best practice agronomy have successfully transitioned mungbean from subsistence crop into a high value export product of broad acre mechanised agriculture.

The Australian breeding program has operated as a co-investment of Queensland Department of Agriculture Fisheries and Forestry (DAFF) and the Grains Research and Development Corporation (GRDC) since 2003. Recent varietal releases such as Crystal, Satin II (2008) and Jade-AU (2013) have delivered 20 and a further 12 percent productivity increase over historical varieties through improved vigour, broad adaptation and foliar disease resistance. Future increases in productivity, reliability and specific adaptation to new production environments will come from understanding and exploiting the physiological components of plant growth and grain yield. This pilot study was conducted to evaluate phenology, biomass, partitioning and yield potential of 25 contrasting commercial varieties, breeding lines and germplasm imported from the AVRDC, World Vegetable Centre.

211	Crop management	FATEMI, Z.	Collection, characterization and evaluation of Moroccan faba bean landraces

Collection, characterization and evaluation of Moroccan faba bean landraces

FATEMI, Z.[1*], Daoui, K.[1], UDUPA, S.M.[2], SOUDI, G.[3], OUABBOU, H.[4], and EL GHADRAOUI, L.[3]. [1]Institut National de la Recherche Agronomique (INRA), P.O. Box BP. 578, Meknès VN 50000, km 13 Route Haj Kaddour, Meknes, Morocco; [2]International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 6299, Rabat, Morocco; [3]Faculté des Sciences et Technologie (FST),Université Sidi Mohamed Ben Abdellah, Fes, Morocco; [4]Institut National de la Recherche Agronomique (INRA), P.O. Box 589, Settat, Morocco. *(zfatemi03@yahoo.fr)

Faba bean (*Vicia faba* L.) is an important food legume crop of Morocco with a multitude of uses. Although, Morocco is among the major producer of this crop in the WANA region, its yield is low and unstable, fluctuating from 180 to 1520 kg/ha. This situation is mainly due to biotic stresses (*Orobanche*, Chocolate spot, *Ascochyta* blight and rust) and abiotic stresses (drought, heat and cold). Climate change further aggravated these problems. This crop is being grown in marginal area by small farmers, mostly using local landraces under rainfed conditions. Genetic variability present in faba bean landraces is crucial to the development of this crop. . Therefore, 68 local populations (*V. faba* L. var. *minor*, *equina* and *major*) were collected during 2011-12 growing season from most of the faba bean growing region of Morocco namely Fez, Taza, Taounate, Chefchaoun and Tetouan regions . These populations were morphologically characterized through ICARDA/IPGRI descriptors, and evaluated for principle agronomical traits. They showed large variability in leaflet number, plant height, pod characteristics (angle, length and number of seeds per pod). Moderate variability was observed for leaflet size and shape, flower color. Based on morphological traits, principal component analysis leaded to grouping these landraces into nine genepools. These Moroccan landraces were also screened for biotic stresses and identified tolerant landraces for chocolate spot. The identified useful variability is being deployed in conventional breeding for genetic improvement of faba bean in national breeding program.

212	Crop management	Fikre, Asnake	Unraveling breeding traits in Ethiopian legume research hastened intensification and economic gains

Unraveling breeding traits in Ethiopian legume research hastened intensification and economic gains

Fikre, ASNAKE.[1*]. *(Tataw71@gmail.com)

The legume industry in Ethiopia is significantly influencing the agricultural system with an area of some 1.8 million ha and production volume enjoying more than 270 million MT production annually. Ethiopia contributes significant volume of legumes globally. Legumes are major source of income, nutrient, farm fertilization and farming system sustainability of the Ethiopian 5 million small holder agrarian households. The market advantage of legumes is pronounced compared to other field crops. In the presence of the huge underlying principles that grain legumes accounted to, breeding efforts have all driven by traits of economic and adaptability functions. Among major legumes faba bean, field pea, chickpea, haricot bean, grasspea, soybean and lentil play overwhelming role in the system. Economic traits includes: seed size in faba bean, lentil and chickpea; seed color in faba bean, chickpea, field pea and haricot bean; nutritional quality parameters in lentil, soybean, haricot bean and grasspea. Along with desired traits development the lines are also been backed by favorable genes for tolerance against the bio-threats of rust (*Uromyces cicer-arietini*) in lentil, bean stem maggot in haricot bean, fusarium wilt *(Fusarium oxysporum fsp ciceris*) and ascochyta blight *(Ascochyta rabiei*) in chickpea, chocolate spot *(Botrytis fabae)* in faba bean by genetic means. The crossing programs work in assemblage of favorable genes that confers adaptability as well as desirable grain produce quality attainment, which in combination with best crop management practices has warranted intensification with a magnitude ranging 3 to 5 tons/ha in well adaptation zones. Over the last four decades the research program has developed some 160 varieties each with defined marketable/consumable trait/s. These improved produce gains is valued between 2000 to 4000USD per hectare has stimulated best production practices that in a decade legume productivity improved by 60% on average.

213	Crop management	Ganga Rao, N.V.P.R	Chickpea breeding and development efforts in Eastern and Southern Africa:achievements and oppoutunities

Chickpea breeding and development efforts in Eastern and Southern Africa:achievements and oppoutunities

Ganga Rao, N.V.P.R.[1*], Ojiewo, Chris.[2], Silim, S.N.[3], Gaur, P.M.[4], Gowda, C.L.L.[4], Moses, Siambi.[1], Monyo, E.S.[1], Fikre, Asnake.[5], Kileo, Robert.[6], Kimurto, Paul.[7], Mahendar, Thudi.[4], and Varshney, R.K.[4]. [1]ICRISAT, P.O.Box-39063, Nairobi, Kenya; [2]ICRISAT, Addis Ababa, Ethiopia; [3]ICARDA-Addis Ababa, Ethiopia; [4]ICRISAT, Patancheru, India; [5]EIAR, Adis Ababa, Ethiopia; [6]LZARDI, Ukiriguru, Tanzania; [7]Egerton University, Njoro, Kenya.
*(n.gangarao@cgiar.org)

In Eastern and Southern Africa(ESA), chickpea is grown on about 493,000 ha. Ethiopia and Tanzania are the major chickpea growing countries by occupying 73% of total ESA area, and minor producing countries are Malawi, Kenya, Eritrea, Sudan and Uganda. Chickpea provides a unique oppourtunity to grow in post-rainy season under residual moisture conditions. Ethiopia is the major chickpea producer and exporter in ESA and during last one decade production(119%) and productivity(78%) have increased substantially. Ethiopia and Tanzania export a sizable quantities of chickpea and earning about 46.6 million $ annually. Chickpea improvement in ESA over the years resulted in release of 40 high yielding varieties with desirable agronomic and quality traits. The major breeding priorities in ESA were high grain yield, resistance to Fusarium wilt, collar rot, dry root rot and ascochyta blight;tolerance to Helicoverpa pod borer, terminal drought and grain quality traits. The current productivity levels in Ethiopia is about 1730 kg/ha and but in all other ESA countries productivity levels are still below 1000 kg/ha. The productivity gains in Ethiopia, providing an oppourtunity for cross learning among neighbouring countries. The new varieties and breeding populations developed by ICRISAT using conventional and molecular breeding approaches have been evaluated in ESA and their adaptability and adoption rates are very high. However, a huge untapped yield potential exists in the currently released as well as pipe line varieties. Better integration of available genomic and

genetic resources in breeding, effective seed production and delivery, intergated crop mangement, wider stakeholder partcipation will provide an oppourtunity to futher enhance on-farm yields.

214	Crop management	Ganga Rao, N.V.P.R	Pigeonpea breeding in Eastern and Southern Africa: achievements and future prospects

Pigeonpea breeding in Eastern and Southern Africa: achievements and future prospects

Ganga Rao, N.V.P.R.[1*], Silim, S.N.[2], Siambi, Moses.[1], Monyo, E.S.[1], Lyimo, Stephen.[3], Ubwe, Rose.[3], Kananji, GAD.[4], Obong, Yuventino.[5], Sameer Kumar, C.V.[6], Gowda, C.L.L.[6], Manuel, Amane.[7], Upadhyaya, H.D.[6], and Varshney, R.K.[6]. [1]ICRISAT, P.O.Box-39063, Nairobi, Kenya; [2]ICARDA-Ethiopia, Addis Ababa; [3]SARI, Arusha, Tanzania; [4]CARS, Lilongwe, Malawi; [5]NgettaZARDI, Lira, Uganda; [6]ICRISAT, Patancheru, India; [7]IIAM, Maputo, Mozambique. *(n.gangarao@cgiar.org)

Pigeonpea is no more an orphan crop in Eastern and southern Africa(ESA), with its multiple benefits to cropping systems, smallholder farmers, consumers and traders. pigeonpea has huge regional and international export potential and india alone imports 506,000 t annually. ESA countries export about 200,000 t of grain per year that worth $ 180 million. During the last two decades, area and production in ESA increased dramatically by 135% and 125%, respectively. Tanzania, Malawi, Mozambique, Kenya and Uganda are the major pigeonpea producers. Tanzania and Malawi are showing the path to success in terms of productivity and production gains that guide other countries to follow. Pigeonpea improvement in ESA started in 1992 and since then 27 high yielding varieties were released and adopted them widely. The major breeding priorities were high grain yield, inter-cropping compatibility, photo-period insensitivity, grain quality, resistance/tolerance to Fusarium wilt, Helicoverpa pod borer and resilience to climate change. ESA has unique genetic diversity and its use in genetic enhancement has paid rich dividends. Tremendous yield gains have been recoreded with the use of new varieties, integated crop management, effective seed systems and sustained market demand. However, a huge gap still exists between realizable and actual yields with present technologies. ICRISAT-Patancheru is utilizing hybrid pigeonpea technology, genomic and genetic resources most effectively. Efforts are being made to use them in ESA breeding program to further elevate yield potentials in the region. A region specific strategy being outlined to bridge the gaps between actual, realized and potential yields using conventional and modern breeding by involving all the stakeholders.

215	Crop management	Gerbu, L.D.	Agronomic approach to mitigate zinc deficiency in the Southern Region of Ethiopia

Agronomic approach to mitigate zinc deficiency in the Southern Region of Ethiopia

Gerbu, LEGESSE HIDOTO.[1*], Ayele, Walelign Worku.[2], Mohamed, Husein.[2], and Tar'an, Bunyamin.[3]. [1]Researcher/student; [2]Researcher/Instractor; [3]Researcher/instractor. *(hidotog@yahoo.com)

Low dietary intake of Zn is the major reason for the prevalence Zn deficiency in the majority of the population of Southern Ethiopia. An experiment in Southern Nations Nationalities and Peoples Region of Ethiopia was conducted to evaluate growth, yield and seed zinc concentration response of chickpea varieties to zinc fertilizer application strategies. Five chickpea varieties (Arerti, Habru, Mastewal, Natoli and local landrace) and three zinc fertilizer application strategies (soil application, seed priming and foliar application) were included in the experiment. There is no significant effect of zinc application strategies on agronomic performance of chickpea. Chickpea seed zinc concentration varied significantly to varieties, application strategies and their interaction. Local landrace was found to be higher in seed zinc concentration followed by Arerti (Kabuli) and Natoli (Desi) varieties. Foliar application of 0.5% ZnSO4.7H2O at early vegetative, flowering and pod filling stages increased seed zinc concentration by more than 25% as compared to soil application and seed priming. Foliar zinc application on local landrace produced the highest

seed zinc concentration (49 ppm) as compared to other treatment interaction.

216	Crop management	Gharti, D.B.	Grain Legumes Research in Nepal: Present Scenario and Future Prospects

Grain Legumes Research in Nepal: Present Scenario and Future Prospects

Gharti, D.B.[1*], Darai, R.[1], Subedi, S.[1], Sarker, A.[2], and Kumar, S.[3]. [1]Nepal Agricultural Research Council, Grain Legumes Research Program, Nepal; [2]South Asia and China Regional Program,International Center for Agricultural Research in the Dry Areas (ICARDA),New Delhi, India; [3]North Africa Platform, ICARDA, Rabat, Morocco. *(dhana_gharti@yahoo.com)

Grain legumes play an important role in Nepalese agriculture contributing towards food and nutritional security, nitrogen economy, crop intensification, diversification and sustainable farming systems and rank fourth in terms of area and fifth in agricultural production. Grain Legumes Research program (GLRP) of Nepal in collaboration with CGIAR centers works for genetic improvement of lentil, chickpea, pigeonpea, soybean, mungbean, blackgram, and cowpea, resulting in development of 35 improved varieties and a dozen of production technologies for different agro-ecological domains. This has led to substantial increase (142%) in grain legumes production, mainly because of 47%area increase and 65%yield increase during the last two and a half decades. The current estimates for area, production and productivity of grain legumes in Nepal are 334,323 ha, 319,770 metric tons and 956kg ha-1, respectively. Lentil is the major grain legume and accounts for 62% of area and 65% production of total grain legumes in Nepal and has emerged as a major export commodity. A number of micro-nutrient rich (iron, zinc and selenium) lentil lines have been identified in collaboration with ICARDA and scaled out under the HarvestPlus Challenge Program. Further efforts are underway for expanding area under lentil, chickpea, fieldpea, and lathyrus in rice-fallow through Village based seed enterprise under OFID/ICARDA program. There is further scope for increase in area, production and productivity of grain legumes in Nepal through development and popularization of suitable varieties and technologies, streamlining community based seed production system, addressing climate change issues and policy reforms for the promotion of legumes.

217	Crop management	Gondwe, T.G	Cowpea production in Malawi

Cowpea production in Malawi

Gondwe, T.G.[1*], Boahen, S.[2], and Chunga, P.Z.[3]. [1]International Institute of Tropical Agriculture, Lusaka, Zambia; [2]International Institute of Tropical Agriculture, Nampula, Mozambique; [3]International Institute of Tropical Agriculture, Lilongwe, Malawi. *(mwatigondwe@gmail.com)

The integration of cowpea (Vigna unguiculata L. Walp) into the continuous maize cropping systems in Malawi has the potential to contribute significantly to food and nutritional security of small holder farmers. Objectives of the study were to identify optimum planting date for selected cowpea genotypes and to identify best genotypes for Lilongwe district. Field experiments were conducted at Chitedze research station during the 2012/2013 and 2013/2014 growing season using 10 cowpea genotypes developed by IITA and one widely grown cowpea variety Sudan-1. The experimental design was a randomized complete block with a plot size of 9 m x 3 m replicated 3 times. Seeds were planted on three different dates at 10 days intervals beginning on 4th January 2013. Data collected include days to 50 % flowering, days to 50% podding, days to 90% podding, number of pods per plant, plant height, biomass and grain yield. Results indicate that high yield for most lines were realized during the second time of planting meaning that mid-January was the best planting time for cowpea in Lilongwe district. IT-97K-390-2 out preformed (2057 kg/ha) all lines including Sudan-1(939 kg/ha) which was the check.

