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01. NEW CONCEPTS IN RICE ROOT BIOLOGY

TOWARDS AN INTEGRATION BETWEEN GENETIC AND FUNCTIONAL GENOMIC APPROACHES IN ROOT RESEARCH IN RICE

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Purpose:

Roots are key organs for plants as transporters of water and nutrients. However, they are complicated to observe. To develop rice varieties with root systems adapted to the target environments (e.g. with a high number of deep, thick and highly branched roots for the upland ecosystem) without direct observation, a better knowledge of the genes involved is necessary. So far, only three genes influencing root architecture or nutrient uptake have been cloned in rice.

Whole genome association mapping (WGAM) offers a fast access to new quantitative trait loci (QTLs) with a better resolution than conventional QTL mapping. Results on several panels are presently available. However, WGAM relies on statistics and its results need further validation using evidences from other approaches, notably functional genomics. The effects of genes with function on root development validated in *Arabidopsis* are being studied in rice (e.g. SHR and SCR or the family of leucine-rich repeat receptor-like kinases in our lab). We will present a summary of all these results.

Approach and methods used:

We are using approaches involving meta-QTL analysis, association mapping, and positional cloning for the genetic side that we compare with the results of orthology between rice and other species and the functional validation of these orthologs in rice for the genomic side.

Key results:

The meta- analysis of QTL studies published up to 2006 led to the identification of several interesting zones but the upgrade of this study up to present mostly confirms what was already known. WGAM that is often conducted in intra-subspecific panels identifies many new markers that are sometimes within candidate genes but more often in linkage disequilibrium with them. When comparing the position of WGAM-derived QTLs to those of known genes derived from functional genomics, only few seem to correspond. The reasons for such a situation will be discussed. The parallel advancement of the positional cloning of a QTL for root depth on chromosome 9 will also be presented.

Synthesis and Applications:

The integration of genetic and functional approaches to identify the genes involved in root architecture and plasticity in rice is likely to lead to the release of mega-varieties with improved root system in the near future.