

Allelic diversity of candidate genes for drought tolerance in a rice reference collection

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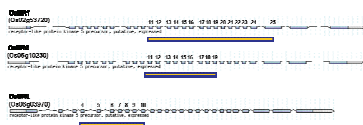
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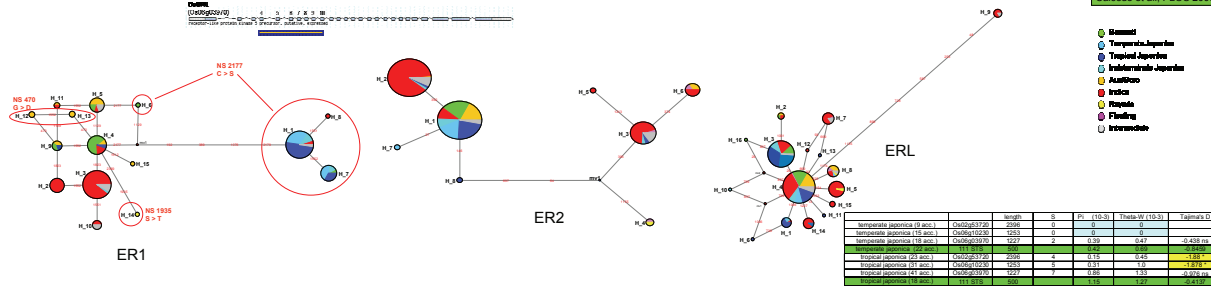
Considering climatic changes, improving crops for drought tolerance is one of the major challenges of plant breeders for the coming years. During domestication and selection events of major food crops in different eco-geographical environments, humankind has generated some selection pressure acting on key adaptive genes that could be still useful for crop improvement. Generation Challenge Program has funded in 2006 - 2008 a commissioned project called "allelic diversity of orthologous candidate genes" (ADOC) aiming to assess the allelic diversity of candidate genes or gene families for drought tolerance, in reference collections of about 300 accessions of seven mandate crops of the CGIARs (rice, barley, sorghum, bean, chickpea, potato and cassava). Here we report results obtained on rice for several genes families, including ASR (ABA-stress ripening), ERECTA and SuSy (sucrose synthase) genes, involved at different steps of drought stress response.

ERECTA



	length	S	Pi (10-3)	Theta-W (10-3)	Tajima's D	
sativa (142 acc.)	Os02g03720	2396	10	1.07	0.76	1.009 ns
sativa (142 acc.)	Os06g10230	1253	9	1.11	1.21	-0.185 ns
sativa (142 acc.)	Os06g03970	1227	17	1.17	2.28	-1.236 ns
sativa (73 acc.)	111 STS	900	2.29	2.11	0.2784	

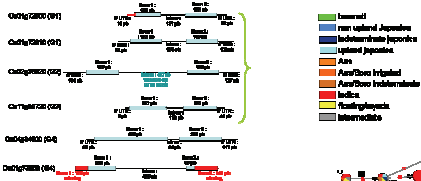
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ERECTA and ERECTA like-genes are functional candidates for stomatal patterning and transpiration efficiency. Those Leucin Rich Repeat + Receptor-Like Kinases are probably involved in signal transduction.

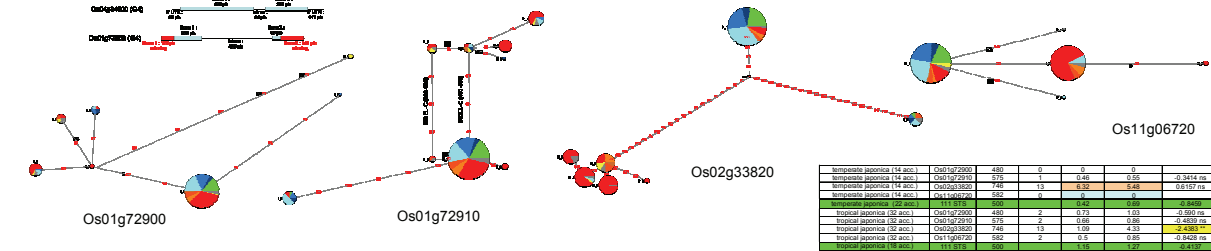
Non synonymous substitutions are found in ER1, and contribute to the differentiation between subgroups. A negative Tajima's D was found in the tropical japonica subgroup for the two ER genes, whereas no departure from neutrality was found for ERL.

