

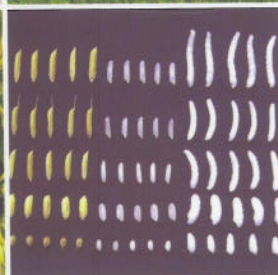
# ABSTRACTS

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## **Progress in genetic improvement of rice drought tolerance and aerobic adaptation**

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Drought is a major constraint in upper rainfed fields, which remain saturated only briefly after rainfall. It is especially damaging around flowering, but also reduces yield if it occurs for extended periods during vegetative growth. Drought risk affects productivity even in favorable years, because it causes farmer to apply sub-optimal amounts of fertilizer. Trials by the IRRI-India Drought Breeding Network in 2005 showed that many widely-grown varieties in rainfed areas, including Swarna, Sambha Mahsuri, MTU 1010, and IR 36, are extremely drought-sensitive. Improvements in drought tolerance are therefore urgently needed by rainfed farmers. Genetic variation in tolerance to both vegetative- and reproductive-stage stress exists in cultivated rice, but few programs select for them directly. Selection for secondary drought-related traits has been proposed under the assumption that they are reliable indicators of tolerance, but most such traits have proven neither more heritable than yield under stress nor highly correlated with it. Recently, genetic analysis of yield per se, in trials in which drought stress is imposed repeatedly during vegetative and reproductive growth, has confirmed that yield under drought is as heritable as non-stress yield. Genotypes have been identified combine high yield potential with higher yield under stress than current widely-grown varieties. For example, IR 74371-46-1-1 yielded 1.3 t ha<sup>-1</sup>, or over twice as much as IR 64 and MTU 1010, under severe lowland stress at Raipur in WS 2005, and also out-yielded them under full irrigation. Small introgressions can result in large tolerance gains. For example, IR 77298-14-1-2, a BC3 derivative of IR 64, out-yields its recurrent parent by 100% under severe lowland stress at IRRI. That one or a few loci can have large effects on drought tolerance was confirmed by QTL analysis of crosses between tolerant and susceptible parents. A single QTL on chromosome 12 accounted for 40% of genetic variation for yield under stress over two years in a population derived from Vandana/Way Rarem. Another, on chromosome 3, explained 20% in IR55419-04/Way Rarem. It is likely that drought-tolerant donor varieties contain many more such alleles, which may be useful in marker-aided breeding (MAB). Selection for yield under aerobic management has produced genotypes with high biomass production and reproductive-stage drought tolerance in aerobic soils. These aerobic-adapted cultivars, usually derived from crosses between lowland HYVs and improved upland rices, can yield 4 t ha<sup>-1</sup> when direct-sown under hydrological conditions in which lowland-adapted varieties yield 2 t ha<sup>-1</sup> or less. Aerobic rice may be useful in reducing drought risk and increasing cropping intensity in upper-toposequence rainfed fields, by permitting establishment at the beginning of the rainy season rather than after sufficient standing water has accumulated for transplanting. Aerobic adaptation, like drought tolerance, appears to be strongly affected by a small number of loci, and may be transferable by MAB. Drought-tolerant and aerobic-adapted varieties are now being developed via direct selection for yield under stress by several South and Southeast Asian programs, and can be expected to have a large impact on rice productivity in drought-prone regions.

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## **Salinity, submergence and nutrient deficiency in rice: bases of tolerance and progress through breeding**

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Abiotic stresses such as submergence, salinity, drought and nutritional disorders are major constraint for rice production across large areas of rainfed rice ecosystems. Notable, these stresses seem to disproportionately affect the predominantly poor farmers in these areas. Our current efforts intend to understand the mechanisms and identify the genetic determinants of tolerance for salinity, submergence and nutritional deficiencies, particularly P and Zn deficiency, with the objective of designing efficient breeding strategies to speed the development of tolerant germplasm. Tolerance to these stresses is complex, involving a number of variable physiological mechanisms. For example, tolerance to salinity

