

BRAINSTORMING SESSION

Group A

Moderated by Jonathan Crouch

Feedback from Group A on Genetic Basis and Breeding Tools

Rapporteur: Sarah Hearne

General comment:

Consider removing capacity building for many topic areas: much of what we discussed was capacity building!

Note: Comments on outsourcing below do not necessarily mean moving outside GCP members but also does not preclude it; simply finding the most time and cost effective way of performing tasks be that genotyping, transformation etc.

Topics were sometimes modified, new topics were also introduced. Each topic was ranked high (H), medium (M) or low (L) priority.

Genetic basis	Understanding allelic diversity Divergent viewpoint within group: <ol style="list-style-type: none">1. Integrate with understanding of regions with QTL; investigate diversity of genomic region2. What alleles?<ol style="list-style-type: none">a. Step back<ol style="list-style-type: none">i. Findii. Utilizeiii. Look across crops M
Genetic basis	LD and association mapping in wheat and other polyploids Need to prove concept first. Continue with existing projects and await outputs L
Genetic basis	Standardized agreed best practices for QTL linkage and association mapping (iMAS) Need overview of packages available with Pros and Cons Isn't this ongoing work? When outputs available? H
Genetic basis	Functional annotated rice genes validated through expression studies,

	mutagenesis and targeted activation/disactivation (and associated easy to use well linked databases)
	<p>Don't start with rice.</p> <p>Start with other crops which have higher levels of drought tolerance. Identify candidates through transcriptome analysis. Come back to rice and other model plants for validation.</p> <p>H</p>
Genetic basis	Linking markers with functional genes
	Group could not interpret comment?
Other suggestions by group	<p>Understand gene order between AND within crops. Link with allelic diversity</p> <p>H</p> <p>Use of system tools should be initiated Could use model pathways initially Harness advances in proteome and metabolome analysis as they become effective. Initiate studies and form linkages. Proof of concept</p> <p>L now H in the future (we need to start testing effectiveness now)</p>
Breeding tools (including MAS)	Strategies for introgressing exotic germplasm
	Questioned whether generation of wide-crosses could be outsourced H
Breeding tools (including MAS)	Low tech low cost assays for NARS across all crops - simple agarose gel-based markers for national programs – sampling methods – DNA extraction
	<p>Group questioned the need for NARS to invest directly in marker assays.</p> <p>Suggestion: Outsource all routine marker work to service labs which have higher throughput and lower cost per data point than NARS could achieve. "DNA can be sent anywhere via DHL". This would improve the quality control and standardization across projects. The important point is the utilization of good data not necessarily the generation of it which can be performed more efficiently in service centres</p> <p>Could support preliminary work in NARS labs so may be some need for modification of assays but not for the bulk of marker work. DNA extraction and sampling methodologies may still need to be implemented.</p>

	<p>What GCP could do now: Provide lists of “service labs” around the world who could offer such services, provide contact details and price: possibly GCP itself could negotiate rates?</p> <p>Could consider small project to investigate DNA extraction methodologies for NARS etc. with a range of technical capacities</p> <p>NARS may want/need training on utilization of data</p> <p>H</p>
Breeding tools (including MAS)	Robust experimental designs and data analysis protocols
	<p>Critical for all: capacity building May be done on a web interface</p> <p>H</p>
Breeding tools (including MAS)	Marker-accelerated breeding with transgenes
	<p>Group question: What transgenes?</p> <p>Alternative suggestion:</p> <p>GCP should ID centers of excellence for transformation that could be utilized by GCP members and others to perform transformation. Different centre may be needed for different crops. Should be able to provide cheaper more efficient transformation. “Don’t reinvent the wheel”.</p> <p>Note to group: We should consider this in the context of national guidelines of those countries where we may wish to deploy products: some national guidelines may state that products should be developed “in-house”. None the less transformation may be done outside for proof of concept.</p> <p>L</p>
Breeding tools (including MAS)	MAS feasibility studies
	<p>Should have national program focus Needs to be more wide focus than drought, some crops marker lack would suggest lack of feasibility for drought MAS but should not preclude MAS for other traits</p>

	H for NARS
Breeding tools (including MAS)	Databases of MAS successes and failures
	Again a critical tool Could include breeding methodologies for MAS: link with experimental design H
Other suggestions by group	Have centralized marker providers: Specialist centers who provide information and possibly primer Should have web interface e.g CIMMYT: Maize, IRRI: Rice, IITA: Cowpea, CIAT: Bean etc. H Ex-post impact assessment of breeding technologies within CG and partners (MAS versus phenotypic selection) Location of bottlenecks for differing crops H