

BRAINSTORMING SESSION

Group B

Moderated by Carmen de Vicente

Feedback from Group B on Genetic Basis

Participants in breakout group:

Peter Stamp (Ethiopia)

Rebecca Nelson (Cornell)

James Gethi (KARI, reporting)

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Genetic basis

Focus on low-input situations, especially if yield under favorable conditions is a handicap to making progress under low-input

Systematically: QTL -> NILs -> genes -> markers

Marker-assisted genetics and physiology for per-se drought

Marker-assisted breeding for available QTL/genes affecting problems with simpler inheritance (pests/diseases/nutrition/etc that constrain adaptation under drought); need good inventory and tools to facilitate

Recognize differences among crops for the strategies that are best taken – make a systematic analysis to guide this

×	What (product)	Why	How
1	Drought: traits that indirectly enhance water-use efficiency	Easier to achieve	Seek tools for improving nematode resistance; disease resistance Nutrient-use efficiency (P-acquisition, N-use efficiency) Salinity tolerance
2	Drought: genetic basis of per se	Need to advance basic understanding	What are the real traits? Dissect, with crop and environment specific approach.

3	Rigorous inventories of existing information and genetic resources	Don't reinvent the wheel; efficient utilization of existing resources and knowledge	Inventory needed traits Inventory donors Inventory of major QTLs for relevant traits Target varieties to be improved
4	Parental lines to enhance drought-related tolerances	Major QTLs are needed	Create elite parental lines with high trait values and identified major QTL
5	Identify genes - >Marker assisted breeding for disease, drought	Reducing cost implied by huge numbers of materials for screening	Identify short list of strong QTLs for marker-assisted exploitation Marker-assisted selection to reduce numbers of materials Fix certain key genes in parental materials?
6	Minor QTLs	These are important too	Introgression lines for high LD; recurrent selection for low LD
7	Genetic stocks, e.g., QTL-NILs	Validation of QTLs Link physiological and genetic analyses Enhance access	Marker-assisted genetic analysis combined with careful physiology