involves sodium exclusion, controlled transport, and sequestering of toxic ions in older tissues and in apoplasts. Tolerance to submergence is particularly associated with ability to accumulate higher levels of non-structural carbohydrates in seedlings prior to submergence, its efficient use during flooding through limited extension growth and ability to retain leaf chlorophyll content for limited photosynthesis during submergence and for faster resumption of growth when water recedes. Tolerance to P deficiency seems to be associated with enhanced ability for P acquisition from hardly available sources, through greater root surface area, enhanced external efficiency or both. Tolerance to these abiotic stress is also associated with the ability to up-regulate the anti-oxidant system to detoxify active oxygen species that accumulates during stress. Major QTLs for salinity (*Saltol*), Submergence (*Sub1*) and P-deficiency tolerance (*Pup1*), were identified in rice using populations developed from contrasting parental lines. These QTLs were further fine-mapped and the respective loci were sequenced/annotated and are being studied through expression and complementation analysis to identify and validate candidate genes underlying tolerance at these loci. For submergence, a cluster of genes identified as Ethylene Responsive Elements (ERFs) were found to be responsible for the tolerant phenotype conferred by *Sub1* locus. Two of these genes, *Sub1B* and *Sub1C*, are invariably present in the *Sub1* region of all rice accessions analyzed but the presence of *Sub1A* is variable with two alleles; a tolerance-specific allele '*Sub1A-1*' and an intolerance-specific allele '*Sub1A-2*'. Overexpression of *Sub1A-1* in an intolerant cultivar conferred enhanced tolerance, indicating that *Sub1A-1* is a primary determinant of submergence tolerance. For *Saltol* and *Pup1*, similar analysis is on-going to identify the genes involved. Parallel efforts aimed at identifying SSR markers that are QTL- /gene-specific to be used in marker assisted backcrossing (MAB) to incorporate these genes into popular, yet, intolerant varieties. Substantial progress was made with *Sub1* locus, which was introgressed into few widely grown cultivars using MAB. The new varieties maintain the high yield and other agronomic properties of the recurrent parents and are tolerant to submergence. Cultivation of these varieties is expected to provide protection against damaging floods and increase the food security for farmers in flood-prone areas. Similar approach is being pursued to incorporate *Saltol* and *Pup1* into popular varieties. The ultimate goal is to integrate these QTLs/genes into suitable varieties in combination dictated by target environments, to develop resilient cultivars for high and stable productivity.

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### Genetic networks underlying drought tolerance in rice: detection, verification and application in breeding

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In a large backcross breeding effort involving three elite lines (IR64, Teqing and a new plant type line, NPT) as recipients, and a diverse set of 20 lines from 11 countries as donors, we developed and screened 68 BC<sub>2</sub>F<sub>2</sub> bulk populations from 42 crosses under severe stresses of two types of drought, the lowland stress at the reproductive stage and chronic stress of upland conditions. A total of 794 DT introgression lines (ILs) were selected. We then tracked the gene flow in the 794 DT ILs by genotyping the ILs with well-distributed SSR markers. A total of 104 genomic regions (bins) across the rice genome were associated with DT or water use efficiency (WUE) in rice detected by 1090 cases of significant excess of donor alleles and homozygotes in the ILs. A high level of allelic diversity at many DT loci was suggested based on differences in gene action and effects of the detected DT loci. Linkage disequilibrium analyses revealed the hierarchy of the multilocus structure of DT loci – the presence of multiple QTL groups, including many perfect association loops, each consisting of multiple unlinked but positively associated DT loci that were co-regulated in response to selection. This result led us to, for the first time, the discovery of the high-confidence genetic networks underlying DT in rice. Results from the progeny testing of the DT ILs under both stress and non-stress conditions indicated that QTLs within association loops acted like single genes with large effects on multiple phenotypes including yield, indicating that these association groups or loops were targets of selection. In the following QTL pyramiding experiments, we analyzed F<sub>2</sub>-derived lines selected under severe drought from crosses between unrelated DT ILs that segregated for more than DT 30 QTLs and progeny tested these lines to verify the identified DT loci and genetic networks.