218	Crop management	Goyal, A.	Chickpea Improvement Program at ICARDA

Chickpea Improvement Program at ICARDA

Goyal, A.[1*], and Hamwieh, A.[2]. [1]International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco; [2]International Center for Agricultural Research in the Dry Areas (ICARDA), Beirut Lebanon. *(a.goyal@cgiar.org)

Chickpea (*Cicer arietinum* L.) is an important food legume crop with worldwide 12.5 m ha and 0.94 t ha-1 productivity. Chickpea is cultivated mostly in the arid and semi-arid regions of the world. India with annual production of 9.2 m t has the distinction of being the largest producer and consumer of chickpea in the world. People in dry areas of South Asia, West Asia, Central Asia, China, North and East Africa and Latin America are dependent on chickpea mainly for food and feed. Chickpea production is challenged by different diseases, insect-pests, environmental stresses, soil problems, and lack of adoption of modern agronomic technologies. The future chickpea breeding program should coop up with the challenges possess by increase in population, climate change and economic instability. Since 1975, the International Center for Agriculture Research in the Dry Areas (ICARDA) has a global mandate for (*Kabuli*) chickpea improvement. In view of the problems in dry areas, ICARDA is working on chickpea to improve the yield potential and to incorporate genes for different biotic and abiotic stresses. The main focus is on improving genotypes for high yield, resistance to *Ascochyta blight* (AB), *Fusarium wilt* (FW), leaf miner, viruses as well as drought, salt, heat, frost and herbicide tolerance, enhancing biological nitrogen fixation and development of best agronomic practices. From 1975 to 2012, more than 10,100 crosses (approximately 273/year) have been made between different genotypes. Among them 3,097 crosses for AB, 1109 for FW, 805 for early maturity, 717 for high yield and 553 crosses for drought tolerance. Based on the strong correlation between ICARDA and the national agriculture research centers, more than 150 varieties have been released successfully.

219	Crop management	Kennedy, P.	Breeding field pea for Australian conditions

Breeding field pea for Australian conditions

Kennedy, P.[1*], Leonforte, A.[1], Armstrong, E.[2], Lines, M.[3], McMurray, L.[4], Pritchard, I.[5], and Rosewarne, G.[1]. [1]Biosciences Research Division, Department of Environment and Primary Industries, Horsham, VIC, Australia; [2]NSW Department of Primary Industries, Wagga Wagga, NSW, Australia; [3]South Australian Research and Development Institute, Clare, SA, Australia; [4]South Australian Research and Development Institute, Clare, SA; [5]Department of Agriculture and Food, Perth, WA, Australia. *(peter.kennedy@depi.vic.gov.au)

Field pea is an important pulse crop in medium to low rainfall cropping regions of Australia with an average of 300,000 ha sown annually. While breeding efforts have delivered superior varieties to industry, significant potential for crop adoption and expansion exists. This expansion is likely to be driven through sustained genetic improvement. The PBA field pea breeding program aims to deliver varieties with improved crop adaptation and increased yield potential and reliability. An important industry breakthrough was the release of variety Kaspa; a broadly adapted, semi dwarf plant type with shatter resistance, lodging resistance, and uniform round (non-dimpled) dun seed. Short term aims of the field pea program are to deliver "Kaspa-type" varieties with improved reliability in short season climates, where field pea production is most likely to expand, while combining improved virus and powdery mildew resistance. The longer term goals are to incorporate complex disease resistance (e.g. blackspot, downy mildew and bacterial blight), with soil salinity tolerance, boron toxicity tolerance, and reproductive frost and drought tolerance into a Kaspa-type plant background. In this poster presentation, we will highlight both recent and forthcoming pea variety releases, which showcase significant gains in many of these areas realised through the effective trait pyramiding achieved in elite plant backgrounds.

220	Crop management	Khalifa, G.E.	Two new faba bean cultivars for the River Nile and Northern states - Sudan

Two new faba bean cultivars for the River Nile and Northern states - Sudan

Khalifa, G.E.[1*], Noha, N.A.M.[1], Tambal, H.A.[2], Hamza, F.E.A.[3], and Awad, S.M.[4]. [1]Agricultural Research Corporation, Hudeiba Research Station, River Nile State; [2]Agricultural Research Corporation, Shendi Research Station, River Nile State; [3]Agricultural Research Corporation, Merowe Research Station, Northern State; [4]Food Research Center-Shambat. Khartoum State. *(gamalhrs@yahoo.com)

Faba bean is known to be one of the most important food legume crops. It is grown mainly in the northern part of Sudan. In the past, nine cultivars were released. Yield potential and seed quality of sixteen faba bean genotypes including the three checks BB7, H.93 and Ed-Damer were evaluated at Hudeiba, Shendi and Merowe Research Farms for four seasons. Reaction to root rot and quality analysis was also evaluated. Results obtained from this investigation indicated that most of the tested genotypes performed well at Merowe and Shendi than Hudeiba. The two medium- seeded genotypes C.98\8 (53.0 g) and C.28\02 (53.0 g) showed stable and significantly higher seed yields than the checks, in addition to their resistance to dry root rot, which are considered among the major biotic stresses in the production areas. The genotypes C.98\8 and C.28\02 were also characterized by good seed quality as they have high crude protein content (24.62 and 27.05%), and short cooking time (45 and 40 min.), respectively.

221	Crop management	KHANAL, N.P.	Impact of Climatic and Socio-economic Factors on Lentil Crop Yield in the Tarai Region of Nepal

Impact of Climatic and Socio-economic Factors on Lentil Crop Yield in the Tarai Region of Nepal

KHANAL, N.P.[1*], MAHARJAN, K.L.[2], SAPKOTA, A.[3], SHARMA, J.N.[4], PANDEY, B.[5], JOSHI, K.D.[6], HARRIS, D.[7], and WITCOMBE, J.R.[8]. [1]Assistant Professor, Graduate School for International Development and Cooperation, Hiroshima University, Japan; [2]Professor, Graduate School for International Development and Cooperation, Hiroshima University; [3]Senior Program Officer, Forum for Rural Welfare and Agricultural Reform for Development (FORWARD), Chitwan, Nepal; [4]Project Officer, Local Initiative for Biodiversity and Development (LI-BIRD), Pokhara, Nepal; [5]Project Officer, Social Upliftment through Participatory Program (SUPPORT) Foundation, Kanchanpur, Nepal; [6]Researech Fellow, Center for Arid Zone Studies, University of Wales, U.K; [7]Manager, Center for Arid Zone Studies, University of Wales, U.K; [8]Professor, Center for Arid Zone Studies, University of Wales, U.K. *(narayankhanal36@gmail.com)

The importance of lentil in livelihoods of people and sustainability of cereal-based cropping system is well recognized. However, there is a wide gap between potential yield and national average yield of this crop in Nepal, and reasons behind it are poorly understood. This paper analyzes the impacts of climatic and socio-economic factors on lentilyield variability using Heckman Selection model. The climate factors considered in this study are maximum temperature, minimum temperature and rainfallcovering the period of 33 years (1976-2010). The socio-economic data were collected from 640 households spreading across the eight *Tarai* districts of Nepal in2010. Result shows that rainfall has significant negative impact on selecting lentil,and its yield. Less performance of lentil in higher rainfall receiving households might be due to substitution of its area with more profitable crops. This argument is supported by negative relationship between lentil and wheat area. Moreover,the combined impact of climate variableson lentil yield for 2015, 2020, 2025 and 2030 has been projected to be increased by3.31%, 6.68%, 10.09%, 13.57%, respectively.This study also shows that households with higher operational land, raising more livestock and with higher annual cash incomes, and realizing higher output price are more likely to grow lentil and realize higher yield.

222	Crop management	Krstic, D	Pigment content of alfalfa established with pea-oat mixture

Pigment content of alfalfa established with pea-oat mixture

Krstic, D.[1*], Eric, P.[1], Antanasovic, S.[1], Mikic, A.[2], and Cupina, B.[1]. [1]University of Novi Sad, Faculty of Agriculture, Trg D. Obradovica 8, 21000 Novi Sad, Serbia; [2]Institute of Field and Vegetable Crops, Maksima Gorkog 30, 21000 Novi Sad, Serbia. *(djordjek@polj.uns.ac.rs)

Problems in perennial forages establishment range from evenness of plant stand to obtain a financial return in the first year.Comparing to small grains, field pea can be a better companion crop for the spring establishment of alfalfa. It is a fast growing and is harvested early and thus reduces the duration of competition and allows light to be transmitted through its canopy. However, alfalfa grown with small grains has higher total yield in the first year. The aim of this study was to use advantage of both nurse crops i.e. to use mixture of field pea and oat as a nurse crop for alfalfa establishment and analyse differences in pigment content of alfalfa in first cut. Trial comprised two sowing years, 2008 and 2009. The factorial component of the experiment included two pea (P) varieties (semi-leafless Jezero and normal-leaf Javor) and their mixture with oat (O) in different proportion (100% P, 90% P/10% O, 80% P/20% O, 70% P/30% O, 100% O). Different cover crop and there mixture as well as weather conditions has effect on pigment content. Two year average has shown that chlorophyll *a* range from 7.32 mg g-1 (100% P) to 8.59 mg g-1 (80% P/20% O). Pure stand of alfalfa has the lowest content of chlorophyll *b* (1.76mg g-1) and the highest content of carotenoids (2.98 mg g-1) compared to other treatments.

223	Crop management	Larbi, A.	Genotype, Rhizobium inoculum and NPK fertilizer effects on soybean grain yield in northern Ghana

Genotype, Rhizobium inoculum and NPK fertilizer effects on soybean grain yield in northern Ghana

Buah, S.S.J.[1], Denwar, N. B.[1], Larbi, A.[2*], and Hoeschle-Zeledon, I.[3]. [1]Savanna Agricultural Research Institute (SARI), Nyankpala, Ghana; [2]International Institute of Tropical Agriculture (IITA), Africa RISING West Africa Project, Tamale, Ghana; [3]International Institute of Tropical Agriculture (IITA), Africa RISING Project, Ibadan, Nigeria. *(a.larbi@cgiar.org)

Soybean is becoming an important cash and oilseed in Ghana because it is relatively drought tolerant and requires lower production inputs. Grain yields are low on farmers' field due partly to limited access to seeds of improve varieties and low soil nutrient levels. The effect of Rhizobium inoculation (R) with and without NPK fertilizer on grain yield of soybean genotypes was evaluated in 2012 and 2013 using a split-plot design with four replicates at Nyankpala, Yendi and Wa in the Guinea savannah zone of northern Ghana. Main plots were five medium-maturing soybean genotypes five medium-maturing soybean genotypes (TGX 1834-5E, TGX 1445-3E, TGX 1448-2E, TGX 1904-6F and Jenguma a released variety); and sub-plots were R with and without NPK-R; 60 kg P2O5 + 30 kg K2O (PK); 25 kg N + 60 kg P2O5 + 30 kg K2O (NPK); and R + 60 kg P2O5 and 30 kg K2O (RPK). Genotype affected ($P<0.05$) grain yield at all locations in 2013. Average grain yield across sites varied from 1302 kg/ha in genotype TGX-1445-3E to 1545 kg/ha TGX-1904-6F. Grain yield varied ($P<0.05$) among the fertilizer and Rhizobium treatment at all locations in both years, ranging from 1359 kg/ha without fertilizer or Rhizobium inoculation to 1581 kg/ha when P and K were applied. The results showed that application of P and K alone or P and K with Rhizobium to genotype 1904-6F will result in higher soybean grain yield in the Guinea savannah zone in northern Ghana.

224	Crop management	Mansur, C.P.	Evaluation of machine harvestable desi chickpea genotypes for high density planting under rainfed ecosystem

Evaluation of machine harvestable desi chickpea genotypes for high density planting under rainfed ecosystem

Mansur, C.P.[1*], Patil, S.B.[2], Gaur, P.M.[3], Salimath, P.M.[4], Alagundagi, S.C.[4], and Salkinkop, S.R.[4]. [1]College of Horticulture, University of Horticultural Sciences (UHS), Bagalkot, Karnataka, India; [2]International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco; [3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India; [4]University of Agricultural Sciences (UAS), Dharwad, Karnataka, India. *(chidanandpm@yahoo.co.in)

Presently mechanical sowing is being adopted in chickpea by farmers, but they are facing problem for mechanical harvesting due to lack of suitable genotypes. Hence, there is need to develop and scruitnize the genotypes with compact and erect plant structure as an alternative to minimize the yield gap by adjusting more number of plants per unit area and also suitable for mechanical harvesting to reduce the drudgery on scarce labour in India. In mechanical harvesting, plant height and first pod height of *desi* chickpea become an important factor. But tall and erect chickpea genotypes are relatively less yielders and further yield can be improved by increasing planting densities. Therefore, keeping this in view, the present investigation was carried out during 2011-12 and 2012-13 at ICRISAT, Patancheru, India.

The results revealed that, the semi-erect genotype, JG-11 planted at 40 per cent higher density followed by 20 per cent higher density produced higher seed yield compared to rest of the treatments. The tall genotype, ICCV-11604 at 40 per cent higher plant density recorded comparable seed yield (2258 kg ha-1) and net returns (Rs. 46,753 ha-1) with JG-11 planted at normal density (2299 kg and Rs. 49,531 ha-1, respectively). The improvement of biological yield to the tune of 5.99 per cent in ICCV-11604 was observed compared to JG-11. Planting tall chickpea genotype ICCV-11604 at higher density of 4.66 lakh ha-1 was found to be optimum for higher yields and is an appropriate agronomic practice to be disseminated to the farming community for obtaining higher productivity in chickpea with minimum production cost.

225	Crop management	MARROU, H.	Crop simulation of grain legumes under Mediterranean conditions using SSM-iLegume: take home lessons for breeding and crop management

Crop simulation of grain legumes under Mediterranean conditions using SSM-iLegume: take home lessons for breeding and crop management

MARROU, H.[1,2*], GHANEM, M.[3], and SINCLAIR, T.R.[2]. [1]Montpellier SupAgro, France; [2]NCSU, USA; [3]ICARDA, Morocco. *(marrou@supagro.inra.fr)

Breeding for traits in the dry environments can be costly, and the results may be appropriate only for the few tested climatic scenarios. Similarly, decisions to change crop management can be risky especially in areas where subsistence agriculture prevails, and the recommendations should be supported by *ex-ante* analyses. Crop models are powerful tools that can offer mechanistic bases for exploring and extrapolating the impact of a given trait or management across are range of environments. However, not all crop models are appropriate for such analyses. Most models are based on unnecessarily complex algorithms disconnected from the biological mechanisms and require "calibration" of parameters in each circumstances to attain "validated" output. A Simple Simulation Model (SSM) has been developed (Soltani and Sinclair, 2012) that avoids this weakness and is based on directly measured parameters for each cultivar to be simulated. SSM has been shown to be robust in simulating various legumes, including soybean and chickpea. Here we report the use of SSM in simulating development, final vegetative mass and yield of two grain legumes: lentil (*Lens culinaris*) and lingot bean (*Phaseolus vulgaris*) under Mediterranean conditions. First, we show how simulations help to identify suitable areas to grow lentils in the Middle-East and West Asia. Second, we investigate productivity increases that can be expected from breeding lentils for drought resistance traits. Finally, we use the model to assess the impact of two management options (residue mulching and adjustment of irrigation

schedules) for lentils and beans in the Middle East and South of France.

