Towards challenging pre-breeding & breeding approaches for the commodity CGIAR Research Programs (CRPs)

Philippe Ellul
Senior Science Officer CGIAR Consortium
International Pre-breeding workshop
Montpellier, February 2-4th 2015
15 CGIAR Centers
<table>
<thead>
<tr>
<th>16 CGIAR Research Programs (CRPs)</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>• MAIZE</strong></td>
</tr>
<tr>
<td><strong>• WHEAT</strong></td>
</tr>
<tr>
<td><strong>• GRiSP (Global Rice Science Partnership)</strong></td>
</tr>
<tr>
<td><strong>• Roots, Tubers &amp; Bananas</strong></td>
</tr>
<tr>
<td><strong>• Dryland Cereals</strong></td>
</tr>
<tr>
<td><strong>• Grain Legumes</strong></td>
</tr>
<tr>
<td><strong>• Livestock &amp; Fish</strong></td>
</tr>
<tr>
<td><strong>• CRP for Managing &amp; Sustaining Crop Collections</strong></td>
</tr>
<tr>
<td><strong>• Policies, Institutions &amp; Market</strong></td>
</tr>
<tr>
<td><strong>• Agriculture for Nutrition &amp; Health</strong></td>
</tr>
<tr>
<td><strong>• Humid Tropics</strong></td>
</tr>
<tr>
<td><strong>• Aquatic Agricultural Systems</strong></td>
</tr>
<tr>
<td><strong>• Dryland Systems</strong></td>
</tr>
<tr>
<td><strong>• Climate Change, Agriculture and Food Security (CCAFS)</strong></td>
</tr>
<tr>
<td><strong>• Forests, Trees and Agroforestry (FTA)</strong></td>
</tr>
<tr>
<td><strong>• Water, Land and Ecosystems (WLE)</strong></td>
</tr>
</tbody>
</table>
Our vision:
A global agri-food system that is more productive, carbon neutral, and provides nutritious options at affordable prices.

Our mission:
To harness science and innovation to meet the multi-sectorial challenges of the 21st century with a focus on enabling the poor and women to benefit from economic growth in the agri-food sector in the face of climate change.

Our goals (System Level Outcomes or SLOs):
1. Reduce poverty
2. Improve food and nutrition security for health
3. Improve natural resource systems and ecosystem services

From Strategic Research Framework (SRF) 2015
From CRP 1\textsuperscript{st} call to 2\textsuperscript{nd} call starting in 2017

Planning for 2015-16 / Extension Proposals

- Independently reviewed by Consortium Office (CO) Science Team and ISPC (Independent Science & Partnership Council)
- 11 Extension Proposals received support from ISPC and CO Science Team; \textbf{the 7 commodity CRPs are in this group}
- Based on ISPC & CO comments and recommendations, Fund Office (FO) identified 3 groups: A, B and C; \textbf{the 7 commodity CRPs are in Group A recommended to be approved by FC}
- Consequences on W1/2 budget allocation for 2015-16
- Approved by Fund Council on 6\textsuperscript{th} November 2014
<table>
<thead>
<tr>
<th>GRiSP</th>
<th>MAIZE</th>
<th>WHEAT</th>
<th>RTB</th>
<th>DC</th>
<th>GL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Technology targeting and evaluation</td>
<td>Sustainable intensification of maize-based farming systems</td>
<td>Maximizing value for money and social inclusivity through prioritization of WHEAT R4D investments</td>
<td>Unlocking the value and use potential of genetic resources</td>
<td>Data, Knowledge &amp; Communication</td>
<td>Managing productivity</td>
</tr>
<tr>
<td>Harnessing genetic diversity</td>
<td>Novel tools, technologies and traits for improving genetic gains and breeding efficiency</td>
<td>Novel diversity to faster adapt wheat to climate change and resource constraints</td>
<td>Accelerating the development and selection of cultivars</td>
<td>Improved Varieties and Hybrids</td>
<td>Trait determination</td>
</tr>
<tr>
<td>Developing improved rice varieties</td>
<td>Stress resilient and nutritious maize</td>
<td>Global partnership to accelerate genetic gain in farmers’ field</td>
<td>Managing priority pests and disease</td>
<td>Integrated Crop Management</td>
<td>Trait deployment</td>
</tr>
<tr>
<td>Sustainable intensification along the rice value chain</td>
<td>Aligning with and strengthening maize seed systems for effective product delivery</td>
<td>Sustainable intensification of wheat-based cropping systems</td>
<td>Making available low-cost, high-quality planting material for farmers</td>
<td>Seed Systems &amp; Input Markets</td>
<td>Seed systems, post-harvest processing, markets and nutrition</td>
</tr>
<tr>
<td>Out-scaling and capacity building</td>
<td>Inclusive and profitable maize futures</td>
<td>Human and institutional capacities for seed systems and scaling-out</td>
<td>Developing tools for more productive, ecologically robust cropping systems</td>
<td>Post-harvest Value and Market Access</td>
<td>Capacity Building and Partnerships</td>
</tr>
<tr>
<td>-</td>
<td></td>
<td></td>
<td>Promoting postharvest technologies, value chains, and market opportunities</td>
<td>Cc1 Knowledge, Impacts, Priorities, and Gender Organisation</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td></td>
<td></td>
<td>Enhancing impact through partnerships</td>
<td>Cc2 Tools and platforms for genotyping and bioinformatics</td>
<td></td>
</tr>
<tr>
<td>-</td>
<td></td>
<td></td>
<td>Result Based Management</td>
<td>Cc3 Management</td>
<td></td>
</tr>
</tbody>
</table>

