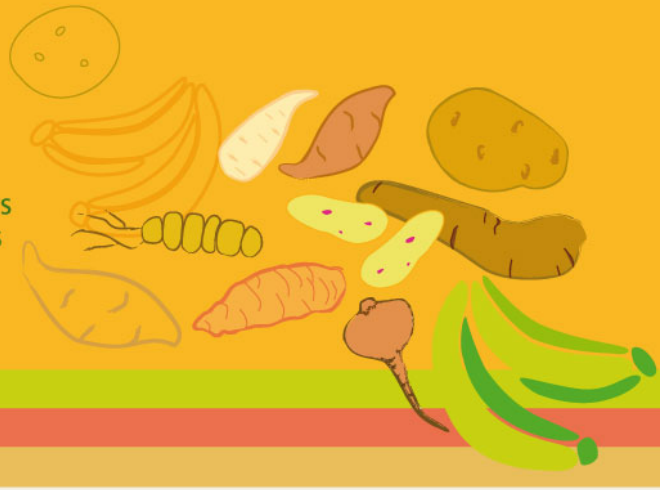
RESEARCH PROGRAM ON Climate Change, Agriculture and Food Security

RESEARCH PROGRAM ON Roots, Tubers and Bananas



# Workshop report:
## Scientific Review and Planning Workshop

### Management of critical pests and diseases through enhanced risk assessment and surveillance and understanding of climate impacts through enhanced modeling

**February** 2013

CIP · Bioversity International · CIAT · IITA · ICRISAT · IRRI · icipe

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The workshop was conducted with the active participation of scientists from the following CG- and affiliated centers as well as from international organizations and universities:

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Workshop Reports aim to disseminate interim climate change, agriculture and food security research and practices and stimulate feedback from the scientific community.

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RTB is a broad alliance of research-for-development stakeholders and partners. Our shared purpose is to exploit the potential of root, tuber, and banana crops for improving nutrition and food security, increasing income and fostering greater gender equity– especially amongst the world's poorest and most vulnerable populations.

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**Acronyms**

| | |
|---|---|
| AI: | Activity index |
| BBTD: | Banana bunchy top disease |
| BMZ: | German Federal Ministry for Economic Cooperation and Development |
| BXW: | Banana Xanthomonas wilt |
| CABI: | Commonwealth Agricultural Bureau International |
| CBSD: | Cassava Brown Streak Disease |
| CCAFS: | CGIAR Research Program on Climate Change, Agriculture and Food Security |
| CC-PD-YLD: | Climate Change Plant Disease Yield Model |
| CG: | Consultative Group |
| CGIAR: | Consultative Group on International Agricultural Research |
| CIAT | International Center for Tropical Agriculture |
| CIDA: | Canadian International Development Agency |
| CIP: | International Potato Center (Centro Internacional de la Papa) |
| CIMMYT: | International Maize and Wheat Improvement Center |
| CLIMEX: | Climate and Population Modeling Software |
| CMD: | Cassava Mosaic Disease |
| GRISP: | Global Rice Science Partnership |
| RTB: | CGIAR Research Program on Roots, Tubers and Bananas |
| CWBD: | Cassava Witches Broom Disease |
| DANIDA: | Danish International Development Agency |
| DNA: | Deoxyribonucleic acid |
| DRC: | Democratic Republic of Congo |
| ELISA: | Enzyme-Linked-Immuno Sorbant-Assay |
| EPPO: | European and Mediterranean Plant Protection Organization |
| ESSP: | Earth System Science Partnership |
| EI: | Ecoclimatic Index |
| ERI: | Establishment risk index |
| EU: | European Union |
| FAO: | Food and Agriculture Organization of the United Nations |
| FERA: | The Food and Environment Research Agency, UK |
| Foc TR4: | Tropcial Race 4 of *Fusarium oxysporum* f.sp. *cubense* |
| GI: | Generation index |
| GIS: | Geographic Information System |
| GPC: | Global Plant Clinic |
| GPS: | Geographic Position System |
| IAPSC: | Inter-African Phytosanitary Council |
| *Icipe*: | International Centre of Insect Physiology and Ecology |
| ICRISAT: | International Crops Research Institute for the Semi-Arid Tropics |
| IFAD: | International Fund for Agricultural Development |
| IITA | International Institute of Tropical Agriculture |
| ILCYM: | Insect Life Cycle Modeling (software) |
| IPDN: | International Plant Diagnostic Network |
| IPPC: | International Plant Protection Convention |
| IRRI: | International Rice Research Center |
| ISPMs: | International Standards for Phytosanitary Measures |
| IWMI: | International Water Management Institute |

| | |
|---|---|
| KSU: | Kansas State University |
| LB: | Late Blight |
| LAMP: | Loop Mediated Isothermal Amplification |
| NARES: | National Agriculture Research and Extension Services |
| NASA/POWER: | National Aeronautics and Space Administration Project on the Prediction of Worldwide Energy Resource |
| NPPO: | National Plant Protection Organizations |
| NDL: | National Diagnostic Laboratories |
| OSU: | Ohio State University |
| PRA: | Pest Risk Analysis |
| PCR: | Polimerase Chain Reaction |
| PLRV: | Potato Leave Roll Virus |
| PROMUSA: | Mobilizing Banana Science for Sustainable Livelihood |
| PVX: | Potato Virus X |
| PVY: | Potato Virus Y |
| RNA: | Ribonucleic acid |
| RPPO: | Regional Plant Protection Organizations |
| Rs: | *Ralstonia solanacearum* |
| RTB: | Roots, Tubers and Bananas |
| SDD: | Species Distribution Data |
| SLU: | Swedish University of Agricultural Science |
| S & SE Asia: | South & Southeast Asia |
| SMS: | Short Message Service |
| SPVD: | Sweet Potato Virus Diseases |
| SVM: | Support Vector Machines |
| UC Davis: | University of California Davis |
| USAID: | United States Agency for International Development |
| USDA-FAS: | United States Department of Agriculture-Foreign Agricultural Service |
| VCG: | Vegetative Compatibility Groups |
| VD: | Virus Diseases |
| WTO-SPS: | World Trade Organization Agreement on the Application of Sanitary and Phytosanitary Measures |

**Abstract**

The workshop was conducted from 10-14 December, 2012 at the International Potato Center, Lima, Peru. It was jointly funded by the research programs on Roots, Tubers, and Banana (RTB) and on Climate Change, Agriculture and Food Security (CCAFS). The workshop successfully linked scientists from CG-Centers (Bioversity, CIAT, CIMMYT, CIP, ICRISAT, IITA, and IRRI) and other stakeholders (CABI, FAO, FERA, *icipe*, UC Davis, University of Leeds, Kansas State University, Ohio State University) working in pest and disease management. Discussions focused on challenges and opportunities to synergize expertise towards improving risk assessments of pests and diseases under current and changing climates in order to target surveillance initiatives as well as to share experiences and develop joint modeling approaches to better understand the effects of climate change on agricultural pests, diseases and crop losses.

The first two days involved a scientific review with 37 presentations covering themes on target pests and diseases, risk assessment, surveillance strategies, modeling under current and future climates, detection and diagnosis, data management and reporting. Intensive group and plenary discussions followed that reached consensus on a harmonized science based framework and planning document for cross-cutting research across CGIAR Research Program 3.4 and CCAFS. A priority list of pests and diseases for RTBs was identified for the development of Pest Risk Analysis (PRA) documents. PRAs are advocated by the International Plant Protection Convention (IPPC) as a dynamic document to which all existing and newly recorded information can be housed and shared to guide International Standards for Phytosanitary Measures (ISPMs). Common modeling tools will be used and system level frameworks established to extend global pest and disease models and improve predictions of risks under climate change. Joint endeavors were discussed to link pest and disease models to crop models as well as to compile shared databanks to house data in appropriate formats for modeling.

Collaborative efforts will be concentrated in pilot sites for which primarily the Kivu region in Sub-Saharan Africa (Burundi, eastern DRC, Rwanda, North-western Tanzania and western Uganda) was identified but sites in Asia for specific banana diseases were also highlighted. This will comprise studies on the current distribution and impact of pests and diseases on RTB and other crops and the application of modeling tools to predict changes under different climates. Predictions will be used to inform and support policy makers in the preparation of national and regional adaptation plans, which will include the development of harmonized protocols for targeted surveillance, sampling and diagnostics. Capacity will be built in national institutions to facilitate the pre-emptive implementation of effective integrated pest and disease management practices to limit spread and new introductions due to increased globalization of trade, human movement and climate change.

This joint workshop was successful at harmonizing different research programs in order to use resources more efficiently and share precious knowledge and experience across CGIAR centers and their partners. The result was to develop an authoritative and synergized logframe with clear products, milestones and outcomes. Further, the foundation has been built for joint proposal development to RTB, CCAFS and for bilateral funded research projects.

**Key words:** *Pest and disease risk assessment, climate change, pest and disease modeling, crop losses, harmonized protocols for surveillance, sampling and diagnostics, networks*

**Acknowledgement**

The financial support provided by the CGIAR research programs CCAFS and RTB is gratefully acknowledged to organize this joint workshop, which allowed discussing and developing a challenging cross-cutting research program among centers and its partners. The workshop organizers are grateful to the invited participants, namely Michael Robson, Andrew Challinor, Karen Garrett, Timothy Holmes, Sally Miller, Orlando Sosa, Julian Smith, and Corinne Valdivia, who made excellent contributions to the scientific review and stimulating our discussions and research planning. Likewise, the participation and contribution from our partners at *icipe* is highly acknowledged. Further, we are thankful to Sonia Santivanez and Diana Salazar for their great logistical support to organize and conduct this workshop.

## 1. Introduction

Within the new structure of the Consultative Group on International Agricultural Research (CGIAR), new defined Research Programs should bring together the research synergies, strengths, and resources from multiple centers to increase efficiencies and enhance impacts in achieving global development goals. The **Roots, Tubers, and Bananas Research Program** (RTB Research Program) is one of these initiatives; it is led by the International Potato Center (CIP) together with its sister centers Bioversity International, International Center for Tropical Agriculture (CIAT), and the International Institute for Tropical Agriculture (IITA). The Research Program on **Climate Change, Agriculture and Food Security** (CCAFS) is led by CIAT. It seeks to overcome the threats to agriculture and food security in a changing climate; exploring new ways of helping vulnerable rural communities adjust to global changes in climate. The approach of CCAFS is to bring together the world's best researchers in agricultural science, climate science, environmental and social sciences to identify and address the most important interactions, synergies and trade-offs between climate change and agriculture.

Endemic and non-endemic pests and plant pathogens are a major threat to the productivity of Roots, Tubers and Bananas (RTB) and all other mandate crops of the CGIAR as systems adapt to changing global needs. These threats persistently challenge food security, income generation and trade with cropping intensification, increased human mobility and climate change challenging our ability to manage plant health. Assessment and forecasting of future shifts in the distribution and impact of plant pests and pathogens combined with early and accurate diagnoses and surveillance at local, regional, and global scales are necessary to deploy pre-emptive mitigation strategies.

The objective of the scientific review and planning workshop was to contribute to:

- Link experts in pest and pathogen ecology, epidemiology, risk analysis, modeling and mapping, detection and surveillance, trade regulations etc. across the globe to identify scientific challenges, to review available resources and set priorities, and to create synergies between CG centers and other stakeholders to efficiently address the challenges of pest risks assessments and surveillance under a changing climate.
- Establish a priority list of pests and pathogens through evaluation of their risk to food security and income generation.
- Develop new modeling tools addressing the effects of climate change on agricultural pests and diseases, and especially assemble and evaluate a general platform for pest and disease risk assessments under climate change.
- Identify and recommend appropriate methods for diagnostics, risk assessments and surveillance.
- Develop a harmonized and shared science based framework and planning document (MTP) for pests and disease risk assessment and modeling and surveillance research that identifies major research products, milestones, and outcomes, target regions, countries and key research teams for future collaborative research and capacity building initiatives.

**2. Scientific review summary**

During the scientific review workshop, a total of 37 presentations were given covering themes on target pests and diseases, risk assessment, surveillance strategies, modeling under current and future climates, detection and diagnosis, data management and reporting (see annex 7.1).

**2.1 Root, tuber and banana target pests and diseases**

A wide range of fungal, viral and bacterial diseases and invertebrate pests affect root, tuber, banana, and plantain (*Musa* spp.) production worldwide. Key pests and diseases may be geographically local while others may have a broader global bearing. Those established in particular areas are undoubtedly of concern, which need to be managed appropriately. However, great concern arises from the potential risk of the introduction into important production regions, where pests and diseases of significance elsewhere, are absent. In some cases pests and diseases present in the centers of origin of the various crops, where they may not be significant constraints where natural suppression through host genetic variability and resistance, and biological means maintain their impact within acceptable thresholds, but may pose significant and as yet unknown threats elsewhere.

A particular threat from Asia for banana is posed by Fusarium wilt (*Fusarium oxysporum* f.sp. *cubense*, *Foc*), Tropical Race 4 (TR4). Currently TR4 is spreading from Southeast Asia and Australia to China and beyond. *Mycosphaerella eumusa* causing banana leaf spot in India and Sri Lanka and Freckle disease caused by *Guignardia musae* are two emerging fungal diseases of importance in the region. Key virus diseases to be aware of include Banana bunchy top disease (BBTD) and banana bract mosaic. Moko and Bugtok, caused by *Ralstonia solanacearum*, are serious banana bacterial diseases but so far limited to the Philippines, while Blood Disease, caused by *Pseudomonas celebensis* (taxonomic identity is being established), are causing epidemics in Indonesia and Malaysia. In Africa, an indigenous bacterium that is spreading across the great lakes region and devastating production is Xanthomonas Wilt (*Xanthomonas campestris* pv. *musacearum*) while *Ralstonia solanacearum* Race 2, that causes Moko disease, is currently restricted to Australia, South Pacific and Latin America. Weevils tend to be the major insect pests affecting banana, while nematodes of various species continue to limit productivity globally.

Although the cassava pest complex is large, the most limiting pests are mites, mealybugs and whiteflies. The recent introduction of cassava mealybugs and mites in Southeast Asia is a cause for concern. Whiteflies (*Bemisia tabaci*) are widely spread pests, directly affecting cassava and acting as virus vectors. Their importance varies between different regions and continents. However, their major risk refers to their capacity to transmit several cassava-related viruses. *Meloidogyne* spp. are likely the key nematode pests affecting all cassava growing regions, but to an unquantified and likely underestimated extent. Several diseases caused by viruses, fungi, bacteria, phytoplasma are also of significant concern. Cassava mosaic disease, Cassava brown streak disease and Cassava frog skin disease are significant among diseases, while antholysis, Super Elongation (*Sphaceloma manihoticola*), and witches broom (Phytoplasma) and Sri Lankan Mosaic Virus from South Asia offer a potential threat elsewhere.

Potato producing farmers in developing countries worldwide contend with about 20 insect pests. The potato tuber moth, *Phthorimaea operculella*, is highly invasive and considered the most damaging potato pest, while the Andean potato tuber moth, *Symmetrischema tangolias,* is less invasive and mostly distributed in the Andean region. Other invasive pests of concern are the Guatemalan potato tuber moth, *Tecia solanivora,* which has so far spread across S America, and reached the Canary Islands. The leaf miner fly *Liriomyza huidobrenis*, is now reported from 66 countries and the bud midge, *Prodiplosis longifilia,* is likely to become more invasive under climate change. The green peach aphid (*Myzus persicae*), the potato aphid (*Macrosiphum euporbiae*) and cutworms (*Agrotis* spp.) occur worldwide and are a key risk for virus infection. The Colorado potato beetle, *Leptinotarsa decemlineata*, which originated in central Mexico, has become the main threat to potato production in developing countries of Central Asia, through to China. The potato cyst nematodes (*Globodera rostochiensis* and *G. pallida*), indigenous to South America, are yet to gain a foothold in Africa and Asia, but would cause significant damage, as demonstrated in Europe, should they become established. Root knot nematodes (*Meloidogyne* spp.) however cause significant damage and affect seed health and quality across potato growing regions, especially in Africa and Asia, where the situation is little understood, along with other damaging nematode species, such as *Ditylenchus* spp. Regarding the large number of pathogens reported from potato, just a few are generally considered the primary agents of disease worldwide. One of the primary potato diseases is late blight caused by *Phytophthora infestans.* The soil- and seed-borne pathogen *Ralstonia solanacearum,* which causes bacterial wilt, is serious in many parts of the developing world, particularly in warm, humid areas. Similarly, a number of viruses also accumulate through generations and participate in seed degeneration; the most important seed degeneration viruses are PVY and PLRV, and to a lesser extent PVX. Others are also widespread and may contribute to degeneration of potatoes, but their presence in developing countries remains poorly quantified. As with bacterial wilt, several other pathogens may be seed- and soil-borne pathogens (e.g. *Rhizoctonia solani, Streptomyces* spp*.* and *Clavibacter michiganensis* subsp. *sepedonicus*) and may participate in seed degeneration, which overall is probably the main biotic constraint to potato productivity in developing countries. The bacterial complex of black leg and soft rot caused by *Pectobacterium* spp. and *Dickeya* spp. can be severe under conducive environmental conditions.

For sweetpotato**,** weevils (*Cylas* spp.) are the most serious insect pests in Central America, Africa and Asia; *C. formicarius* is found globally, whereas *C. puncticollis* and *C. brunneus* are reported only from Africa. These are considered as the main target pests although a large complex of pests may occur regionally, e.g. in East Africa consisting of stem and root feeders defoliators, and virus vectors. Nematodes, particularly *Meloidogyne* spp. and *Rotylenchulus* spp., are a significant problem in many sweetpotato producing areas, but are often overlooked or misdiagnosed. The major disease problem of sweetpotato globally results from viruses, which often occur in a complex reducing yield considerably. Of about 30 known sweetpotato infecting viruses the most widespread are Sweet potato feathery mottle virus and Sweet potato virus C, and Sweet potato chlorotic stunt virus. Sweetpotato begomoviruses or 'sweepoviruses' have recently been found to be common worldwide, but remain relatively little studied. Numerous bacteria and fungi, including *Ceratocystis fimbriata, Altenaria bataticola, Elsinoe batatas, Fusarium solani, F. oxysporum, R. solanacearum, Rhizopus stolonifer, Diplodia gossypina*, *Macrophomina phaseolina, Streptomyces ipomoeae, Dickeya* spp*.* and *E. chrysanthemi* have also been reported to cause various types of root or stem rot diseases or foliar blemishes, although they are much less important on a global scale and/or only important locally.

Yam (*Dioscorea* spp.) is a favoured staple crop in West Africa, gaining in importance in Asia and Americas. Various pests and disease affect this crop of which viruses are a particular threat, especially for seed degeneration. Anthracnose (*Colletotrichum gloeosporioides*) can be especially destructive to susceptible cultivars. The yam nematode, *Scutellonema bradys*, endemic to West Africa, and *Pratylenchus coffeae* in Central America cause serious damage to tubers, especially during storage, which leads to seed degeneration. *Meloidogyne* spp. nematodes are prevalent across yam growing regions and lead to quality and production losses.

### 2.2 Pest, disease and weed risk assessments and modeling under current and future climates

#### 2.2.1 Crop modeling

Crop models used in combination with climate models can help to predict future changes in growing conditions and crop yield due to climate change. One approach is to predict a plausible impact of climate change on crop production in a given year in the future, using a climate change scenario, which is a set of assumptions about drivers of future global emissions. Modeling exercises have had success in exploring plausible climate change impacts, increasingly using ensemble methods and crop model inter-comparisons to address uncertainty. Uncertainty remains about a number of aspects, including the implications of downscaling and climate model bias, as well as the speed with which climate change will occur, which depends on different scenarios of emissions. It is also possible to explore how agricultural systems adapt to a gradient of climate change, regardless of the exact timing of change.

To improve crop modeling effort to estimate impacts of climate change, adaptation options and responses to climate variability, integration with pest models is important. Crop losses due to insects are a major way in which climate change will have an impact on agricultural productivity. Mechanistic and empirical (statistical, machine learning) approaches can be combined to achieve this integration (Colbach, 2010). Fuzzy logic or similar rule-based approaches could be used to process inputs from insect and crop models to map changes in a relatively simple way.

On the other hand, also mechanistic methods are necessary. Some models have been proposed to integrate crop and insect simulation, but little in terms of a generic model has been achieved and for many crops and pests such models are not available.

