

Group D

Outputs for Discussion
Moderated by Hei Leung

	Category	Output
1	Genetic basis/understanding	LD in wheat
1		Support characterization and use of wild genetic resources
1		A core set of germplasm for each crop with molecular and trait characterization
1		Expression analysis under field-relevant conditions
1		Investment in drought response (gene expression analysis) in non-cereals
2	Breeding tools/protocols	Homologous recombination for allele replacement
2		Hormone assay
2		SNPs in candidate genes, especially drought tolerance
2		Assure phenotype protocols are field relevant and use in genomics and gene discovery
2		Novel alleles and sources identified for drought, diseases, and nutrition
2		TILLING for vegetatively propagated crops
2		Improved drought tolerance pyramided with drought tolerance by MAB
2		Breeding activities linked to HarvestPlus
2		GIS to characterize environments
2		Phenotyping protocols for drought
3	Data management/software	Support for large datasets
3		Simulation tools for breeders
3		Access to analytical tools (open-source)
3		Germplasm sampling procedures available on Web
3		Data extraction tools
3		Functional integrated info platform for each crop
3		software and quality control
3		User-friendly informatics tools, on-line crop resource centers
3		Internet-independent bioinformatics tools
3		Timely access to data
4	Traits	Understanding of durable resistance
4		Drought tolerance in root crops
4		Root-related traits related to water-use efficiency, including soil and insect pests and parasitic weeds; nutrient use efficiency
4		Drought tolerance
4		Root development and physiology under stress
4		Enhanced methods to assay root traits
4		Combining drought and biotic stress tolerance
5	Training/capacity	Database use

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	building	
5		Project scientist training
5		Enlarge training programs (sabbaticals) for NARS scientists
5		Apply genomics to global conservation strategies and breeding programs
5		Extend phenotyping network concept to other crop types
5		Breeders trained in molecular biology and molecular biologists trained in breeding
5		Association mapping, sampling strategies
6	Policy and IPR	Enhanced germplasm access
6		IPR protection of stakeholders
6		Agreed policy framework by GCP members
6		Matching fund for GCP members to max. impact and responsibility of participating institutions
7	Genetic and genomic resources	Genomic resources: EST libraries for all 22 CGIAR crops, incl. orphans
7		CSSL sets in orphan crops
7		SSR markers sets for multiple crops
7		Use of proteomics, with emphasis on biochemistry and physiology
7		Transgenics for functional genomics
7		Metabolic pathways analysis as breeding tool
7		Diversity panel used for multiple traits in crop species