**CRP Extension Proposals 2015-16**
<table>
<thead>
<tr>
<th>GRiSP</th>
<th>MAIZE</th>
<th>WHEAT</th>
<th>RTB</th>
<th>DC</th>
<th>GL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Technology targeting and evaluation</td>
<td>Sustainable intensification of maize-based farming systems</td>
<td>Maximizing value for money and social inclusivity through prioritization of WHEAT R4D investments</td>
<td>Unlocking the value and use potential of genetic resources</td>
<td>Data, Knowledge &amp; Communication</td>
<td>Managing productivity</td>
</tr>
<tr>
<td>Harnessing genetic diversity</td>
<td>Novel tools, technologies and traits for improving genetic gains and breeding efficiency</td>
<td>Novel diversity to faster adapt wheat to climate change and resource constraints</td>
<td>Accelerating the development and selection of cultivars</td>
<td>Improved Varieties and Hybrids</td>
<td>Trait determination</td>
</tr>
<tr>
<td>Developing improved rice varieties</td>
<td>Stress resilient and nutritious maize</td>
<td>Global partnership to accelerate genetic gain in farmers’ field</td>
<td>Managing priority pests and disease</td>
<td>Integrated Crop Management</td>
<td>Trait deployment</td>
</tr>
<tr>
<td>Sustainable intensification along the rice value chains</td>
<td>Aligning with and strengthening maize seed systems for effective product delivery</td>
<td>Sustainable intensification of wheat-based cropping systems</td>
<td>Making available low-cost, high-quality planting material for farmers</td>
<td>Seed Systems &amp; Input Markets</td>
<td>Seed systems, post-harvest processing, markets and nutrition</td>
</tr>
<tr>
<td>Out-scaling and capacity building</td>
<td>Inclusive and profitable maize futures</td>
<td>Human and institutional capacities for seed systems and scaling-out</td>
<td>Developing tools for more productive, ecologically robust cropping systems</td>
<td>Post-harvest Value and Market Access</td>
<td>Capacity Building and Partnerships</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CRP Extension Proposals 2015-16</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Promoting postharvest technologies, value chains, and market opportunities

Enhancing impact through partnerships

Cc2 Tools and platforms for genotyping and bioinformatics

Result Based Management

Cc3 Management
+25 crops, 7 CRPs, 1 pipeline...