### 2.2.2 Disease modeling

Two basic types of plant disease models exist that are of interest in relation to climate change studies. The first comprises plant disease forecasters where information about disease outbreaks or an increase in intensity based on information about the weather or climate, crop and pathogen. Some of the oldest of these models forecast potato late blight and have been evolving for almost a century (Van Everdingen, 1926; Beaumont, 1947), generally drawing on temperature and humidity as the most important predictors. However, newer approaches more suited to work with climate change have been developed, such as metamodeling as developed by Sparks et al. (2011). The second type of plant disease model considered is crop loss models. Typically these models are closely related to crop growth models and may indeed have a crop growth model component within them, e.g. RICEPEST (Willocquet et al. 2000; 2002) and WHEATPEST (Willocquet et al. 2008). Both types of models are instructive when considering climate change; the first group of models can be used as predictors for changes in disease intensity due to climate and other changes that can be incorporated into the model. These results can be used to identify future disease hot spots and help instruct strategic decisions. The second group can be used with results from the first to look at the possible changes in yield losses and effects of control methods. The International Potato Center (CIP) and partners have used both conventional forecasting models (Hijmanns et al. 2000) and the metamodeling approach of Sparks et al. (2011) to evaluate the effects of climate change on potato late blight at different spatial scales and globally. The International Rice Research Institute (IRRI) has used the crop loss models mentioned above to study climate change effects on rice and wheat cropping systems.

### 2.2.3 Insect pest modeling

Changes in temperature and humidity are perceived as the two most important climatic factors expected to affect insect development, reproduction and survival. This might lead to range expansion of a native pest into new areas, as well as increased damage potential from invasive alien species. There are also potential negative effects of increasing temperatures on the expression of host plant resistance, including the expression of transgenes. Furthermore, it is expected that climate change may influence established biological control by de-regulating natural enemy-pest interactions, because of a higher sensitivity of higher trophic levels to climatic variability or of different temperature optima compared with pests. Different modeling approaches to capture these changes and predict various scenarios were presented. While none of the models can be considered perfect in fitting all the needs, there are multiple ways in modeling the distribution of insect species under different climate scenarios.

The Insect Life Cycle Modeling (ILCYM) software developed by CIP is a platform requiring minimal user induction (Sporleder et al., 2013; Tonnang et al., 2012). ILCYM supports the development of process-based temperature-driven and age-stage structured insect phenology models and applies these models in a GIS environment for insect species distribution and risk mapping. For studying the effects of climate change on insects, the software provides downscaled future climate scenarios from different projections and has been used to predict potential impacts on the risk and future distribution of the potato tuber moth, *Phthorimaea operculella* (Kroschel et al., 2013). The CLIMEX software is a flexible modeling and mapping tool used to estimate the climatic suitability for a species based on observations of the geographical distribution and seasonal abundance, and on the species' growth response under experimentally manipulated conditions. The climatic suitability is measured through the Ecoclimatic Index (EI), which reflects the annual balance between population growth during favorable seasons and mortality during unfavorable seasons. Basically, the population growth is calculated based on temperature, moisture and light indices and the mortality on extremely cold, dry, hot and wet conditions. CLIMEX is an appropriate alternative for species, which do not have comprehensive lifecycle data generated or available (Suthers and Maywald, 2005; Parsa et al., 2012; Jaramillo et al., 2011).

Other tools like MaxEnt and Support Vector Machines (SVM) are based on the interaction of occurrence records of species (presence-only) and the environment (features). MaxEnt estimates the probability of presence of species conditioned by the environment, based on a maximum entropy probability distribution; meanwhile, SVM is a useful technique for data classification based on supervised learning methods (kernel). These methods have demonstrated success across a wide taxonomic range. They are very useful as a first approximation to the understanding of the distribution of the species, when there is not enough knowledge of the lifecycle and the biology of the species. Considering the existence of a multitude of tools, it was agreed that at least three software packages will be selected and individually applied for each insect in order to derive an 'ensemble model'. Another suggestion was to use published information as input data into ILCYM.

#### 2.2.4 Platform for pest and disease risk assessments under climate change

Common features of platforms where discussed to support risk assessment under climate change, as described also in a scoping study recently prepared for CCAFS and which is under revision by workshop participants for joint publication. For example, ILCYM provides a platform for accessing relevant weather variables from baseline and future climate scenarios, and using these as input for models of insect responses to weather variables. IRRI also developed weather and climate databases. Other components of a platform include general frameworks for construction of decision support systems to support climate change adaptation and further support the potential for index insurance to buffer farmer exposure to risk under climate change

### 2.3 Risk based surveillance

Orlando Sosa presented the global regulatory framework of the International Plant Protection Convention (IPPC). The IPPC, with its secretariat at FAO, is an international agreement on plant health with 177 current signatories that aims to protect cultivated and wild plants by preventing the introduction and spread of pests. The governing body – the Commission on Phytosanitary Measures - adopts International Standards for Phytosanitary Measures (ISPMs), which are recognized by the WTO-SPS agreement. The IPPC uses Pest Risk Analysis (PRA) as the basis by which countries prepare the requirements to trade commodities and protect plant resources. PRAs underscore the importance of surveillance and diagnostics and the preparation of national lists of regulated pests. Mike Robson of the Plant Production and Protection Division in FAO outlined the main drivers of pest and disease spread, including weather/climate, production practices, "biological events" and movement of material (including through trade). Pest and disease constraints need to be addressed in an integrated manner (from crop selection, land preparation and planting; water availability; soil fertility management; weed management etc.) within diverse cropping systems by the farmer, with least collateral impact on the environment/natural resources. These integrated approaches might involve improved or resistant varieties, biological control of pests, cultural control (such as changing planting times, removing alternate hosts, and rogueing) or chemical control with less hazardous chemical products. Climate change is just one of the many driving forces alongside land use management, cropping systems, inappropriate use of pesticides, abiotic stresses, pest evolution etc. To safeguard food security; risk based surveillance must consider communities that are most vulnerable, due to their dependence on particular cropping systems, and must be supported by policy makers. Julian Smith, FERA UK, further developed discussions based on what policies are being addressed by risk based surveillance and what level of confidence is required to satisfy those policies. Careful attention is needed to decide how risk based surveillance is deployed when there are cost, labor and technical implications associated with sampling and testing, both spatially and temporally. For example: absence of a pest in seed to satisfy certification schemes, or surveys to establish pest prevalence and spread, or testing for mycotoxins distributed heterogeneously in traded products; are affected by the ease in which the target can be diagnosed/detected, and the availability of technical capacity and funds.

### 2.4 Current surveillance strategies

Gus Molina of Bioversity highlighted that for banana early diagnoses of pests and diseases was critical in preventing pathogen dissemination and to preclude incursions. Focusing on the quarantine pathogen tropical race 4 (TR4) of *Fusarium oxysporum* f.sp. *cubense* (*Foc*), the causal agent of Fusarium wilt of bananas; a molecular diagnostic method has been developed to enable detection in symptomatic and asymptomatic banana, soil and water. Further, characterisation of the pathogen present in Asia into different Vegetative Compatibility Groups (VCG) has been achieved. VCG1213/16 comprises TR4 and was shown to be the dominant VCG from samples collected in China, Indonesia, Malaysia, Philippines, and Taiwan. In order, to increase capacity for early detection in countries where TR4 does not yet exist, awareness campaigns and training courses on diagnosis, surveillance and management of TR4 have been initiated in Latin and South America. These results are a key step towards designing policies and measures to prevent further spread of TR4 through effective quarantine measures and targeted surveillance. Jan Kreuze of CIP highlighted that for potato and sweet potato several diseases and insect pests had been historically monitored. In fact, at CIP's inception a number of countrywide disease surveys by expert consultants were commissioned and remain today the only geographic record of a number of diseases. Surveillance efforts have targeted the critically important pathogen; *Phytophthora infestans*, the causal agent of late blight. Within the context of the global initiative on late blight, major pathogen strains have been mapped and more recently there have been efforts to link with the Euroblight initiative. There are a myriad of viruses that effect sweet potato in Africa so diagnoses are being done using a novel technology based on siRNA sequencing to assemble 'viromes'. This shows viral diversity and variability across the continent which can be used to define containment measures and guide further research into impact and significance of identified viral entities. Surveys have been used to determine the incidence and effect of insect pests of potato and sweet potato and to identify natural enemies e.g. spread from introductions in Kenya of *Copidosoma koehleri,* a parasitoid of the potato tuber moth (*Phthorimaea operculella*), and also secondary pests, that have been previously overlooked e.g. leafminer fly (*Liriomyza huidobrensis*) in Nepal. Fen Beed of IITA focused more on practical mechanisms for surveillance in Africa and how to target surveillance activities when resources are limited. Topics covered included the design and implementation of spatial surveys to represent landscapes, production of easy to interpret GIS maps, interpolation of GPS linked datasets, going public exercises, media based awareness campaigns, community based actions, use of SMS alerts and Java based surveys for mobile phones, farmer field schools and how these can be feasibly and sustainably supported by appropriate (rapid, precise and practical) diagnostic capacities. It was recognized that many surveillance schemes were instigated by discrete projects, specific to certain diseases, crops and locations. For CGIAR

Research Program 3.4 future surveillance strategies should focus on minimizing the risk of exotic diseases becoming introduced or new variants of existing diseases becoming established.

**2.5 Detection and diagnostics**

A set of presentations was made spanning from traditional symptom recognition based methods mediated by mobile plant clinics to classical techniques ranging from the use of microscopy, ELISA, culturing and pathogenicity tests, through to novel methods such as isothermal amplification methods (LAMP), microarrays and massive parallel sequencing approaches.

Plantwise (formerly Global Plant Clinic, GPC) helps developing countries to establish an integrated plant health system. This system links the farmer with an integrated support network, consisting of input suppliers (e.g. pesticide manufacturers), diagnostic laboratories, researchers, national plant protection organizations (NPPOs) and policy makers. Plantwise clinics are made accessible to farmers by holding them on a regular basis in a prominent local meeting place, such as a market. When the farmer has a problem with a crop, he/she can bring a sample along to the plant clinic. At the clinic a trained 'plant doctor' listens to the farmer, examines the sample, diagnoses the problem based on visual symptoms and signs and offers a suggested treatment. Diagnosis is not always straightforward. Plantwise helps link clinics with diagnostic laboratories and other resources they need. A free service is available for eligible clients in developing countries. The service, based at CABI in the UK, receives more than 500 samples each year from more than 80 countries. Plantwise is closely involved in surveillance and identification of new diseases and has published 31 new disease records with its global partners since 2001, 11 from Africa alone.

In the laboratory, classical techniques range from the use of microscopy to culturing and pathogenicity tests. Most classical laboratory methods require a great deal of experience on the part of the practitioner, and may be very time- and space-consuming. Serological assays have been used for diagnosis of diseases caused by viruses for so long that they may be considered “classical”, and are important tools in the field and laboratory. New formats such as lateral flow devices have made point of care field diagnosis of diseases feasible, but are still limited regarding sensitivity and lack of available antibodies for all diseases. Still, improved selective media, diagnostic reference materials such as on-line image libraries and Lucid keys, and laptop- and smartphone-based microscopes are among the innovations in classical methods that continue to improve the speed and quality of plant pathogen diagnostics. Experiences with the use of pictures taken by farmers using smartphones has generally not been very successful due to the low quality of the pictures taken.

PCR based methods (including real-time, degenerate and multiplex) have gained a prominent place in pest diagnostics over the last 25 years and have proven robust and sensitive in identifying known and in some cases new pests under laboratory conditions. However, whilst we have become increasingly competent at laboratory diagnostics for known pathogens, we have struggled to achieve the same levels of specificity and sensitivity with field diagnostics, where ELISA-based technologies have been foremost retained. Loop Mediated Isothermal Amplification (LAMP) is essentially the same as PCR in that it relies on primers designed to target and amplify nucleic acid sequence, but differs in one major area in that the amplification reaction proceeds at a steady temperature (~60°C); as opposed to PCR cycling. As an outcome of this difference the infrastructure needed to support LAMP is much less, limited to a hot block or low cost re-usable heat-packs. Reagents can be lyophilized and the products of LAMP can be viewed on a gel, or on a dipstick styled Lateral Flow Device, and thus the diagnostics can be performed in a lab of basic infrastructure or in a field. Several examples of LAMP based technologies were provided. The challenges to bring the technology to field use rely on optimizing the way of detecting positive reactions (closed tube system to avoid contamination) and developing of simple enough nucleic acid extractions that can be used under field conditions. A new small low-cost device called Gene-Z, was presented, which is a new, simple, low-cost, hand-held platform for diagnosing emerging infectious diseases caused by plant pathogens, such as fungi, bacteria and virus. This portable isothermal platform is operated by an iPod Touch or Google Android tablet. It is uses micro-fluidic chips with dehydrated primers for isothermal amplification (such as LAMP) enabling the simultaneous testing of 4 samples for 15 different components each.

DNA barcoding is a taxonomic method that uses a short genetic marker, amplified by PCR by generic primers, in an organism's DNA, the sequence of which is used as a molecular 'barcode', to identify it as belonging to a particular species. DNA barcoding has arisen as a robust and standardized approach to species identification, and has recently been applied to identifying plant pests and diseases. Although DNA barcoding is a powerful tool, circumventing the need for ever rarer specialized taxonomist to identify pest species, experience has shown it is still limited by lack of verified and curated barcode sequences for most important pests and a relatively complex and expensive procedure, limiting its application to specialized laboratories.

The power of nucleic sequencing has transformed over the past 5 years. What used to take weeks, months or years is now achievable in hours and days. Commonly referred to as a next generation sequencing (NGS), one application is the unbiased amplification of nucleic acid sequence that is present in a sample that can then be interrogated for 'signature sequences' of interest. This approach may be used to identify the signatures of unknown pests without recourse for a priori knowledge. Several examples from CIP and FERA were presented. The power of modern high throughput DNA sequencers is now also enabling a new generation of virological studies in which metagenomes of ecosystems can be determined to understand evolution and variability of viruses. Work where the technology is used to determine the 'virome' of sweetpotato throughout Africa was presented. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. Such technologies however are still too expensive and knowledge intensive to be applied by most national diagnostic laboratories (NDL).

Platforms for the sensitive detection of multiple viruses at the same time such as microarrays may be practical and efficient solutions for NDLs with the need to test many plants against many viruses with sufficient sensitivity. ClonDiag tube arrays are able to detect up to 80 features with sensitivity approximating PCR and require only a cheap scanner or can even be read by smartphone pictures. Preliminary results for potato and sweetpotato were presented.

### 2.6 Data management and reporting

Risk assessment and surveillance efforts routinely generate, or utilize, volumes of relatively homogenous data with the potential to streamline preventive efforts in pest and disease management. Species distribution data (SDD) ranks foremost in importance among them. CABI's Crop Protection Compendium is the most comprehensive pest and disease SDD database available to date, and it is freely accessible online via the CABI's Plantwise knowledge bank. Additional data of relevance to prevention efforts include pest phenology data and climate station data; both routinely used to model species distributions, predicting climatic suitability for the establishment of a species.

SDD is gathered by multiple mechanisms. CABI's plant doctors, for example, passively receive samples of diseased plants or insects to provide diagnostic and advice. Their observations are then recorded in a database with approximate location data. Most common, however, is active surveillance, conducted by one or more experts with more specific monitoring goals (e.g., monitoring the invasion of cassava mealybugs in Asia). Active surveillance can be sustainably and meaningfully scaled up via diagnostic networks such as the International Plant Diagnostic Network (IPDN) led and presented by Dr. Miller of Ohio State University.

To best take advantage of the potential of risk assessment and surveillance data several challenges must be overcome. Top among them is the need to integrate highly distributed data generated by the diverse mechanisms discussed above. The potential exists to develop data collection or management standards that would streamline the integration of data collected in the future. CABI's Plantwise, for example, has developed guidelines for what they call an "Ideal" pest distribution dataset, which could be used as a starting point for a more comprehensive or appropriate data management protocol. An additional challenge is to make data more broadly available for browsing, analysis and decision-making. One model discussed is that of Trendalyzer, an information visualization tool developed by Hans Rosling's Gapminder Foundation. The disadvantage of this tool, however, is that it is not geographically explicit; hence, an important imperative will be to develop a tool that could facilitate discovery specifically for SDD.

## 3. Research planning and workshop results

### 3.1 Pest risk analysis and surveillance for target pests and diseases

Intensive workshop discussions on PRA to help guide surveillance strategies for pests and diseases facilitated the development of an action plan to characterize and manage risk due to RTB pests and diseases and their potential invasion to new areas. It was recognized that increased risk due to pest and pathogen introductions result from increased globalization of trade, human movement and climate change. To address this risk and to take pre-emptive action to mitigate pest and disease introductions the group endorsed the development and implementation of PRAs as advocated by the International Plant Protection Convention (IPPC). The benefit of a PRA is to document all known information to help guide intervention strategies and to identify research gaps. As new information becomes available this is used to update PRA documents to ensure that all appropriate knowledge is housed in a single location that is freely available to all in order to support the ISPMS of the IPPC. Initial steps were taken to strengthen collaborative ties between CGIAR RTB crop protection experts and the Secretariat of the IPPC at FAO. It was recognized that capacity building exercises were needed to develop and implement PRAs through training NPPOs and linking with RPPOs such as IAPSC.

#### 3.1.1 Prioritization of key pests and pathogens

Workshop participants reached a consensus on the selection of priority pests and diseases of RTB for the development of PRA. This was based on pests and pathogens that were currently causing severe losses to crop yield and economic impacts in locations that were restricted but where expertise existed from within the group. The intention was to populate PRAs with information that would help to inform intervention strategies to prevent the introduction and spread of these pests and diseases in other areas; e.g. the Guatemalan potato tuber moth from South America recently introduced to the Canary Islands in Africa and other European countries; cassava mosaic and cassava brown streak from Africa to elsewhere and conversely witches broom to Africa from South America and Asia etc. Furthermore, the intention was to develop PRAs for use in countries and regions currently afflicted by the targeted pests and diseases and to further refine the information in PRA based on their experiences. Consideration was also made of the linkages between regulated quarantine pests and pathogens as defined by the IPPC and targeted pests and diseases of RTB for PRA e.g. BBTV in order to create synergy in efforts. Priority insect pests selected are the tomato (and potato) leaf miner, *Tuta absoluta*, the Guatemalan potato tuber moth, *Tecia solanivora*, and the cassava green mite, *Mononychellus mcgregori/tanajoa*. Likewise the following diseases were prioritized: BXW, Foc TR4, CBSD, CMD, SPVD, CWBD, LB, Rs, Blood disease, and BBTV.

#### 3.1.2 Risk-based surveillance

Funds for surveillance are limited, particularly in developing countries so there is a need to target surveillance activities to specific regions, pests and diseases based on an evaluation of risk of introduction or spread. Therefore, surveillance strategies for the identified critically important pests and diseases of RTB will be based upon protocols that quantify risk as defined in PRAs. These protocols will allow us to set species-specific surveillance priorities in space and time, to optimize the allocation of our human and financial resources. Results from surveillance will be used to further refine risk analyses protocols and PRAs in order to better guide and justify future surveillance initiatives. A critical factor is also to ensure that standardized surveillance techniques are used to ensure that samples collected are from spatially representative locations and that complimentary surveys, separated by space or time, produce results that can be directly compared. In addition to physically visiting farmers' fields innovative methods will be used, as developed by CABI, such as community based mobile plant clinics and going public exercises to harness information on the potential presence of targeted pests and pathogens. Furthermore, results from surveillance, particularly when temporally separated will inform and measure the impact of interventions deployed to eradicate, contain, and limit the spread or introduction of pests and diseases. Surveillance based exercises determined by risk analyses will encompass epidemiological knowledge for each targeted pest or disease of RTB crops. Furthermore, the dependency of populations on any given RTB crop for their calorific dependence and food security will be combined with knowledge of pest and disease presence, spread and potential impact in order to assess risk and prioritize when and where surveys are undertaken. The successful eradication and containment of selected pests and diseases of RTB crops depends on the ability to detect new infections and low-density populations which will dictate the development of species-specific diagnostic methods that are practical, robust, precise and cost effective.

#### 3.1.3 Development of diagnostic tools for selected pests and diseases

As recognition of symptoms in the field may be insufficient to diagnose the causal pest or pathogen of disease it is necessary to have support from laboratory or field based diagnostics. For example, the two key species of cassava mealybugs are very difficult to tell apart by non-experts and CBSD is very difficult to detect based on aerial symptoms alone. If appropriate diagnostic methods are not available then a priority is to develop them. Both serological and molecular methods for diagnostics will be deployed based on which species of pest or disease is being analyzed and what is the preferred method based on national capacities or experience. If no experience of either diagnostic method resides in the targeted areas for surveys then support will be provided by CGIAR centers and advanced research institutes and training provided to national partners. The use of field based diagnostic methods such as immunological lateral flow devices will be used if already developed and available. Another method that can be used is portable kits to capture pathogen DNA in the field that can be transferred across country borders without SPS regulations; as it is only the DNA and not a viable organism capable of causing infections that is transferred. The benefit of using such kits is to provide samples from different countries for expert diagnoses using the same method, staff at the same time using optimized protocols to ensure comparability of results. The centralized diagnostic facility can be used to transfer capacity to staff of other laboratories. A critical factor is also to ensure that standardized sampling and diagnostic protocols are developed and implemented and that training is provided to ensure equivalent capacities are created. This can be enforced through the likes of proficiency or ring testing of standard samples for each pest or pathogen.

