Summary of brainstorming sessions (Rice/*Musa*)

Participants

Population session: ~25

Bottle neck session: ~20

Facilitators

Alain Ghesquiere

Hei Leung

Genetic Population Development to optimize genetic analysis and breeding

Guide to discussion

- Address complex traits
- Resolve complex combinations/networks of genes, not simple genetic control
- Unlock diversity
- Contribute to long-term genetic diversity platform

Taking Stocks

Concentrate on

- Well-managed
- Publicly accessible
- High-quality
- Relevance to drought research

Population	Feature	Produced and accessible at	GCP support
Chr Segmental Substitution Lines (CSSL)	**2 *sativa* x *glabberima* libraries 4 wild inter-specific libraries**	**CIAT/IRD**	**+++**
	4 japonica x indica libraries	**NIAS, Japan**	
RIL (tolerant x sensitive, including DH lines)	**~ 6 commonly used populations**	**IRRI, CIRAD/IRD**	
Advanced breeding populations	**•Advanced breeding lines •NERICA series •Recurrent selection program**	**IRRI, WARDA CIAT, CIRAD, IRD**	**+**
Introgression lines	***glabberima* x *sativa***	**CIAT, IRRI, WARDA**	
Mutants	**Insertions/activations Deletions**	**International Rice Functional Genomics Consortium**	**+**

Desirable and feasible objectives

To serve 2 main objectives

- **Ability to map QTL for drought tolerance (complex traits) at 2-5 cM (0.5-2 Mb) resolution**
- **Ability to extract lines suitable for pre-breeding**

Generation

Feasible activities

Nested Association Mapping (NAM) populations

- Similar to maize NAM populations but with emphasis on “underused” genomes (glaberrima and wild species)
- Use ~25 starter lines crossed to a common parent
- Produce about 5000 RIL (200 lines per cross)

Multi-parental Advanced Generation Intercross (MAGIC)

- 8-16 founder lines
- Scalable
- High resolution
- Scramble background, aid QTL detection with high epistatic interaction

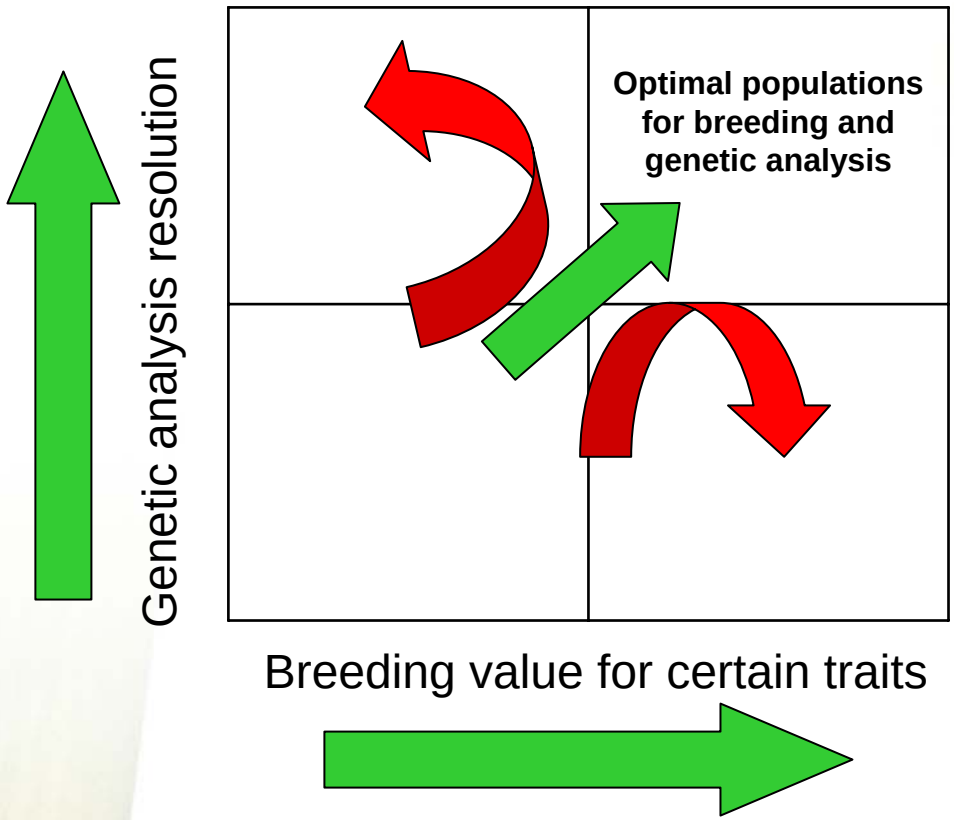
Issues:

