

Genomic regions associated with drought tolerance in upland rice landraces: linking experimental data from QTL mapping and EST sequencing

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Increasing yield while maintaining environmentally friendly production stands as a great challenge for the research of economically important crops. Rice (*Oryza sativa* L.) is a crop of great social and economic importance in Brazil. The discovery of mechanisms which lead to better water use efficiency, maintaining or increasing plant yield, is strategically important for breeding programs in countries where a significant part of the production is carried on a rain fed, upland (“aerobic”) environment. In order to identify QTLs associated with grain yield under drought conditions, accessions belonging to a rice drought tolerance core collection were selected and used for the construction of populations of recombinant inbred lines (RILs). One of these populations, originated from the crossing Chorinho x Puteca, was used for microsatellite map construction and QTL mapping of yield and morphological traits under drought stress. QTLs for yield and yield components under drought stress were mapped on five rice chromosomes. One QTL for plant height, with a strong effect on phenotypic variation (42%), was mapped on chromosome 3. This genomic region flanks the *OsDWARF* gene, which is involved in brassinosteroid metabolism. *OsDWARF* mutants show abnormal development and growth due to problems with cell organization of tissues involved in leaf growth. Therefore, this QTL is a potential candidate for further analyses to assess its role in drought tolerance mechanisms in rice and for potential use in marker assisted selection programs. In addition, QTL mapping data were compared with the identification, annotation and physical map location data of transcription factors detected by EST sequencing of subtractive cDNA libraries from root and stem tissues of two varieties from the rice germplasm bank maintained by Embrapa. Prata Ligeiro – a drought tolerant upland rice landrace – and IRAT20, a drought sensitive variety were used in this analysis. EST data were subjected to annotation and their location on the rice genome, as well as their co-location with QTLs for drought tolerance traits in rice, were determined by *in silico* analyses. Such results illustrate how advanced genomic tools can assist in the process of aggregating value to crop genetic resources. By coupling genomic tools such as sequencing, QTL mapping and gene expression data with thorough phenotyping in several phases of the study, crop germplasm can be deployed in breeding programs according to a pre-defined purpose.

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