GB managers
Pre-breeder
Other researchers
- Genebanks & passport data
- Genotyping/genomic data (GbS, Reseq.)
- Phenotypic data
- Geo-location data

Plant researchers
Pre-breeder
Breeders
- Mapping lines
- QTL discovery
- Gene discovery
- Trait performance
- SNP discovery
- DHs

Breeders
Pre-breeder
Implementers/technicians
- SNP validation
- MAS
- Gene pyramiding
- Multi-location field trials
- DHs

Seed researchers & Implementers
- Seed delivery
- Seed Quality Control
- Seed technologies
- Pathogen detection
- Germination, vigor testing
- Seed lots homogeneity
- Logistic for seed distribution

Multidisc. Res. (ecology, social sciences,...)
- Foresight
- Cropping systems
- Value chain
- Scaling out
- Post harvesting technologies
- Capacity building
- Other SAI approaches

CGIAR is a global research partnership for a food secure future
From managing & sustaining crop collections to research

<table>
<thead>
<tr>
<th>Organization</th>
<th>Crop Collections</th>
<th>Accessions</th>
</tr>
</thead>
<tbody>
<tr>
<td>AfricaRice</td>
<td>Rice</td>
<td>20,000</td>
</tr>
<tr>
<td>Bioversity</td>
<td>Banana, Plantain</td>
<td>1,298</td>
</tr>
<tr>
<td>CIAT</td>
<td>Beans, Cassava, Tropical forages</td>
<td>65,635</td>
</tr>
<tr>
<td>CIMMYT</td>
<td>Maize, Wheat</td>
<td>155,129</td>
</tr>
<tr>
<td>CIP</td>
<td>Potato, Sweet potato, Andean Roots &amp; Tubers</td>
<td>16,495</td>
</tr>
<tr>
<td>ICARDA</td>
<td>Grain legumes, Wheat, Barley, Forage &amp; range crops</td>
<td>135,406</td>
</tr>
<tr>
<td>ICRAF</td>
<td>Trees</td>
<td>5,144</td>
</tr>
<tr>
<td>ICRISAT</td>
<td>Dryland cereals, Grain cereals</td>
<td>156,313</td>
</tr>
<tr>
<td>IITA</td>
<td>Banana, Plantain, Maize, Cowpea, Cassava, Yam</td>
<td>28,286</td>
</tr>
<tr>
<td>ILRI</td>
<td>Tropical forages</td>
<td>18,291</td>
</tr>
<tr>
<td>IRRI</td>
<td>Rice</td>
<td>116,817</td>
</tr>
<tr>
<td><strong>Total</strong></td>
<td></td>
<td><strong>712,568</strong></td>
</tr>
</tbody>
</table>
Screening Biological Nitrification Inhibition (BNI) in tropical pasture grasses


- Con – control plots
- Soy – soybean
- Pm – Panicum maximum
- BMul – Brachiaria hybrid cv. Mulato (apomictic hybrid that contains germplasm from B. ruiziensis, B. decumbens and B. brizantha, but NOT from B. humidicola)
- Bh-679 – B. humidicola accession CIAT 679 (standard cultivar Tully)
- Bh-16888 – B. humidicola

Ammonium oxidation rate in soil (mg NO₂⁻-N/kg soil/d)

0.00  0.05  0.10  0.15  0.20  0.25

Con  Soy  Pm  BMul  Bh-679 Bh-16888
Adoption of Brachiaria hybrids*

*Total area planted
= 479,000 ha

(estimate based on seed sales assuming 7 kg seed/ha)

Kindly provided by Peters Michael (CIAT/Livestock & Fish) and Tom Randolph (ILRI/ Livestock & Fish)
Screening wild species of *Oryza spp.*

**Useful Traits**

- Insect resistance
- Disease resistance
- Tolerance of abiotic stresses
- QTLs for yield
- Nutrition?
- Industrial uses?

*O. officinalis*  
*O. ridleyi*  
*O. alta*  
*O. minuta*  
*O. brachyanta*  
*O. rufipogon*  
*O. longistaminata*

Kindly provided by Dr. Bas Bouman (IRRI/GRiSP)

*CGIAR is a global research partnership for a food secure future*
Transfer of salt tolerance from *Oryza coarctata*

15 years of crossing produced 1 viable plant!

