

P6.11 - Molecular diversity and variation of *Sub1* gene expression in relation to submergence tolerance in rice

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Breeding for improving submergence tolerance in rice cultivars is a major objective for flood prone areas of Asia. A cluster of three ERF like genes at the SUB1 locus (chromosome 9) has been identified from a rice variety, FR13A that confer tolerance to complete submergence for about 14 days. Genetic diversity is one of the important issues to find out additional sources of tolerance to submergence. Further, SUB1 gene-expression differences contributing to phenotypic variation are useful to understand the mechanisms of submergence tolerance. In the present investigations, SSR-based clustering among 160 flood-prone rice accessions and expression studies of *Sub1A* and *Sub1C* loci (conferring submergence tolerance) were undertaken, using semi-quantitative RT-PCR method. Microsatellite cluster analysis at 30 SSR loci grouped the varieties into four major clusters (based on geographical origin) and four sub-clusters. SSR-based clustering and submergence screening indicated that a diverse collection of accessions could provide additional diversity and submergence tolerance sources for further studies. SNPs study generated three patterns at *Sub1A* locus and four patterns found at *Sub1C* locus. Of the eight haplotypes (combination of SNPs), A1C1 haplotype was most tolerant than other haplotypes, indicating major role of *Sub1A1* and *Sub1C1* alleles for the tolerance. Haplotype specific expression of two ERF genes indicated that allelic expression variation affected the tolerance level of different haplotypes, differentially. In tolerant varieties (IR40931), the highest expressed gene was *Sub1A*; while expression level of *Sub1C* was low. In susceptible Fulkari, the highest-expressed gene was *Sub1C* and the *Sub1A* was not expressed. In moderately tolerant varieties (Motorsail and Kottamali) both *Sub1A* and *Sub1C* transcripts were up-regulated by submergence. These studies also demonstrated that two hybrids had unequal expression of *Sub1A* and *Sub1C* alleles that also affected the elongation patterns differentially. Selection of hybrid 2 (Kalukanda/Swarna *Sub1*) might led to improvement of tolerance in presence of moderate level of elongation having balanced level of *Sub1A* and *Sub1C* transcripts. These finding could be used as a new innovation to develop intermediate tall improved rice varieties with submergence tolerance for flood prone rice areas of south-east Asia, where adaptation of semi-dwarf rice varieties are limited.

P6.12 - Maize genetic transformation with the *SbMATE*, aluminum tolerance gene isolated from sorghum

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The toxicity of aluminum (Al³⁺) is a major limiting factor for plant growth in acid soils which represent 68% or 250 million hectares of Brazilian territory and nearly 50% of arable land on the planet. Recently, in sorghum was identified and isolated by positional cloning technique and comparative genomics, a major aluminum tolerance gene, called *SbMATE*. This gene encodes a member of a membrane transporters family responsible for efflux of citrate in roots of sorghum. The present research test the hypothesis of the use of this gene for the generation of transgenic maize cultivars with higher levels of adaptation to acid soils. Callus of maize line Hi-II, were transformed via *Agrobacterium tumefaciens* with the gene *SbMATE*. The gene construction used *SbMATE* gene under the control of the ubiquitin promoter and bar gene driven by CaMV35S promoter. Transformed cells were selected in media containing the herbicide ammonium glufosinate. From the five transgenic plants containing the bar gene four also had the *SbMATE*. The presence of these genes has been shown by PCR specific primers. The high expression in these four plants has been shown by Real-time PCR analysis comparing non-transgenic plants of the same genotype. Results have demonstrated an effect of the sorghum *SbMATE* gene in maize which would bring a great impact in the acidic soils agriculture around the world.

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