- good for animal genetics but may not be good for plants where large populations can be made easier
- Lots of crossing work

In both cases, selection of parental lines important to determine relative utility for genetic analysis and/or breeding

Generation

Selection of parental lines will determine relative utility for genetic analysis and/or breeding



Issues discussed

- Take advantage of breeding lines in gene discovery
- Different loci will be found to be important in different parents – how do we handle this?
- Emphasis on response to selection
- Need to couple with phenotyping
  - Need for strict protocols & adherence to protocols in drought trials
  - Need to phenotype across diverse environments

GCP research bottlenecks towards crop Improvement

Demand	Offer/Facilitate	GCP can directly contribute
1. Understanding Target Population Environment (TPE)	- Linkage with other program - Extensive GxE analysis	Can be incorporated in projects as validation or demonstration of usefulness in breeding progress
2. Trait packages needed, in addition to drought	- Define trait packages with regions/ecosystem • Upland • Rainfed/Marginal areas • Irrigated Example of companion traits in upland rice: o Tolerance to acid soil o Disease resistance o Weed competitiveness	• Support traits pyramiding • Marker tools • Support specific companion traits (in addition to drought tolerance)

Generation

GCP research bottlenecks towards crop Improvement

3. Capacity building • **Infrastructure for screening nursery and phenotyping for drought response** • **Tool kits (ready-to-use marker systems, diagnostic kits, phenotyping protocols)** • **Human resources**	**- Coordinate testing for drought evaluation centers (ecosystem)** **- Shuttle research/training activities (emphasis on drought)** **- Facilities (equipment, building on site)** **- Recognize different kinds of phenotyping (sophistication) for** **a) genetic analysis** **b) breeding**	**Genotyping Support Service** **Phenotyping Support Service** **Provide diagnostic markers** **Support shuttle research training**
4. Resolving trait complexity		**Projects to understand drought tolerance/QTL mechanism, physiological/genetics** **Establish high-confident QTL**

Generation

GCP Research Bottlenecks towards crop Improvement

5. Policy changes to facilitate varietal release and market access of improved varieties	• **National Seed System** - **"Release system of varieties"** • **Linkage with policy makers** • **Establish "Substantial Equivalence" for backcross materials to fast-track release**	**What GCP can contribute?**
6. Germplasm exchange and dissemination	• **Working through International Breeding Network and International Treaty** • **Exchange/dissemination within country**	
7. Relation with **(a) Private sector** **(b) Delivery of good seed**	• **linkage with PASS** • **linkage with SME** **Example: small hybrid rice companies** **- providing inbred parents** **- F1 seed production** **- distribution/marketing** **- decrease seed cost**	

Generation

Which options for GCP populations in *Musa* ?

- Development and utilization of segregating populations
- Develop additional (SSR, DArT, SNP…) markers
- Development and saturation of molecular linkage maps

- Bac end sequencing.
- Anchor physical map to genetic map

- Increase microsynteny studies with rice Arabidopsis and other models

How to overcome bottlenecks towards crop improvement in *Musa*

- Phenotyping the reference collection in at least three locations (with different ecosystems).
- Multilocation trials of improved material for biotic and abiotic stresses
- Training in phenotyping for drought (PSS)
- Incorporate drought tolerance to already well accepted cultivars in dry areas (e.g. South India, Ethiopia and North East Brazil).
- Promote exchange of breeding materials between Musa breeders.