226	Crop management	McMurray, L.S.	High levels of metribuzin tolerance developed in lentil

High levels of metribuzin tolerance developed in lentil

McMurray, L.S.[1,2,3*], Vandenberg, A.[3], Preston, C.[2], Mao, D.[1], Meier, K.[3], and Paull, J.[2]. [1]South Australian Research and Development Institute; [2]University of Adelaide; [3]University of Saskatchewan. *(larn.mcmurray@sa.gov.au)

Lentil (*Lens culinaris* Medikus) is a significant winter pulse crop in southern Australia with more than 150,000 ha sown annually. Weeds are a major limitation to production. Metribuzin is a broad spectrum herbicide, but low crop safety exists in lentil. The development of herbicide tolerant cultivars is considered a viable strategy to improving weed control in lentil. Two approaches, run in parallel, were used to develop lentil germplasm with improved metribuzin tolerance.

Over 750 diverse lentil lines were screened using a hydroponic sand assay method. Only a few lines were identified with low herbicide damage symptoms. Over 200 mutated (M) M3 and M4 PBA Flash lines identified from M2 and M3 field metribuzin screens, along with the best lines from above, were sprayed with metribuzin (215 g a.i./ha) at the 5 leaf stage in unreplicated weed spray chamber screens. Four M4 PBA Flash lines and germplasm lines USSR-05-05 and SP1333 showed higher levels of tolerance compared to the control line PBA Flash.

A controlled environment dose response experiment with these six lines and PBA Flash was conducted with metribuzin applied at the 5 leaf stage at 0, 142.5, 285, 570, 855, 1140, 2280, 4560 g a.i/ha. Biomass reduction of PBA Flash at the lowest rate was 70% and higher than that of the tolerant selections (0 - 32%). Mutant line 11SVHM043 showed the highest level of tolerance with no biomass reduction at the 1140 rate (greater than 5x label rate) and only a 43% reduction at the highest rate. Field validation and crossing with elite Australian lentil germplasm has commenced utilising the highest level of tolerance discovered.

227	Crop management	Monyo, E.S	Achievements, Challenges and Lessons in Enhancing Productivity and Production of Major Tropical Legumes for sub-Saharan Africa and South Asia

Achievements, Challenges and Lessons in Enhancing Productivity and Production of Major Tropical Legumes for sub-Saharan Africa and South Asia

Monyo, E.S.[1*], Ndjeunga, J.[2], Upadhyaya, H.[3], Boukar, O.[4], Mukankusi, C.[5], Gaur, P.[3], SameerKumar, C.[3], Agrama, H.[6], Rubyogo, J.[7], Gangarao, NPVR.[1], Varshney, R.[3], Gowda, CLL.[3], KumaraCharyulu, D.[3], Arega, A.[6], Katungi, E.[5], Siambi, M.[1], Okori, P.[8], Desmae, H.[9], Beebe, S.[10], Myer, M.[3], Kamara, A.[4], Boahen, S.[11], and Ajeigbe, H.[12]. [1]ICRISAT, United Nations Avenue, Gigiri, Box 39063, Nairobi 00623, Kenya; [2]ICRISAT, BP12404, Niamey, Niger; [3]ICRISAT, Patancheru, AP 502324, India; [4]IITA, Kano, Nigeria; [5]CIAT, Kampala, Uganda; [6]IITA, Chitedze Research Station, Lilongwe, Malawi; [7]CIAT, Selian Agricultural Research Institute, Arusha, Tanzania; [8]ICRISAT, Chitedze Research Station, Lilongwe, Malawi; [9]ICRISAT, BP 320, Bamako; [10]CIAT, Cali, Colombia; [11]IITA, Nampula, Mozambique; [12]ICRISAT, Kano, Nigeria. *(e.monyo@cgiar.org)

Tropical Legumes II (TL-II) seeks to improve the livelihoods of 60 million smallholder farmers (SHF) in 15 countries through enhanced productivity of chickpeas, common beans, cowpeas, groundnut, pigeonpeas and soybeans. It is implemented by ICRISAT, CIAT and IITA in collaboration wih NARS of Burkina Faso, Ghana, Mali, Niger, Nigeria, Senegal, Ethiopia, Kenya, Malawi, Mozambique, Tanzania, Uganda, Zimbabwe, Bangladesh and India. The project is designed to help SHF overcome constraints such as drought, pests, diseases and lack of seed of improved varieties. TL-II is expected to enhance productivity by at least 20% through increased adoption covering 30% of legume area,

strengthen national breeding programs and generate at least $1.3 billion in added value as a result. Significant achievements have been made. Active breeding programs are now in place in all 15 countries. 129 new varieties have been released and are fast replacing old ruling varieties. 37 national partners were trained to MSc and PhD. More than 258,000 tons improved seed was produced between 2007-2013, enough to reach 51.6 million farmers in 5kg packs. Innovative approaches to target the poor - especially women such as small seed packs, seed loans and decentralized production schemes were promoted. Since 2007, improved varieties disseminated have been adopted on 2,007,889 ha and generated US$513 million from project funding and nearly $2 billion from project and partners investiments. In effect, for each dollar invested, the project generates $11 with direct project investment or $39 with partnership's investment. These successes and associated challenges will be discussed.

228	Crop management	Mukong, J.M.	Production, Trade and Consumption of Legumes in Sub - Saharan Africa.Suggested strategies to ensure sustainable and more profitable production.

Production, Trade and Consumption of Legumes in Sub - Saharan Africa.Suggested strategies to ensure sustainable and more profitable production.

Mukong, J.M.[1*]. [1]Seeds and Medicinal Plants Research Centre, Bamenda. *(mukongmbah@yahoo.com)

Food legumes play a vital role by being a source of income and livelihood for millions of people in the world. They contribute to the alleviation of malnutrition among resource farmers and the population. The aim of this work is to outline factors that affect production and marketing in Sub-Saharan Africa and to suggest strategies to ensure sustainable and more profitable production. Food legumes contribute to the sustainability of cropping systems and soil fertility. Cowpea and dry beans are the two main food legume crops grown in Sub-Saharan Africa. Area harvested under all food legumes was more than 28 million ha in 2011-12, representing 34% of the global food legume area harvested. Yields are low compared to other developing and developed countries .Low and Poor yield discourages many farmers. The future of the legume crop sector remains positive in Sub-Saharan Africa if these crops get the required policy attention in terms of research and institutional infrastructure. The question is what should be the research and development strategy that would increase profitability and environmental resilience of legume crop production and minimize risk to the farmers in order to sustain their interest. There is an urgent need to domesticate high-value species and integrate them into the system in order to enhance the system's diversity and profitability, develop disease-resistant varieties and develop an enabling policy environment addressing food legume marketing and plants protection.

229	Crop management	Mukong, J.M.	The role of Rhizobium-Legume Symbiosis in agricultural soil in Arid Regions

The role of Rhizobium-Legume Symbiosis in agricultural soil in Arid Regions

Mukong, J.M.[1,2*]. [1]Seeds and Medicinal Plants Research Centre; [2]Benevolent Education and Rural Development Society. *(mukongmbah@yahoo.com)

Biological N2 fixation is a major source of N input in agricultural soils including those in arid regions. The major N2-fixing systems are the symbiotic systems, which can play a significant role in improving the fertility and productivity of low-N soils. The Rhizobium-legume symbioses have received most attention and have been examined extensively. The behavior of some N2-fixing systems under severe environmental conditions such as salt stress, drought stress, acidity, alkalinity, nutrient deficiency, fertilizers, heavy metals, and pesticides is reviewed. These major stress factors suppress the growth and symbiotic characteristics of most rhizobia; however, several strains, distributed among various species of rhizobia, are tolerant to stress effects. Some strains of rhizobia form effective (N2-fixing) symbioses with their host legumes under salt, heat, and acid stresses, and can sometimes do so under the effect of heavy

metals. Reclamation and improvement of the fertility of arid lands by application of organic (manure and sewage sludge) and inorganic (synthetic) fertilizers are expensive and can be a source of pollution. The Rhizobium-legume (herb or tree) symbiosis is suggested to be the ideal solution to the improvement of soil fertility and the rehabilitation of arid lands and is an important direction for future research.

230	Crop management	Narits, L.	The new protein crops in Estonian conditions

The new protein crops in Estonian conditions

Narits, L.[1*]. [1]Estonian Crop Research Institute. *(lea.narits@etki.ee)

Vegetable protein has a very important role in a healthy diet. In Estonian fields hundreds of years field pea (*Pisum sativum* L.) and faba bean (*Vicia faba* L.) have been cultivated for food. During the last century cultivation of garden pea (*Pisum sativum spp. sativum* L.) for green seeds and common bean (*Phaseolus vulgaris* L.) for greed pods have been widespread in home garden. Estonian Crop Research Institute has carried out field trials with different pulses to enlarge the assortment of legumes and thus locally cultivated healthier food choices and to encourage new people to grow various kinds of protein crops. Spring type crops with shorter growing period were selected for trials (2011-2013) to be tested for Estonian climatic condition. Promising results have been obtained with the brown lentil (*Lens cultivaris* L.) - average protein 28.36% DM, red lentil (*Lens cultivaris* L.) - 29.48%, soybean (*Glycine max* (L.) Merr.) - 36.19% and chickpea (*Cicer arietinum* L.) - 17.93%.

231	Crop management	Nyandoro, R.	Efficacy of fungicidal seed dressings to manage fusarium root rot of soybean in southern Alberta, Canada.

Efficacy of fungicidal seed dressings to manage fusarium root rot of soybean in southern Alberta, Canada.

Nyandoro, R.[1*], Chang, K.F.[2], Hwang, S.F.[2], Strelkov, S.E.[1], Turnbull, G.D.[2], howard, R.J.[3], and Harding, M.W.[3]. [1]Department of Agricultural, Food and Nutritional Science, University of Alberta, Edmonton, AB T6G 2P5, Canada; [2]Crop Diversification Centre North, Alberta Agriculture and Rural Development (AARD), Edmonton, AB T5Y 6H3, Canada; [3]Crop Diversification Centre South, Alberta Agriculture and Rural Development (AARD), Brooks, AB T1R 1E6, Canada. *(nyandoro@ualberta.ca)

Soybean (*Glycine max*) has potential for inclusion in crop rotations in Alberta owing to its relatively high returns and availability of short season cultivars. It is, however, threatened by root rot disease caused by *Fusarium* spp. Experiments were conducted in the 2012 and 2013 summer seasons under greenhouse and field conditions to evaluate the efficacy of seed treatment fungicides (Apron Maxx, Rancona Summit + Maxim 5FS, Rancona Summit, Evergol Energy, Trilex Evergol, Vitaflo 280, Rancona Summit + Maxim 5FS + Vibrance, Vitaflo 280 + Apron, and Vibrance + Apron) against *Fusarium avenaceum* on soybean cultivar TH29002RR. Experiments were arranged in randomized complete block design with fungicides as treatments, along with inoculated and disease-free controls. Seeds that were treated with RanSumMx (Rancona Summit + Maxim), Rancona Summit, Apron Maxx, and Evergol Energy resulted in significantly higher crop emergence rates compared with the inoculated control treatment under field conditions ($P \leq 0.05$), while in the greenhouse, seed treatments with RanSumMx, Vitaflo Apron, Evergol Energy, Vitaflo280, and RanSumMxVb (Rancona Summit + Maxim + Vibrance) had the highest crop emergence ($P \leq 0.05$). Similarly, treatment with RanSumMx, The Rancona Summit, Trilex Evergol, Evergol Energy, or Apron Maxx resulted in the highest soybean grain yields (2.81, 2.62, 2.58, 2.57 and 2.57 t/ha, respectively). While some fungicides were quite effective against root rot, the highest yield (2.81 t/ha) in the field was observed on plants grown from disease-free untreated seeds, suggesting that fungicidal seed treatment still falls short of the 100% crop protection desired by farmers.

232	Crop management	Ogoke, I.J.	Underutilized Grain legumes of Nigeria

Underutilized Grain legumes of Nigeria

Ogoke, I.J.[1*], and Ngwuta, A.A.[1]. [1]Department of Crop Science and Technology, Federal University of Technology Owerri, PMB 1526, Owerri, Imo State, Nigeria. *(ogoke_ij@yahoo.com)

Grain legumes are important as food and feed. They also contribute to the sustainability of cropping systems within which crops are produced in Nigeria through their effects on atmospheric nitrogen fixation, and soil physical properties. In addition, being indigenous species, they are well adapted to climatic and abiotic conditions of the different agro-ecologies of Nigeria. Particularly, these species are less prone to damages by prevalent pests and diseases. Consequently, these germplasms are invaluable in the development of varieties that are well adapted to the ecological zones relative to pests and disease resistances. The production and utilization of these indigenous leguminous grain species including *Mucuna* sp, *Vigna* sp, *Vigna subterranean*, *Stenostylis sternocarpa*, *Phaseolus Lunatus*, among others, have continued to dwindle in Nigeria. Also, not much research has been focused on their improvements, cultivation and utilization. Hence their categorization as underutilized or neglected crops. They are, however, important in addressing the challenges of food security, health and income generation in Nigeria.

233	Crop management	Olson, M.A.	Progress on the development of mung bean [Vigna radiata (L.) R. Wilczek] cultivars for commercial production in Alberta

Progress on the development of mung bean [Vigna radiata (L.) R. Wilczek] cultivars for commercial production in Alberta

Olson, M.A.[1*], Bandara, M.[1], Kruger, A.[1], Howard, R.[1], Harding, M.[1], Bing, D.J.[2], and Chatterton,, S.[2]. [1]Alberta Agriculture and Rural Development; [2]Agriculture and Agri-Food Canada. *(mark.olson@gov.ab.ca)

Mung bean [*Vigna radiata* (L.) R. Wilczek] is a grain legume crop cultivated across Asia for its edible seeds and sprouts. This warm-season crop also has a favorable market demand in North America, particularly for sprout production. Field evaluations of over 200 exotic, cultivated, mung bean genotype(s) were conducted in Brooks and Bow Island in 2006 in Alberta, where relatively warm long growing seasons exist and irrigation is available. Based on preliminary assessments, 33 genotypes were selected and further evaluated for days to maturity and seed yields in Brooks and Bow Island, Alberta, and Morden, Manitoba in 2007 and 2008. Four genotypes (CHN-4, CN 33520, Morden Mung, and VC 6372) consistently yielded from 514-735 kg seed ha-1 with a maturity range of 102 -104 days. All of these genotypes, however, were susceptible to halo blight caused by *Pseudomonas syringae* pv. *phaseolicola*. This disease could be controlled somewhat by seed treatment with Apron Maxx (Fludioxonil + Metalaxyl-M), followed by foliar applications of copper oxide fungicides. A mutated population, derived from the variety AC Harosprout after treatment with ethyl methanesulfonate, was evaluated extensively for maturation, growth habit, halo blight resistance and seed yield in southern Alberta. Based on assessments, 36 entries, including mutant lines, were evaluated at Brooks and Bow Island. Thirteen lines produced seed yields ranging from 1300 to 1660 kg ha-1 with a maturity of 96 to 99 days in 2012. Further evaluations using the three most promising lines from these trials, and some on-farm field assessments, are in progress.

234	Crop management	Ortega, P.F.	Yield response to plant populations in three chickpea cultivars under subsurface drip irrigation system.

Yield response to plant populations in three chickpea cultivars under subsurface drip irrigation system.