#### 3.1.4 Establishment of diagnostic networks

An important initiative to facilitate training, protocol and PRA development and information sharing is the creation of functional networks. Models developed by the International Plant Diagnostic Network (IPDN) in East and West Africa, Central America and Asia will be disseminated to target areas with the focus of selected pests and pathogens for RTB crops. IPDN will enable connections to taxonomists and diagnosticians around the world who can help with the identification of unknowns in the field based on symptoms and following lab based diagnostics. Further, portals managed by CABI Plantwise and FAO will be harnessed to create platforms for information sharing and to link to other information sources.

### 3.1.5 Knowledge bank

Outreach will be a fundamental part of our endeavors. An output will be to create a one stop knowledge bank that will house all data and documents generated by this initiative including (1) surveillance protocols (2) sampling protocols (3) diagnostic protocols (4) species distribution data (5) pest and pathogen phenology data (6) modeling results and predicted distribution maps and (7) PRAs.

### 3.1.6 Specific workshop results on PRA and surveillance for target pests and diseases (Product line 1, logframe)

Emerging, re-emerging and endemic insect pests and plant pathogens continue to challenge our ability to safeguard the health worldwide of root and tuber crops. Further, globalization, climate change, increased human mobility, and pathogen and vector evolution have combined to increase the spread of invasive plant pathogens. Assessments of the risks posed by pests and diseases combined with surveillance on local, regional, and global scales plus rapid and precise diagnoses are needed to predict outbreaks and allow time for development and application of pre-emptive mitigation strategies. Four interdependent products have been designed and milestones developed to address these issues through harnessing expertise from among CGIAR centers and their respective partner networks.

**Product (1.1): Pest Risk Analysis (PRA) concluded for target pests (Tomato and potato leaf miner, *Tuta absoluta*; Guatemalan potato tuber moth, *Tecia solanivora*; cassava green mite, *Mononychellus mcgregori/tanajoa*) (2015)**

Targeted pests were selected for their high potential of global economic importance but still relatively restricted distribution (see list of priority pests in annex 7.3). Hence, they were chosen as foci of preventive efforts under our research theme. The approach will be comprehensive, including both risk analysis and risk management. Insect pest modeling and risk mapping will become a major component in the PRA.

To achieve this product four milestones have been developed: a. *Literature review and stakeholder consultations* (2013); b. *Life table data and distribution data compiled* (2013-2014); c. *Risk maps developed and validated* (2014-2015); d. *PRAs finalized and disseminated* (2015)

Information gathering is essential part of PRA. High quality and completeness of information is important to properly assess the risk and make appropriate management decisions or recommendations. We will prepare fact sheets for the species under our considerations using a wide range of information sources (scientific literature, previous PRAs, official files, data bases (CABI), etc. We will consult stakeholders (e.g., National Plant Protection Offices) to get specific country information. We intend to develop a standard protocol to geo-reference and digitize this data so that it becomes readily available for pest risk analysis and modeling endeavors. Pest phenology models will be the basis for developing global and regional risks maps being an important part of PRA. If not available, life table studies will be conducted or existing phenological data compiled and risk maps developed using ILCYM and/or CLIMEX. Initial protocols have been developed by the International Potato Center (CIP) under their ILCYM software development initiative.

Main outcomes: NPPO, EPPO, NARES will use science-based information in regulating target pests in international trade and national quarantine.

Key CGIAR staff are Kroschel (CIP), Parsa (CIAT), Hanna (IITA), and Samira (*icipe*). Technical backstopping in development and implementation of PRAs will be provided by partners of IPPC (FAO). Funding will be sourced from RTB.

**Product (1.2): PRAs and surveillance strategies developed for the targeted pathogens* (BXW; Foc; CBSD; CMD; SPVD; CWBD; LB; Rs; Blood disease; BBTV) (2015)**

*Banana diseases are BXW = *Xanthomonas campestris* pv. *musacearum*, Foc = *Fusarium oxysporum* f.sp. *cubense*, Rs = *Ralstonia solanacearum*; Blood disease = another bacterial pathogen of uncertain taxonomy; BBTV = bunchy top virus; Cassava diseases are CBSD = brown streak virus, CMD = mosaic virus, CWBD = witches broom; Sweet Potato = SPVD = virus diseases; Potato disease is LB = late blight caused by *Phytophthora infestans.*

These diseases were targeted because they currently pose tremendous losses to production and because they are limited in their current locations and thus to combat them and prevent introductions unified global action is required. For example BXW is restricted to great lakes region of Africa, CMD and CBSD to Africa, CWBD to Americas, whereas Rs (Race 2 Biovar 1 and known as Moko Disease) does not exist in Africa but is found in North, Central and South America, Caribbean and Philippines. Other forms of Rs attack potato (Race 1 and 3). BBTV and LB are present in several regions but in different forms with varied degrees of virulence. A particular threat from Asia for banana (as it kills the exported Cavendish clones) is posed by Tropical Race 4 (TR4) of Foc, which is spreading from Southeast Asia and Australia to Indonesia, Malaysia, China and beyond. SPVD occur in complexes and their identities, impacts and geographical distributions are only now beginning to be unraveled through advanced diagnostics.

Future surveillance strategies for such critically important diseases of root and tuber crops must be based upon protocols that address risk, that become refined as experiences are accrued. Such practices can be housed in open access working documents such as Pest Risk Analyses (PRA) to increase information sharing between countries, regions and continents potentially facing the same threats. While the practice of using PRAs is advocated by the International Plant Protection Convention (IPPC), as set out under its various International Standards for Phytosanitary Measures (ISPMs), they are not routinely used in developing countries. PRAs attempt to bring in risk assessment and risk management and qualitative *versus* quantitative judgments, but also share features about risk related to pest and disease entry, establishment, spread, the emergence of new variants and their consequences. Each also strives to bring together a state-of-knowledge through a desk review of literature on what is known and not known and to attribute risk and uncertainty to these knowledge sets. Therefore, PRAs can be used to highlight when and where targeted surveillance activities are undertaken. Results from such surveillance schemes can be used to take appropriate actions to limit risk and to revise the PRA for any given disease (or group of diseases based around a particular RTB crop).

To achieve this product four milestones have been developed: a. *Literature review and stakeholder consultations* (2013); b. *PRAs developed and disseminated* (2014); c. *Targeted capacity building in PRAs to NPPOs* (2014); d. *Surveillance strategies developed based on distribution maps* (2015). Once available information has been documented into the format of an IPPC approved PRA training areas will be identified for targeted surveillance and this will be undertaken by lead CGIAR staff and their NARs partners in 3 areas; Kivu region of great lakes region in Africa, Northern Andes, Indonesia. Kivu will be a focal area because of the presence of Bioversity, CIAT, CIP, IITA and their partners and because of the high demand as staple foods and for income generation for banana, cassava, potato and sweet potato. The Kivu region is assigned as North Western Tanzania, Burundi, Rwanda, eastern DRC and Western Uganda. North Andes include Peru, Colombia and Ecuador where CIP and CIAT are based. Indonesia is selected because of the presence of Foc TR4 and Blood disease of banana. Following training in development of PRAs the NPPOs based in the above regions will undertake better informed surveillance strategies and results generated will be used to guide policy and research prioritization.

Main outcomes: NPPO and researchers use information for better informed surveillance, policy and research prioritization.

Key CGIAR staff are Forbes, Kreuze (CIP); Beed, Legg, Kumar (IITA); Alvarez, Aritua (CIAT); Molina, Karamura (Bioversity).Technical backstopping in development and implementation of PRAs will be provided by partners of FERA and IPPC (FAO). FERA and OSU will also provide technical backstopping in development and implementation of field and lab based diagnostic methods. As a critical component of RTB funds will be sourced from this Research Program and also from FAO to support the mandate of IPPC.

**Product (1.3): Evaluate and document risk that pathogen population evolution will threaten RTBs; cassava (CMD and CBSD), potato & tomato (LB and Rs) and sweet potato (VD) and banana (BXW, Rs, Blood disease, Foc) (2020)**

Critical diseases listed are as defined in 3.1.1.4. Because there is a focus for this output on linking diagnostic platforms Rs characterization will encompass potato and banana and also be linked to tomato where there is a wealth of knowledge. This output serves to better predict and record the likelihood of the emergence of new variants of selected diseases and to take pre-emptive action to curtail introductions and epidemics.

To achieve this product eight milestones have been developed: a. *Sampling plans developed to collect representative data compatible with modeling and repository* (2013); b. *Develop field based diagnostic assays for target diseases* (2014); c. *Samples and collections made from all hosts (cultivated and wild)* (2014); d. *Pathogen populations characterized genotypically and phenotypically* (2015); e. *Pathogenicity profiles of sampled isolates determined* (2015); f. *Map (Genetic and phenotypic description including pathotypes) of Rs on banana in Asia/South America developed* (2016); g. *Map (Genetic and phenotypic description including pathotypes) of cassava (CMD and CBSD), potato & tomato (LB and Rs) and sweet potato (virus) and banana (BXW also Ethiopia) in Kivu region* (2016); h. *Phenotypic (race and VCG) and genetic description of the population of Foc on banana in target area of Kivu, Indonesia and Brazil* (2017).

The milestones above are interlinked and self-explanatory but it is important to note the following clarifications to each: a. Live samples to be collated in reference collections and used to develop diagnostic methods that encompass all variation; b. Visual symptom recognition supported by the likes of immunological lateral flow devices or use of pathogen DNA capture kits in field for PCR based diagnostics in centralized laboratories; c. To encompass all variation of targeted pathogens prior to when new variants attack crops; this will involve deep sequencing for viruses and will be linked to the new RTB seed degeneration project; d. Genetic constitution plus expression based on environment; e. Ability to cause disease when tested against differential cultivars differing in resistance; f. To be led by Bioversity; g. To be led by all CGIAR partners and in addition to Kivu the country of origin for the bacterium that causes BXW will be included i.e. Ethiopia; h. To be led by Bioversity for Indonesia and Brazil and co-led by IITA and Bioversity for Kivu.

Main outcomes: Better targeted resistance breeding, management strategies, and phytosanitary measures implemented.

Lead CGIAR staff are Forbes, Kreuze (CIP); Beed, Legg, Kumar (IITA); Alvarez, Aritua (CIAT); Dita, Molina, Karamura (Bioversity). Technical support for diagnostics and variant characterization from partners of FERA, OSU and LSU; and for PRA IPPC (FAO) will be involved. Outcomes will include better targeted resistance breeding, deployment of appropriate pre-emptive management strategies and implementation of phytosanitary measures. Funds will be sought from RTB and also USAID and USDA-FAS due to their support for developing informed SPS strategies.

**Product (1.4): One stop shop for data storage on pest and pathogens, queries and visualization with a front page in the RTB web page (2015)**

This output serves to collate all of the available information on known pests and diseases of RTB in an accessible format at a single location. This will offer a massive advancement to link what are currently discrete databases managed by individual projects or CGIAR centers to benefit a global understanding of the distribution, impact and variance of critical pests and diseases of RTB crops. This information will help to guide the development of PRA documents and to target surveillance activities and prioritize research investments.

To achieve this product three milestones have been developed: a. *Each CG center to assess credibility of datasets for their mandate crops* (2014); b. *Contract GIS/data platform specialist to manage activities (probably based at CIAT)* (2013); c. *Platform implemented for housing data; data in modeling useful format, including host (cultivar & resistance) information, farming system information* (2015).

Main outcomes: Scientist and policy makers access and use data for research and to better inform decision making and prioritization.

This global undertaking will help to make accessible previously fragmented information to all scientists and policy makers to better inform decision making and investment prioritization. Lead CGIAR staff for predictive results from disease modeling initiatives are Garrett (KSU) and Sparks (IRRI); for current pathogen profiles are Forbes, Kreuze (CIP); Vandenbergh (Bioversity); Legg, Beed, Kumar (IITA); and for insect modeling and pest profiles are Kroschel (CIP), Parsa (CIAT), Hanna, Legg, Tamò (IITA), Calberto (Bioversity). Support will be provided by sources of data to include CABI Plantwise, PROMUSA, Euroblight, Rustmapper, CIAT trial database, Australian biosecurity database. Funds will be sourced from RTB and also potentially CABI Plantwise or FAO.

### 3.2 Modeling climate impacts on potential future insect pest risks and distribution

#### 3.2.1 Development and selection of modeling tools

Current tools to predict potential species distributions have some limitations. Statistical models such as MaxEnt are easy to use and freely available. However, they can be subject to strong sampling biases when data is limited. This may be the case for many of our priority species. On the other hand, mechanistic models are less subject to biases, but the only tool currently available, CLIMEX, is very costly and potentially also challenging for the average user. Hence, there is an imperative and opportunity to strengthen the ILCYM (Insect Life Cycle Modeling) platform, developed under the leadership of CIP, to complement current alternatives to infer potential distributions, under both current and future climate scenarios. The RTB and CCAFS insect modeling team has a demonstrated expertise in the development and application of statistical (e.g., MaxEnt), mechanistic (e.g., CLIMEX, and process-oriented fully temperature-driven and age-stage structured insect phenology models supported by ILCYM. Taking advantage of appropriately formatted and collated data for species distribution and phenology, improved and robust ensemble models combining the concepts behind the different modeling approaches will be developed to predict and map future distribution for the targeted priority pests for RTB and other crops.

#### 3.2.2 Standardization and digitalization of existing current distribution data

Workshop participants recognized that, while there was an availability of discrete information sources on the distribution of pests that included “grey” literature, reports from projects, insect museums and pathogen germplasm collections, and general web citations; there was a need to formularize all data to ensure it was credible and for it to be stored at a single site that was publically available. The recommendation was to develop a standard protocol to geo-reference and digitize this data so that it becomes readily available for pest risk analysis and modeling endeavors.

#### 3.2.3 Standardization and collection of pest phenology data

In addition to species distribution data, phenology data is of particular importance to assess potential risks and impacts of insect pests. Existing phenology data for priority pests will be catalogued and protocols developed to systematically generate new data for key priority pests in a format that is suitable for modeling initiatives (e.g. CLIMEX and ILCYM). Preliminary protocols have been developed by the International Potato Center (CIP) under the ILCYM initiative.

#### 3.2.4 Assessments of climate impacts on regional scales

The developed modeling tools have been shown to be useful for predictions over a large geographic range. However, predictions in a smaller geographical range especially in mountainous regions are hampered by the lack of quality regional weather data sets and reliable downscaling options. To overcome these limitations, the "*Index interpolator"* was recently developed as a sub-module in ILCYM software, which inputs daily minimum and maximum temperature data and simultaneously calculates the three risk indices (establishment index, *ERI*, generation index, *GI,* and activity index, *AI*) location by location. The analyses of the indices are at high spatial (pixel size of 90 m) and temporal resolution (daily data) that enables capturing the insect population potential establishment, distribution and abundance on small regional scales at an altitude gradient. Altitudinal gradients with gradual changes in climates, pests and host suitability can ideally be used to assess current and future climate impacts on pest distribution and risks. The East African highlands in the Lake Kivu region (Burundi, eastern DRC, Rwanda, North-western Tanzania and western Uganda) with the extensive production of several RTB crops such as potato, cassava, sweet potato and banana as well as of crops under the mandate of other CGIAR (e.g., maize, CIMMYT) and affiliated centers (e.g., horticultural crops, icipe) offer a good opportunity for collaborative efforts to assess the impacts of climate change on insect pests (and diseases). However, the availability of present and historical weather data needs to be assessed and infrastructure built up and meteorological data records strengthened.

#### 3.2.5 Assessments of climate impacts on crop yields

New opportunities exist to make progress in the area of linking pest/disease models and mechanistic crop models. A detailed generic insect population model is available, ILCYM (developed by CIP). A generic crop model, InfoCrop, will be available in R in 2013 (implemented by Bioversity). There is an opportunity to use these recent advances and address the crop-insect model integration challenge in an innovative way and allowing for relatively easy integration into GIS and climate models by non-specialists (using R in all cases).

#### 3.2.6 Specific workshop results on modeling climate impacts on potential future insect pest risks and distribution (Product line 2, see logframe)

**Product (2.1): Pest models extended and improved and risk maps compiled, validated and stored in one common databank (2016)**

The data bank on pest models needs to be extended to be able to predict potential climate impacts on a wide range of pests of RTB and other crops including horticultural crops. These models will be needed for global and regional risk assessments and will be especially applied in the regional endeavor to understand climate impacts and prepare for adaptation in the Kivu region, which have been selected as pilot region (see product 2.3).

To achieve this product, three milestones have been developed: a. *Geo-referenced pest distribution data for at least 20 arthropod target species* (2013-2014); b. *ILCYM extended by a new module to make use of published mean life table data in the development of phenology models* (2014); c. *Life table data compiled for at least 10 pests of RTB and other crops (Spiraling whitefly*, B. tabaci A & B type, Cosmopolites sordidus, *Banana Aphid* (*BBTV*) Pentalonia nigronervosa, Chilo partellus, Busseola fusca, Scirpophaga incertulas, Helicoverpa armigera, Maruca vitrata) (2013-2015); d. *3 modeling tools validated for generating risk maps under current and future climate scenarios of at least 10 species (5 RTB pests, and 5 pests of other crops)* (2013-2015); e. *Pest ensemble models developed for each pest species* (2015-2016); f. *Life table data and risk maps stored in one common data bank (e.g., as part of ILCYM) and made available* (2013-2016).

Geo-referencing of pest distribution data is important for model validation and for applying mechanistic modeling approaches (e.g., for generating maps using CLIMEX). The generation and compilation of life table data, which are the basic inputs in ILCYM software, is time consuming. However, often life table studies have been undertaken for many pests but only mean values have been published which limits their direct use for developing phenology models for pest risk assessments. ILCYM will be extended by a sub-module which can use mean published life-table data. Modeling outputs will be validated by comparing models developed from mean values only or from full data sets of mean values and their standard deviations. Main output of this product are life table studies and data for risk assessments of many important pests of RTBs (RTB) and other crops (e.g., maize, CIMMYT, sorghum, ICRISAT etc.). All participating centers will be trained in the application and use of ILCYM and other modeling software (CLIMEX) to have the capacity in the application and use of different modeling approaches. Modeling outputs (risk maps) generated by different modeling approaches will be validated and compared. Based on this, pest ensemble models will be developed and tested.

Outcomes: Researchers in RTB and CCAFS are trained in the application of pest modeling and risk assessments studies and have pest models developed for their mandate crops; these models are made available for NARC for regional and site specific pest assessments.

Key CGIAR staffs are Kroschel (CIP), Parsa (CIAT), Hanna, Legg, Tamò (IITA), Calberto (Bioversity), Ekesi (icipe), Tadele (CIMMYT), F. Horgan (IRRI), H. Sharma (ICRISAT), Srinivasan (AVRDC), CABI. Funding will be sourced from RTB and CCAFS.

**Product (2.2): Regional pest distribution and incidence maps developed, related RTB crop losses analyzed, and impacts of pest risks in RTBs and other crops on livelihoods under current and future climate scenarios analyzed and documented for pilot countries and sites (2015)**

According to a species specific temperature requirement, the insect pest distribution and abundance changes at altitude gradients. Impacts of climate change on insect pests can be therefore best understood by studying the temperature-dependent pest distribution at regional or local scales at altitude gradients and predict climate impacts on future pest distribution and abundance and related crop losses using pest phenology modeling and regional risk mapping at high resolution. Impacts on crop yields and famers' livelihoods can be also extrapolated and forecasted. These kinds of studies can be best undertaken in agroecologies of mountainous regions of Africa and the Andes. The Kivu region in Africa (Burundi, Rwanda and Uganda) will be our focal area of research because of the presence of all RTB centers (Bioversity, CIAT, CIP, IITA), CCAFS (e.g., CIMMYT), *icipe* and their partners and because of the high demand of staple foods and for income generation for banana, cassava, potato, sweet potato, maize and horticultural crops.

