Molecular breeding of stress tolerant rice: From genes to farmer's fields.

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Rice is the most important staple food in the world and is the main and sometimes the only food available for poor people in Asia. Poor farmers usually don't have access to fertile agricultural land and irrigation, i.e. they grow rice under unfavorable, rainfed conditions with little or no access to fertilizer and chemicals controlling pests and diseases. Productivity in rainfed systems is accordingly low and constrained by various biotic (e.g. blast, bacterial blight, tungro) and abiotic stresses (e.g. drought, submergence, salinity, and nutrient deficiencies).

At the International Rice Research Institute (IRRI) we are addressing these problems by performing screenings under stress in order to identify tolerant varieties and to map the underlying QTL(s). Fine mapped QTLs can than be introgressed into widely grown rice varieties by marker assisted breeding. Following this approach, we have fine mapped a major QTL for submergence tolerance (*sub1*) and are currently developing submergence tolerant versions of important Asian rice varieties (e.g. IR64-sub1). Sequencing of the *Sub1* locus in the tolerant parent revealed the presence of three ERF-type transcription factor genes (*Sub1A*, *Sub1B* and *Sub1C*). The *Sub1A* gene was subsequently identified as the major determinant of submergence tolerance by transgenic and other approaches. Importantly, *Sub1A* is absent from the Nipponbare (ssp. *japonica*) genome and, though present, not clearly annotated in the available ssp. *indica* genomic sequence (93-11) demonstrating the importance of sequencing QTLs in the respective tolerant donor parent. Preliminary data suggest that *Sub1A* is specifically down regulated in intolerant accessions by an intolerant specific promoter element, and that miRNAs might play a role in downstream gene regulation in tolerant varieties.

Following the same approach, we have mapped and sequenced a major QTL that confers tolerance to phosphorus (P) deficiency under upland conditions. *Phosphorus uptake 1* (*Pup1*) is located on Chr.12, in a region overlapping with a major QTL for drought tolerance (yield under drought) that was recently mapped at IRRI. We are currently addressing a possible interaction of *Pup1* and drought tolerance. Sequence analyses of the *Pup1* locus in the tolerant donor variety (Kasalath) revealed that the Kasalath *Pup1* region is about twice as large compared to the corresponding region in Nipponbare, with large numbers of transposons, unclear gene models and Kasalath specific genes. The absence of genes obviously related to P-uptake or P-mobilization made it additionally difficult to short list candidate genes for a functional assessment.