Ortega, P.F.[1*], Fierros, G.A. .[2], Padilla, I. .[3], Acosta, J.A.[4], Valenzuela, V. .[5], and Aguilar, B.Z. .[6]. [1]INIFAP-CECH. Blvd. Pascual Encinas Félix #21, Col. La Manga, Hermosillo, Sonora, México, 83200; [2]INIFAP-CECH; [3]CENEB-INIFAP;

[4]CEBAJ-INIFAP; [5]INIFAP-CEVACU; [6]INIFAP-CEBAJ. *(ortegampedro@gmail.com)

Chickpea (*Cicer arietinum* L.) is well adapted to semiarid areas of Northwest area of Mexico. A study was conducted to examine yield response of three chickpea cultivars to plant populations under subsurface dip irrigation system. Tequi 98 (late, semivining growth habit), Blanco Sinaloa 92 (medium early, semivining) and Blanoro (medium early, semierect growth habit) were evaluated in raised beds at 1.6 m, with two rows 0.4 m apart. Plant populations evaluated were 7.5, 10, 12.5, 15 and 17.5 plants·m-2. For Tequi 98, there were no statistical differences for seed yield on plant populations from 10 to 17 plants·m-2, and treatment of 7.5 plants·m-2 reduced seed yield in 12%; whereas for Blanco Sinaloa 92, no differences in yield were found for any of the plant populations evaluated. For Blanoro, the semierect type of plant, results indicate that from 12.5 to 17 plants·m-2 there was no statistical differences among treatments. Low plant populations affected seed yield 14% and 33% under plant populations of 10 and 7.5 plants·m-2, respectively. Plant populations evaluated did not affect either seed size or quality.

235	Crop management	Pajic, V.	ASSESSING THE EFFECTS OF GROUP 14 HERBICIDES ON LENTIL USING IMAGING TECHNOLOGY

ASSESSING THE EFFECTS OF GROUP 14 HERBICIDES ON LENTIL USING IMAGING TECHNOLOGY

Pajic, V.[1*], Noble, S.[2], Bett, K.[1], and Vandenberg, A.[1]. [1]Department of Plant Sciences/Crop Development Centre, University of Saskatchewan; [2]College of Engineering, University of Saskatchewan. *(vlp251@mail.usask.ca)

Developments around smaller and cheaper multispectral and hyperspectral sensors are enabling imaging technology to be used increasingly in plant research. Group 14 herbicides, such as sulfentrazone and fluthiacet methyl, cause the destruction of cell membranes, with symptoms that appear as burned plant tissues which occurs within hours or days of application of the herbicide. This research is focused on investigating the possible use of imaging technology to quantify injuries caused by group 14 herbicides. Effects will be examined on a whole plot level in the field conditions (with a multispectral sensor Tetracam ADC Micro mounted on a UAV) and on an individual plant level in a controlled environment (with a hyperspectral sensor). In the field, control (unsprayed) and three treatments of sulfentrazone will be used to examine the response of seven varieties of lentil. In the controlled environment, fluthiacet methyl will be used to screen diverse lentil germplasm for response. Among numerous indices which can be extrapolated from multi- and hyper- spectral images, the Normalized Difference Vegetation Index (NDVI) will be used as it is an excellent estimator of plant stress. NDVI is calculated with spectral reflectance values acquired in the red and near-infrared regions. Group 14 herbicides cause significant reduction of NDVI value at the whole plant as well as at the whole plot level. Imaging technology appears to be a very good tool for assessing damage caused by group 14 herbicides in lentil, and will facilitate further breeding work towards the development of lentils tolerant to group 14 herbicides.

236	Crop management	Patil , S.B.	MACHINE HARVEST: An economical method of chickpea harvesting

MACHINE HARVEST: An economical method of chickpea harvesting

Patil, S.B.[1*], Mansur, C.P.[2], Gaur, P.M.[3], Goyal, A.[1], and Alagundagi, S.C.[4]. [1]International Center for Agricultural Research in the Dry Areas (ICARDA), Rabat, Morocco; [2]University of Horticultural Sciences (UHS), Bagalkot, Karnataka, India; [3]International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru, Andhra Pradesh, India; [4]University of Agricultural Sciences (UAS), Dharwad, Karnataka, India. *(s.patil@cgiar.org)

An economically harvesting method is very important for any crop to reduce the production cost and to perform timely operation. Machine harvest is a better option in comparison to manual harvest as it saves time and labor. Chickpea is a very important food legume crop in India and its production cost is very high mainly due to manual harvest. Plant height and first pod height are the important factors for machine harvest in chickpea as lower pod height affects the

speed of harvest and potential crop loss through pod passing underneath the machine cutter bar. The performance of four tall and one semi-erect chickpea genotype was compard for both manual and machine harvest at ICRISAT-India. The results of machine harvest indicated lower harvest losses for tall genotypes (ranging 2.64 to 4.96%) and higher loss(20%) for semi-erect genotype as compared to manual harvest (3.12 to 5.40%). The actual field capacity was lower under manual harvest (one labor can harvest 0.004 to 0.008 ha h-1) than machine harvest (0.24 to 0.36 ha h-1). Tall genotypes had highest actual and theoretical field capacity with relatively minimum cost for harvesting compared to semi-erect genotype and gave US$ 43.36 to 46.57 ha-1 an additional benefit in machine harvest over manual. In semi-erect genotype, it was negative (US$ 113.76 ha-1) with maximum monetary value of loss (US$ 189.24 ha-1). The results suggest that tall chickpea genotypes are better suited for machine harvest with reduced harvest losses, higher field capacity and reduced production cost.

237	Crop management	Rahman, M.M.	Lentils in conservation agriculture: Relay cropping in Bangladesh

Lentils in conservation agriculture: Relay cropping in Bangladesh

Rahman, M.M.[1*], Malik, A.I.[2], Flower, K.[3], Ali, O.[4], and Erskine, W.[2]. [1]International Rice Research Institute, Dhaka, Bangladesh; [2]Centre for Plant Genetics and Breeding, The University of Western Australia, Australia; [3]School of Plant Biology, Faculty of Sciences, The University of Western Australia, Australia; [4]Bangladesh Agricultural Research Institute, Bangladesh. *(m.m.rahman@irri.org)

Pulse production within rice based cropping systems has declined due to competition from more remunerative crops like rice in Eastern India and Bangladesh. There is scope to regain lentil production using the conservation agriculture practice of no tillage/relay sowing to replace the current farmer practice of multiple tillage before cropping (sole cropping). Relay-sowing – broadcasting lentil into standing rice ~ three weeks before harvest (without cultivation) - was evaluated on-station with six early-flowering lines and check cultivars in two seasons, and on-farm with one cultivar at two locations. The early-flowering lentil lines did not achieve an economic yield (< 1.0 t ha-1) with relay sowing; whereas the check cultivar produced an economic average yield of relay-sown lentil on-station of 1.4 t ha-1 in two seasons. On farmers' fields, relay-sowing gave an average yield advantage of up to 64% over sole cropping. This was mainly because the relay could be sown at the optimum time, whereas the sole crop was sown later than optimal. Relay sowing also has an economic advantage through reducing the cultivation cost (land preparation) over sole cropping of lentil by 40%. The study demonstrates the yield benefit of relay sowing on to full-season standing transplanted monsoonal rice.

238	Crop management	Shirtliffe, S.J.	Integrated Weed Management in Lentil for Control of Herbicide Resistant Weeds

Integrated Weed Management in Lentil for Control of Herbicide Resistant Weeds

Redlick, C.[1], Willenborg, C.[2], Johnson, E.N.[3], and Shirtliffe, S.J.[2*]. [1]Dow Agrosciences; [2]University of Saskatchewan; [3]AAFC Scott. *(steve.shirtliffe@usask.ca)

The occurrence of group II herbicide resistance in wild mustard and kochia threatens lentil production. The objectives of this project was to determine optimum management of herbicide resistant broadleaf weeds in lentil through a combination of physical, chemical and cultural methods as well as developing an integrated weed management program that will reduce herbicide selection pressure in lentil. An integrated weed management system that combined high seeding rates, Heat, ½ rate of Sencor and rotary hoeing resulted in lentil yield equivalent to full rate of Sencor. The optimum seeding rate in the extra-small red lentil class may be a function of the weed control system. A more robust weed control system will probably require a higher seeding rate and incorporate alternative weed control

strategies. Economically the 260 seed m-2 seeding rate of extra-small red lentils was the most profitable. Even in a year with very high levels of disease we did not find yield decreases because of higher seeding rates. Preliminary studies indicate that a fall application of Edge and spring rotary hoeing can be effective in controlling kochia populations. Finally fluthiacet-methyl can effectively control mustard and provides superior weed control when extra-small red lentils are seeded at higher than normal seeding rates.

239	Crop management	Solórzano Vega, E	BROAD BEAN VARIABILITY (Vicia faba L.) IN THE HIGH VALLEY OF MEXICO: COLLECTION AND DOCUMENTATION.

BROAD BEAN VARIABILITY (*Vicia faba* L.) IN THE HIGH VALLEY OF MEXICO: COLLECTION AND DOCUMENTATION.

Solórzano Vega, E.[1*], Vázquez Carrillo, M.G.[2], Márquez Sánchez, A.R.[1], Legaria, J.P.[2], Sandoval-Gamiño, J.[1], López, C.G.[1], and García Hernández, G.[1]. [1]Plant Science Department. Autonomous University of Chapingo. Km 36.5 Road Mexico - Texcoco. Chapingo, Texcoco, Mexico. C. P- 56200; [2]INIFAP. *(esteban_solorzano@yahoo.com)

The purpose of this study was the phenotypic and agronomic characterization of variability in broad bean landraces grown in the high valleys of Mexico. The analyzed characteristics of the plant, such as size, color and shape of the pods and seeds; protein, tannins cooking time; viability, size and shape of pollen, stomata; size and shape of the root and its relation to the aerial part. Isozyme variability studies and molecular markers were also performed. Yields were evaluated in dry grain and its interaction with the environment. Likewise, the production conditions were analyzed and the characteristics of temperature, precipitation and altitude above sea level were determined. There were significant differences for almost all of the measured characteristics, that seed size is predominantly 20 to 30 mm in length. The cooking time was 82 minutes to 44 minutes away. Wide variability in the content of tannins in the testa and protein, significant differences were found between collections. Significant differences in the number of stomata on the beam, distance between stomata were found on the underside. Concerning the root volume found that 85 % of the root is distributed in strata 0 -15 and 15-30 cm deep and there is a 37.3 % reduction in leaf area and 9.2 % in root length under drought. There is a 1:1 relationship between the length of the main stem and root length (LT: LRZ) in the two systems (dry and wet).

240	Crop management	Solórzano Vega, E.	"CARMEN" NEW VARIETY OF FIELD BEAN (Vicia faba minor) FOR THE HIGH VALLEY OF MEXICO

"CARMEN" NEW VARIETY OF FIELD BEAN (*Vicia faba minor*) FOR THE HIGH VALLEY OF MEXICO

Solórzano Vega, E.[1*]. [1]Crops Science Academy, Department of Plant Science. Autonomous University of Chapingo. Km 36.5 Carretera Mexico - Texcoco. Chapingo, Texcoco, Mexico. *(esteban_solorzano@yahoo.com)

Carmen is a new variety of field bean (*Vicia faba* L.) in Mexico, with an average seed size about two cm length (2 g/seed), corresponding to the minor variety, which in Mexico is unknown materially, with a biological cycle about 150 days from planting to harvest, seed small, acceptable performance and cold resistant making it an excellent choice for winter crops and better performance with oat in intercropin system, The aim of this paper is to describe the morphological and agronomic characteristics of the Carmen range after 10 years of work on it. Get a proper field bean variety with acceptable performance condition like alone crop production and planting interspersed with small grains in winter. Through this work is to obtain: the description of the morphological characteristics, based on field beans issued by Internarional Union for Protection of New Plant Varieties (UPOV, 2002). The variations quantified were: plant height, leaf area, number of pods, seeds and weight. Two samplings at two different phenological stages were performed and finally the yield per plant and per unit area (m2) was quantified. From some of the evaluated data is obtained that Carmen range is 123.5 cm plant height, where the flower and tie the first sheath is located at a height of

35.1 cm. Producing sheath from node 10 to 22 on average and average amount of up to 52 pods per plant, which usually has an average of 4 kills branches.

241	Crop management	Subedi, M	Effect of pre-harvest desiccants on seed germination and vigour of red lentil cultivar CDC Maxim

Effect of pre-harvest desiccants on seed germination and vigour of red lentil cultivar CDC Maxim

Subedi, M.[1*], Willenborg, C.[1], and Vandenberg, A.[1]. [1]Department of Plant Sciences, University of Saskatchewan, SK, Canada. *(mas248@mail.usask.ca)

Lentil (*Lens culinaris* Medik.), is a major pulse crop grown in Western Canada. Lentil growers usually apply desiccants to facilitate harvesting operations and to minimize harvest losses. Information on the impact of pre-harvest desiccants on post-harvest lentil seed germination and vigour is limited. Field studies were conducted at two sites, Scott and Kernen-Saskatoon in Saskatchewan in 2012 and 2013, to evaluate the effects of glyphosate (900 g a.e. ha -1), ET-pyraflufen (10 or 20 g a.i ha -1), glufosinate (300 or 600 g a.i. ha -1), flumioxazin (105 or 210 g a.i. ha-1), saflufenacil (36 or 50 g a.i. ha-1), diquat (207.5 or 415 g a.i. ha-1) applied alone or as tank mix with glyphosate on seed germination and seed vigour of the widely grown red lentil cultivar CDC Maxim. Treatments were arranged in randomized complete block design with four replicates at each location. In 2012, at both sites, glyphosate applied alone or as tank mix with other herbicides significantly reduced seed germination and seed vigour. Glyphosate applied alone and as tank mix with other herbicides reduced mean seed germination and seed vigour of lentil by 23.5% and 16.5% at Kernen and 20.0% and 7.8% at Scott compared to the respective untreated controls. No such adverse effect of desiccants on seed germination and vigour were observed in 2013. In summary, these results suggest that sole application of glyphosate or tank mixes of desiccants with glyphosate decrease the seed quality. The seeds may not suitable for seed production purpose.

242	Crop management	Tay, J.	Effects of Sowing Date of Yield and Yield Components of Green Chickpea

Effects of Sowing Date of Yield and Yield Components of Green Chickpea

Tay, J.[1*]. [1]Centro Regional de Investigación Quilamapu,INIA. Casilla 426, Chillán,Chile. *(jtay@inia.cl)

The production of Green Chickpea can be an opportunity, for Chilean Frozen Food Industry, a new product that would be added to the list of vegetables legumes, such green peas,green bean, shelled bean and green faba bean. The purpose of this poster is to show the effect of five sowing dates (first week of August to end of September) on green chickpea yield and yield components, with the cultivar Alfa INIA. The research was carried out during 2013, in Chillán (36° 32´S;71° 55´W), south central of Chile. The experiment was a RCB design, with four replications. The experimental plots were of 3 x 5 m planted at row spacings of 0.60 m. The results showed that were significant difference among sowing dates, related to plant height, numbers of pods per plant and green grain yield. The highest green grain yield were obtained witth sowing date from half to end of september.

243	Crop management	Tazawa, J	Study of Soybean Cultivars and Sowing Time for Organic Soybean Cultivation in Japan.

Study of Soybean Cultivars and Sowing Time for Organic Soybean Cultivation in Japan.

