Water stress is responsible for significant losses in rice production. A deep and thick root system was clearly shown to be correlated with a better yield under water stress situations in rice. A large number of candidate genes co-localizing with QTLs for root morphology have been detected. Nevertheless, the most valuable genes and alleles to improve drought tolerance still remain to be identified.

Our goal is to survey rice genetic resources to identify genes and alleles contributing to a deeper, thicker and faster root development using a combination of approaches such as meta QTL analysis, population genetics, association mapping and transcriptomics.

Method

We sequenced segments of 8 candidate genes and surveyed their allelic and haplotypic diversity in a panel of 32 rice accessions representative of O. sativa 4 isozymic groups. The level of genetic variation at the nucleotide level was estimated as nucleotide polymorphism (θ) and nucleotide diversity (π). θ and π were calculated for coding regions, for non coding regions and for the whole gene. The neutrality of mutation was tested employing Tajima’s D test for the whole set of accessions as well as for the two main varietal groups.

Six out of the 8 genes had sequences of good quality for the 32 accessions. Among these 6 genes, IAA8 exhibited the highest diversity (π=5.52.10⁻³). Tajima’s test of neutrality of mutations in IAA8 revealed a significant departure from neutral expectations. D was significant for japonica varieties and correlated to phenotypic results on root development through association analysis. This value is negative indicating an excess of rare alleles. The tests were not significant for the other genes.

The gene IAA8 shows 4 haplotypes. Haplotype 1 is the most frequent (56%) whereas haplotype 4 is the scarcest (3%). Indica and japonica could be discriminated based on their haplotypes. The number of haplotypes was higher among indicas than among japonicas.

The correlation between the function of IAA8 and the selection evidences allows considering IAA8 as a good candidate gene for root development in tropical japonica. We could distinguish isozymic groups based on the haplotypic organization. This bipolarity was reported with neutral markers such as isozymes, RFLP, SSR (Glaszman, 1987; Garris et al., 2005) but it is not always the case.

The polymorphism of IAA8 and its promoter will be assessed in an extended population of 200 tropical japonica accessions and correlated to phenotypic results on root development through association mapping. The level and tissue localization of the gene expression will be investigated.