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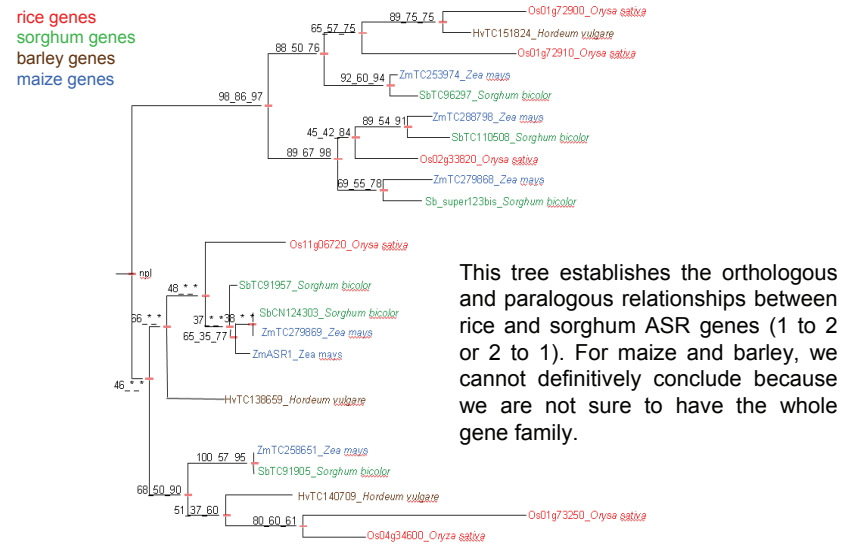
ABSTRACT

Drought is a major abiotic stress. Many candidate genes have been proposed during the last years to explain aspects of tolerance to drought stress, for a specific crop and in a specific environment. However, the relation between gene structural polymorphism and functional diversity is seldom clear. In a program founded by GCP (Generation Challenge Program) we are currently producing a dataset of allelic diversity at orthologous candidate genes for drought tolerance in rice, sorghum and barley.

The ASR (ABA, Stress and Ripening) gene family is one of the target genes chosen in this program. Many evidences show the implication of this family in drought tolerance, notably the co-localization between ASR1 locus and a QTL directly linked to drought tolerance in maize (Jeanneau et al., 2002) and the increase in ASR transcript level under osmotic stress in rice (Vaidyanathan et al., 1999).

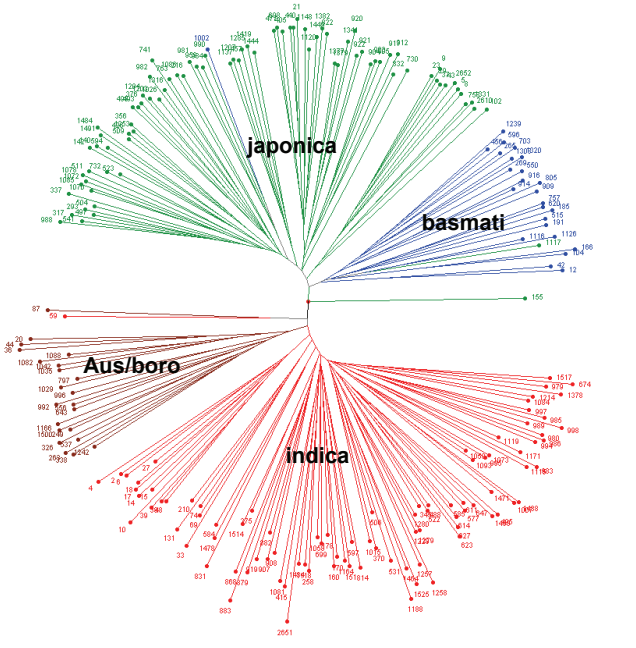
We gathered all sequences available in the databases on this gene family. Based on phylogenetic relationships between genes, orthologous genes were identified. In a second step, their whole sequence polymorphism was assessed in a collection of 222 reference accessions for each crop already characterized with neutral markers. The first analysis of allelic diversity in rice shows different pattern of haplotypes between genes. Is there any link with the adaptation of some rice accessions to water-stress? To answer this question, we will search for traces of selection within these genes.

Phylogenetic analysis of the six ASR of rice, the six ASR of sorghum, three ASR of barley and six ASR of maize. (FIGENIX pipeline)

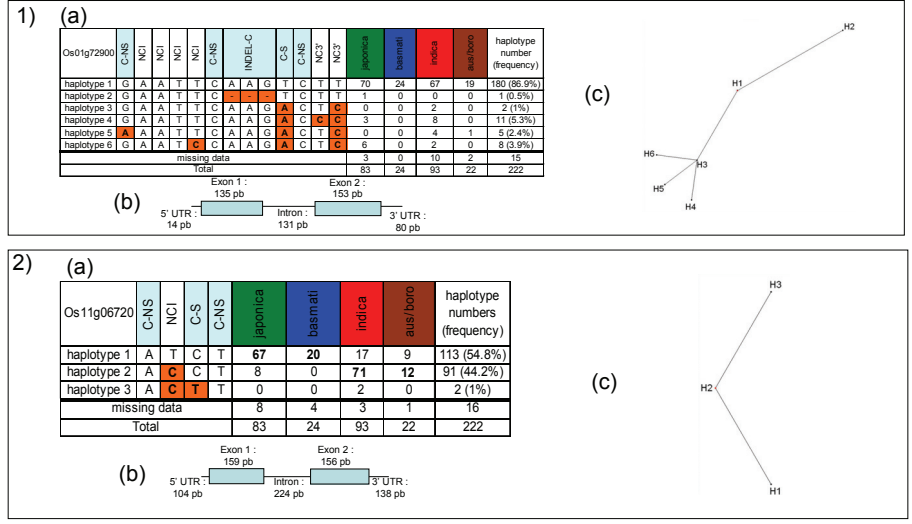


FOCUS IN RICE

Structure of the rice collection (222 accessions) analyzed with 48 SSR markers (GCP. 2005-01a).



Haplotype analysis of two ASR genes in the rice collection : 1) Os01g72900, 2) Os11g06720. (a) Different haplotypes and their repartitions in the four major groups of the rice collection, C-NS : non synonymous substitution in the coding region, C-S : synonymous substitution in the coding region, INDEL-C : insertion or deletion in coding region, NCI : substitution in the intron and NC-3' : substitution in the 3' UTR. (b) structure of the sequences analyzed. (c) unrooted parcimony tree of the haplotypes.



The rice population is highly structured in four clear groups corresponding to isozymic groups (Glaszmann, 1987) : japonica (VI), basmati (V) in one hand and indica (I), aus/boro (II) on the other hand. Two others small groups include Rayada (IV) and Badhoia (III).

In the ASR gene family, the haplotype diversity of Os11g06720 is correlated with population structure, while the haplotype diversity of Os01g72900 is not.

Is there any link between nucleotide polymorphism and the adaptation of some rice accessions to water stress?

Prospect : To answer this question, we will have to analyze the collection taking into account ecotype adaptation and not only isozymic groups. Some isozymic groups include accessions with different adaptation to water stress (e.g temperate japonicas adapted to the irrigated ecosystem and tropical japonicas adapted to the upland ecosystem). We will analyze the haplotype structure in the four others genes of the ASR gene family in rice, the six ASR genes in sorghum and the three in barley. We will investigate ASR genes families evolution, by comparing expectations of the neutral equilibrium model to the patterns of our genetics data with Tajima's D statistic and HKA test. To eliminate the effect of demographic history, we will calibrate these tests genome-wide with a hundred genes based on other studies.