*IR56 (No Salt)*

*IR56 (EC 24)*

*O. coarctata (EC 24)*

*F₁ IR56 x O. coarctata (EC 24)*

*BC₁ IR56 x O. coarctata//IR56 (EC 24)*

Kindly provided by Dr. Bas Bouman (IRRI/GRiSP)
Creating mapping populations for QTLs/genes discovery

1) F1 + one or several selfings
   • F2 populations
   • Recombinant Inbred Lines (RILs)
   • Intermated Recombinant Inbred Lines (IRILs) # Heterogenous Inbred Families (HIFs)

2) F1 + several backcrosses BCn (n= 6 to 10)
   • Near Isogenic Lines (NILs)
   • Introgression Lines (ILs)
   • Chromosomes Substitution Lines (CSLs)
   • Back-cross Inbred Lines (BILs)

3) Multiparent Advanced Generation Inter-Cross (MAGIC)
Population genomic and genome-wide association studies of agroclimatic traits in sorghum

Geoffrey P. Morris¹,², Punna Rams,³, Santosh P. Deshpande,³ C. Thomas Hash,⁴ Trushar Shah,⁶ Hari D. Upadhyaya,⁶ Oscar Riera-Lizarazu,⁵ Patrick J. Brown,⁵ Charlotte B. Acharya,⁵ Sharon E. Mitchell,⁵ James Harriman,⁵ Jeffrey C. Glaubitz,⁵ Edward S. Buckler,⁶,⁷,⁸ and Stephen Kresovich⁹

¹Department of Biological Sciences, University of South Carolina, Columbia, SC 29208; ²International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Hyderabad 502 324, Andhra Pradesh, India; ³ICRISAT-Sador, BP 12404 Niamey, Niger; ⁴Department of Crop Sciences, University of Illinois, Urbana, IL 61801; ⁵Institute for Genomic Diversity and Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY 14853; and ⁶Agricultural Research Service, Department of Agriculture, Ithaca, NY 14853

Edited by Ronald L. Phillips, University of Minnesota, St. Paul, MN, and approved November 21, 2012 (received for review September 14, 2012)

Accelerating crop improvement in sorghum, a staple food for people in semiarid regions across the developing world, is key to ensuring global food security in the context of climate change. To facilitate gene discovery and molecular breeding in sorghum, we have characterized ~265,000 single nucleotide polymorphisms (SNPs) in 971 worldwide accessions that have adapted to diverse agroclimatic conditions. Using this genome-wide SNP map, we have characterized population structure with respect to geographic origin and morphological type and identified patterns of ancient crop diffusion to diverse agroclimatic regions across Africa and Asia. To better understand the genomic patterns of diversification in sorghum, we quantified variation in nucleotide diversity, linkage disequilibrium, and recombination rates across the genome. Analyzing nucleotide diversity in landraces, we find evidence of selective sweeps around starch metabolism genes, whereas in landrace-derived introgression lines, we find introgressions around known height and maturity loci. To identify additional loci underlying variation in major agroclimatic traits, we performed genome-wide association studies (GWAS) on plant height components and inflorescence architecture. GWAS maps several classical loci for plant height, candidate genes for inflorescence architecture, and candidate genes for inflorescence architecture. Finally, we trace the independent spread of multiple haplotypes carrying alleles for short stature and low inflorescence branches. This genome-wide map of SNP variation in sorghum provides a basis for crop improvement through marker-assisted breeding and genomic selection.

Sorghum bicolor | quantitative trait locus | adaptation

CGIAR is a global research partnership for a food secure future
Upstream research partnership & Seeds of Discovery

- **Maize**: ~27,000 accessions in CIMMYT’s genebank
  - Developed new GbS method for composite DNA samples (30 plants per accession); the method simultaneously
    - Quantifies allele frequencies within accessions (SNP), and
    - Estimates genetic distances among accessions (PAV)
  - Completed the sequencing of 20,000 accessions → diversity analysis in progress
- **Wheat**: ~140,000 accessions in CIMMYT’s genebank
  - Completed sequencing of 42,000 accessions
  - Data being used to assemble AM panels

From Peter Wenzl, SeeD Project leader at CIMMYT
Upstream research partnership & SeeD

1. Molecular alleles
   - Underutilized sources of **genetic variation**
   - Selection imprints
   - Heterotic patterns (maize)
   - Hidden translocations (wheat)
   - Rare recombinants

2. Novel alleles and allele donors
   - Novel, beneficial **alleles, haplotypes**
   - **Markers** linked to loci and alleles that control priority traits
   - Genetically distinct ‘**donor accessions**’

3. ‘Bridging germplasm’
   - **Breeder-ready lines and populations** with new, beneficial alleles
   - Molecular **markers** linked to beneficial alleles and statistical **models** for estimating breeding values to accelerate genetic progress in breeding programs

