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Rice root genetic architecture: meta-analysis from a QTL database

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The genetic architecture of rice root system has been extensively studied by teams interested in improving drought resistance of rice. Many papers have been published in the last 10 years on QTL detection for root parameters in several populations. These combined data could be extremely helpful for candidate gene identification or QTL cloning provided an easy access to the whole data is possible.

Our objective was to store the relevant data in an easy to query database and synthesize these results in a way useful for geneticists interested in rice root system through a metaQTL analysis.

We extracted from 24 papers all relevant information on QTLs controlling root parameters. A database of 689 QTLs for 29 traits detected in 12 populations was constituted. The physical position on the pseudochromosomes of the markers flanking the QTLs was determined. For this purpose, Gramene data or sequence information were used when available. Otherwise, as in the case of AFLPs, the nearest marker with a known sequence was used. An overview of the number of QTLs in segments of 5 Mb covering the whole genome is presented. Areas with a large density of QTLs for any given traits were further explored through a meta-QTL analysis approach using the software package BioMercator. The method allowed us to determine the likely number of true QTLs in these areas using an Akaike information criterion, and estimate their position. The consensus QTL confidence interval was generally reduced.

Existing bioinformatics tools such as OrygenesDB (<http://orygenesdb.cirad.fr/>) can be used to list the genes underlying consensus QTL confidence intervals.

The QTL basic information will be soon available to the scientific community in Tropgene database. (<http://tropgenedb.cirad.fr/>). Complex queries on the experimental conditions in which QTL were detected will be possible. Beside root data, the database includes similar data on other drought avoidance or drought tolerance traits.