

Evaluation of Genetic Diversity in Rice (*Oryza Sativa* L.) for Direct Seeding Traits Using SSR Markers

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ABSTRACT

Molecular markers are useful tools for evaluating genetic diversity and determining cultivar identity. The purpose of the present study was to evaluate the genetic diversity within a diverse collection of rice accessions, and to determine differences in the patterns of diversity. Forty eight rice genotypes of particular interest *i.e* to direct seeding were evaluated for genetic diversity using SSR markers linked to ten traits of direct seeding. The results indicated that among SSR markers used, 10 SSR loci were polymorphic and produced 36 alleles. The number of alleles per locus generated by each marker varied from 2 to 5 alleles with an average of 3.6 alleles per locus. The polymorphic information content (PIC) values ranged from 0.305 to 0.797 with an average of 0.628. Out of the 10 polymorphic SSR markers used, 8 markers were highly informative (PIC > 0.50), 2 markers were informative (0.25 < PIC < 0.50). Highly significant correlation coefficient was found between PIC values and the number of alleles detected per locus ($r=0.925^{**}$). The SSR markers RM201, RM263 and RM5509 were the highest polymorphic markers in current study. The Jaccard's similarity coefficients among the studied genotypes ranged from 0.1 to 1. The 48 rice genotypes were grouped into six major clusters at 35 % similarity level. Cluster II was the largest with 11 genotypes followed by clusters III and I with seven and six genotypes respectively.

Key words: *Direct seeded rice, Molecular diversity, SSR markers.*