Tazawa, J.[1*], and Miura, S.[1]. [1]National Agriculture and Food Research Organization. *(jtazawa@affrc.go.jp)

The ratio of the organic cultivating area is 0.4% to the total agricultural cropping field area in Japan, though the organic area is increasing gradually. The Japanese government is promoting the expansion of organic farming area up to 1% by 2019. As the organic soybean field has not increased for a few years, expansion is important. Field

experiments for organic soybean cultivation were conducted for 3 years. We focused on the characteristics of soybean cultivars and sowing time. Yield under organic conditions is better in the late mature cultivar, 'Fukuyutaka' than the early mature 'Tachinagaha'. Correlation between sowing time and the yield indicated that early mid-July was the best period to sow seeds for organic soybean, though the best sowing season in the Kanto area, east part of Japan, is usually the middle to end of June. Two of the biggest problems of soybean cultivation are insects and weeds. Seed weight and damaged seed ratio had a positive correlation. The longer the accumulated temperature from flowering to maturing periods, the higher the damaged seed ratio. Weed control by intertillage and molding at 2 and 4 weeks after sowing was as effective as conventional methods with chemical herbicide. We found that selecting the soybean cultivars which have small seed weight and low accumulated temperature between flowering to maturing, and cultivating with late sowing and early twice intertillage and molding, are effective for organic soybean production.

244	Crop management	Valenzuela-Herrera, V.	JUMBO 2010, new large seeded chickpea cultivar for the state of Sinaloa, Mexico

JUMBO 2010, new large seeded chickpea cultivar for the state of Sinaloa, Mexico

Valenzuela-Herrera, V.[1*], Manjarrez-Sandoval, P.[1], Acosta-Gallegos, J.A.[2], Ramírez-Soto, M.[1], Padilla-Valenzuela, I.[3], Ortega-Murrieta, P.F.[4], and Fierros-Leyva, G.A.[4]. [1]INIFAP-CEVACU Km 17.5 Carretera Culiacan-ElDorado. CP. 80000, Culiacan, sinaloa Mexico; [2]INIFAP-CEBAJ; [3]INIFAP-CENEB; [4]INIFAP-CECH.
*(valenzuela.victor@inifap.gob.mx)

The chickpea produced in the Northwest region of Mexico is of the Kabuli type, of pronounced angular shape and large seed size. The production of chickpea in this region is mainly intended for exportation towards Europe, the Middle East and some other Mediterranean countries. Jumbo 2010 is a new cultivar developed from the single cross of Dwelley x Blanco Sinaloa-92. During its development the selection from the F2 onwards was based on root-rot resistance in a wilt-sick plot and large light cream-colored seeds. Leaves are composite of large leaflets of semi-opaque green color, flowers are white and pods are large, during seed filling the pod size is 28 x 15 mm of medium intensity green color. The seed of Jumbo is extra large, with 36 to 38 seeds per 30 g, of round-angular shape. The five-year average seed yield in Sinaloa was 2.400 kg/ha, 200 kg above the commercial check Blanco Sinaloa 92, 97% of its yield meets the 9 mm exportation size. Jumbo 2010 is resistant to the prevalent races of *Fusarium oxysporum* pv *ciceris*, but susceptible to the leaf miner (*Lyriomiza* sp). At the Bajio region in Central Mexico, Jumbo 2010 was the only cultivar with a yield of 2.0 ton/ha for two years under limited irrigation and delayed January-February planting, while the yield of Blanco Sinaloa 92 was 1.3 ton/ha. In this region Jumbo 2010 has shown susceptibility to Ascochyta blight when planted during the rainy season.

245	Crop management	Vance, W.	Alleviating abiotic constraints to rainfed winter chickpea production- An example for small holder farms in the High Barind Tract of Bangladesh

Alleviating abiotic constraints to rainfed winter chickpea production- An example for small holder farms in the High Barind Tract of Bangladesh

Vance, W.[1*], Bell, R.W.[1], Johansen, C.[2], and Haque, M.E.[3]. [1]School of Veterinary and Life Sciences, Murdoch University, Perth WA; [2]Agricultural Consultant, 15 Westgate Court, Leeming, Perth, WA; [3]International Development Enterprises- Bangladesh (iDE). *(w.vance@murdoch.edu.au)

Studies were carried out in the High Barind Tract of Bangladesh to determine constraints to chickpea (*Cicer arietinum* L.) production during the winter season. Chickpea is grown on residual soil moisture usually after rice (*Oryza sativa* L.) transplanted in puddled soil in the preceding rainy season. In this chickpea production system, drying surface soils can limit crop establishment and then the crop may be exposed to sub-optimal conditions (both high and low

temperatures, low soil water content) during subsequent growth stages.

Over three years, field and glasshouse experiments investigated the constraints to chickpea crop establishment and growth and agronomic solutions to mitigate these constraints. The experiments targeted one technology advancement, mechanised one-pass row sowing by minimum tillage, and one agronomic management technique, time of sowing. The minimum tillage technology allowed timely planting of chickpea into soil at water contents (15 to 24 % g/g) that did not limit crop establishment. Glasshouse studies confirmed that chickpea emergence was possible between soil water contents of 12 to 24 % (g/g). Late sown crops were likely to be exposed to low temperatures (<15°C) during early growth, limiting biomass formation, and were also likely to be exposed to high temperatures (>35°C) from podding to maturity, resulting in depressed grain yields. From these experiments the recommended sowing time in this region, considering chickpeas' requirements for soil water and temperature for successful crop establishment and high yield, is between 30 November and 10 December.

246	Genomics and Genetics	Caron C.	A bioinformatic pipeline for automation of genotype by sequencing analysis of large, complex genomes

A bioinformatic pipeline for automation of genotype by sequencing analysis of large, complex genomes

Caron, C.[1*], Ramsay, L.[1], Sanderson, LA.[1], and Bett, KE.[1]. [1]Department of Plant Sciences, University of Saskatchewan, 51 Campus Dr., Saskatoon, SK, Canada. *(carolyn.caron@usask.ca)

Genotyping by sequencing (GBS) has become a low-cost and efficient method for genotyping of multiple individuals using genome-wide molecular marker discovery. Analysis of raw GBS data to discover SNP genotypes is currently a multi-step process requiring the use of various bioinformatic command-line tools. A pipeline has been developed to automate this process while providing informative summaries at each step. This pipeline divides GBS analysis into four steps: (1) de-multiplexing of samples, (2) trimming of adaptor sequences and low-quality bases using Trimmomatic, (3) alignment of reads against a reference genome sequence using Bowtie2, and (4) raw variant calls made using the SAMtools package. This approach is beneficial for users with varying levels of command-line experience as it eases the learning curve for the required tools while still providing flexibility. Furthermore, the summaries generated enable users to evaluate the data produced by each step for biological validity, thus making this pipeline efficient for high-throughput GBS analysis while still ensuring data validity can be evaluated.

247	Genomics and Genetics	Diaz-Castro E	Application of Novel SNP Markers to Re-examine Common Bacterial Blight Resistance in OAC Rex

Application of Novel SNP Markers to Re-examine Common Bacterial Blight Resistance in OAC Rex

Diaz-Castro, E.[1*], Khanal, R.[2], Perry, G.[1], Xie, W.[1], Navabi, A.[1], and Pauls, K.P.[1]. [1]Department of Plant Agriculture, University of Guelph; [2]Agriculture and Agri-Food Canada. *(ediazcas@uoguelph.ca)

Common Bacterial Blight (CBB; caused by *Xanthomonas axonopodis pv. phaseoli*) is a major constrain in production of dry beans (*Phaseolus vulgaris* L.), worldwide. The objective of this study was to identify the genomic regions contributing to CBB resistance in OAC Rex, a derivative of interspecific crosses with *P. acutifolius*. A population of 81 recombinant inbred lines (RILs) of the cross between OAC Rex and OAC Seaforth (susceptible) were phenotyped in artificially-inoculated field nurseries in Southwest Ontario in 2011 and 2013. The population was genotyped using 7043 Single Nucleotide Polymorphism (SNP) markers, from which 1556 were polymorphic between the two parental lines. A linkage map was constructed and aligned with the physical map of the SNP markers in the reference bean genome sequence. The alignment of the linkage map was consistent with the physical positions of the SNPs in the bean genome except for PV03, PV09 and PV11, where alignment discrepancies were observed in sections of the chromosomes. Composite Interval mapping identified a cluster of SNP markers in the vicinity of the major CBB QTL

on PV08 at 123 cM accounting for 22% of the variation. Other QTL, with smaller effects, were identified on PV01 at 21 cM, PV02 at 47 cM, PV6 at 47 cM, and PV11 at 259 cM, accounting for 5, 6, 6, and 4% of the variation, respectively. The identified SNPs can be used to develop new markers for selection in bean breeding programs and to identify CBB resistance candidate genes, which may have been introgressed from *P. acutifolius*

248	Seeds and Nutrition	Jha, A.B.	Folate profiles in diverse cultivars of common bean, lentil, chickpea and pea by LC-MS/MS

Folate profiles in diverse cultivars of common bean, lentil, chickpea and pea by LC-MS/MS

Jha, A.B.[1*], Diapari, M.[1], Ashokkumar, K.[1], Ambrose, S.J.[2], Zhang, H.[2], Tar'an, B.[1], Bett, K.E.[1], Vandenberg, A.[1], Warkentin, T.D.[1], and Purves, R.W.[1,2]. [1]Crop Development Centre/Department of Plant Sciences, University of Saskatchewan, 51 Campus Drive, Saskatoon, SK S7N 5A8, Canada; [2]ACRD, National Research Council, 110 Gymnasium Place, Saskatoon, SK S7N 4K9, Canada. *(ambuj.jha@usask.ca)

Knowledge of the diversity in folate profiles of pulse crop cultivars grown in contrasting locations in western Canada was not available. With this objective, folate concentration was measured in four cultivars each of common bean, lentil, chickpea and pea with a long term breeding objective to produce pulse crops rich in folates. Using liquid chromatography coupled with mass spectrometry (LC-MS/MS), six different folates were quantified in all crops. Analysis of variance showed significant differences in the concentration of six folates based on genotype and location. Significant differences in the relative proportion of the six folates were observed among the crops, and to a lesser extent among cultivars within crops. Chickpea with an average of 471 µg/100 g had the highest concentration of total folate followed by common bean (192 µg/100 g), lentil (153 µg/100 g), and pea (26 µg/100 g). Among folates, 5-methyltetrahydrofolate was the major folate in common bean and pea, whereas 5-formyltetrahydrofolate was predominant in lentil and chickpea. Useful variation detected among the four cultivars evaluated in each crop will set the stage for wider surveys of variation and expanded breeding activities for biofortification of pulse crops.

249	Genomics and Genetics	JOHNSON, PYARE LAL	Variability and Stability analysis for seed yield and its components in chickpea (Cicer arietinum L.)

Variability and Stability analysis for seed yield and its components in chickpea (Cicer arietinum L.)

JOHNSON, PYARE LAL.[1*], SAI, Shailja.[1], Nanda, Hem Chand.[1], Sharma, Raj Narayan.[1], Chandrakar, Hemendra Kumar.[1], and NAIR, SUNIL KUMAR.[1]. [1]Indira Gandhi Krishi Vishwavidyalaya. *(pyare_johnson@yahoo.com)

The genotypic coefficient of variation (GCV) was maximum for the characters *viz.,* biological yield plant-1, 100-seed weight, seed yield plant-1, seed volume, hydration capacity seed-1, hydration index and swelling index in E1, E2, E3 and E4. Pods plant-1 in E1, E2 and E3 and primary branches plant-1 in E2 and E3. GCV for seed yield was high which imparts good scope for yield improvement through direct selection in chickpea. High heritability coupled with high genetic advance was recorded in characters *viz.,* 100-seed weight, seed volume, hydration capacity seed-1, hydration index and swelling index in E1, E2, E3 and E4 and pods plant-1 in E1 and E2. Biological yield plant-1 in E2, E3 and E4 and primary branches plant-1 in E2 and E3 and plant height in E3, which indicates that the heritability is due to additive gene action and the selection based on these character may be effective. The genotype JG 11 was stable for primary branches plant-1 over all environments. GCP 101 was stable for biological yield plant-1. Vaibhav, Indira Chana-1 and JGK 1 were stable for 100-seed weight. JG 14, Indira Chana-1, JG 74 and GCP 101were stable for seed yield plant-1 and JG 14 and JG 74 were stable for harvest index over all the environments.

250	Genomics and Genetics	Kaur, S.	Characterisation of genetic diversity in lentil germplasm (Lens culinaris L.) by SNP genotyping

Characterisation of genetic diversity in lentil germplasm (Lens culinaris L.) by SNP genotyping

Lombardi, M.[1], Cogan, N.O.I.[1], Forster, J.W.[1,2], Materne, M.[1], and Kaur, S.[1*]. [1]Department of Environment and Primary Industries, Victoria, Australia; [2]La Trobe University, Bundoora, Victoria 3086, Australia. *(sukhjiwan.kaur@depi.vic.gov.au)

Characterization of the genetic diversity of germplasm is essential for the efficient organization and utilization of breeding material. Knowing the genetic relationships among cultivars is critical for breeders to select potential genotypes for breeding purposes. The identification of diversity in germplasm collections is of particular importance for lentil breeding, where limited diversity exists due to population bottlenecks. In addition many of the lentil cultivars have limited pedigree information, so further inbreeding is a significant risk. The aim of this study was to assess the levels of genetic diversity within the lentil germplasm using a set of landraces and commercial cultivars. A custom 384-SNP set was selected using SNPs discovered from transcriptome data generated from key lentil cultivars which was the used to genotype a total of 524 accessions of lentil sourced from Australian Grains Genebank (AGG). These included 392 landraces and 132 commercial cultivars originated from USA, Canada and China.

To display the genetic relationships among different lentil accessions, a Principle Coordinate Analysis (PCoA) was carried out. The results of this study indicated a low level of diversity within lentil lines. Furthermore, data was also analysed using software program STRUCTURE to understand the similarities and differences among different lentil accessions as well as to validate pedigree relationships.

251	Genomics and Genetics	Khamassi Khalil	The use of KASPAR-SNP Marker to analyze the genetic structure and diversity of A Tunisian field bean (Vicia faba L. var minor) germoplasme collection in comparison to global genetic diversity and German frost and drought tolerant breeding lines.

The use of KASPAR-SNP Marker to analyze the genetic structure and diversity of A Tunisian field bean (Vicia faba L. var minor) germoplasme collection in comparison to global genetic diversity and German frost and drought tolerant breeding lines.

khamassi, KHALIL.[1,2,3*], Mohamed, B. Ali .[1,4,5], Ben Jeddi, Faysal.[2], Bett, Kirsten.[1], Vanderberg, Albert.[1], Link, Wolfgan.[5], and O' Sullivan, Donal. M. .[3,6]. [1]University of Saskatchewan, Plant science Department, Saskatoon, Canada; [2]University of Carthage, National Agronomic Institute of Tunisia (INAT), Laboratory of horticultural Sciences,Tunisia; [3]National Institute of Agricultural Botany (NIAB), Cambridge, UK; [4]Agronomy Department, College of Agriculture, Assiut University, Assiut, Egypt; [5]Göttingen University, Department of Crop Sciences, Gottingen, Germany; [6]School of Agriculture, Policy and Development, University of Reading, Reading, UK. *(khalil.khamassi@usask.ca)

252	Biotic Stress	Maguire K. L.	Combined approach to Foot Rot of peas

Combined approach to Foot Rot of peas

Maguire, K. L.[1*], and Charlton, A.[2]. [1]Processors and Growers Research Organisation, Peterborough, UK; [2]The Food and Environment Research Agency, Sand Hutton, York, UK. *(kerry@pgro.org)

Foot rot is becoming an increasing problem for peas grown in the UK. Although peas are grown in rotation one year in five there are increasing incidences of foot rot in both vining and combining peas. Vining peas are concentrated in areas close to the factories as the crop needs to be frozen within 150 minutes of harvest, and therefore land close to the factories is favoured for growing peas with an associated risk of increased incidence of foot rot in these areas.