ASR



	length	S	Pi (10-3)	Theta-W (10-3)	Tajima's D	
sativa (214 accessions)	Os01g2990	490	9	1.22	3.16	-1.3788 ns
sativa (214 acc.)	Os01g2910	575	6	1.13	0.78	-0.7159 ns
sativa (214 acc.)	Os02g33820	742	22	8.96	4.99	2.1472*
sativa (214 acc.)	Os11g06720	582	4	0.88	1.16	-0.4246 ns
sativa (73 acc.)	111 STS	500	2.29	2.11	0.2784	

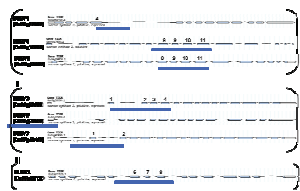
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Some ASR (ABA Stress and Ripening) proteins are supposedly involved in drought stress tolerance either through a role as hydrophilin (monomeric form) or their Zn-dependent DNA binding activity (on an hexose transporter). They act in the crosstalk between ABA and sugar metabolism.

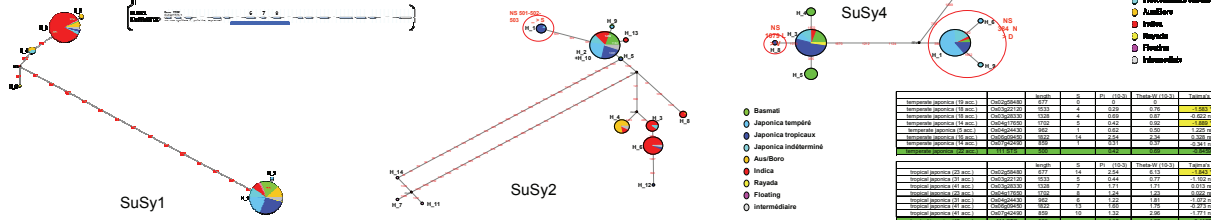
A very high level of polymorphism is found for Os02g3380, enhanced by the insertion of a MITE within the intron. Positive D is found in *Oryza sativa* and a negative D in tropical japonica, suggesting a balanced selection at the species level but purifying selection for tropical japonica subgroup. Os11g06720 (orthologous to maize ASR1, positional candidate for ASR) is highly conserved, with only two major haplotypes. A similar pattern with a major haplotype is identified for two genes in tandem on chromosome 1.

Susy



	length	S	Pi (10-3)	Theta-W (10-3)	Tajima's D	
sativa (256 accessions)	Os02g05490	677	16	1.29	4.84	4.175 ns
sativa (232 acc.)	Os03g28320	1533	35	1.99	3.91	-1.366 ns
sativa (220 acc.)	Os03g28330	1328	8	1.84	1.0	1.825 ns
sativa (178 acc.)	Os04g17650	1702	12	1.77	1.22	-1.129 ns
sativa (179 acc.)	Os05g02430	962	9	1.57	1.63	-0.882 ns
sativa (226 acc.)	Os06g09450	1822	50	2.84	4.73	-1.176 ns
sativa (218 acc.)	Os07g42490	859	13	5.05	2.54	2.423*
sativa (73 acc.)	111 STS	900	2.29	2.11	0.2784	

Caicedo et al., PLOS 2007



Sucrose synthase genes like other ones involved in sugar metabolism are involved in sugar remobilisation, osmotic adjustment and growth regulation under drought conditions. Different levels of polymorphism are found, depending on the members of the gene family.

Here again some significant positive D values are found for two SuSy genes, but negative values are found when considering different subgroups.

Tropical (mainly upland rice) and temperate (mainly irrigated rice) japonica subgroups seem to present distinct haplotypes for SuSy 3 and SuSy 4. Haplotype distribution in relation to hydrologic conditions remains to be studied.

Candidate gene diversity has been identified in a highly structured rice reference collection. Within a gene family, different diversity patterns have been highlighted in this study. Generally the (neutral) population structure is still evident from the haplotype network, but a few genes present a significant departure from neutrality, when considering the whole population of *Oryza sativa* or the different subgroups individually. Implication in term of crop adaptation to specific hydrologic growth conditions is still difficult to address at this stage, but specific subgroups like japonica may be used for association mapping with drought tolerance traits (temperate japonica being mainly anaerobic and tropical japonica being mainly upland cultivars). Natural polymorphism associated with adaptation to cropping systems in different environments may then be used for crop improvement.

Diversity analysis of *Oryza rufipogon* and *Oryza nivara* as been initiated for some genes and will provide additional information on the evolution of those gene families during domestication.