Comparative allele diversity of candidate genes for drought tolerance in GCP crops

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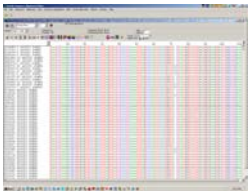
A Allelic



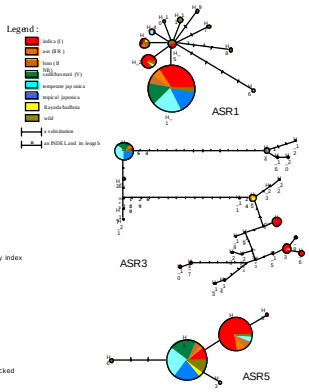
	ASR (1/g)	VIN	ERECTA	Orab-2a(1/g)	SUSY	SPS	TOTAL
Rice	5/6	2/2	3/3 (3 fg/a)	1/1	7/7 (2 fg/a)	1/1	19/20
Sorghum	6/6	2/2	3/3 (1 to 2 fg/a)	1/1 ?	9?5 (2fg/a) -1	1/1	18/18
Barley	3/3	2/3	2/2 (2fg/a)	1/1	2/2 (2 fg/a)	1/1	12/13
Cassava	2/2		1/1 (2 fg/a)		4/4 (2fg/a)	1/1	8/8
Potato	3/3		2/2 (2 fg/a)		2/2 (2fg/a)	1/1	8/10
Chickpea	1/1		1/1 (2fg/a) ?	1/1 (2 pa/a)	0/2	1/2	4/7
Beans	2/2		1/1 (2 fg/a)	2/2	2/2		7/7
TOTAL	2.2/2.3	7/7	13/13	6/6	2.2/2.4	6/11	76/82

Number of genes for which we have generated allelic sequences, for at least one fragment. NB: For rice SPS only 1 orthologous group will be sequenced. When completed, we should have data on more than 80 different genes.

We are generating a set of allelic sequences for 6 gene families across seven species

D Diversity

Rice reference set

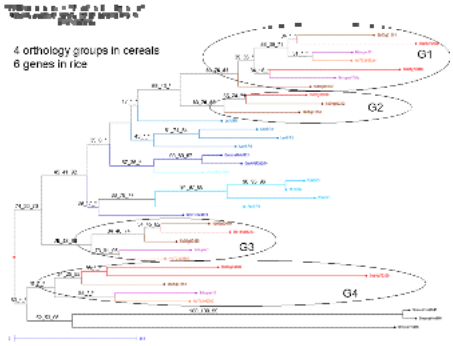


Haplotype networks of 3 rice ASR genes

Reference sets of 300 accessions have been validated and should be available for phenotyping.

Population structure often interferes in haplotype patterns

O Orthologous

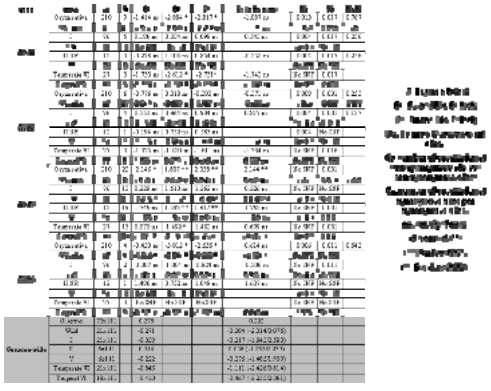


ASR phylogeny

Orthology relationships were identified for monocots / dicots. COS markers can be derived.

Some new genes have been identified in non-model species

C Candidate genes



Neutrality tests for rice ASR genes

Diversity / evolutionary pattern may reveal population history and/or some selective pressure, related to adaptative traits, acting on some genes

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