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Allelic Diversity At Orthologous Candidate Genes For Drought Tolerance In Cereal Crops: Example Of The ASR Gene Family.

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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 and the increase in ASR transcript level under osmotic stress in rice. We gathered all sequences available in the databases on this gene family. We used these sequences to design consensus primers in order to amplify all genes of this family in the three cereals. Based on phylogenetic relationships between genes, orthologous genes are identified. In a second step, their whole sequence polymorphism is assessed in a DNA bank of 283 reference accessions for each crop already characterized with neutral markers. The first analysis of allelic diversity shows that some rice ASR genes are on purifying selection and other may be on relaxed selection. This reference germplasm could allow testing association between genes polymorphism and trait variability.