Combining peas do not have these restrictions but there is still an increasing disease problem. Foot rot is caused by *Fusarium spp.* and *Phoma medicaginis.* In recent years *Aphanomyces euteiches* has also become a contributing factor to this disease complex. In a combined approach the incidence of these pathogens is being identified and monitored as well as testing varieties for resistance.

253	Crop management	Nagaraji S	Nutrient-efficient, resilient and sustainable legumes for prosperity in the drylands

Nutrient-efficient, resilient and sustainable legumes for prosperity in the drylands

Ellis, N.[1,2], Nagaraji, S.[1,2*], Beebe, S.[3], Ghanem, M.[4], Okori, P.[2], Chaturvedi, SK.[5], Tamo, M.[6], Agrawal, SK.[4], Gaur, P.[2], Gopalakrishnan, S.[2], Kumar, CVS.[2], Varshney, R.[2], and Njuguna, EM.[2]. [1]CGIAR Research Program on Grain Legumes; [2]ICRISAT; [3]CIAT; [4]ICARDA; [5]Indian Institute of Pulses Research; [6]IITA. *(n.satish@cgiar.org)

The CGIAR Research Program on Grain Legumes is an ambitious international program to improve eight legume crops that are vital to the health, prosperity and resilience of millions of poor people across the developing world – especially children and women, who are the most vulnerable to malnutrition.

Grain legumes are protein rich and affordable foods. Protein sourced from grain legumes costs one-fifth as much as protein from milk. These are also vital sources of micronutrients such as iron.In addition to feeding their households, many poor grain legume farming families derive vital income by selling part of their crop. They are often primarily cultivated by women in Africa, providing a strategic window for focusing research benefits towards women – also benefiting the children who depend on them.

Smallholders generally cannot afford to buy enough chemical nitrogen fertilizer; as a result the yields of their crops are very low. A stellar advantage of grain legumes is their capacity to biologically convert nitrogen from the atmosphere into nitrogen in the soil – in other words, creating free fertilizer out of thin air.

A second major environmental benefit is that grain legume crops diversify typical farming systems. Greater diversity increases food and income security: if one crop fails due to drought or pests, another may rescue the total farm operation.

The research program is a partnership among four members of the CGIAR Consortium: ICRISAT as lead center, CIAT, ICARDA and IITA, along with several public and private institutes and organizations, governments, and farmers worldwide.

254	Biotic Stress	Odeny DA	SCREENING GROUNDNUT RECOMBINANT INBRED LINES FOR RESPONSE TO EARLY LEAF SPOT: TOWARDS MARKER ASSISTED SELECTION IN ZAMBIA

SCREENING GROUNDNUT RECOMBINANT INBRED LINES FOR RESPONSE TO EARLY LEAF SPOT: TOWARDS MARKER ASSISTED SELECTION IN ZAMBIA

Tembo, E.[1], Harvey, C.[2], Njoroge, S.[2], Mweetwa, AM.[1], Tembo, L.[1], Kaimoyo, E.[1], Monyo, ES.[3], and Odeny, DA.[3*]. [1]School of Agricultural Sciences, University of Zambia, Box 32379, Lusaka, Zambia; [2]ICRISAT-Lilongwe, P.O Box 1096, Lilongwe, Malawi; [3]ICRISAT-Nairobi, P.O Box 39063 – 00623, Nairobi, Kenya. *(d.odeny@cgiar.org)

Groundnut (*Arachis hypogaea* L.) is an important global oilseed crop and a major source of protein and vitamins in many rural areas of Africa. In Zambia, production of groundnut is limited by several factors with Early Leaf Spot (ELS) (*Cercospora Arachidicola* Hori) as one of the major destructive diseases. Development of ELS resistant varieties is the most effective and economical strategy for managing the disease. To gain a better understanding of the genes

involved in the resistance to ELS, a total of one hundred and ten (110) F8 Recombinant Inbred Lines (RILs) (Robut 33-1× ICGV-SM 95714) were screened under field conditions using artificial inoculation. Disease scoring was done on four plants randomly selected from each RIL family using a 1-9 scale at 60, 75, 90 and 100 days after planting. The mean scores for each RIL at each scoring date were used to calculate the area under disease progress curve (AUDPC). The AUDPCs ranged from 72.5 to 225 score-days with a mean of 147.75 and a population standard deviation of 36.69. Based on the normal distribution curve, the AUDPCs were used to categorize the RIL families as resistant, medium resistant, medium susceptible or susceptible. Chi-square test confirmed the expected Mendelian 1:1 segregation of the F8 RILs to ELS further justifying their subsequent use in Quantitative Trait Loci (QTL) analysis.

255	Seeds and Nutrition	Reza M	Can Fe-chelating bacteria increase bioavailable Fe-content in lentil (Lens culinaris L.)?

Can Fe-chelating bacteria increase bioavailable Fe-content in lentil (Lens culinaris L.)?

Reza, M.[1,2*]. [1]J.R. de Freitas; [2]F.L. Walley. *(m.reza@usask.ca)

Iron (Fe) deficiency in human nutrition is prevalent worldwide, particularly in developing countries. Legumes including lentil (*Lens culinaris* L.) are an important source of protein and are consumed worldwide. Iron bio-fortification of legumes can be an effective approach to increase Fe-bioavailability in areas affected by Fe deficiencies. The objective of this study is to isolate Fe-chelating soil bacteria and assess their potential to improve Fe-uptake of lentil. Soil samples, collected in areas cultivated to lentil from eight different locations in Saskatchewan, were used in a growth chamber study in which lentil (CDC Milestone) was grown and Fe-chelating bacteria were isolated. Preliminary results indicate that Fe-chelating bacteria colonize the rhizosphere and/or endorhizosphere of lentil. Approximately 200 potential Fe-chelating strains have been isolated from plant parts using nutrient media. Studies designed to assess the effect of Fe-chelating bacteria on iron acquisition of lentil are currently in progress.

256	Seeds and Nutrition	Singhal A.	Effect of Genotype and Environment on Compositional and Functional Attributes of Fababean Protein Isolates

Effect of Genotype and Environment on Compositional and Functional Attributes of Fababean Protein Isolates

Singhal, A.[1*], Vandenberg, B.[2], Tyler, R.T.[1], and Nickerson, M.T.[1]. [1]Department of Food and Bioproduct Sciences, University of Saskatchewan, Saskatoon, SK, Canada; [2]Crop Development Center, University of Saskatchewan, Saskatoon, SK, Canada. *(ats945@mail.usask.ca)

Grain legumes (pulses) such as pea, chickpea, bean and fababean represent good sources of protein, carbohydrate and dietary fibre, and are associated with several nutritional and health benefits. Fababean (*Vicia faba* L.) is typically high in carbohydrate (~57%), protein (~24%) and dietary fibre (~20%), and also is low in fat (1-2%). The overall goal of this study was to investigate the compositional and functional attributes of fababean protein isolates prepared from a variety of genotypes grown in several years and locations, with the aim of identifying whether genotype or environment, or both, had significant impacts on the characteristics of the isolates. Isolates were prepared by alkali extraction, isoelectric precipitation and freeze drying from CDC Fatima, Taboar, SSNS-1, FB9-4, FB18-20, Snowbird and Snowdrop fababean genotypes grown in various locations within Saskatchewan, Alberta and Manitoba (Canada) in the 2011 and 2012 growing seasons. Significant differences ($p<0.05$) were observed among genotypes with respect to the yield, protein content and legumin/vicilin ratio (Lg/Vn) of, protein recovery in, and the surface tension, foaming capacity, creaming stability, emulsion activity and stability indices, and zeta potential of the isolates. The correlation between the protein content and Lg/Vn ratio of the isolates was significant for FB9-4 only ($r=-0.96$, $p<0.05$). The results indicate that the compositional and functional attributes of fababean protein isolates were impacted to varying

degrees by genotype. Knowledge gained from this study may aid in the selection of fababean seed lots better suited for the production of protein isolates with superior compositional and functional attributes.

257	Genomics and Genetics	Turner F	Exploring genomic contributions in a common bacterial blight resistant navy bean population

Exploring genomic contributions in a common bacterial blight resistant navy bean population

Turner, F.[1*], Pauls, P.[1], and Navabi, A.[1]. [1]University of Guelph. *(fturner@uoguelph.ca)

The Ontario navy bean breeding program has released several varieties resistant to common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. phaseoli. Resistance is derived from two interspecific crosses with *Phaseolous acutifolius* (tepary bean) and is conditioned by several loci on different chromosomes. While the contribution of *P. acutifolius* to the common bean genome has been thoroughly studied in the context of CBB resistance, little is known about its possible contribution to other important agronomic traits. A greater understanding of tepary introgression in the genomes of these lines could identify genes and alleles contributing to important traits in Ontario's bean breeding germplasm and inform future breeding programs of such material's desirability. In this study, a population developed from a cross between two resistant parents, Rexeter and Apex, three-way crossed to a susceptible parent with no tepary introgression, Compass, (Compass2*//Rexeter/Apex) was used. In a preliminary study, twenty F1 genotypes, their parents and, the two tepary plant introductions (PI319443 and PI440795) were screened with a panel of 5830 SNPs. Graphical genotyping was used to compare potential sources of introgression where genomic regions were identical by state to their tepary ancestors and the genetic distances of this population from tepary bean and its parents were compared to CBB susceptibility values obtained by image analysis of *X. axonopodis* pv. phaseoli infected leaves. F1s which segregated into groups with greater similarity to Rexeter and Apex, their resistant parents, were also more resistant to CBB than those that segregated into groups with Compass, their susceptible parent.

258	Crop management	Hamidou Falalou	Drought tolerant and dual purpose genotypes of groundnut for high productivity and effective crop-livestock system in Sahelian zones of West and central Africa

Drought tolerant and dual purpose genotypes of groundnut for high productivity and effective crop-livestock system in Sahelian zones of West and central Africa

Hamidou Falalou, Halilou Oumarou, Vincent Vadez. ICRISAT Niamey Niger, BP 12404Email : f.hamidou@cgair.org

Mixed crop-livestock is the prevailing system in the Sahelian countries of west and central Africa (WCA). Crops residues are used to feed animals. As productivity is influenced mainly by drought, heat, low soil fertility and cultivar choice, drought tolerant and dual purpose groundnut varieties selection could boost crop and livestock productivity and increase smallholder livelihood and income earning in WCA.
For identifying high yielding (pods and haulm) and drought tolerant varieties, two experiments were conducted in the field during rainy seasons and two during the summer seasons at the ICRISAT Sahelian Centre (ISC) in Sadore, Niger (13 N, 2 E). 268 genotypes of ICRISAT groundnut reference collection along with 9 farmers' preferred varieties (FPV). One additional experiment on 20 contrasting genotypes was conducted in lysimetre system in rainy season. The experimental design was a complete randomized bloc. An intermittent drought was imposed at flowering stage. Pod and haulm yield decreased up to respectively 56 and 30% due to drought stress. Our findings showed that genotypes ICG 8751, ICG 3140, ICGV 97182, ICG 12697, 55-437, ICG 15287, ICG 434, ICGV 01232, ICGV 02266 and ICGV88145 revealed drought tolerant. Under well water conditions, genotypes ICGV 01232, ICG 8751 and ICG 434 produced more pods (10%) and haulm (37%) than 55-437 (FPV drought tolerant check). Under drought stress, ICGV 97182 and ICG 434 revealed higher pod yield (9%) than 55-437 while ICGV 02266, ICG 8751 and ICG 434 showed

higher haulm yield (21%) than 55-437. ICGV 97182, ICG 8751 and ICG 434 showed higher roots length density than 55-437. Thus, these findings indicates that ICG 434 revealed drought tolerant and dual purpose genotype under well watered and drought conditions while ICGV 97182, ICG 8751 revealed higher yielding than 55-437 under drought stress. Drought tolerance related traits revealed different across genotypes and seasons

259	Crop management	Abdulkadir Aydoğan	Comparison of Kabuli chickpea (*Cicer arietinum* L.) Cultivars with the Fern and Unifoliate leaf Traits for Parameter of Physical Quality

Comparison of Kabuli chickpea (*Cicer arietinum* L.) Cultivars with the Fern and Unifoliate leaf Traits for Parameter of Physical Quality

Abdulkadir Aydoğan[1], Cemalettin Y. Çiftçi[2].
[1]Tarla Bitkileri Merkez Araştırma Enstitüsü, Ankara; [2] Ankara Ü. Ziraat Fakültesi Tarla Bitkileri Ana Bilim Dalı (akadir602000@yahoo.com)

The research was carried out to compare Kabuli chickpea (*Cicer arietinum* L.) Cultivars with the fern and Unifoliate leaf Traits for parameter of Physical Quality. The study was conducted in 2010 and 2011 under Ankara condition. In the study, 20 cultivars and lines which are consists of 10 to each leaf type was used as materials. Experiment was conducted in a randomized comlete block design with split plot and with three replications.In the study, fern and Unifoliate leaved cultivars and lines were evaluated for protein content of seed, dry and wet weight of seeds, water absorption capacity and index, dry and wet volume, swelling capacity and index, cooking time and sieve analysis.There were no statistically significant differences except dry weight in wet weight of seeds, water absorption capacity and index, dry and wet volume, swelling capacity and index, cooking time and sieve analysis.

