Status of Genomic Selection in Forages

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Current Status at CIAT

• Brachiaria breeding pipeline
  • Evaluation of testcross progenies (3000 hybrids)
  • ‘Best bets’ screened for:
    • Reproductive mode, biotic/abiotic stress & quality (150-200 hybrids)
    • Forage biomass, seed yield and persistence (~100 hybrids)
    • Advanced trials (25-30 hybrids)
    • Grazing trials and seed multiplication (1-3 hybrids)
  • MAS for apomixis

Cultivar Release!!!

Yr 1
Yr 2
Yr 3

Yr 3-4
Yr 4-6
Yr 7-8
Yr 9-10
Opportunities for Genomic Selection

- Improved selection accuracy without adding years to the recurrent selection cycle
  - Selection of sexual mothers for the next cycle of RS currently made after first year spaced plant evaluation
- Flowering time selection
  - Genotypes with inappropriate flowering in advanced trials as not possible to select for in Colombia (0° lat)
- Selection of ‘best bet’ hybrids for Africa
  - Phenotyping the TP across regions

Yr 1
Yr 3
Yr 2

Yr 3-4
Yr 4-6
Yr 7-8
Yr 9-10

Cultivar Release!!!
Current Status and Prospects for Genomic Selection at ILRI

• Forage genebank
  • 19,210 accessions (grasses, legumes & fodder trees)
  • E.g. Napier grass (the most widely grown cut & carry forage)
    • Extensively phenotyped over a number of years
      • Morphology, forage biomass, drought tolerance, nutritive value, smut and stunt resistance (KALRO)
    • Clonally propagated crop
    • Gene discovery proposal (RNAseq, GBS and AM)
  • E.g. Lablab (fast growing, high yielding dual purpose crop with wide adaptability and a large amount of variation)
    • Phentotyped for crop residue (yield and quality) and tradeoff with grain yield
New Tools and Challenges

- **Tools:**
  - First saturated genetic maps of Brachiaria *spp.* by GBS
  - Markers for apomixis and aluminum resistance
  - Diploid *B. ruiziziensis* reference genome (with TGAC)
    - 2015/2016 funding for MatePairs, PacBio reads & annotation
  - Pearl millet reference genome for Napier grass

- **Challenges:**
  - Investment in high quality plant phenotyping
  - Rapid standardized GBS protocols or a SNP platform
  - Statistical models for heterozygous polyploids
    - links to RTB crops
better lives through livestock

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