To achieve this product, seven milestones have been developed: a. *Harmonize and standardize survey methodologies and tools* (2013); b. *Surveys conducted and completed* (2013-2015); c. *Regional climatic data collected and stored in databank* (2013-2014); d. *ILCYM's Index interpolator to develop regional risks maps further improved and validated in the Andean region* (2013-2014); e. *Data analyzed and digitalized* (2014-2015); f. *Phenology models applied to generate regional risk maps in ILCYM for important pests of RTBs and others (maize, horticultural crops)* (2014-2015); g. *Regional pest impacts on livelihoods analyzed* (2015-2016).

Survey regions, methodologies and tools will be harmonized among all partners to assess pest incidence and severity in RTBs and other crops at an altitude gradient in the Kivu region; data collection will be done in several years and seasons to receive a representative data collection under different climates. A large number of climate stations for temperature and precipitation will be installed in the defined survey regions and completed by secondary data records. ILCYM's Index interpolator will become an important tool in developing high resolution pest risk (distribution and abundance) maps. The Index interpolator will be further validated with climate and pest incidence data from the Andean region to have an overall robust tool available; this will also consider a tool to analysis the impact of precipitation. For a wide range of economic important pests in all RTBs, maize and horticultural crops, selected by each partner, regional risk maps under current and future climates will be developed and potential impacts on crop losses and livelihoods estimated.

Outcomes: NARES and policy makers understand impact of climate change on agricultural systems and livelihood in the Kivu region and use information for adaptation planning.

Key CGIAR staff are Kroschel (CIP), Parsa (CIAT), Hanna (IITA), Calberto (Bioversity), Ekesi (*icipe*), Tadele (CIMMYT), and partners from CABI. Funding will be sourced from RTB, CCAFS and bilateral (e.g., BMZ).

**Product (2.3): Climate Change impacts on pest induced crop losses estimated (2018)**

InfoCrop will need to be integrated with ILCYM. The resulting model needs to be validated with empirical data or co-validated against existing, more crop-specific models. Potato and banana have been selected as the crops to work on initially.

To achieve this product, three milestones have been developed. *a. Implement a crop model for banana, potato and other crops in R (based on InfoCrop) in order to interface with ILCYM* (2013-2014)*; b. Link InfoCrop and ILCYM in order to provide a mechanistic model to estimate crop losses due to pests* (2014-2015)*; c. Estimate crop losses using AgTrials data, InfoCrop-ILCYM and other methods* (2015-2016)*; d. Capacity building in impact assessment using the developed tools* (2017)*; e. Integration of developed modeling tools for crop loss estimation in monitoring and surveillance systems in at least two crops* (2017-2018).

The implementation of InfoCrop and ILCYM will be harmonized and documentation will be improved to make code reuse possible. Data from Product 2.1 will be used to calibrate and validate models.

Outcomes: NARES and policy makers have better predictive tools for monitoring and surveillance and adaptation planning, enabling a detailed ex ante evaluation of different management and adaptation options. NARES and international scientists will have tools in a commonly used open source environment, facilitating scientific exchange and collaborative innovation.

Key CGIAR staff are Van Etten and Calberto (Bioversity), Kroschel (CIP), and Aggarwal (IWMI). Partnerships will be built with universities to integrate PhD students (e.g., University of Leeds, UK; University of Hohenheim, Germany). Funding will be sourced from RTB, CCAFS and bilateral.

### 3.3 Modeling climate impacts on potential future disease risks and distribution

Plant pathogens cause important losses in major food crops globally, and can be particularly difficult to manage in areas where food insecurity and limited farmer training are risk factors. Weather drives the level of disease risk, so climate change will modify disease risk in ways that may challenge farmers' ability to adapt. Modeling climate change effects on disease supports prioritization by researchers, policy makers, and educators by identifying where the most important challenges to plant disease management are likely to occur.

More than 15M ha area is rainfed in South Asia, covering Pakistan, India, Nepal, Bengladesh, and Myanmar. This system provides more than 65% of cereals (principally rice) and legumes (chickpea, pigeonpea, etc.), hence it is very important for food security and nutritional security. In this system rice is grown in the rainy season and legumes normally follow rice in the post-rainy season utilizing residual moisture left after rice production, and potatoes are also an important component of this system. Among several crops, chickpea as a food legume is found to be most suitable as a second crop with greater potential in the rainfed sown soon after the harvest of rice. In this system chickpea, flower and set seed on the continuously receding residual moisture, thus becomes vulnerable to diseases that are predisposed by drought stress. This is a common phenomenon in the last 20 years, and it will be important to understand how the future risks in this system are influenced by climate change. The latest IPCC 2007 report indicates that rainfed systems will be particularly vulnerable to climate change. The effect of climate change may already be apparent, not only in terms of declining rice yields, but also in terms of the emergence and changing scenarios for diseases. Key diseases are brown spot (*Cochliobolus miyabeanus*, Anamorph: *Bipolaris oryzae*) and leaf blast of rice (*Magnaporthe oryzae*, Anamorph: *Pyricularia oryzae*), Fusarium wilt (*Fusarium udum*) and Phytophthora blight (*Phytophthora drechsleri* f. sp. *cajani*) of pigeonpea, and Fusarium wilt (*Fusarium oxysporum* f. sp. *ciceris*) and dry root rot (*Rhizoctonia bataticola*) of chickpea, and late blight seed degenerative diseases of potato. Together these diseases are capable of reducing grain yield by 10-100% in legumes, frequently reducing yield by 40%. This system is an important focus because of important disease losses, susceptibility to climate change, and also because there are sufficient data available for these systems to support its use as a model for analysis in cropping systems more broadly. IRRI has a model for rice yield loss, RICEPEST (Willocquet et al. 2000, 2002), that has been validated for this rice production system for current conditions, data from the production oriented survey of India with information related to cropping systems and diseases at the district level, NASA/POWER weather data that have been bias-corrected and downscaled to $0.25^o$ resolution for matching district level data in India, and GIS capabilities to support climate analyses. ICRISAT has been working in the area for 40 years and has accumulated sizeable data sets for weather and diseases of legume crops that can be used to construct models of the relationship between weather and crop losses.

#### 3.3.1 Specific workshop results on modeling climate impacts on potential future disease risks and distribution (Product line 3, see logframe)

The following outputs have been designed to contribute to solutions to this problem. They are designed to support collaborative research work in the Kivu region as well as in South Asia. A systems approach will be important for understanding how this cropping system may shift under climate change, what forms of adaptation are likely as rainy seasons shift, and what support will be needed to help farmers adapt more efficiently. Most climate change scenario analyses have focused on individual pests or diseases, or at least individual crops. We will provide a new framework for climate change analysis of diseases in cropping systems and proof of concept for integration across four CGIAR centers.

**Product (3.1): Risk of epidemics to RTB crops resulting from climate change (CBSD, CMD; SPVD; BXW, BBTV, Rs, Sigatoka; LB) analyzed and documented (2015)**

Critical diseases listed are as defined in 3.1.1.4 and also included are black and yellow Sigatoka and a relative that causes leaf speckle (caused by *Mycosphaerella fijiensis*, *Mycosphaerella musicola* and *Mycosphaerella eumusa*, respectively). This output serves to better inform likely risk of disease epidemics due to changes in climate and to thus take pre-emptive action to prevent disease emergence or introductions in environments with climatic conditions that are conducive.

To achieve this product, three milestones have been developed: a. *Collate available data in format appropriate for modeling* (2013); b. *Effect of climate change on late blight severity in Kivu determined* (2014); c. *Develop model parameters and estimate risk of invasion based on conducive climates* (2015).

There are discrete datasets restricted to projects or CGIAR centers so the first task is to organize this information into a format that is accessible to all and suitable for modeling exercises. Guidance will be provided by partners at KSU and IRRI on the required format for modeling and each CGIAR lead contributor will be responsible for collating datasets that they are aware of. Because, studies on LB are more advanced and better coordinated previously than for other targeted diseases, a major milestone for the Kivu region in 2014 will be to predict effects of climate change. Based on the 2014 milestone for LB and on knowledge of the epidemiology of targeted pathogens model parameters for each will be developed and used to predict the risk of invasion to areas recognized as having conducive climates. Such predictions will be used to better inform national and regional surveillance strategies and results generated will be used to guide policy and research prioritization and to further refine model parameters. Targeted regions are Kivu region for all targeted diseases for cassava, sweet potato and potato diseases and for banana; BXW and BBTV and for S&SE Asia targeted diseases are LB for potato and Rs and Sigatoka for banana.

Outcomes: NPPO and researchers use information for better informed surveillance, policy and research prioritization.

Lead CGIAR staff are Forbes, Kreuze (CIP); Molina (Bioversity); Beed, Hannah, Legg (IITA) and technical backstopping in pathogen variation and diagnostic methods will be provided by FERA and OSU. Funds will be sought from RTB (based in importance of targeted crops to this Research Program) and from CCAFS (because of climate change predictions through modeling) and potentially from the private sector for *Mycosphaerella* spp. in S&SE Asia.

**Product (3.2): Develop a generic disease modeling platform for the analysis of climate change effects on crop disease and resulting yield loss**

To achieve this product, three milestones have been developed: a. *Data sets assembled and cleaned* (2013); b. *Grain legume model for CC-PD-YLD assembled and rice model implemented* (2014); c. *Generic CC-PD-YLD model platform assembled* (2015)

We will begin by assembling the relevant weather, disease, and socioeconomic data sets for the initial modeling region, drawing on data maintained by IRRI, ICRISAT, CIP, and Bioversity, and cleaning and formatting it for the purposes of this study. We will prepare and cross-validate a new grain legume model for the effects of climate change on plant disease and yield loss. This new model, along with existing models of rice disease and yield loss, will be applied to study the initial test system. In the course of preparing the grain legume model, we will develop a more general modeling platform for broader use in modeling disease and yield loss for plant diseases in general. This new broader modeling platform will build on the valuable traits of ILCYM and current rice models.

Outcomes: NARES and policy makers understand impact of climate change on agricultural systems and livelihood.

Key research team (Sparks) IRRI, (Pande and Sharma) ICRISAT, (Forbes) CIP, (Garrett) KSU, (Valdivia) U Missouri, NARES, Van Etten (Bioversity), Aggarwal (CCAFS). Funds will be sought from CCAFS, GRISP, Grain Legumes, and RTB.

**Product (3.3): A new system level framework (protocols and methodologies) established for analysis of climate change effects on crop diseases in cropping systems of multiple crop species**

To achieve this product, three milestones have been developed, building on product (3.2) and with the same research team: a. *Establish framework for cropping system synthesis* (2013); b. *Develop system-level model for rainfed rice-grain legume-potato system* (2014); c. *Synthesis of system-level model outputs and implications shared* (2015)

First, we will develop a framework for analysis of multiple diseases in a cropping system with multiple crop species. This will require consideration of how diseases interact, and how the timing of planting of different crop species will influence disease risk. Second, we will apply this system-level analysis to the rain-fed rice-grain legume-potato systems. This will provide estimates of climate change impacts that include system-level interactions rather than simply reductionist analyses of single diseases in single crop species. The results will by synthesized and generalized for application in other cropping systems, to provide a general framework for whole-system synthesis.

Outcomes: NARES and policy makers understand impact of climate change on agricultural systems and livelihood.

Key research team (Sparks) IRRI, (Pande and Sharma) ICRISAT, (Forbes) CIP, (Garrett) KSU, (Valdivia) U Missouri, NARES, Van Etten (Bioversity), Aggarwal (CCAFS). Funds will be sought from CCAFS, GRISP, Grain Legumes, and RTB.

### 3.4 Platform for pest and disease risk assessments and modeling under climate change

A CCAFS scoping study has been drafted, addressing 'Priorities to address pests and diseases in agricultural adaptation to climate variability and change in the tropics'. This scoping study follows on a CCAFS project by the scoping study team published as Garrett, K. A., A. Dobson, J. Kroschel, B. Natarajan, S. Orlandini, H. E. Z. Tonnang, and C. Valdivia. 2013. The effects of climate variability and the color of weather time series on agricultural diseases and pests, and decision making for their management. Agricultural and Forest Meteorology 170:216–227. The scoping study is being revised by the original authors and new contributors from the workshop to incorporate the workshop insights. The main message is that it will be desirable for the CGIAR centers and their research partners to look for points of synergy, such that the center scientists minimize redundancy in addressing this problem, drawing on common tools for modeling frameworks, databases, and translation of models for climate change scenario analyses, the construction of decision support systems/early warning systems, and potentially the construction of index insurance programs. A diagram illustrating the framework is included in the abstract by Garrett and the scoping study team (see annex 2: Book of abstracts).

**4. Logframe: "Management of critical pests and diseases through enhanced risk assessment and surveillance and understanding of climate impacts through enhanced modeling"**

| Products | Milestones | Outcomes | Target region & key countries | Research team (CG) and key partners | Funding |
|---|---|---|---|---|---|
| **Product line 1: Pest Risk Analysis (PRA) and Surveillance for targeted Pests and Diseases** | | | | | |
| 1.1: PRA concluded for target pests (Tomato leaf miner, *Tuta absoluta*; Guatemalan potato tuber moth, *Tecia solanivora*; cassava green mite, Mononychellus mcgregori/tanajoa) (2015) | a. Literature review and stakeholder consultations (2013)<br>b. Life table data and distribution data compiled (2013-2014)<br>c. Risk maps developed and validated (2014-2015)<br>d. PRAs finalized and disseminated (2015) | NPPO use information in regulating target pests and diseases; International trade, EPPO, NARES, | Africa, Asia, South America | Kroschel (CIP), Parsa (CIAT), Hanna (IITA), Samira (*icipe),* FAO, CABI | icipe-BMZ; RTB, |
| 1.2: PRAs and surveillance strategies developed for targeted pathogens (BXW, Foc, Rs, Blood disease, BBTV; CBSD, CMD, CWBD; SPVD; LB) (2015) | a. Literature review and stakeholder consultations (2013)<br>b. PRAs developed and disseminated (2014)<br>c. Targeted capacity building in PRAs to NPPOs (2014)<br>d. Surveillance strategies developed based on distribution maps (2015) | NPPO and researchers use information for better informed surveillance, policy and research prioritization | Kivu region, Northern Andes, Indonesia | Forbes, Kreuze (CIP); Beed, Legg, Kumar (IITA); Alvarez, Aritua (CIAT); Molina, Karamura (Bioversity); Smith (FERA); Miller (OSU); Sossa (IPPC) | RTB, FAO |
| 1.3: Evaluate and document risk that pathogen population evolution will threaten RTBs; cassava (CMD and CBSD), potato & tomato (LB, Rs and virus for potato) and sweet potato (VD) and banana (BXW, Rs, Blood disease, Foc) (2020) | a. Sampling plans developed to collect representative data compatible with modeling and repository (2013)<br>b. Develop field based diagnostic assays for target diseases (2014)<br>c. Samples and collections made from all hosts (cultivated and wild) – linked with seed degeneration via deep sequencing (2014)<br>d. Pathogen populations characterized genotypically and phenotypically (2015)<br>e. Pathogenicity profiles of sampled isolates determined (2015)<br>f. Map (Genetic and phenotypic description including pathotypes) of Rs on banana in | Better targeted resistance breeding, management strategies, and phytosanitary measures implemented. | Indonesia, Brasil, Kivu | Forbes, Kreuze (CIP); Beed, Legg, Kumar (IITA); Alvarez, Aritua (CIAT); Dita, Molina, Karamura (Bioversity); Smith (FERA); Miller (OSU); Sossa (IPPC); Yuen (SLU),Viljoen (SUN) | RTB; USAID; USDA-FAS |

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|---|---|---|---|---|---|
| | Asia/South America developed (2016)<br>g. Map (Genetic and phenotypic description including pathotypes) of cassava (CMD and CBSD), potato & tomato (LB and Rs) and sweet potato (virus) and banana (BXW also Ethiopia) in Kivu region (2016)<br>h. Phenotypic (race and VCG) and genetic description of the population of Foc on banana in target area of Kivu, Indonesia and Brasil (2017) | | | | |
| 1.4: One stop shop for data storage on pathogens, queries and visualization with a front page in the RTB web page (2015) | a. Each CG center to assess credibility of datasets for their mandate crops (2014)<br>b. Contract GIS/data platform specialist to manage activities (probably based at CIAT) (2013)<br>c. Platform implemented for housing data; data in modeling useful format, including host (cultivar & resistance) information, farming system information (2015) | Scientist & policy makers access and use data for research and to better inform decision making and prioritization | Global | Garrett (KSU); Sparks (IRRI); Forbes, Kreuze, Kroschel (CIP); Vandenbergh, Calberto (Bioversity); Legg, Beed, Kumar , Hanna, Tamò (IITA); Parsa (CIAT); Smith (FERA); Miller (OSU); CABI Plantwise, PROMUSA, Euroblight, Rustmapper, CIAT trialdatabase, Australian biosecurity database | RTB; CABI-plantwise, FAO |
| **Product line 2: Modeling climate impacts on potential future insect pest risks and distribution** | | | | | |
| 2.1: Pest models extended and improved and risk maps compiled, validated and stored in one common databank (2016) | a. Geo-referenced pest distribution data for at least 20 arthropod target species (2013-2014)<br>b. ILCYM extended by a new module to make use of published mean life table data in the development of phenology models (2014)<br>c. Life table data compiled for at least 10 pests of RTB and other crops (Spiraling whitefly, *B. tabaci* A & B type, *Cosmopolites sordidus*, Banana Aphid (BBTV) *Pentalonia nigronervosa*, *Chilo partellus, Busseola fusca, Scirpophaga incertulas, Helicoverpa armigera, Maruca* | Researchers in RTB and CCAFS are trained in the application of pest modeling and risk assessments studies and have pest models developed for their mandate crops; these models are made available | Global, pilot site in East Africa (Great Lake region) | Kroschel (CIP), Parsa (CIAT), Hanna, Legg, Tamo (IITA), Calberto (Bioversity), Ekesi (icipe), Tadele (CIMMYT), F. Horgan (IRRI), H. Sharma (ICRISAT, Srinivasan (AVRDC), CABI | RTB, CCAFS |

| | | | | | |
|---|---|---|---|---|---|
| | *vitrata*) (2013-2015)<br>d. 3 modeling tools validated for generating risk maps under current and future climate scenarios of at least 10 species (5 RTB pests, and 5 pests of other crops) (2013-2015)<br>e. Pest ensemble models developed for each pest species (2015-2016) f. Life table data and risk maps stored in one common data bank (e.g., as part of ILCYM) and made available (2013-2016) | for NARC for regional and site specific pest assessments. | | | |
| 2.2: Regional pest distribution and incidence maps developed, related crop losses analyzed, and impacts of pest risks in RTBs and other crops on livelihoods under current and future climate scenarios analyzed and documented for pilot countries and sites in Africa (2016) | a. Harmonize and standardize survey methodologies and tools (2013)<br>b. Surveys conducted and completed (2013-2015)<br>c. Regional climatic data collected and stored in databank (2013-2014)<br>d. ILCYM's Index interpolator to develop regional risks maps further improved and validated in the Andean region (2013-2014)<br>e. Survey data analyzed and digitalized (2014-2015)<br>f. Phenology models applied to generate regional risk maps in ILCYM for important pests of RTBs and others (maize, horticultural crops) (2014-2015)<br>g. Regional pest impacts on livelihoods analyzed (2015-2016) | NARES and policy makers understand impact of climate change on agricultural systems and livelihood in the Kivu region and use information for adaptation planning | Kivu pilot region (Burundi, Rwanda, Eastern DRC, Southwaest Uganda); Andean region for model parametrizati on | Kroschel (CIP), Parsa (CIAT), Hanna, Legg (IITA),Calberto (Bioversity), Ekesi (icipe), Tadele (CIMMYT), CABI | RTB, CCAFS |

| | | | | | |
|---|---|---|---|---|---|
| 2.3: Climate change impacts on pest induced crop losses estimated (2018) | a. Implement a crop model for banana, potato and other crops in R (based on InfoCrop) in order to interface with ILCYM (2013-2014)<br>b. Link InfoCrop and ILCYM in order to provide a mechanistic model to estimate crop losses due to pests (2014-2015)<br>c. Estimate crop losses using AgTrials data, InfoCrop-ILCYM and other methods (2015-2016)<br>d. Capacity building in impact assessment using the developed tools (2017)<br>e. Integration of developed modelling tools for crop loss estimation in monitoring and surveillance systems in at least two crops (2017-2018) | Agricultural researchers have access to tools that allow them to estimate crop losses with scientifically grounded methods. NARES are trained to perform crop loss estimates using weather and future climate data in order to evaluate ex ante different crop and pest management options. | Global | Calberto (Bioversity), Van Etten (Bioversity), Kroschel (CIP); IMWI, University of Leeds, Hohenheim | RTB, CCAFS |
| **Product line 3: Modeling climate impacts on potential future disease risks and distribution** | | | | | |
| 3.1: Risk of epidemics to RTB crops resulting from climate changes (CBSD, CMD; SPVD; BXW, BBTV, Rs, Sigatoka; LB) analyzed and documented (2015) | a. Collate available data in format appropriate for modelling (2013)<br>b. Effect of climate change on late blight severity in Kivu determined (2014)<br>c. Develop model parameters and estimate risk of invasion based on conducive climates (2015) | NPPO and researchers use information for better informed surveillance, policy and research prioritization | Kivu region; S&SE Asia | Garrett (KSU); Sparks (IRRI); Forbes, Kreuze (CIP); Molina (Bioversity); Beed, Hannah, Legg (IITA); Smith (FERA); Miller (OSU) | RTB; CCAFS; private sector |
| 3.2: Develop a generic disease modeling platform for the analysis of climate change effects on crop disease and resulting yield loss | a. Data sets assembled and cleaned (2013)<br>b. Grain legume model for CC-PD-YLD assembled and rice model implemented (2014)<br>c. Generic CC-PD-YLD model platform assembled (2015) | NARES and policy makers understand impact of climate change on agricultural systems and livelihood | Global | (Sparks) IRRI, (Pande and Sharma) ICRISAT, (Forbes) CIP, (Garrett) KSU, (Valdivia) U Missouri, NARES, Van Etten (Bioversity) | CCAFS, GRISP, Grain Legumes, RTB |

| | | | | | |
|---|---|---|---|---|---|
| 3.3: A new system level framework (protocols and methodologies) established for analysis of climate change effects on crop diseases in cropping systems of multiple crop species | a. Establish framework for cropping system synthesis (2013)<br>b. Develop system-level model for rainfed rice-grain legume-potato system (2014)<br>c. Synthesis of system-level model outputs and implications shared (2015) | NARES and policy makers understand impact of climate change on agricultural systems and livelihood | Global, pilot sites in South Asia | (Sparks) IRRI, (Pande and Sharma) ICRISAT, (Forbes) CIP, (Garrett) KSU, (Valdivia) U Missouri, NARES, Van Etten (Bioversity) | CCAFS, GRISP, Grain Legumes, RTB |