LIST OF PARTICIPANTS

#	Surname	First Name	Affiliation	Country
1	Abd El-Rahman,	Rehab	FCRI-ARC	Egypt
2	Abdi	Ketema Daba	University of Saskatchewan	Canada
3	Acosta-Gallegos	Jorge	Instituto Nacional de Investigaciones Forestales, Agricolas y Pecuarias	Mexico
4	Adhikari	Kedar	The University of Sydney	Australia
5	Adhikari	Elina	North Dakota State University	USA
6	Agblor	Kofi	Crop Development Centre University of Saskatchewan	Canada
7	Agrama	Hesham	International Institute of Tropical Agriculture (IITA)	Zambia
8	Agrawal	Shiv Kumar	International Centre for Agricultural Research in the Dry Areas (ICARDA), P.O. Box/6299, Rabat-Instituts, Morocco	Morocco
9	Agunbiade	Tolulope	University of Iliniois at Urbana-Champaign	USA
10	Ali	Omar	Bangladesh Agricultural Research Institute, Gazipur Bangladesh	Bangladesh
11	Ali	Mohamed	Postdoctoral research fellow	Canada
12	Al-Katib	Omer	Pulse Trading	Canada
13	Andaloussi	Fouad	INRA	Morocco
14	Andersen	Stig U.	Aarhus University	Denmark
15	Antanasovic	Svetlana	University of Novi Sad, Faculty of Agriculture	Serbia
16	Araujo	Susana	Tropical Research Institute (IICT)	Portugal
17	Arganosa	Gene	Crop Development Centre, University of Saskatchewan	Canada
18	Arntfield	Susan	Department of Food Science University of Manitoba	Canada
19	Arrighi	Jean-Francois	Laboratoire des Symbioses Tropicales et Mediterraneennes (LSTM) IRD	France
20	Arwin	Arwin	Center for Application Isotopes Radiation - National Nuclear Energy Agency Indonesia	Indonesia
21	Atkins	Craig	School of Plant Biology, The University of Western Australia	Australia
22	Aubert	Grégoire	INRA	France
23	Badana Mudiyanselange	Shermy	UNIVERSITY OF SASKATCHEWAN	Canada
24	Bai	Yonghe	Dow AgroSciences/Dow Chemical Company	USA
25	Bandara	Manjula	Alberta Agriculture and Rural Development	Canada
26	Bangar	Parminderjit	University of Saskatchewan	Canada

27	Banniza	Sabine	University of Saskatchewan	Canada
28	Baranger	Alain	INRA	France
29	Barker	Chris	Genome Prairie	Canada
30	Barlow	Brent	University of Saskatchewan	Canada
31	Batley	Jacqueline	University of Queensland	Australia
32	Bazghaleh	Navid	University of Saskatchewan Agriculture and Agri-Food Canada	Canada
33	Beebe	Stephen	CIAT	USA
34	Bellucci	Elisa	Università Politecnica delle Marche D3A-Dipartimento di Scienze Agrarie, Alimentari e Ambientali, Ancona, Itally	Italy
35	Berger	Jens	CSIRO Plant Industry	Australia
36	Beshir	Hussien Mohammed	University of Saskatchewan	Canada
37	Bett	Kirstin	University of Saskatchewan	Canada
38	Bhadauria	Vijai	University of Saskatchewan	Canada
39	Bhardwaj	Harbans	VIRGINIA STATE UNIVERSITY	USA
40	Bhatnagar-Mathur	Pooja	ICRISAT	India
41	Blade	Stan	Alberta Innovates/University of Alberta	Canada
42	Boukar	Ousmane	International Institute of Tropical Agriculture (IITA)	Nigeria
43	Bourgault	Maryse	University of Melbourne	Australia
44	Boutet	Gilles	French National Institute for Agricultural Research	France
45	Bowness	Robyne	Alberta Agriculture and Rural Development	Canada
46	Buchwaldt	Lone	AAFC	Canada
47	Bueckert	Rosalind	University of Saskatchewan	Canada
48	Bukun	Bekir	Dicle Univresity	Turkey
49	Burstin	Judith	INRA	France
50	Cannon	Ethalinda	Iowa State University	USA
51	Cannon	Steven	USDA-ARS	USA
52	Caron	Carolyn	University of Saskatchewan	Canada
53	Caudillo	Kiela	University of Saskatchewan	Canada
54	Chahota	Rakesh	CSK Himachal Pradesh Agricultural University- Palampur-176062 (HP)	India
55	Chan	Crystal	C2 Management	Canada
56	Chang	Kan-Fa	Alberta Agriculture and Rural Development	Canada
57	Chatterton	Syama	Agriculture and Agri-Food Canada	Canada
58	Chaturvedi	Sushil	Indian Institute of Pulses Research, Kanpur (India)	India
59	Chen	Li-An	University of Saskatchewan	Canada
60	Chen	Jianghua	Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences	China (PRC)
61	Chen	Weidong	USDA ARS	USA
62	Cheng	Xuzhen	Institute of Crop Sciences, China Academy of Agriculture Sciences	China (PRC)
63	Cho	Cheryl	University of Saskatchewan	Canada
64	Close	Timothy	Department of Botany & Plant Sciences, University of California	USA

65	Conner	Robert	Agriculture & Agri-Food Canada	Canada
66	Cook	Douglas	University of California-Davis	USA
67	Coyne	Clarice	USDA	USA
68	Crahay	Jacques	Cosucra Groupe Warcoing SA	Belgium
69	Cupina	Branko	University of Novi Sad, Faculty of Agriculture	Serbia
70	Daoui	Khalid	Nationa Institute for Agricultural Research	Morocco
71	Dastmalchi	Mehran	University of Western Ontario	Canada
72	Davies	Phil	South Australian Research and Development Institute	Australia
73	Dempewolf	Hannes	Global Crop Diversity Trust	Germany
74	Denton	Matthew	The University of Adelaide	Australia
75	Deokar	Amit	University of Saskatchewan	Canada
76	Desgroux	Aurore	INRA Rennes	France
77	Desilva	Devini	University of Saskatchewan	Canada
78	Dhaubhadel	Sangeeta	Agriculture and Agri-Food Canada	Canada
79	Diapari	Marwan	University of Saskatchewan	Canada
80	Diaz Castro	Esteban	University of Guelph	Canada
81	Dickstein	Rebecca	Department of Biological Sciences University of North Texas	USA
82	Diederichsen	Axel	Plant Gene Resources of Canada - Agriculture and Agri-Food Canada	Canada
83	Dokken-Bouchard	Faye	Saskatchewan Ministry of Agriculture	Canada
84	Domoney	Claire	John Innes Centre	United Kingdom
85	Douglas	Col	DAFF	Australia
86	Driedger	Darcy	Alberta Agriculture and Rural Development	Canada
87	Duc	Gerard	Institut National de la Recherche Agronomique	France
88	Durkin	Jonathan	AAFC	Canada
89	Edwards	Dave	University of Queensland	Australia
90	Ehlers	Jeffrey	The Bill & Melinda Gates Foundation	USA
91	El Bouhssini	Mustapha	International Central for Agricultural Research in the Dry Areas (ICARDA)	Morocco
92	Eleouet	Morgane	Aberystwyth University	United Kingdom
93	Ellis	Noel		India
94	Emmrich	Peter	John Innes Centre Department of Metabolic Biology	United Kingdom
95	Erskine	William	Centre for Plant Genetics and Breeding (PGB), The University of Western Australia	Australia
96	Fatemi	Zain El Abidine	National Institute for Agriculture Research	Morocco
97	Fatokun	Christian	International Institute of Tropical Agriculture (IITA)	Nigeria
98	Fedko	Alexander	ARD	Canada
99	Ferhatoglu	Yurdagul	University of Saskatchewan	Canada
100	Fevereiro	Pedro	Instituto de Tecnologia Química e Biológica - UNL	Portugal
101	Fikre	Asnake	Ethiopian Institute of Agricultural Research (EIAR)	Ethiopia
102	Fischbuch	Leanne	Alberta Pulse Growers Commission	Canada

103	Fletcher	Allison	Saskatchewan Pulse Growers	Canada
104	Friesen	Laurie	Research Program Manager, SPG	Canada
105	Gaad	Djouher	National Research Center for Biotechnology	USA
106	Gaikwad	Nikhil	SHIVAJI UNIVERSITY, KOLHAPUR, MAHARASHTRA, INDIA 416 004	India
107	Gali	Kishore	University of Saskatchewan	Canada
108	Gaur	Pooran	International Crops Research Institute for the Semi-Arid Tropics(ICRISAT)	India
109	Gerbu	Legesse Hidoto	Agricultural research Institute & Hawassa University	Canada
110	Gharti	Dhan	NARC, Grain Legumes Research program, Rampur, Chitwan, Nepal	Nepal
111	Gillard	Chris	Department of Plant Agriculture, University of Guelph	Canada
112	Giller	Ken E.	Wageningen University	Netherlands
113	Gina	Boux	Cigi	Canada
114	Gondwe	Therese	International Institute of Tropical Agriculture (IITA)	Zambia
115	Goyal	Aakash	Scientist D, Genetics & Plant Breeding International Center for Agriculture in the Dry Areas (ICARDA) PO Box 6299, Station Exp. INRA-Quich, Rue Hafiane Rabat-Institutes,Rabat, 10112 Morocco Cherkaoui. Agdal Cell: +212-691911542	Morocco
116	Grant	David	USDA-ARS	USA
117	Grusak	Michael	USDA-ARS Children's Nutrition Research Center	USA
118	Guo	Yong	Institute of Crop Sciences, Chinese Academy of Agricultural Sciences	China (PRC)
119	Gupta	Priyanka	ICARDA, ICARDA-INRA Rabat, Morocco	Morocco
120	Guy	Stephen	Washington State University	USA
121	Hacikamiloglu	Beybin	Harran University, Agricultural Faculty	Turkey
122	Hamidou	Falalou	ICRISAT	Niger
123	Hamwieh	Aladdin	international Center for Agricultural Research in the Dry Areas ICARDA, P.O. Box 114/5055, Beirut, Lebanon	Egypt
124	Hassan	Fathi	Leibniz University Hannover Institute of Plant Genetics, Department of Plant Biotechnology	Germany
125	Hawkins	Glen	DISeeds Inc	Canada
126	Hecht	Valerie	University of Tasmania	Australia
127	Henriquez	Boris	Alberta Agriculture and Rural Development	Canada
128	Henriquez	Maria Antonia	Agriculture and Agri-Food Canada	Canada
129	Hernandez	Georgina	Center for Genomic Science/ National University of Mexico	Mexico
130	Hobson	Kristy	New South Wales Department of Primary Industries	Australia
131	Hofer	Julie	ICRISAT	India
132	Hoisington	Dave	University of Georgia	USA
133	Holub	Eric	University of Warwick School of Life Sciences	United Kingdom
134	Hood-Niefer	Shannon		Canada
135	Hoover	Ratnajothi	DEPT OF BIOCHEMISTRY MEMORIAL UNIVERSITY OF NEWFOUNDLAND	Canada
136	Hou	Anfu	Agriculture & Agri-Food Canada	Canada
137	Hoy	Christy	Alberta Agriculture	Canada

138	Hu	Jinguo	USDA-ARS	USA
139	Huang	Shaoming	University of Saskatchewan	Canada
140	Hwang	Sheau-Fang	Alberta Agriculture and Rural Development	Canada
141	Ibrahim	Hossam Eidin	Department, Faculty of Agriculture, Alexandria University, Alexandria-21545, EGYPT	Egypt
142	Idrissi	Omar	- Institut National de la Recherche Agronomique du Maroc, CRRA de Settat -Morocco. - Plant Production Unit, Faculty of BioScience Engineering, Ghent University-Belgium.	Belgium
143	Igrejas	Gilberto	University of Trás-os-Montes and Alto Douro Department of Genetics and Biotechnology Institute for Biotechnology and Bioengineering Centre of Genomics and Biotechnology	Portugal
144	Iheanyi	Ogoke	Federal University of Technology Owerri, Owerri, Imo State, Nigeria	Nigeria
145	Ilk	Nadine	The Sainsbury Laboratory (TSL)	England, United Kingdom
146	Isobe	Sachiko	Kazusa DNA Research Institute	Japan
147	Jackson	Scott	The University of Georgia	USA
148	Jacobsen	Hans-Joerg	Leibniz-Universität Hannover	Germany
149	Jaillais	Benoit	INRA	France
150	Jain	Parul	University of Saskatchewan	Canada
151	Jamie	O'Rourke	USDA-ARS	USA
152	Jang	Hyun-Ju	Seoul National University	Korea
153	Janine	Croser	Centre for Plant Genetics and Breeding, The University of Western Australia	Australia
154	Javadi	Firouzeh	Kyushu University	Japan
155	Jendoubi	Wadra	University of Carthage, Field Crop Laboratory, National Institute for Agricultural Research of Tunisia (INRAT), rue Hédi Karray, 2080 – Tunisia	Tunisia
156	Jha	Ambuj	University of Saskatchewan	Canada
157	Jiang	Yunfei	University of Saskatchewan	Canada
158	Jimenez-Lopez	Jose	The UWA Institute of Agriculture, The University of Western Australia	Australia
159	Jogloy	Sanun	Plant Sci. Dept.,Agri.,Khon Kaen Univ.,	Thailand
160	Johnson	Pyare	Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India	India
161	Joshi	Jaya	University of Western Onterio	Canada
162	Joshi	Trupti	University of Missouri Columbia	USA
163	Juan	Osorno	NORTH DAKOTA STATE UNIVERSITY DEPARTMENT OF PLANT SCIENCES	USA
164	Junko	Tazawa	National Agriculture and Food Research Organizaion	Japan
165	Kahlon	Jagroop Gill	AFNS, University of Alberta	Canada
166	Kahn	Michael	Agricultural Research Center Washington State University	USA
167	Kamphuis	Lars	CSIRO Plant Industry/The UWA Institute of Agriculture	Australia
168	Kang	BeomKyu	National Institute Of Crop Science	Korea
169	Kang	Yang Jae	Seoul National University	Korea
170	Kapoor	Karan	University of Saskatchewan	Canada
171	Karen	Cichy	USDA-ARS	USA
172	Kaur	Parwinder	The University of Western Australia	Australia

173	Kaur	Sukhjiwan	Department of Environment and Primary Industries	Australia
174	Kaur	Jagmeet	Punjab Agricultural University, Ludhiana, India	India
175	Kawaguchi	Masayoshi	National Institute for Basic Biology	Japan
176	Keatinge	John	AVRDC - The World Vegetable Center	Taiwan (ROC)
177	Keller	Wilf	Ag-West Bio Inc.	Canada
178	Kemal	Seid	ICARDA-Ethiopia Office	Ethiopia
179	Kennedy	Peter	Department of Environment and Primary Industries, Victoria, Australia	Australia
180	Kessler	Dallas	Plant Gene Resources of Canada	Canada
181	Khadke	Shivram	Smt. Kasturbai Walchand College, Sangli, M.S. India	India
182	Khalifa	Gamal El Kheir	ARC	Sudan
183	Khamassi	Khalil	University of Saskatchewan	Canada
184	Khanal	Narayan	Graduate School for International Development and Cooperation, Hiroshima University	Japan
185	Kharrat	Mohamed	ICARDA	Morocco
186	Khazaei	Hamid	PhD candidate	Finland
187	Kim	Moon Young	Seoul National University	Korea
188	Kim	Sue	Seoul National University	Korea
189	Kim	Sungup	RDA	Korea
190	Kisha	Ted	USDA-ARS	USA
191	Knight	Diane	University of Saskatchewan	Canada
192	Kreplak	Jonathan	INRA	France
193	Krstic	Dorde	University of Novi Sad, Faculty of Agriculture	Serbia
194	Kruger	Arthur	Alberta Agriculture and Rural Development	Canada
195	Kumar	Jitendra	Indian Institute of Pulses Research, Kanpur-208024, U.P., India	India
196	Kumari	Safaa	ICARDA	Tunisia
197	Kundu	Shudhangshu	University of Saskatchewan	Canada
198	Larbi	Asamoah	International Institute of Tropical Agriculture	Ghana
199	Lavaud	Clement	INRA Rennes - IGEPP	France
200	Laxmipathi Gowda	C	ICRISAT	India
201	Lee	Suk-Ha	Seoul National University	Korea
202	Lee	Yeong-Ho	Seoul National University	Korea
203	Lelandais	Christine	Université Paris 7 CNRS	Canada
204	Li	Wenbin	Northeast Agricultural University	Canada
205	Li	Hongjie	ShanDong Shofine Seed Technology CO.,LTD	China (PRC)
206	Li	Zenglu	University of Georgia	USA
207	Lichtenzveig	Judith	Curtin University	Australia
208	Lightfoot	David	Genomics Facility, Dept of Plant Soil and Agric Systems	USA
209	Lindsay	Donna	University of Saskatchewan	Canada
210	Liu	Xiaofei	University of Saskatchewan	Canada

