IDENTIFICATION OF THE GENOMIC REGIONS ASSOCIATED WITH PHOSPHORUS DEFICIENCY TOLERANCE IN SRI LANKAN RICE GERMPLASM FOR MARKER ASSISTED BREEDING

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Rice (*Oryza sativa* L.) is indispensible as the staple food for more than 50 % of the human population. The demand for rice is steadily growing. Increasing rice productivity is quite challenging and affected by many factors such as limitations of nutrients in the soil. Phosphorous (P) is the most limiting macro nutrient in rice growing soils worldwide due to the fixation of P by metal ions such as Fe^{3+} and Al^{3+}. Farmers tend to apply P fertilizer in large quantities to achieve their yield targets but that is often leading to increased cost of production, environmental pollution and health hazards. Therefore, the production of P deficiency (PD) tolerant rice varieties through molecular marker assisted breeding (MAB) is identified as the most promising and sustainable solution.

Breeding of rice for PD tolerance in Sri Lanka is still in infancy although it is internationally well studied. A quantitative trait locus (QTL), *Pup1* for PD tolerance is reported and molecular markers are available to use in MAB. A japonica rice cultivar, *Nipponbare* and Indonesian landrace *Kasalath* was used for these studies. These information cannot be directly used in MAB of rice in Sri Lanka and validation of *Pup1* haplotypes with respect to the degree of PD forbearance in Sri Lankan rice germplasm is a prerequisite. The present research project was aimed to set up a platform for MAB of rice in Sri Lanka for PD tolerance.

A set of 30 rice landraces and varieties was screened for PD tolerance using the parameters such as plant height, number of tillers, shoot dry weight, shoot P concentration, shoot P uptake and P use efficiency and multiple statistical procedures. A scoring system was developed to score the PD tolerance of rice varieties; 3 - tolerant, 2 - moderately tolerant and 1 - sensitive in which three classes were identified. The improved genotype H-4 is the highest PD tolerant variety. Haplotype analysis was conducted using 23 DNA markers, 30 rice genotypes and the reference PD tolerant landrace *Kasalath* and PD sensitive landrace *Nipponbare* revealed 31 haplotypes indicating very high diversity within *Pup1* region. The sequence analysis of codominant region *K20* revealed very high level of sequence polymorphism and five clusters where unique haplotypes were detected in the highest tolerant H-4, *Murungakayan* and H-10 within the Sri Lankan rice germplasm which are different from *Kasalath* group. The genetic analysis based on the segregating population revealed that most of the traits follow quantitative inheritance and the associated color change due to P starvation, epistatic dihybrid ratios, very high heterosis and heritability indicating the higher chance of mapping QTLs effectively. The bulk segregant analysis (BSA) revealed the potential of applying marker alleles for marker assisted selection and to DNA marker analysis within the *K46* region provides the background to detect the highest tolerant cultivars separately from the tolerant cultivars for PD. The results obtained from the present study would undoubtedly contribute to the improvement of rice production.