## 5. Conclusions

The workshop was successful at harmonizing cross-cutting research among two CGIAR research programs (CCAFS and RTB) by developing and harmonizing a synergized logframe with clear product lines (1. Pest risk analysis (PRA) and surveillance for pests and diseases; 2. Modeling climate impacts on potential future insect pest risks and distribution; 3. Modeling climate impacts on potential future disease risks and distribution), strategic research products, milestones and developing outcomes in order to use resources more efficiently and share precious knowledge and experience across centers and their partners. Product line 1 clearly relates to cross-cutting research output and outcome development for RTB. Instead, product development for product line 2 and 3 seeks for strong collaborative efforts among centers of both research programs, RTB and CCAFS, and its various partners to tackle identified challenges and better understand climate impacts on pests and diseases across crops and regions through enhanced modeling and to use predictions to inform and support policy makers in the preparation of national and regional adaptation plans. It is proposed to concentrate collaborative efforts in pilot sites of Africa and Asia. For final product development, a period of 3-5 years has been planned, which demands long-term funding from CGIAR Research Programs (CCAFS and/or RTB) complemented through bilateral funded projects.

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**7. Annexes**

**8.1 Program and book of abstract**

**Scientific Review and Planning Workshop**

**"Management of critical pests and diseases of RTBs through enhanced risk assessment and surveillance (RTB)"**

**"Modeling climate impacts on pests and diseases"**

**Program**

**&**

**Book of Abstracts**

10-14 December 2012

Lima, Peru

**Program**

| Monday, December 10 | |
|---|---|
| 08:00 - 08:30 | Registration |
| 08:30 - 08:45 | Welcome note by P. Donini (DDG-Research) |
| 08:45 - 09:15 | Introduction into workshop objectives and program (J. Kroschel, F. Beed) |
| 09:15 - 09:30 | Self introduction of participants |
| **Theme 1:** | **Target pests and diseases: justification and distribution (Chair: J. Smith)** |
| 09:30 - 10:00 | Banana and plantain: target pests and diseases (P. Lepoint) |
| 10:00 - 10:30 | Cassava: target pests and diseases (B. Herrera) |
| 10:30 - 11:00 | *Coffee break* |
| 11:00 - 11:30 | Potato and sweetpotato: target pests and diseases (J. Kroschel, J. Kreuze) |
| 11:30 - 12:00 | Banana, cassava and yam: target pests and diseases (F. Beed) |
| **Theme 2:** | **Pest, disease and weed risk assessment and modeling under current and future climates (Chairs: J. Kroschel & K. Garrett)** |
| 12:00 – 12:30 | Predicting crop risks under climate change: progress and opportunities (A. Challinor, via skype) |
| 12:30 – 13:30 | *Lunch* |
| 13:30 – 13:45 | Platform for pest and disease risk assessments under climate change (K. Garrett) |
| 13:45 – 14:00 | Climate change adaption in disease management: a framework for evaluating the likely utility of decision support systems and index insurance (K. Garrett) |
| 14:00 – 14:15 | Disease risk assessments and modeling at IRRI (A. Sparks) |
| 14:15 – 14:30 | Disease risk assessments and modeling at CIP (G. Forbes) |
| 14:30 – 14:45 | Insect pest risk assessments using phenology modeling (J. Kroschel) |
| 14:45 – 15:00 | Insect Life Cycle Modeling (ILCYM) software for phenology models development and life table parameters estimation (H. Tonnang) |
| 15:00 – 15:15 | *Coffee break* |
| 15:15 – 15:30 | Spatial analysis tools in ILCYM software for risk assessment (H. Juarez) |
| 15:30 – 15:45 | Weed and pest risk assessments with Maxent (R. Simon) |
| 15:45 – 16:00 | Linking crop and pest models for assessing risks on crop losses using intelligent systems (H. Tonnang) |
| 16:00 – 16:15 | Towards an integration of crop simulation and insect population dynamics models to estimate climate change impact on productivity due to insect pests (G. Calberto, J. van Etten) |
| 16:15 – 16:30 | Risk assessments and modeling at CIAT (S. Parsa) |
| 16:30 – 16:45 | Risk assessments and modeling at CIMMYT (P. Likhayo) |
| 16:45 – 17:00 | Risk assessments and modeling  of biotic stresses in ICRISAT mandate crops (H. Sharma) |
| 17:00 – 17:15 | Pest Risk assessments and activities in modeling impacts of climate change on pest dynamics at *icipe* (S. Subramanian) |
| 17:15 – 17:30 | Risk assessments and modeling: IITA (M. Tamo) |
| 17:30 – 17:45 | Drivers of Change and Adaptive Capacities in the Andes |
| 17:45 – 18:15 | *Open discussion* |
| 18:15 | *Cocktail in CIP's garden* |

| Tuesday, December 11 | |
|---|---|
| **Theme 3:** | **Risk based surveillance (Skype presentation plus q & a) (Chair: F. Beed)** |
| 08:00 – 08:45 | Regulation of pest to protect trade and plant health (FAO-IPPC-O. Sosa) |
| 08:45 – 09:15 | Targeted surveillance to promote food security (FAO-AGP-M. Robson) |
| 09:15 – 09:30 | Sampling strategies for trade shipments (J. Smith) |
| 09:30 – 10:00 | *Open discussion* |
| 10:00 – 10:30 | *Coffee break* |
| **Theme 4:** | **Current surveillance strategies (Chair: J. Kroschel)** |
| 10:30 – 10:45 | Current surveillance strategies for banana pests and diseases (M. Dita) |
| 10:45 – 11:00 | Current surveillance strategies for potato and sweet potato pests and diseases (G. Forbes) |
| 11:00 – 11:15 | Current surveillance strategies for banana, cassava and yam pests and diseases (F. Beed) |
| 11:15 – 12:00 | *Open discussion* |
| 12:00 – 13:00 | *Lunch* |
| **Theme 5:** | **Detection and diagnostics (Chair: M. Tamo)** |
| 13:00 –13:15 | Symptom recognition mediated by mobile plant clinics (T. Holmes) |
| 13:15 –13:30 | Classical disease and pest diagnostic methods (S. Miller) |
| 13:30 –13:45 | Barcoding for pathogens and insect pests (J. Kreuze) |
| 13:45 –14:00 | Virus disease detection methods (J. Kreuze) |
| 14:00 –14:15 | LAMP and next generation sequencing (J. Smith) |
| 14:15 – 15:00 | A new low-cost diagnostic tool for detecting regulated (quarantine) cassava and banana diseases (E. Alvarez) |
| 15:00 –15:15 | *Open discussion* |
| 15:15 – 15:45 | *Coffee break* |
| **Theme 6:** | **Data management and reporting (Chair: S. Parsa)** |
| 15:45 – 16:00 | Plantwise knowledge bank (T. Holmes) |
| 16:00 – 16:15 | Valuing pest risk analysis in pest outbreak prevention (J. Smith) |
| 16:15 – 16:30 | Networks for diagnostics and capacity building (S. Miller) |
| 16:00 – 16:45 | Climate data management for species distribution models (H. Juarez) |
| 16:45 – 17:00 | Innovations to increase efficiency of data management (R. Simon) |
| 17:00 – 17:30 | *Open discussion* |
| **Wednesday, December 12** | |
| 08:00 – 08:30 | Orientation to group work and outputs (J. Kroschel, F. Beed) |
| 08:30 – 10:00 | Working group A:**Targeting** |
| Group A1: | Targeting priority pests for RTB & CCAFS |
| Group A2: | Targeting priority pests for RTB & CCAFS |
| Group A3: | Targeting priority diseases for RTB & CCAFS |
| Group A4: | Targeting priority diseases for RTB & CCAFS |
| 10:00 – 10:30 | *Coffee break* |
| 10:00 – 10:20 | Reporting to plenary: group A1 & A2 |
| 10:20 – 10:40 | Reporting to plenary: group A3 & A4 |
| 10:40 – 12:10 | Working group B:**Capacity and needs for modeling** |
| Group B1: | Modeling of pests |
| Group B2: | Modeling of pests |

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| Group B3: | Modeling of diseases |
| Group B4: | Modeling of diseases |
| 12:10 – 12:30 | Reporting to plenary: group B1 & B2 |
| 12:30 – 12:50 | Reporting to plenary: group B3 & B4 |
| 12:50 – 14:00 | *Lunch* |
| 14:00 – 15:30 | Working group C:**Capacity and needs for risk assessment under current and future climates** |
| Group C1: | Risk assessments for pests |
| Group C2: | Risk assessments for pests |
| Group C3: | Risk assessments for diseases |
| Group C4: | Risk assessments for diseases |
| 15:30 – 16:00 | *Coffee break* |
| 16:00 – 16:20 | Reporting to plenary: group C1 & C2 |
| 16:20 – 16:40 | Reporting to plenary: group C3 & C4 |
| 16:20 – 17:00 | Open discussion (J. Kroschel, F. Beed) |
| **Thursday, December 13** | |
| 08:00 – 08:30 | Orientation to group work and outputs (J. Kroschel, F. Beed) |
| 08:30 – 10:00 | Working group D:**Risk based surveillance strategies** |
| Group D1: | Risk based surveillance for pests |
| Group D2: | Risk based surveillance for pests |
| Group D3: | Risk based surveillance for diseases |
| Group D4: | Risk based surveillance for diseases |
| 10:00 – 10:30 | *Coffee break* |
| 10:00 – 10:20 | Reporting to plenary: group D1 & D2 |
| 10:20 – 10:40 | Reporting to plenary: group D3 & D4 |
| 10:40 – 11:40 | Working group E:**Detection and diagnostics** |
| Group E1: | Detection and diagnostics of pests |
| Group E2: | Detection and diagnostics of pests |
| Group E3: | Detection and diagnostics of diseases |
| Group E4: | Detection and diagnostics of diseases |
| 11:40 – 12:00 | Reporting to plenary: group E1 & E2 |
| 12:00 – 12:20 | Reporting to plenary: group E3 & E4 |
| 12:20 – 13:30 | *Lunch* |
| 13:30 – 14:30 | Working group F: **Data management and reporting** |
| Group F1: | Data management and reporting |
| Group F2: | Data management and reporting |
| Group F3: | Data management and reporting |
| Group F4: | Data management and reporting |
| 14:30 – 14:50 | Reporting to plenary: group F1 & F2 |
| 14:50 – 15:10 | Reporting to plenary: group F3 & F4 |
| 15:10 – 15:40 | *Coffee break* |
| 15:40 – 17:00 | Working group G:**Planning of products, milestones, outcomes, and responsibilities** |
| Group G1: | RTB Theme 3 |

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| Group G2: | RTB Theme 3 |
| Group G3: | CCAFS |
| Group G4: | CCAFS |
| **Friday, December 14** | |
| 08:30 – 09:00 | Orientation to group work and outputs (J. Kroschel, F. Beed) |
| 09:00 – 10:30 | Working group G (cont.): **Planning of products, milestones, outcomes, and responsibilities** |
| Group G1: | RTB Theme 3 |
| Group G2: | RTB Theme 3 |
| Group G3: | CCAFS |
| Group G4: | CCAFS |
| 10:30 – 11:00 | *Coffee break* |
| 11:00 – 11:20 | Reporting to plenary: group G1 & G2 |
| 11:20 – 11:40 | Reporting to plenary: group G3 & G4 |
| 11:40 – 12:30 | Final discussion; assignment of responsibilities; plan to disseminate for refinement and development of proposals |
| 12:30 – 14:00 | *Lunch & Faire well cocktail* |
| | *DEPARTURE* |

# THEME 1

## TARGET PESTS AND DISEASES:

## JUSTIFICATION AND DISTRIBUTION

**Banana and plantain: target pests and diseases**

**P. Lepoint[1], M. Dita[2], A. Molina[4], C. Staver[3], G. Blomme[1], E. Karamura[1]**

[1]Bioversity International Africa, [2]South America, [3]Montpellier, [4]Asia

A wide range of pests and diseases including fungal, viral and bacterial diseases, and nematodes and weevils affect banana and plantain (*Musa* spp.) production worldwide. In Asia, the primary center of origin of *Musa* spp., the major fungal diseases affecting bananas consist of Fusarium wilt (*Fusarium oxysporum* f.sp. *cubense*, *Foc*) including its most virulent strain the Tropical Race 4 (TR4) and black sigatoka (*Mycosphaerella fijienis*). *Mycosphaerella eumusa* causing banana leaf spot in India and Sri Lanka and Freckle disease caused by *Guignardia musae* are two emerging fungal diseases of importance in the region. Key virus diseases in Asia include Banana bunchy top disease (BBTD) and banana bract mosaic. Moko and Bugtok caused by (*Ralstonia solanacearum*) are serious banana bacterial diseases but so far limited to the Philippines, while Blood Disease caused by *Pseudomonas celebensis* (taxonomic identity is being established) are causing epidemics in Indonesia and Malaysia. Latin America and the Caribbean (LAC), although neither the center of origin of bananas nor a center of domestication or secondary diversity, grow 28% of the global *Musa* production and seven countries of the region are in the top 10 banana exporting nations. In spite of considerable technical change in recent decades, bananas in LAC continue to face important challenges for sustainable pest and disease management of *Foc*, banana rust thrips (*Chaetanaphothrips signipennis*), Erwinia soft rot (*Dickeya* spp.) and Moko (*Ralstonia solanacearum*). While the latter are specific to certain production systems, *M. fijienis* is still the major phytosanitary challenge for banana production in LAC and Foc TR4 and BBTD are listed as quarantine diseases. In Africa, center of secondary diversification for the East African Highland bananas (EAHB) and plantain, key pests and diseases include BBTD, banana Xanthomonas wilt (XW), black sigatoka, weevils and nematodes, of which some singly or in various combinations cause major damage in Cavendish, EAHB and plantain systems significantly reducing yield. The continent is dominated by smallholder systems, often perennial and subtended by informal seed systems with minimum attention to seed quality. Foc TR4 is equally listed as a quarantine disease in Africa whereas XW is endemic to the African continent and was first described on *Musa* in 1974. A systematic prioritization of banana pests and diseases is currently under way to guide research investment. Steps include mapping of cultivar group/production system, estimation of yield impacts of pests and diseases, review of current production practices, technology under use and costs of production.

## Cassava: target pests and diseases

**B.V. Herrera Campo, J.M. Pardo**

Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia

Cassava production worldwide is significantly affected by pests and diseases. Although the cassava pest complex is large, the most limiting pests are mites, mealybugs and whiteflies. Several caused by viruses, fungi, bacteria, phytoplasma are also of significant concern. CIAT's phytosanitary research has focused on a few species, prioritized on their economic impact and their potential risk of introduction into important production centers, where they are absent. Recent efforts have been made in order to know the current and the potential distribution of cassava green mite, cassava mealybug and the whitefly, regarding pests, and Cassava Mosaic disease, Cassava Brown Streak disease and Cassava frog skin disease, concerning to diseases. Cassava mealybugs and mites are present in South America, their origin center, and Africa, where they caused considerable losses after being introduced in 1970´s. They were successfully controlled in late 1980´s. Regardless the large absent of these pest in Southeast Asia, cassava production areas become threatened in the last years, due to recent introduction of the cassava mealybug and a cassava mite in this area. Results from species distribution models carried out at CIAT show that environmental conditions ensure the potential establishment of these pests. Whiteflies are widely spread pests, directly affecting cassava. Their importance varies between different regions and continents. However, their major risk refers to their capacity to transmit several cassava-related viruses. Most important diseases affecting cassava in Africa are Cassava Mosaic disease and Cassava Brown Streak disease. The former´s distribution embraces the entire cassava belt in Africa and the western coast of India where cassava is cultivated. The latter was largely confined to the Eastern coast of the continent but recently has moved to other central places in the continent. Cassava Frog Skin disease is an important constraint to cassava production in some areas of Latin America and cassava bacterial blight is the major issue in Asia.

## Potato and sweetpotato: target pests

**J. Kroschel**

International Potato Center (CIP), Lima, Peru

Potato producing farmers in developing countries worldwide have to contend with about 20 insect pests. The potato tuber moth, *Phthorimaea operculella*, and the Andean potato tuber moth, *Symmetrischema tangolias,* have evolved in the center of potato origin. *P. operculella* has become very invasive and is reported from more than 90 countries worldwide. It is considered the most damaging potato pest in the developing world. The Andean potato tuber moth is widely distributed in the Andean region; it is less invasive but has been also reported outside its range of origin; e.g., Australia. The Guatemalan potato tuber moth, *Tecia solanivora,* started invading South America in 1983 and reached Ecuador in 1996. In 2000, it reached the Canary Islands (Tenerife) and is considered major threat to potato production of southern Europe. The leaf miner fly *Liriomyza huidobrenis*, also of neotropical origin, is reported today from 66 countries; recently we could report its occurrence in Nepal. The bud midge, *Prodiplosis longifilia,* can be very damaging and is likely to become more invasive under climate change. The green peach aphid (*Myzus persicae*), the potato aphid (*Macrosiphum euporbiae*) and cutworms (*Agrotis* spp.) are found worldwide. Aphids are mainly a risk for virus infection and seed degeneration. Cutworms are extremely polyphagous and damaging in the Hindu Kush-Himalaya. The Colorado potato beetle, *Leptinotarsa decemlineata*, which originated in central Mexico, has become the main threat to potato production in developing countries of Central Asia, the Caucasus, and has also been reported from western China.

Sweetpotato weevils (*Cylas* sp.) are the most serious insect pests of sweetpotato in Central America, Africa and Asia; *C. formicarius* is found globally, whereas *C. puncticollis* and *C. brunneus* are reported only from Africa. These are considered as the main target pests although a large complex of pests may occur regionally, e.g. in East Africa consisting of: (i) stem and root feeders, (ii) defoliators, and (iii) virus transmitters.