211	Loader	Tara	Cigi	Canada
212	Long	Jennifer	USAID	USA
213	Lozano	Rafael	University of Almeria Spain	Spain
214	Lu	John	Agriculture and Agri-Food Canada	Canada
215	Lucas	Mitchell	University of California Riverside	USA
216	Lui	Sara		Canada
217	Lulsdorf	Monika	University of Saskatchewan	Canada
218	Maalouf	Fouad	ICARDA	Egypt
219	Madhavan Nair	Ramakrishnan	AVRDC - The World Vegetable Center	India
220	Madrid-Herrero	Eva	Institute for Sustainable Agriculture, CSIC	Spain
221	Maguire	Kerry	Processors and Growers Research Organisation	United Kingdom
222	Maharjan	Keshav	Gradaute School for International Development and Cooperation, Hiroshima University	Japan
223	Malik	Al Imran	University of Western Australia	Australia
224	Mamidi	Sujan	North Dakota State University	USA
225	Maren	Friesen	Michigan State University	USA
226	Marrou	Helene	North Carolina State University (NCSU)	France
227	Marsolais	Frederic	Agriculture and Agri-Food Canada Southern Crop Protection and Food Research Centre	Canada
228	Mascarenhas	Lisette	Director of Research and Development, SPG	Canada
229	Mbah	Mukong Julius	SEEDS AND MEDICINAL PLANTS RESEARCH CENTRE, Bamenda	Cameroon
230	McBreairty	Laura	University of Saskatchewan	Canada
231	McGee	Rebecca	USDA-ARS, Washington State University	USA
232	McLaren	Debra	Agriculture and Agri-Food Canada	Canada
233	McMurray	Larn	South Australian research and Development Institute	Canada
234	McPhee	Kevin	North Dakota State University	USA
235	Meier	Kendra	University of Saskatchewan	Canada
236	Mendiola	Javier	University of Delaware	USA
237	Mengistu	Molla	University of Saskatchewan	Canada
238	Metzner	Ralf	Forschungszentrum Juelich	Germany
239	Michel	Ghanem	International Center for Agricultural Research in the Dry Areas (ICARDA)	Belgium
240	Miklas	Phillip	USDA-ARS	USA
241	Mirali	Mahla	U of S	Canada
242	Mishra	Neelu	Indian Institute of Pulses Research	India
243	Mobini	Saeid	Crop Development Center	Canada
244	Mohsenzadeh	Eliza	University of Saskatchewan	Canada
245	Monteros	Maria	Noble Foundation	USA
246	Monyo	Emmanuel	ICRISAT	Kenya
247	Morrall	Robin	University of Saskatchewan	Canada
248	Muehlbauer	Fred	Washington State University	USA

249	Muel	Frederic	CETIOM	France
250	Murray	Jeremy	John Innes Centre Project Leader	United Kingdom
251	Mysore	Kirankumar	The Samuel Roberts Noble Foundation	USA
252	Nadigatla	Ganga Rao	ICRISAT-Nairobi	Kenya
253	Nagaraji	Satish	ICRISAT	India
254	Nandy	Sushmita	Saskatchewan Ministry of Agriculture	Canada
255	Narits	Lea	Estonian Crop Research Institute	Estonia
256	Nath	Rajib	Bidhan Chandra Krishi Viswavidyalaya, MOHANPUR-741252, West Bengal, India.	India
257	Navarro Borrell	Adriana	University of Saskatchewan	Canada
258	Nayyar	Harsh	Panjab University Botany Department Chandigarh India	India
259	Ndjeunga	Jupiter	ICRISAT - Niamey	Niger
260	Nelson	Matthew	The University of Western Australia	Australia
261	Nelson	Rex	United States Dept. of Agriculture, Agricultural Research Service	USA
262	Nyandoro	Ronald	University of Alberta	Canada
263	Odeny	Damaris	ICRISAT Nairobi	Kenya
264	Okori	Patrick	ICRISAT - Malawi	Malawi
265	Olson	Mark	Alberta Agriculture and Rural Development	Canada
266	Ortega	Pedro	INIFAP	Mexico
267	Ozga	Jocelyn	University of Alberta	Canada
268	Pasche	Julie	North Dakota State University	USA
269	Pastor-Corrales	Marcial	USDA/ARS	USA
270	Pasupuleti	Janila	ICRISAT	India
271	Patil	Somanagouda	International Centre for Agricultural Research in the Dry Areas, P.O. Box/6299, Rabat-Instituts, Morocco.	Morocco
272	Pauls	K. Peter	University of Guelph	Canada
273	Penmetsa	R. Varma	University of California at Davis, Dept. of Plant Pathology	USA
274	Perez de la Vega	Marcelino	Universidad de Leon	Spain
275	Perry	Gregory	University of Guelph	Canada
276	Phillip	McClean	North Dakota State University	USA
277	Pilet-Nayel	Marie-Laure	INRA	France
278	Podder	Rajib	University of Saskatchewan	Canada
279	Porch	Timothy	USDA-ARS	Puerto Rico
280	Potts	Carl	Executive Director, SPG	Canada
281	Powell	Tracy	US Agency for International Development, Bureau for Food Security	USA
282	Rachaputi	Rao (RCN)	Queensland Alliance for Agriculture and Food Innovation (QAAFI) The University of Queensland	Australia
283	Rahman	Matiur	International Rice Research Institute – IRRI	Bangladesh
284	Rajendran	Karthika	International Centre for Agricultural Research in the Dry Areas (ICARDA), P.O. Box/6299, Rabat-Instituts, Morocco.	Morocco
285	Rameau	Catherine	INRA	France

286	Ramirez	Milagros	INIFAP	Mexico
287	Ramsay	Larissa	University of Saskatchewan	Canada
288	Rana	Jai Chand	National Bureau of Plant Genetic Resources, Regional Station, Phagli, Shimla - HP	India
289	Ratet	Pascal	Institut des Sciences du végétal, CNRS	France
290	Rathore	Abhishek	ICRISAT, India	India
291	Reynaldo	Yadira	Florida International University	USA
292	Reza	Md Mortuza	University of Saskatchewan	Canada
293	Rezaei	Mohammad	University of Saskatchewan	Canada
294	Risula	Dale	Saskatchewan Ministry of Agriculture	Canada
295	Rodda	Matthew	Department of Environment and Primary Industries, Victoria, Australia	Australia
296	Roorkiwal	Manish	ICRISAT	India
297	Rothwell	Shane	Lancaster University	United Kingdom
298	Rubiales	Diego	Institute for Sustainable Agriculture, CSIC	Spain
299	Rubyogo	Jean Claude	International Center for Tropical Agriculture (CIAT)	Tanzania
300	Rueda	Janice	American Pulse Association	USA
301	Saha	Shyamali	University of Saskatchewan	Canada
302	Sameer Kumar	Chanda Venkata	ICRISAT	India
303	Samineni	Srinivasan	ICRISAT	India
304	Sanderson	Lacey-Anne	University of Saskatchewan	Canada
305	Santalla	Marta	Misión Biológica de Galicia, Consejo Superior de Investigaciones Científicas	Spain
306	Saraf	Meenu	Department of Microbiology and Biotechnology,Gujarat University,Ahmedabad	India
307	Sari	Ehsan	University of Saskatchewan	Canada
308	Sarker	Ashutosh	ICARDA	India
309	Sass	Olaf Andreas Gerhard	Norddeutsche Pflanzenzucht Hans-Georg Lembke KG	Germany
310	Saxena	Rachit	ICRISAT	India
311	Schafleitner	Roland	AVRDC-The World Vegetable Center	Taiwan (ROC)
312	Schlegel	Vicki	University of Nebraska-Lincoln	USA
313	Scholz	Todd	USA Dry Pea & Lentil Council	USA
314	Schroder	Stephan	North Dakota State University Department of Plant Sciences	USA
315	Seetha	Anitha	ICRISAT-Lilongwe	Malawi
316	Sen Gupta	Debjyoti	Ph D candidate, NDSU, Fargo	USA
317	Sharma	Hari	ICRISAT	India
318	Sharma	Kiran	ICRISAT	India
319	Shirtliffe	Steve	University of Saskatchewan	Canada
320	Shunmugam	Arun	University of Saskatchewan	Canada
321	Si	Ping	The University of Western Australia	Australia
322	Siambi	Moses	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT)	Kenya

323	Siddique	Kadambot	The University of Western Australia	Australia
324	Simons	Kristin	North Dakota State University	USA
325	Singh	Narendra	Indian Institute of Pulses Research	India
326	Singh	Renu	Department of Sciences, JCD Memorial College, JCDV, Sirsa, Haryana	India
327	Singh	Sarvjeet	Punjab Agricultural University, Ludhiana, India	India
328	Singhal	Ashish	University of Saskatchewan	Canada
329	Sivachandra Kumar	Nimllash Thangam	University of Saskatchewan	Canada
330	Slater	Susan	University of Saskatchewan	Canada
331	Smitchger	Jamin	Montana State University	USA
332	Smykal	Petr	Palacky University in Olomouc	Czech Republic
333	Soans	Chandrasen	Illumina, Inc.	USA
334	Solorzano	Esteban	UNIVERSIDAD AUTONOMA CHAPINGO	Mexico
335	Souter	Jodi	University of Saskatchewan	Canada
336	Sparvoli	Francesca	Institute of Agricultural Biology and Biotechnology (IBBA), National Research Council (CNR)	Italy
337	Steele	Kelly	Arizona State University	USA
338	Stonehouse	Robert	University of Saskatchewan	Canada
339	Stougaard	Jens	Aarhus University	Denmark
340	Subedi	Maya	University of Saskatchewan	Canada
341	Sudheesh	Shimna	Department of Environment and Primary Industries	Australia
342	Susek	Karolina	Institute of Plant Genetics, Polish Academy of Sciences Department of Genomics Legume Structural and Functional Genomics Team	Poland
343	Szczyglowski	Krzysztof	Agriculture and Agri-Food Canada	Canada
344	Tamo	Manuele	International Institute of Tropical Agriculture (IITA)	Benin
345	Tar'an	Bunyamin	University of Saskatchewan	Canada
346	Tay	Juan	INIA CHILE	Chile
347	Tenuta	Mario	University of Manitoba	Canada
348	Thompson	John	University of Southern Queensland	Australia
349	Thompson	Richard	INRA, UMR1347 AGROECOLOGIE INRA CENTRE DE DIJON	France
350	Thudi	Mahendar	International Crops Research Institute for the Semi-Arid Tropics	India
351	Tian	Jing	Institute of Cereal and Oil Crops, Hebei Academy of Agricultural and Forestry Sciences	China (PRC)
352	Tiffin	Peter	Univ. of Minnesota	USA
353	Tikle	Ashok	Rajamata Vijayaraje Scindia Krishi Vishwa Vidyalaya GWALIOR	India
354	Timmerman-Vaughan	Gail	Plant and Food Research	New Zealand
355	Todd	Christopher	University of Saskatchewan	Canada
356	Toms	Shirley	Senior Research Program Manager, SPG	Canada
357	Tremorin	Denis	Pulse Canada	Canada
358	Tromas	Alexandre	Agriculture and Agri-Food Canada	Canada
359	Trujillo	Diana	University of Minnesota	USA

360	Turner	Fawn	University of Guelph	Canada
361	Udupa	Sripada	International Centre for Agricultural Research in the Dry Areas, P.O. Box/6299, Rabat-Instituts, Morocco	Morocco
362	Upadhyaya	Hari	International Crops Research Institute for the Semi Arid Tropics (ICRISAT)	India
363	Vance	Wendy	School of Veterinary and Life Sciences Murdoch Univeristy	Australia
364	Vandemark	George	United States Department of Agriculture	USA
365	Vandenberg	Bert	University of Saskatchewan	Canada
366	Varshney	Rajeev	ICRISAT, India	India
367	Vasconcelos	Marta Wilton	Escola Superior de Biotecnologia da Universidade Católica Portuguesa	Portugal
368	Vaz Patto	Maria Carlota	ITQB, Instituto de Tecnologia Quimica e Biologica	Portugal
369	Verdier	Jerome	Shanghai Plant Stress Center, CAS	China (PRC)
370	Verma	Neha	University of Saskatchewan	Canada
371	Vijayan	Perumal	University of Saskatchewan	Canada
372	Vinodan	Rajandran	University of Tasmania	Australia
373	Vladimir	Pajic	University of Saskatchewan	Canada
374	von Wettberg	Eric	Florida International University	USA
375	Walker	Jenn	Alberta Pulse Growers	Canada
376	Walley	Fran	Dept. Soil Science University of Saskatchewan	Canada
377	Wang	Ning	Canadian Grain Commission	Canada
378	Wang	Shuping	ShanDong Shofine Seed Technology Co.Ltd.	China (PRC)
379	Wang	Jianping	University of Florida	USA
380	Warale	Rushikesh	University of Saskatchewan	Canada
381	Warkentin	Tom	University of Saskatchewan	Canada
382	Weeden	Norman	Montana State University	USA
383	Weller	Jim	University of Tasmania School of Biological Sciences	Australia
384	Wen	Jiangqi	The Samuel Roberts Noble Foundation	USA
385	Widders	Irvin	Legume Innovation Lab Michigan State University	USA
386	Wiesinger	Jason	USDA-ARS, Michigan State University	USA
387	Wijesinghe	Avanthi	University of Saskatchewan	Canada
388	Wilker	Jennifer	University of Guelph	Canada
389	Wisler	Gail	United States Department of Agriculture	USA
390	Wolde-Meskel	Endalkachew	N2Africa Project (Hawassa University)	Ethiopia
391	Wolko	Bogdan	Institute of Plant Genetics, Polish Academy of Sciences Legume Structural and Functional Genomics Team	Poland
392	Wong	Melissa	University of Saskatchewan	Canada
393	Woo	Sheridan	University of Naples "Federico II", Department of Agriculture, Section of Biology and Protection of Agricultural and Forest Systems	Italy
394	Wood	Jennifer	NSW Department of Primary Industries	Australia
395	Yang	Aijun	CSIRO Plant Industry	Australia
396	Yang	Shi	University of Adelaide	Australia

397	Yang	Chao		Canada
398	Yang	Kai	College of Plant Science and Technology , Beijing University of Agriculture	China (PRC)
399	Yang	Tianquan	Xishuangbanna Tropical Botanical Garden, Chinese Academy of Sciences	China (PRC)
400	Young	Nevin	Department of Plant Pathology Department of Plant Biology University of Minnesota	USA
401	Youssef	Chvan	Grande école: Agrocampus ouest- Angers- France	France
402	Yu Hua	He	Yunnan Academy of Agricultural Sciences	China (PRC)
403	Yuan	Hai Ying	Crop Development Centre, University of Saskatchewan	Canada
404	Yuliasti	Yuliasti	Center of Application Isotopes Radiation- National Nuclear Energy Agency of Indonesia	Indonesia
405	Zahradka	Peter	University of Manitoba/Canadian Centre for Agri-Food Research in Health and Medicine	Canada
406	Zhang	Xinyu	Department of Plant Agriculture, University of Guelph	Canada
407	Zhou	Qixing	Crop Diversification Centre North, Alberta Agriculturea and Rural Development	Canada
408	Zhu	Hongyan	University of Kentucky	USA
409	Zou	Xiaolu	Southern crop protection and food research center, Agriculture and Agri-Food Canada	Canada

Compiled by Bunyamin Tar'an