New breeding approaches and technologies; new tools such as GS

Elite germplasm selected by breeders
Pipeline approach & partnership strategy

Discovery phase
- New concept of product, service, or process

Proof of concept phase
- Testing of proof of concept in real world / controlled conditions (n=1000s)

Pilot phase
- Multi-location release/trials for smallholder’s benefit (n=100,000s)

Scaling up phase
- Release for scaling up & adoption in different locations (n=1,000,000s)

Science partnerships
Development partnerships

CGIAR is a global research partnership for a food secure future
SLOs & partnership strategy

- Reduced poverty
- Improve food and nutrition security for health
- Improve natural resource systems & ecosystem services

Number of Partners

- National institution for agricultural extension (0.1%)
- Financing institution (0.8%)
- Advisory services (1.6%)
- Foundation (1.7%)
- Development organization (2.0%)
- Farmers organization (2.5%)
- Regional organization (3.2%)
- International organization (3.8%)
- International agricultural research center (6.6%)
- Private company (7.5%)
- Government (10.3%)
- Non-governmental organization (11.8%)
- Academic institution (22.4%)
- National research institution (25.7%)

CGIAR is a global research partnership for a food secure future
Pre-breeders & private sector?
Pre-breeder melon, Nunhems Bangalore (India)

The pre-breeder will support the mainstream breeding by:
• Developing material(s) and gene pools with specific traits, ready to be used in the breeding programs.
• Developing the respective breeding populations to be used in breeding for developing specific markers or other molecular tools.
• Developing genetic knowledge to improve selection efficiency.
• Creating & implementing phenotyping methodology.

He/She will be responsible for developing genetic material enhancing the germplasm of melons, strong emphasis on complex trait studies, trait introgression activities, goals and team strategies related to trait handling, trait testing and resulting actions, meeting time-lines and cost effectiveness.

Applicant should possess M.Sc/ Ph.D in plant breeding and genetics/horticulture with specialisation in vegetable breeding with 3 to 5 years experience in vegetable (preferably melon) breeding.

Must have in depth working knowledge of horticulture, agronomy, genetics, pathology, statistics, physiology, molecular genetics and cell biology.
Pre-breeder for Cucurbitaceae, VCo (Vilmorin & Co)

The primary responsibilities for this position include, but are not limited to the identification and introduction of valuable new traits into cucurbit crops to support the main stream breeding, to involve the following:

- Creation, maintenance & valorization of genetic resources: genetic mapping population, EMS populations, ILL, core collections.
- Strong emphasis on complex trait studies, via use of classical (bi-parental crosses) or novel QTL approach (LD, multi parental crosses.); creation of relevant material and process.
- Creation & implementation of phenotyping methodology.
- Coordination and completion of VCo cucurbitaceae pre-breeding upon priority; represent VCo in all molecular pre-breeding projects: internal VCo, or w/ external partners.

PhD in Plant Breeding, Statistical Genetics, Plant Genetics. Experience with:
- collecting and analyzing experimental data, genetic statistics, and experimental design.
- relevant statistical software required.
- field and greenhouse work required.
- with vegetable crops is desirable, but not required.
- Lab experience recommended but not required: pathology, molecular, cell.
CRPs and pre-breeding

⇒ Commodity CRPs are increasing their pre-breeding activities
⇒ Pre-breeder’s role is defined differently by Crop/Center/CRP (harmonization?)
⇒ Pre-breeding supports the mainstream breeding

- Evaluate accessions & old landraces for specific traits
- Create, maintain & valorise PGRs (mapping population, EMS populations, etc)
- Develop original mapping populations via classical (bi-parental crosses) or novel QTL approaches (LD, multi parental crosses)
- Identify QTLs/genes and Molecular Markers (discovery, validation)
- Develop innovative genetic knowledge/tools to improve selection (eg Reverse Breeding, Tilling by NGS, etc...)
- Create & implement phenotyping methodology
- Manage multidisciplinary projects
- Other? in situ conservation, participatory breeding, domestication, crop evolution, etc...
CRPs and pre-breeding

⇒ Strengthen links between genebank managers, researchers in physiology, pathology, genomics, bioinformatics, quantitative genetics, intellectual property, social sciences, etc... - and breeding.
Thanks