## Potato and sweetpotato: target diseases

**J. Kreuze, G. Forbes, L. Gutarra**

International Potato Center (CIP), Lima, Peru

A very large number of pathogens have been reported in association with potato production, but a smaller number of them are generally considered to the primary agents of disease worldwide. One of the primary potato diseases is late blight caused by the oomycete pathogen *Phytophthora infestans.* Late blight is a global problem and its significance in terms of both yield loss and fungicide usages has been estimated to be over 10 billion USD annually. Bacterial wilt, caused by *Ralstonia solanacearum* is a major disease in many parts of the developing world, particularly in warm, humid areas. *R. solanacearum* is a soilborne pathogen mainly transmitted through tuber seed leading to a condition often referred to as seed degeneration. Similarly, a number of viruses also accumulate through generations and participate in seed degeneration; the most important seed degeneration viruses are PVY and PLRV, and to a lesser extent PVX. Other mild viruses such as PVS, PVM, PVA, PVV are also widespread and may contribute to degeneration of potatoes, but their presence in developing countries has not been systematically surveyed in many places and the effect on yields poorly quantified. Surveys on native potatoes in Peru and Ecuador determined the high incidence of PVX and PVS viruses however their infection not always were related to decreased performance on some native varieties. Several other viruses such as APMV, PYVV, APLV, PYV, PVT, AMV, PAMV, and PBRSV are only important in Latin America whereas Potato spindle tuber viroid and phytoplasma diseases may be of importance locally in some regions. As with bacterial wilt, several pathogens may be seed- and soilborne pathogens (e.g. *Rhizoctonia solani, Streptomyces* spp*.* and *Clavibacter michiganensis* subsp. *sepedonicus*) and may participate in seed degeneration, which overall is probably the main biotic constraint to potato productivity in developing countries. There are several diseases which have local importance, and may also be considered quarantine problems. Powdery scab, caused by *Spongospora subterranea* and potato wart, caused by *Synchtrium endobioticum,* are diseases caused by pathogens with a great survival capacity reason by wich they are very difficult to manage. The bacterial complex of black leg and soft rot caused by *Pectobacterium* spp. and *Dickeya* spp. can be extremely severe under the conducive environmental conditions, although we are unaware that *Dickeya* spp*.* have been reported in developing countries. Nematodes of the species *Globodera* spp. in temperate regions and highlands and *Melodoigyne* spp. in warm areas are widespread and can cause significant damage also by increasing the incidence of other bacterial and fungal diseases on roots.

The major disease problem of sweetpotato on a worldwide scale is caused by viruses which often occur in a complex reducing yield considerably. Of the about 30 known sweetpotato infecting viruses the most widespread are Sweet potato feathery mottle virus and Sweet potato virus C, and Sweet potato chlorotic stunt virus (SPCSV). Recently it has been realized that sweetpotato begomoviruses or ‘sweepoviruses’ are also very common worldwide, although their impact is not clear yet as they have been relatively little studied. Whereas most sweetpotato infecting viruses (with the exception of SPCSV) often cause no, or only mild symptoms in most sweetpotato cultivars, mixed infection with SPCSV causes increased titers with all currently investigated viruses and severe disease complexes with many of them. Therefore SPCSV is probably the single most serious disease problem for sweetpotato worldwide. Nematodes (particularly *Meloidogyne* spp.) are also a significant problem in many sweetpotato producing areas. Numerous bacteria and fungi, including *Ceratocystis fimbriata, Altenaria bataticola, Elsinoe batatas, Fusarium solani, F. oxysporum, R. solanacearum, Rhizopus stolonifer, Diplodia* gossypina, *Macrophomina phaseolina, Streptomyces ipomoeae, Dickeya sp.(E. chrysanthemi)* have also been reported to cause various types of root or stem rot diseases or foliar blemishes, although they are much less important on a global scale and/or only important locally.

## Banana, cassava and yam: target pests and diseases

**F. Beed**

International Institute for Tropical Agriculture (IITA), Dar es Salaam, Tanzania

Cassava is a staple food across Africa, banana across the great lakes region and yam is a favored food in West Africa. All three crops are of critical importance to food security and income generation to Africa. While cassava and banana have been introduced to Africa from Latin America and Asia, respectively, yam is indigenous. The productivity of all three crops is threatened by current and emerging pests and diseases that are indigenous to Africa, and further, due to the potential introduction of other pests and diseases from elsewhere in the world. Taking cassava as an example; indigenous pathogens and pests include African cassava mosaic virus, East African cassava mosaic virus complex, South African cassava mosaic virus, whiteflies, fungal diseases and root scales. However, some of the most devastating viruses have restricted distribution such as brown streak, Ugandan brown streak virus and East African mosaic virus – Uganda (EACMV-UG). Exotic pests that are now established on cassava in Africa include Green spider mite (*Mononychellus tanajoa*), Cassava mealy bug, (*Phenacoccus manihoti*), Cassava Bacterial Blight (*Xanthomonas axonopodis*) and Indian cassava mosaic virus. While important pests and pathogens not present in Africa but present in South America include; common mosaic virus, green mosaic virus, vein virus, X virus, Frog Skin Disease, antholysis, Super Elongation (*Sphaceloma manihoticola*) and from southeast Asia; witches broom (Phytoplasma) and from South Asia; Sri Lankan mosaic virus.

For banana an indigenous bacterium that is spreading across the great lakes region and devastating production is Xanthomonas Wilt (*Xanthomonas campestris* pv. *musacearum*) while another bacterium, *Ralstonia solanacearum* Race 2, that causes Moko disease, is currently restricted to Australia, South Pacific and Latin America. A fungal disease caused by *Fusarium oxysporum* f.sp *cubense* is divided into different races based on which clones are attacked. Races 1 and 2 are already established in Africa; race 1 attacks clones of AAA, AAB, ABB and AAAA while race 2 attacks ABB and AAAA clones. Perhaps the greatest threat to banana production in Africa, and potentially the world, is Tropical race 4 (TR4) of this fungus. This is because it kills all clones susceptible to race 1 and 2 plus cultivars in the Cavendish clones (AAA) which were specifically bred for resistance to race 1. Currently TR4 is spreading from Southeast Asia and Australia to China and beyond. Another disease, caused by a virus, that is increasingly devastating all clones of banana in Africa, is a variant of Banana Bunchy Top Disease that is more virulent than other forms elsewhere in the world.

A risk assessment will be provided, based on distribution and impact of pests and diseases of cassava, banana and yam, to prioritize those that justify management interventions such as targeted surveillance, to prevent their introduction, establishment and spread.

## THEME 2

## PEST, DISEASE AND WEEK RISK ASSESSMENT

## AND MODELING UNDER CURRENT

## AND FUTURE CLIMATES

**Predicting crops risks under climate change: progress and opportunities**

**A. Challinor**

University of Leeds, UK

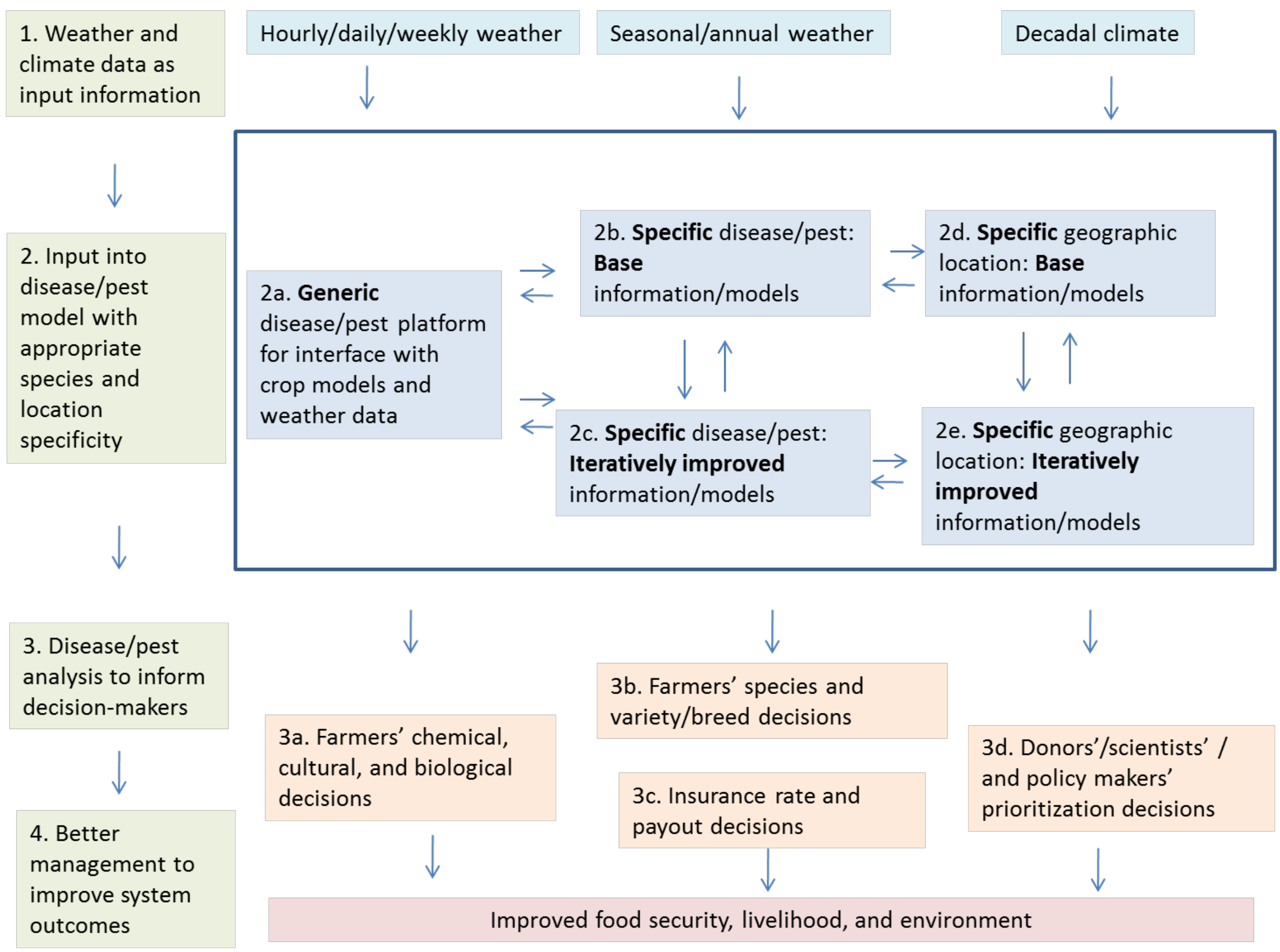
Over the last decade, there have been significant advances in the combined simulation of climate and crop yield. Ensemble techniques to quantify uncertainty are now routinely used, and crop model inter-comparisons' are starting to occur. After a review of these techniques, two areas for future development are suggested: i. greater integration of crop models with models of pests and diseases; ii. greater awareness of the uncertainties inherent in downscaling and climate model bias correction; and ii. re-framing the way in which uncertainty is presented in order to obtain robust information on when changes are expected to occur.

## Platform for pest and disease risk assessments under climate change

**K. Garrett and CCAFS scoping study team**

Kansas State University

Based on the scoping study, we recommend that CCAFS participants work together to assemble and evaluate a general platform for pest and disease models, to the extent useful. Points for synergy would include: 1. Use of shared global and regional weather and climate databases as input; 2. Use of shared programs for predicting losses to pests and disease, where the core models will differ from one pest/disease to another, but the general programming structure for estimating risk and yield losses can be similar; 3. Use of shared conceptual frameworks for how the core pest/disease models can be used in within-season forecasting, seasonal forecasting, scenario analysis and prioritization, and potential index insurance programs; 4. Use of shared platforms for communicating results to stakeholders; 5. Use of shared methodologies for evaluating the impact of CCAFS activities and forming strategies to increase impact.



## Climate change adaptation in disease management: a framework for evaluating the likely utility of decision support systems and index insurance

**K. Garrett, G.M. Ramirez, B. Natarajan**

Kansas State University

The same core models of the relationship between weather and loss to viruses are needed for climate change scenario analysis, decision support systems (DSS), and other potential applications such as index insurance. We have developed a framework for evaluating the likely effectiveness of DSS and index insurance for pests and diseases, as a function of a number of key factors. First, we consider the time series of weather conditions, in terms of baseline temporal autocorrelation and the type of non-stationarity imposed by climate change, and how these patterns make DSS and index insurance more and less feasible. Second, the framework within which the DSS is constructed is considered, in terms of the number of years of data available and how good initial parameter estimates are. We use these system traits to identify parameter combinations or scenarios where DSS and index insurance are likely to be effective or not. We are beginning the work of placing particular diseases and geographic locations in the theoretical parameter space. Ultimately we plan to use this framework to identify pathosystems and locations that are particularly good targets for implementing tools such as DSS and index insurance. We also are addressing the general question of when DSS developed in baseline climate scenarios can still work well in new climate scenarios, versus when DSS must be modified to maintain utility.

## Disease risk assessments and modeling at IRRI

**A. Sparks**

International Rice Research Institute (IRRI), Los Banos, The Philippines

IRRI is actively working to better understand and mitigate uncertainty in rice yields due to short and long-term changes in weather patterns and concurrent shifts in pest and disease severity and distribution. This work focuses both on in-field research and modeling efforts. In-field research is being undertaken to characterize change in diseases due to the transformation of production situations and provide data for modeling efforts. Currently two models are being developed and used by IRRI. EPIRICE predicts the severity of unmanaged epidemics for five rice diseases using weather data. RICEPEST is a mechanistic model capable of simulating yield losses due to six diseases, three insect injuries and a range of weeds using weather and field observation data. Using these models it is possible to estimate relative risks and yield losses under current and future climate conditions for select pests and diseases.

## Disease risk assessments and modeling at CIP

**G. Forbes, J. Kreuze**

International Potato Center (CIP), Lima, Peru

In CIP, plant disease risk modeling and assessment has been primarily limited to potato late blight with some recent activities on potato and sweet potato viruses. Late blight has been modeled at the plot level for research purposes using a process based simulation model. Late blight risk is also estimated at the plot level using simple decision support systems adapted low input farmers. At a larger scale, a disease forecasting model was incorporated into a geographical information system (GIS); this gave the potential for estimating potential disease intensity at various spatial scales. This technology has since been modified to use geo-referenced weather data of much lower temporal resolution, and has been used to estimate effects of climate change. Pathogen evolution for pathogenicity has been of major concern at CIP and efforts to estimate risk are currently underway. Risk of late blight pathogen evolution for fungicide insensitivity has been monitored, which can also provide some degree of predictability because of the clonal nature of the pathogen. Overall risk to farmer health and environment has been estimated using the environmental impact quotient. Recently siRNA technology is being used to monitor viruses in sweet potato and to a lesser degree potato, which can provide insight into the risk of emerging diseases. This technology is discussed more in the session on monitoring.

## Insect pest risk assessments using phenology modeling

**J. Kroschel, H. Tonnang, H. Juarez**

International Potato Center (CIP), Lima, Peru

Temperature has a strong and direct influence on insect development, reproduction and survival and is considered under climate change the dominant abiotic factor directly affecting herbivorous insects (pests). It is also expected that climate change may dissociate predator-prey relationships, because of a higher sensitivity of higher trophic levels to climatic variability or of different temperature optima compared with pests. Two modeling approaches are used to understand and predict effects of increasing temperature on insects: the inductive modeling approach uses the combination of occurrence records and environmental variables and through the application of climate match functions it estimates the establishment potential of a species to new areas. Limitations are that it does not consider detailed biological characteristics of the insect in the modeling framework. It uses degree day models which describe the linear development of insects using the accumulation of temperature above the min. temperature threshold. However, due to the non-linearity of the development curve degree-day models are poor predictors of insect development. Advantages are that it can use minimal data sets and simple functions to describe the species' response to temperature and other climatic factors, which allow quite quick assessments. Software programs which support such kind of modeling are CLIMEX, BIOCLIM and others. The deductive modeling approach uses a process-based climatic response model (i.e., phenology model) for a particular insect species of interest. The temperature dependency of insects is applied in a process-oriented framework; forecasting the potential distribution of insect species is completely independent of observed occurrences. The Insect Life Cycle Modeling (ILCYM) software, developed by CIP, supports the development of process-based temperature-driven and age-stage structured insect phenology models and applies these models in a GIS environment for insect species distribution and risk mapping. For studying the effects of climate change on insects the software provides downscaled future climate scenarios from different projections (e.g., SRES-A1B of the year 2050). The potato tuber moth will be used as an example to demonstrate modeling outputs and global and regional risk maps.

## Insect Life Cycle Modeling (ILCYM) software for phenology models development and life table parameters estimation

**H. Tonnang, H. Juarez, J. Kroschel**

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The relationship between aspects of insects' life-history (development, survival, reproduction, etc.) and environmental variables (temperature) can be well described by process-based phenology models. The present paper describes the model builder of the Insect Life Cycle Modeling (ILCYM) software as a tool to support the development of process-based temperature-driven and age-stage structured insect phenology models. ILCYM's model builder contains a library of several empirical linear and nonlinear models, including the derivations of the biophysical models which have been proposed to define critical temperatures of insects' development. Several statistical measures are provided for the estimation of parameters and the comparison models. Additionally, phenology models can be applied for estimating insect population increase and abundance using deterministic and stochastic simulations under constant and fluctuating temperatures. Outputs of the simulations are life table parameters that include net reproduction rate, mean generation time, intrinsic rate of increase, finite rate of increase and the doubling time. Through these analyses, the biology and temperature requirements of insects can be defined, as well as the effects of different diets or host plants on insects' life table parameters. ILCYM also supports investigation between natural enemies (e.g., parasitoids) interactions and its target pests as well as the natural enemy potential control efficiency in integrated pest management system. Further, possible outbreaks of pest populations in relation to changes in temperature can be simulated.

**Spatial analysis tools in ILCYM software for risk assessments**

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ILCYM is an open-source computer-aided tool built on R and Java codes and linked to uDig platform, which is a basic geographic information system (GIS). The software package consists of three modules the "*model builder*", the "*validation and simulation*", and the "*potential population distribution and risk mapping*". This paper only focuses on the GIS component of ILCYM. Under this later module, insect phenology models are simulated in a defined area according to grid-specific daily/monthly temperatures obtained from available databases. Outputs of the simulations are used for calculating life table parameters that include: the net reproduction rate, mean generation time, intrinsic rate of increase, finite rate of increase and the doubling time. From life table parameters, three indices are estimated (the establishment risk index (*EI*), the generation index (*GI*) and the activity index (*AI*)) and mapped for assessing the potential population distribution and abundance of a particular species. Several functionalities for vector (dbf to shape, raster to points, raster to polygons, extract by points, etc.) and raster analysis (merge, cut, mask, aggregate/disaggregate, re-class, describe, raster calculator, etc.) are part of the ILCYM-GIS component. Such tools improve the manipulation of large datasets and help ILCYM's users in analyzing and visualizing the risk assessment maps. Additionally, a sub-module (*index interpolator*) for analysing the index at higher spatial (pixel size of 90m) and temporal resolution (daily data) for capturing small-scale of insect population distribution and abundance is also presented.

## Weed and pest risk assessments with Maxent

**R. Simon**

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Distribution modeling of biological species is an important tool for biologists to understand and predict past, current or future presence based on typically few observations on the ground. Applications include species under threats like climate change or predictions of epidemic outbreaks of organisms damaging to health or food production. Three main classes of modeling tools are available: a) mechanistic models like the EcoCrop approach; b) process oriented models like ILCYM or c) probabilistic or machine learning tools like MaxEnt. There is currently no consensus on a best modeling tool or approach across biological taxa for different reasons. These include for regression approaches the problem of presence only data - that is, the need for absence data. However, assumption or imputation of absence data is unreliable. Similarly, data obtained under laboratory conditions may not be of value for extrapolation under in-situ conditions since many organisms act like integrative sensors. Therefore, the predictive value of independent variables like temperature may be changed. However, recently the maximum entropy approach as implemented in MaxEnt has shown success across a wide taxonomic range. We therefore review the basic algorithm of Maxent and compare it to the other two approaches. We use it for three applications: a) predicting the distribution of a wild potato species with a well defined habitat; b) a weedy potato species and c) for predicting one insect species (*Phthorimea operculella*).

## Linking crop and pest models for assessing risks on crop losses using intelligent systems

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Proper estimation of actual crop yield with the help of computer assisted simulation models requires detailed quantitative knowledge of the interactions between the crop and its pests. Because of the complexity of such systems, most crop growth models do not include routines for the simulation of damage caused by pests. In this paper, novel ways for linking pest and crop models via intelligent systems are presented. A detailed example of linking the Insect Life Cycle Modeling (ILCYM) software to a potato crop model using fuzzy logic system is given. The framework is based on coupling pest damage of various types into the crop model. Coupling points are identified in the model for simulating damage to leaves, stems, roots, seeds, whole plants, and to the supply of assimilate. This intelligent model coupling is being developed and will be tested by simulating potato yield with measured pest damage levels due to *Liriomyza huidobrensis* (foliar feeding insect) and *Phthorimaea operculella* (foliar and tuber insect) and comparing observed and simulated crop growth and yield results. Such approach for coupling pests with crop models has potential for extending the practical applications of crop models to a broad range of problems.

## Towards an integration of crop simulation and insect population dynamics models to estimate climate change impact on productivity due to insect pests

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Climate change will affect the incidence and distribution of plant pests. The range of many insects' species will expand or shift their distribution and new combinations of pests and diseases may emerge as natural ecosystems are altered by changes in weather variability and the occurrence of extreme weather events. More needs to be known about these changes to adapt production systems and pest management strategies. Research based on systematic experimentation is expensive and time consuming, especially given the urgency of climate change impacts. Moreover, perennial crops need extended observation and large areas for experimentation. Simulation models can complement experimental approaches to assess the possible effects of climate on pests and, ultimately, on crop productivity. However, to do this for a wide range of crops and varieties, we need crop models integrated with insect population dynamics. The aim of our research is to integrate two existing models to achieve this goal, making use of existing models for banana. We report on two activities that contribute to this overall aim: (1) a preliminary co-validation of ILCYM for banana weevil (*Cosmopolites sordidus*), comparing with an existing model COSMOS and using data derived from the literature, and (2) a reimplementation in R of InfoCrop, a generic, daily time step crop model, which has been used for perennial crops. We also discuss the prospect of integrating InfoCrop and ILCYM, and further (co-)validation of this approach.

## Risk Assessment and Modeling: CIAT

**S. Parsa**

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Under the pest risk analysis paradigm, risk assessment is the obligate prerequisite for risk management. The process for risk assessment is often divided into three steps: (1) pest categorization, (2) assessment of the probability of introduction and spread, and (3) assessment of the potential economic consequences. Risk assessment work at CIAT has focused on the second of these steps; more specifically, on environmental suitability assessments via species distribution modeling. Both statistical and mechanistic models have been used to assess global environmental suitability for critical cassava pests and diseases. Our approach has been integrative; taking advantage of ensemble modeling techniques and joint inductive-deductive approaches to derive the "best" risk maps given available data. Ongoing efforts seek to refine modeling expertise; but more importantly, to broaden capacities for pest risk assessment and analysis.

**Risk Assessment and Modeling: CIMMYT**

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Climate change will contribute to increased prevalence of insect pests in many agro –ecosystems. The spotted stem borer (Crambidae: Lepidotera), maize weevil and the larger grain borer (Bostrichidae: Coleoptera), are key economically important pests of maize that impacts on millions of African's livelihoods. The former infests cereal crops in the field while the latter two attacks cereal grain in storage. Larger grain borer is an invasive exotic pest that has shown resistance to commonly used insecticide and its expansion to new area could threaten the grain industry and contribution of agriculture to the GDP due to its feeding activities in converting grains into flour. Further, the new range of expansions could present economic impacts through increased seed and insecticide costs and food security. The focus will be directed towards generating missing gaps in life tables' data, based on literature review, to estimate the pest threshold requirements for development time, fecundity and longevity using Insect Life Cycle Modeling (ILCYM) software to project potential future ranges under changing climate. The data will be generated under temperature conditions of 10 – 35$^{o}$C in steps of 5$^{o}$C and humidity of 40 -75 % in steps of 5% in the laboratory.

## Risk Assessment and Modeling of Biotic Stresses in ICRISAT Mandate Crops

**H.C. Sharma, S. Pande, M. Sharma, H.K. Sudini, R. Sharma, G.V. R. Rao**

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Climate change is likely to make rainfed agriculture even more risk prone in the semi-arid tropics (SAT), and the crop and pest management systems need to adapt to these changes at a faster pace in the near future. However, the exact nature of these changes is quite uncertain. The major areas of our research effort on insect pests is focused on and predicting potential risks, changes in geographical distribution, and modeling population dynamics of legume pod borers, *Helicoverpa armigera*, *Maruca vitrata*, defoliators, *Spodoptera litura* and *S. exigua*, spotted stem borer, *Chilo partellus*, and sorghum head bugs, *Calocoris angstatus* and *Eurystylus oldi*. We are also studying the effects of climate change on pest incidence and population dynamics of the target pests and their natural enemies. In grain legumes, the historical information on wilt and dry root rot in chickpea; and wilt, sterility mosaic, and *Phytophthora* blight in pigeonpea as impacted by climate change is being analysed to predict the likely effects of climate change on disease severity in these crops. Investigations are also in progress on the effect of epidemiological parameters on *Phytophthora* blight disease development in pigeonpea under greenhouse conditions. In dryland cereals, blast disease caused by *Magnaporthe grisea* has emerged as a new threat to pearl millet production in India. We are studying the effect of weather variables on blast development in pearl millet. In groundnut, we will validate a model for the severity of late leaf spot. The studies on climate effects on biotic stresses are aimed at gaining a better understanding of the effect of climate variability and global warming on pest – host – environment interactions to develop strategies for mitigating the effects of climate change on crop production in the SAT Asia and Africa.

**Pest Risk Assessments and activities on modeling impacts of climate change on pest dynamics at icipe**

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Indigenous and invasive insect pests and diseases are key constraints to crop productivity and better livelihoods in Africa. Dynamics of these pests, diseases and their natural enemies are influenced by several biotic and abiotic factors. Climate change affects these biotic and abiotic factors and thereby disturbs their entire dynamics. Globalization and movement of commodities and communities across borders has increased the risk of accidental introductions of Alien Invasive Species (AIS) that negatively impact on agriculture. This is exacerbated by ineffective natural regulatory factors. Surveillance and pest risk assessments for development of develop timely management strategies were undertaken at *icipe* for indigenous and invasive species such as cereal stem borers including *Chilo partellus* and *Busseola fusca*; fruit flies including *Bactrocera invadens*; the tomato red spider mite, *Tetranychus evansi*; red palm weevil, *Rhynchophorus ferrugineus*; the coffee berry borer *Hypothenemus hampei* and *Iris yellow spot virus.* Ecological Niche Modeling like Maximum Entropy (MAXENT), Genetic Algorithm for Rule Set Production (GARP) and Climate and population modeling software (CLIMEX) were used for predicting pest distributions and risk assessments. The modeling approach also guides exploration for potential natural enemies for introduction into Africa for biological control of the target pests. *icipe* in collaboration with International Potato Center (CIP) is elucidating the impact of climate change on pest and disease dynamics through pest risk mapping with temperature dependent life table-data based insect phenology models using Insect Life Cycle Modeling software (ILCYM) for cereal stem borers and their parasitoids, western flower thrips and *Liriomyza* leafminers. Similar activities are also planned with the diamondback moth and their parasitoids, bean flower thrips, natural enemies of the coffee berry borer, avocado thrips and fruit borers. Montane ecosystems are characterized by graded changes in regional climate and associated agro-ecologies across altitudes and can act as surrogates for future climate change scenarios. *icipe* is evaluating the dynamics of key pests of maize, coffee, crucifers and avocado across altitudes in three montane ecosystems of East Africa. Such dynamics will be modeled with downscaled weather data sets derived from a network of existing and newly installed automatic weather stations and data loggers across altitudes to predict impacts of climate change. Predictions using ecological niche- and phenology modeling will be compared and refined with other geospatial data layers such as plant and soil characteristics, hydrology, crop seasonality, land cover and land use-changes*.* The uncertainties of various climate change models will be assessed with a Multi-model Ensemble using the CORDEX–Africa program. The optimal models will be used to predict target species distribution in present, past and future climate change scenarios.

## Risk Assessment and Modeling: IITA

**M. Tamò, F. Beed, G. Goergen, R. Hanna, D. Coyne, P. van Asten, J. Legg**

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Recent and current efforts at IITA to assess risks due to the various biotic stresses, arthropod pests and diseases, are presented for different cropping systems. In the case of cassava arthropod pests, the focus is on temperature-mediated interactions between the pest and its natural enemy which has been introduced to keep the former under control. Modeling approaches are currently on-going for the cassava mealybug *Phenacoccus manihoti* and its hymenopteran parasitoid *Anagyrus lopezi*, the green mite *Mononychellus tanajoae* and its phytoseiid predator *Thyphlodromalus aripo*, the fruit fly *Bactrocera invadens* and its parasitoid *Fopius arisanus*, and the banana aphid *Pentalonia nigronervosa* as a single species model. Preliminary results from these studies indicate a higher risk for natural enemies to be affected by increasing temperatures due to their generally smaller size than the pest. Also, possible asynchronization of the pest-natural enemy is being investigated. In cowpea, experiments have just begun to assess the complex interactions between different drought regimes, beneficial microorganisms such as the endophytic entomopathogenic fungus *Beauveria bassiana* and mycorrhiza, the cowpea plant and one of its key pests, the legume pod borer *Maruca vitrata*. The first sowing date in the rain-out shelter has been harvested, and the data show a negative correlation between the intensity of drought stress and infestation by the pod borer. Cowpea plant co-inoculated with both the endophyte and mycorrhiza were less affected by the drought, and had also less damage by the pod borer. Detection of the endophyte in various plant tissues (roots, leaves, flowers and pods) will be carried out by PCR using *B. bassiana* specific SCAR markers. The experiment is planned to continue until March 2013, and is currently replicated under field conditions. For banana weevils *Cosmopolites sordidus*, our data suggest a positive correlation between temperature and yield loss attributable to increased infestation levels by the weevil. Also, the range of expansion of the weevil in higher altitudes needs to be investigated in more details. This is also the case for white flies attacking cassava and transmitting the devastating CMV and CBSV. With a change in climate and ambient temperature, so likely will the distribution of nematode pests. The three major groups of nematode pests, cyst, root knot and lesion nematodes, have already been predicted to expand in their geographical range according to World Bank studies. However, a major impact of climate change will be through more irregular or reduced availability of water. Under lower water availability nematode damage to roots will further limit water access by plants, in effect exacerbating the effects of climate change. Thus, while there is general consensus for a greater need of drought resistant crops and varieties, a similar, or greater need for root pest and disease resistance is also needed, but often overlooked. A further impact of climate change will be through expanded ranges of nematodes due to changes in temperature. The potential impact of *Radopholus similis* on bananas in the East African Central Highlands illustrates this well. Currently, the nematode occurs only up to approximately 1400 m asl, due to temperature limits. A rise in temperature would result in a corresponding rise in *R. similis* damage at higher altitudes. For plant viruses, the main thrust of our efforts is concentrating on diagnosis for disease surveillance and early warning, and developing mitigating the climate change effects on disease emergence and outbreaks.

**Drivers of Change and Adaptive Capacities in the Andes**

**Corinne Valdivia, University of Missouri, USA**

A research program on adapting to change in landscapes of the Andes [1] identifies climate change as one significant driver of change in the production systems and livelihood strategies of farmers. Increase temperatures are allowing farmers to introduce new varieties, changing farming systems. Simultaneously the intensity of dry periods and rainfall are also shocks to the production system. The impacts and issues at the local level are influenced by geography, ecology and market access. Population growth and resulting land fragmentation, have reduced the fallow period in some regions. Farmers perceive that pests and diseases are a high threat to their livelihoods at the local level. Adaptive capacities can be strengthened through translational research (participatory, interdisciplinary and involving stakeholders and local decision makers). The intersection of climate and livelihoods implies development of risk management strategies. The uncertainty grows when climate conditions change, which has an effect on how people make decisions. We find that the dread and risk felt by decision makers in the Altiplano are shaped by geography and level of food insecurity. The higher the uncertainty and insecurity, the lower the trust of new information and ability to adopt. Linking knowledge systems through participatory processes facilitates development of capacity to adapt to new contexts. Participatory process facilitate the mutual learning, and the focus on short term, linking risk management with medium and long term adaptation, can facilitate action by vulnerable decision makers.

[1] Sustainable Agriculture and Natural Resource Management Collaborative Research Support Program (SANREM CRSP) Co-PIs include: J. Gilles & P. Motavalli, University of Missouri; Karen Garrett, Kansas State University; Anji Seth, University of Connecticut; Elizabeth Jiménez, Universidad de la Cordillera; Jorge Cusicanqui, Universidad Mayor San Andres; Javier Aguilera, and Miguel Angel Gonzales, PROINPA; Cecilia Turin and Edith Fernandez Baca, Universidad Nacional Agraria La Molina

## THEME 3

## RISK BASED SURVEILLANCE

**Regulation of pest to protect trade and plant health**

**O. Sosa**

FAO-IPPC, Rome, Italy

The International Plant Protection Convention is an international agreement on plant health with 177 current signatories. It aims to protect cultivated and wild plants by preventing the introduction and spread of pests. The Secretariat of the IPPC is provided by the Food and Agriculture Organization of the United Nations. The IPPC provides an international framework for plant protection that includes developing International Standards for Phytosanitary Measures (ISPMs) for safeguarding plant resources. The IPPC is recognized by the WTO-SPS agreement as the standard setting organization for global plant health. The presentation will highlight key definitions used in the convention with relevant to pest regulation and introduces the IPPC framework for pest regulation. It will underscore the key activity of Pest Risk Analysis as the basis countries by which countries prepare the requirements to trade commodities and protect plant resources in their territories. The principal steps involved in the PRA will be briefly reviewed. It underscores the importance of pest surveillance and pest diagnostics as key to support the conduct of PRA and the preparation of regulated pest lists and by extension key enabling activities for countries to regulate pests.

# Targeted surveillance to promote food security

**Mike Robson**

FAO-AGP, Rome, Italy

## Sampling strategies for trade shipments

**J. Smith**

Food and Environment Research Agency (FERA), Sand Hutton, York, UK

Plant pathologists often give undue emphasis to the efficacy of the diagnostics and insufficient attention to how the diagnostics can be applied. Yet the challenges associated with sampling and the positioning of the diagnostic in time and space are considerable and fundamental to realising the value of a diagnostic test. In this context a critical initial question relates to what is it I need to be able to say; what is the policy position I need to support. And there are many questions that will require distinct sampling and testing approaches. By example of a few: Freeness from a pest in seed, or for a level of tolerance, as with seed certification schemes; in a pest survey to establish prevalence of a common pest, or to ascertain if a pest is absent or of limited distribution; to assess for GM or aflatoxin contamination in grain shipments; inspection regimes at portside for purposes on regulation and monitoring of trade. Layered on these questions is consideration of the target. How easy is it to diagnose? Is it likely to be uniformly distributed or clumped? The lack of homogeneity of aflatoxin in grain provides for particular challenge in sampling. Then there is the layer of resources, both human and infrastructure, and what is practicable and affordable, relating to issues of a governments willingness to accept the costs of testing, or if the costs can be borne by, or shared with, the private sector. These factors all boil down to a position of what is it I need to be able to prove and what uncertainty can I support in my answer i.e. do I have to be with 95% confidence in detecting a zero, 1 or 5% level of pest prevalence in grain or in seed, or in stating an area is free of a named pest. Brief review of some of these aspects will be given.

## THEME 4

## CURRENT SURVEILLANCE STRATEGIES

## Current surveillance strategies for banana pests and diseases

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Early diagnostic of plant diseases is a critical step for preventing pathogen dissemination, precluding incursions into areas where the disease has not been observed and reducing the inoculum pressure. This is especially true for tropical race 4 (TR4) of *Fusarium oxysporum* f.sp. *cubense* (*Foc*), the causal agent of Fusarium wilt of bananas. *Foc* TR4 is a quarantine pathogen in many *Musa* spp. producing regions of the world and considered a major threat to the banana industry. Trading of symptomless, but infected banana planting material, movement of machinery with adhering infested soil and contaminated irrigation water facilitate the spread of *Foc*. A PCR-based detection tool for TR4 has been developed and subsequently improved (nested and qPRCs) enabling detection at different levels, including symptomatic and symptomless banana tissues, soil and water. In parallel, the use of Vegetative Compatibility Group (VCG) pairing with international VCG-tester sets has enabled the identification of nine VCGs (1213/16, 0120/15, 0121, 0123, 0124/5, 0126, 0128, 01218, 01220) in Asia. VCG1213/16, the group that comprises *Foc* TR4, was the dominant VCG from samples collected in China, Indonesia, Malaysia, Philippines, and Taiwan but not found in samples from the other countries. VCG 0124/5, a VCG associated to *Foc* Race 1, was the dominant VCG in samples from India, Bangladesh, Cambodia, Sri Lanka, Vietnam, and Thailand. No *Foc* infection of banana was found in Papua New Guinea. Awareness campaigns coupled with training courses on diagnostic, surveillance and management of TR4 have been carried out by Bioversity International and National Plant Health organizations in Latin America and several countries (Mexico, Nicaragua, Costa Rica, Cuba, Colombia, Ecuador) have been already capacitated. These results are a key step towards designing policies and measures to prevent further spread of TR4 through effective quarantine measures.

## Current surveillance strategies for potato and sweet potato pests and diseases

**J. Kreuze, G. Forbes, J. Kroschel**

International Potato Center (CIP), Lima, Peru

Several diseases and insect pests of potato and sweet potato have been monitored throughout the history of CIP. After its inception, CIP commissioned a number of country wide disease surveys by expert consultants. These remain today the only geographic record of a number of diseases. One of the most concerted efforts to monitor a pathogen in CIP has been that of *Phytophthora infestans*, the causal agent of late blight. Within the context of the global initiative on late blight, CIP and partners mapped major pathogen strains, sometimes by direct evaluation, but also by reviewing published pathogen population studies. More recently there has been an effort to link this pathogen monitoring with the Euroblight initiative. For viruses, CIP is currently applying a technology based on siRNA sequencing and assembly to determine the 'virome' of sweetpotato throughout Africa. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. The same technique has been used at a smaller scale to identify potato and yam bean viruses in Peru. Incidence and damage of insect pests of potato have been surveyed recently in Ecuador, Peru, Nepal and Kenya along with collections and identifications of natural enemies; likewise for sweetpotato in Africa in Kenya, Rwanda and Uganda. Major results of the surveys are the presence of serious secondary pests in the Andean region, which had been overlooked previously; the confirmation of the introduction of the invasive leafminer fly, *Liriomyza huidobrensis*, in Nepal; the confirmation of establishment and wider distribution of *Copidosoma koehleri,* parasitoid of the potato tuber moth, *Phthorimaea operculella*, which was introduced to Kenya in the 1970s. Further surveys are planned for different potato systems in Africa.

## Current surveillance strategies for banana, cassava and yam pests and diseases

**F. Beed**

International Institute for Tropical Agriculture (IITA), Dar es Salaam, Tanzania

In an optimal world, the distribution, spread and impact of pests and diseases would be nationally documented and updated using results from routine surveillance to facilitate regional pre-emptive management interventions. Alas, this is not the reality and particularly not for African countries where resources and diagnostic capacities are limited. Therefore, cost effective and practical surveillance mechanisms are needed. Further, mechanisms are needed to disseminate results from surveillance exercises as widely and efficiently as possible. Different methods that have been tested will be reviewed, including design and implementation of spatial surveys to represent landscapes and production of easy to interpret GIS maps, going public exercises, media based awareness campaigns, community based actions, use of SMS alerts and java based surveys for mobile phones, farmer field schools and how these can be feasibly and sustainably supported by appropriate (rapid, precise and practical) diagnostic capacities.

Many surveillance schemes have been instigated by discrete projects but often these are only active as long as there is funding. The future aim for surveillance strategies for critically important diseases of cassava, banana and yam is to target locations and mechanisms for surveillance and to link these to protocols that become refined as experiences are accrued. Such practices can be housed in open access working documents such as Pest Risk Analyses (PRA) to increase information sharing between countries, regions and continents potentially facing the same threats. Sustainability of such mechanisms would be ensured if the public and private sector recognized their benefit to realizing their common interests and therefore contributed funds.

Nematode pests are a good example of where surveillance mechanisms need to become more robust as they often go unmonitored and yet they cause devastating diseases in their own right and also exacerbate the impact of other biotic and abiotic stresses. Some species have been highlighted for monitoring for quarantine purposes due to their status as serious pests on key crops, such as *Meloidogyne chitwooodi*. However, the status of many nematode pests in many areas is poorly understood. Species such as *Meloidogyne enterolobii* appears to be an aggressive pest of numerous crops, but due to difficulties with its identification, and a limited nematology capacity across the world, knowledge of distribution and impact is limited. While the critically important nematodes for cassava, banana and yam have been prioritized during session 1, emerging nematode species also need to be considered and offer the potential to discuss novel surveillance methods such as barcoding soil biota? For example, the yam nematode, *Scutellonema bradys*, has recently been recovered from potato in West Africa, and shown to cause severe damage to production and quality. However, its distribution on potato, varietal susceptibility, and its environmental plasticity is virtually unknown.

## THEME 5

## DETECTION AND DIAGNOSTICS

## Symptom recognition mediated by mobile plant clinics

**T. Holmes**

CABI, UK

Plantwise helps developing countries to establish an integrated plant health system. This system links the farmer – via a plant clinic - with an integrated support network, consisting of input suppliers (e.g. pesticide manufacturers), diagnostic laboratories, researchers, national plant protection organizations (NPPOs) and policy makers. Plantwise clinics are made accessible to farmers by holding them on a regular basis in a prominent local meeting place, such as a market. When the farmer has a problem with a crop, he/she can bring a sample along to the plant clinic. At the clinic a trained 'plant doctor' listens to the farmer, examines the sample, diagnoses the problem and offers a suggested treatment. Treatment suggestions are made with five key things in mind. Is the treatment: effective?; practical?; locally available and farmer-friendly?; economic?; and safe?. IPM practices are often the approaches that fulfill these criteria most successfully. The correct chemicals are recommended only when necessary; brand-names are avoided. With access to these services farmers can tackle pests and diseases and produce healthy crops and productive yields. With successful harvests farmers can feed and support their families. Diagnosis is not always straightforward. Sometimes plant doctors need to send samples to a laboratory (in exactly the same way that a family doctor sends samples to a hospital laboratory). Plantwise helps link clinics with diagnostic laboratories and other resources they need. We offer comprehensive support in disease identification and management. We work with all crops in all countries, particularly tropical crops, and offer expert identification services for fungi, bacteria, nematodes, viruses and phytoplasmas. A free service is available for eligible clients in developing countries. The service, based at CABI in the UK, receives more than 500 samples each year from more than 80 countries. Plantwise (formerly Global Plant Clinic (GPC)) is closely involved in surveillance and identification of new diseases and has published 31 new disease records with its global partners since 2001, 11 from Africa alone.

## Classical Disease and Pest Diagnostic Methods

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On a practical level the majority of plant disease and pest diagnoses are based on classical diagnostic methods. Field diagnoses rely on evaluation of symptoms and signs, usually aided by no more than experience, a good hand lens and reference materials. In the laboratory, classical techniques range from the use of microscopy to culturing and pathogenicity tests. Most classical laboratory methods require a great deal of experience on the part of the practitioner, and may be very time- and space- consuming. For insect pests and nematodes, classical identification is largely based on observation of specific physical characteristics. For plant diseases, a suite of structured tests, many based on light microscopy, differentiate potential causal agents into basic pathogen groups, in a process generally referred to as triage. For example, a simple bacterial streaming test differentiates bacterial pathogens from other groups of pathogens and abiotic disorders. A specific series of tests is then carried out depending on the results of the streaming test and the host plant. After a positive streaming test, culturing on general and selective media, sub-culturing, simple determinative biochemical tests, and a hypersensitive reaction (HR) test in tobacco are often sufficient to identify bacterial pathogens to the genus level. Production of key structures in and on plant tissues often allow for identification of fungal and oomycete pathogens to the genus level, but follow-up with culturing and further tests may be necessary. Serological assays have been used for diagnosis of diseases caused by viruses for so long that they may be considered “classical”, and are important tools in the field and laboratory. Improved selective media, diagnostic reference materials such as on-line image libraries and Lucid keys, and laptop- and smartphone-based microscopes are among the innovations in classical methods that continue to improve the speed and quality of plant pathogen diagnostics.

## Barcoding for pathogens and insect pests

**J. Kreuze**

International Potato Center (CIP), Lima, Peru

DNA barcoding is a taxonomic method that uses a short genetic marker in an organism's DNA to identify it as belonging to a particular species. Although the DNA sequences of related species are generally very similar, there are differences to be found. The part of the DNA sequence that is different is specific to that particular organism and forms a unique and specific molecular DNA barcode. DNA barcoding has arisen as a robust and standardized approach to species identification. Through the project QBOL, DNA barcoding has been developed for plant health diagnostics generating DNA barcodes and an associated database of key disease and pest species.

## Virus disease detection methods

**J. Kreuze**

International Potato Center (CIP), Lima, Peru

For many years now CIP has produces a set of kits based on ELISA for the detection of key potato and sweetpotato viruses and bacterial wilt. These kits have the benefit of being easy to use, require minimum equipment and are easy to interpret. However the downside is that they are limited in their sensitivity and only detect a subset of all known viruses of these crops.

The power of modern high throughput DNA sequencers is enabling a new generation of virological studies in which metagenomes of ecosystems can be determined to understand evolution and variability of viruses. We are currently applying a technology based on siRNA sequencing and assembly to determine the 'virome' of sweetpotato throughout Africa. Results of such surveys enable us to get a glimpse of viral diversity and variability across the continent, inform us of viral distribution on which to base containment measures and guide further research into impact and significance of identified viral entities. Such technologies however are still too expensive and knowledge intensive to be applied by most national diagnostic laboratories (NDL) which still mostly rely on ELISA and sometimes PCR methods for testing single viruses at a time. Platforms for the sensitive detection of multiple viruses at the same time such as microarrays may be practical and efficient solutions for NDLs with the need to test many plants against many viruses with sufficient sensitivity. Results from validation experiments of ClonDiag tube arrays for potato and sweetpotato will be presented. On the other hand, for diagnostics at the field level, simple and straight forward methods are needed that are robust, require minimum equipment but still are sensitive and easy to interpret. Loop-mediated isothermal Amplification (LAMP) is a highly sensitive and specific nucleic acid amplification method that does not to require complex thermal cycling equipment. Reagents can be lyophilized and reactions performed with low cost re-usable heat-packs, whereas color changes or lateral flow devices may be used to identify positive reactions. The challenges to bring the technology to field use rely on optimizing the way of detecting positive reactions and developing of simple enough nucleic acid extractions that can be used under field conditions.

## LAMP and next generation sequencing

**J. Smith**

Food and Environment Research Agency (FERA), Sand Hutton, York, UK

As a general direction of travel, crop pest diagnostics have seen a move from antibody based diagnostics (eg ELISA) to nucleic acid based PCR and real-time PCR, with stepwise progression realised in sensitivity, specificity, robustness and facility for design and redesign. However, whilst we have become increasingly competent at laboratory diagnostics for known pathogens, we have struggled to achieve the same levels of specificity and sensitivity with field diagnostics, where ELISA-based technologies have been foremost retained, and we remain at a loss of how to identify or provide surveillance against unknown pathogens. Recent advances in sequencing and amplification chemistries have however, provided a step change in these two areas. Loop Mediated Isothermal Amplification (LAMP) is essentially the same as PCR in that it relies on primers designed to target and amplify nucleic acid sequence, but differs in one major area in that the amplification reaction proceeds at a steady temperature (~60°C); as opposed to PCR cycling. As an outcome of this difference the infrastructure needed to support LAMP is much less, limited to a hot block. The products of LAMP can be viewed on a gel, or on a dip-stick styled Lateral Flow Device, and thus the diagnostics can be performed in a lab of basic infrastructure or in a field. The power of nucleic sequencing has transformed over the past 5 years. What used to take weeks, months or years is now achievable in hours and days. Commonly referred to as a next generation sequencing (NGS), one application is the unbiased amplification of nucleic acid sequence that is present in a sample that can then be interrogated for 'signature sequences' of interest. This approach may be used to identify the signatures of unknown pests without recourse for a priori knowledge. By brief example of Cassava Brown Streak Disease and Maize Lethal Necrosis Disease example will be provided on LAMP and NGS, for the development of a diagnostic suited for basic lab or field and in discovery of an unknown pathogen, respectively.

### A new low-cost diagnostic tool for detecting regulated (quarantine) cassava and banana diseases

**E. Alvarez**

International Center for Tropical Agriculture (CIAT), Cali, Colombia

Cassava and banana are important staple food for millions of people worldwide. In South Asia and LAC, sustainable cassava and banana production, respectively, is currently threatened by the proliferation of emerging diseases. Unchecked, they threaten the livelihoods of small farmers for whom cassava and banana may be their only means of generating income. Climate change aggravates the problem, influencing disease distribution and incidence. Sustainability needs to be fostered for this and future generations through effective, innovative, and improved technologies. Traditional processes for identifying plant pathogens can take days, even weeks, preventing timely decision-making while allowing problems to advance. We therefore propose develop and implement an innovative diagnostic technology for cassava and banana protection: a small low-cost device called Gene-Z, which is a new, simple, low-cost, hand-held platform for diagnosing emerging infectious diseases caused by plant pathogens, such as fungi, bacteria and virus. This portable isothermal platform is operated by an iPod Touch or Google Android tablet. It performs genetic analyses on microRNAs and other genetic markers. It is fast (10 to 30 min), highly specific, insensitive to PCR inhibitors, does not require complicated DNA extraction protocols, and can be used in the field. The Gen Z technology will contribute towards strategies that respond to challenges of food security and climate change.

## THEME 6

## DATA MANAGEMENT AND REPORTING

## Plantwise knowledge bank

**T. Holmes**

CABI, UK

Plant doctors, extension workers and researchers all need access to the latest information in order to be able to best assist the farmer. Plantwise offers online diagnosis and treatment support information as well as practical on the ground training for potential plant doctors. As a result of helping farmers Plantwise collects valuable data about plant pest and disease distribution that is shared with the participating countries. Working with the relevant NPPO (National Plant Protection Organization) Plantwise will publish validated pest and disease distribution data. This information, harnessed effectively, can form this basis of an early warning system alerting the plant health community to a change in distribution of existing pests/diseases or the threat of a disease in a new region. Data gathering from plant clinics is currently the focus of two pilot approaches: a paper form-based system with translation to a digital format away from the clinic; and a mobile tablet/smartphone/pc system with direct data entry at the clinic. Both approaches have challenges in: provision of equipment, ease of use and scalability. It may emerge that multiple approaches are useful; a toolkit from which the most appropriate system for a country or region can be chosen. In fact it is likely that a one-size-fits-all solution is not achievable. The Plantwise Knowledge Bank will help with the local, national and regional fight against pests and diseases. In addition to local distribution data captured at the clinics Plantwise will capture data about new pests and diseases from scientists, published sources and official bodies, and map this information in greater detail than ever before. Working with partners this data will be combined with the best information in the field to provide a comprehensive knowledge bank on crops, pests, diseases and weeds.

**Valuing Pest Risk Analysis in pest outbreak prevention**

**J. Smith**

Food and Environment Research Agency (FERA), Sand Hutton, York, UK

A signature of a successful and resilient cropping system is one which invests in pest outbreak prevention more than cure, where actions are taken that prevent an outbreak or mitigate an outbreak as to make its impact insignificant. It is thus a major objective of governments to anticipate future pest threats (either new, emerging, or evolved) and to mitigate accordingly. Unfortunately, for Africa, and many developing countries, the track-record for pest outbreak prevention provides for example of having achieved too-little too late. Yet with an increase in trade, trade-routes and the influence of climate change the likelihood of future new events is high. The challenge for all countries is to promote free-trade and mitigate pest risks and, where pest risks are seen, to implement measures that are not disproportionate and based on the good evidence as would otherwise contravene WTO guidance. To facilitate in these processes of attributing pest risk to trade, and in providing the evidence required for policy development of phytosanitary measures, the practice of Pest Risk Analysis (PRA) is advocated by the International Plant Protection Convention (IPPC) as set out under its various International Standards for Phytosanitary Measures (ISPMs). In review of PRA literature many schemes are evident as preferred by countries and regions. These variously attempt to bring in risk assessment and risk management and qualitative *versus* quantitative judgements, but also share features about risk related to entry, establishment, spread and consequences. Each also strives to bring together a state-of-knowledge through a desk review of literature on what is known and not known and to attribute risk and uncertainty to these knowledge sets. Further a good PRA may aim to set-out a research agenda and provide for a communication of findings in formats that are both technical and non-technical, for targeted audiences. In this talk example will be made of two PRAs that have been led on by Fera in recent years progressing states-of knowledge for the causal agents of Cassava Brown Streak Disease of cassava and Banana Xanthomonas Wilt of banana.

## Networks for diagnostics and capacity building

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Early and accurate diagnoses and effective pathogen surveillance are necessary on local, regional and global scales to identify invasive species, predict disease outbreaks and allow timely deployment of appropriate mitigation strategies. The quality of plant disease diagnoses and ultimately their usefulness in both plant safeguarding and disease management decision-making is a function of 1) human resources, 2) technology and 3) infrastructure. For all but the most simple and obvious diagnostic problems, well-trained individuals, readily available technology and/or adequate infrastructure for conducting diagnostic tests and protocols are required. However, significant gaps in capacity to diagnose plant diseases exist in both the developing and developed world. The lack of human capital will not be remedied in the near future by a large influx of well-trained diagnosticians. Therefore, sharing of expertise across borders through well-supported networks can compensate for the lack of human capacity in a given country. For example, the International Plant Diagnostic Network (IPDN), established in 2004, assists local diagnosticians through training, diagnostic technology research and development, preparation and sourcing of reference materials and sharing of diagnostic expertise in 12 countries. The expertise of individuals within networks is a rich source of knowledge for development of diagnostic protocols appropriate to various levels of physical and human capacity. Such standardized operating procedures provide guidance on diagnostics for important pests and diseases and engender confidence in the outcomes of the diagnostic processes. Focused regional workshops introduce classical and modern diagnostic methods at a reasonable cost, and provide much needed networking opportunities. Short-term intensive training results in greater knowledge acquisition through repeated practice and exposure to a wide array of plant problems. Both types of training also improve capacity to identify invasive species and therefore mobilize prevention and/or management efforts.

## Climate data management for species distribution models

**H. Juarez, H. Tonnang, J. Kroschel**

International Potato Center (CIP), Lima, Peru

Climate has long been considered as the primary factor constraining potential distribution of many organisms. Proper climate data storage, manipulation and dissemination are therefore the backbones for species distribution models. However, available data bases are characterized by missing values, and other factors leading to numerous data anomalies. Serious care is therefore required during their inclusion into models. Most available tools use 'climate surfaces' for different scenarios. Climate surfaces at very high resolution are essential for studies in mountain environments and areas with great change in gradients. Available data bases contain information for several scenarios at different spatial resolutions starting from 10 arc-minute (18 km) to 30 arc-second (0.9 km). The aim here is to explain how modeling tools manage these datasets using Insect Life Cycle Modeling (ILCYM) software, Maximum entropy (MaxEnt) and CLIMEX for illustrations.

## Innovations to increase efficiency of data management

**R. Simon**

International Potato Center (CIP), Lima, Peru

Amongst the principal challenges for data management and reporting in the context of pest and disease monitoring will be the ability to handle highly distributed data since a classical global monitoring schema would typically rely on a large number of local human observers (like crowd-sourcing) or also on smart specialized sensors. Alternatively or complementary remote sensing data could be used for pest and disease monitoring. This leads us to the second challenge of high volume data in the form of images or fine-grained time series data from sensors in weather stations. As indicated, the data may come from a variety of data collecting devices (like laptops, smartphones, mobile sensors, micro-drones, satellites) hence the need for unified communication and data format protocols. The last challenge is to make these data available for browsing, analysis and decision-making in a highly responsive and in a near real-time manner. In this paper we will review informatics tools for these purposes. These include: a) physical infrastructure with high accessibility and availability; b) efficient data structures for near real-time data discovery, integration, analysis and high availability; c) efficient statistical algorithms and platforms that can handle large datasets; d) data standards that facilitate the analysis; and e) highly automatable statistical reporting tools. Finally, an example scenario briefly shows the integration of these components to address the above listed challenges in data management.

**7.2 List of participants**

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**7.3 Prioritization of insect pests by crop and center**

Priority: Dark gray: 1st, Light gray: 2nd; Gray: 3rd priority

| Pests | Crops | Current presence | Potential risk of spread to | PRA required | PR assessment and modeling | Surveillance needed/ detection tools available (mol. tools) | Data and capacity availability | Center (s) |
|---|---|---|---|---|---|---|---|---|
| Guatemalan potato tuber moth, *Tecia solanivora* | Potato | Latin America, Canary Island | SSA, Asia, South America | Yes | Yes | Yes/ Not developed | Phenology available | CIP, NARS and other stakeholders |
| Tomato leafminer, *Tuta absoluta* | Tomato, potato, Solanaceae crops | Latin America, Mediterranean region, some African countries | SSA, Asia | Yes | Yes | Yes/Yes | Phenology needs to be developed | CIP, *icipe* and IITA |
| *Mononychellus mcgregori/ tanajoa* | Cassava | Asia, LAC | Africa and Asia | Yes | Yes | Yes/ Not developed | Phenology needs to be understood | CIAT and IITA |
| Whiteflies | Cassava, Potato, sweet potato and polyphagous | Asia, Africa and LAC | Global Climate change risks need to be done | No | Yes | Yes (East Africa) Need to look at diagnostic tool | Phenology under development | IITA, *icipe* CIAT, CIP |
| *Cosmopolites sordidus* | Banana | East Africa, South Asia and Global | - | No | Yes at regional scale | Yes | Phenology need to be developed | Bioversity, IITA |
| Cereal Stemborer complex: *Chilo partellu, Busseola fusca* | Rice, Maize and Sorghum | East Africa and South Asia | Climate change range expansion to temperate climates | No | *Yes* | No | Under development *Chilo partellus* data from ICRISAT | ICRISAT, ICIPE, IITA, CYMMYT, Africarice, IRRI |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| *Helicoverpa /Maruca (Pod borers)* | Polyphagous | Asia and Africa | Climate change range expansion to temperate climates LAC | | *Yes* | | | ICRISAT, icipe, IITA, AVRDC |
| Banana Aphid (BBTV) *Pentalonia nigronervosa* | Banana | Global | - | No | Yes | Yes | Phenology under development | Bioversity and IITA |
| Bud midge, *Prodiplosis longifila* | Potato, Polyphagous | LAC; coast of Peru; Florida | SSA, Asia | Yes | Yes | Yes/ Not developed | Phenology needs to be developed | CIP |
| Potato Cyst Nematode *Globodera* spp. | Potato and polyphagous | LAC, Asia, South Africa | SSA | Yes | Yes | Yes | | IITA and CIP |
| *Phenococcus manihoti – Cassava mealybug* | Cassava | LAC, Africa, Asia | Asia | No | Under development | Yes in Asia | Phenology under development | CIAT and IITA |
| Sweet potato weevil - *Cylas formicarius* | Sweet potato | CA, Asia, Kenya?? | South America and Africa | Yes | Under development | Yes | Phenology under development | CIP |
| Banana Nematode – *Pratylenchus coffeae* | Banana | Global | Yes regional spread EAH | No | Yes | Yes Diagnostic tool under development | Under development | IITA and Bioversity |
| Papaya mealybug, *Phaenococcus marginatus* | Polyphagous | CA (Mexico) Asia, Africa | Asia, Africa | No | Yes at regional scale for Biological control | Yes Diagnostic tools needed | Phenology needs to be developed | IITA |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Vectors of maize lethal necrosis virus, *Frankliniella williamsi* and Cereal Aphid | Maize | China, East Africa | Africa and Asia | Yes | Yes | Yes | Phenology needs to be developed | *icipe* and CYMMYT Co funds from CGIAR maize program |
| *Millet headminer - Heliocheilus albipunctella* | Pearl Millet | West Africa | Asia | - | Yes | No | Phenology needs to be developed | ICRISAT |
| *Aproarema modicella* | Groundnut | Asia | Africa | Yes for Africa | Yes | Yes | Phenology available | ICRISAT |
| *Sorghum shootfly* | Sorghum | Asia and Africa | Americas and Australia | Yes for America and Australia | Yes | No | Phenology available | ICRISAT |
| *M. graminicola* | Rice | Asia | Climate change or change in status related to water availability | Yes | Yes | Yes | Phenology needs to be validated | IRRI, IITA |
| Root Knot nematode | Across crops | Global | Change in relation to climate, production | Yes in Africa | Yes in Africa | Yes in Africa | Phenology for various situations required | IITA |

**7.4 Workshop participants group photo**


**First row** (from left to right: Beatriz Herrera (CIAT-CCAFS), Jan Kreuze (CIP), Sevgan Subramanian (*icipe*), Sally Miller (OSU), Hari Sharma (ICRISAT), Jürgen Kroschel (CIP), Elisabeth Alvarez (CIAT), Paddy Likhayo (CIMMYT), Agustin Molina (BIOVERSITY)

**Second row**: Fen Beed (IITA), Danny Coyne (IITA), Adam Sparks (IRRI), Manuel Tamò (IITA), Karen Garrett (KSU), Komi Fiaboe (icipe), Suresh Pande (ICRISAT), Pascale Lepoint (BIOVERSITY), Timothy Holmes (CABI)

**Third row**: Henri Tonnang (CIP), Reinhard Simon (CIP), Manuel Pardo (CIAT), Peter Kromann (CIP), Julian Smith (FERA), Greg Forbes (CIP)

A broad alliance of research-for-development stakeholders & partners