

DII 01 Genetic basis of some traditional rice cultivars of Sri Lanka

Ranawake A.L.,¹ Mori N.²

¹Department of Agricultural Biology, Faculty of Agriculture, ²Laboratory of Plant Genetics, Graduate school of Science and Technology, Kobe University, Japan

Genetic basis of 84 traditional rice cultivars, two *Japonica* rice cultivars and one *Indica* rice cultivar developed at Hokuriku research station, Japan was assessed using 11 SSR markers. SSR markers are co-dominant and therefore amplified DNA fragments represent different allele and different banding patterns scored as different genotypes. Total of 73 alleles were revealed in these 11 SSR markers indicating that all the markers used in the study were polymorphic. *Japonica* rice variety *Nipponbare* was included in the study for amplification and analysis. Banding patterns identified in this variety were used as reference material to score the different alleles in the rice cultivars studied. All the 11 SSR markers amplified visible DNA bands for the rice cultivars. The highest numbers of alleles (13) were recorded in locus RM 493 and the lowest numbers of alleles (2) were recorded in the locus RM 507. The average SSR markers were 6.6 alleles per locus. The allele frequency data indicated that all the loci were polymorphic in the rice cultivars used. Three rice cultivars (*Kalu Bala wee*, *Bg 35-2*, *Koopon Sivappu*) clustered in one group and all the other 81 traditional rice cultivars were differentiated with that group. *Japonica* rice cultivar *Nipponbare* was clustered with traditional rice cultivar *Handiran*, showing similarities in genetic basis of these two cultivars. *Japonica* rice cultivar *Nipponbare* and *Handiran* had the longest spacial distance from all the other rice cultivars while the other *Japonica* rice cultivar *Hyugokithanishiki* was clustered with less distance than that of *Nipponbare*. *Valihandiran* and *Welihandiran* were clustered with close spacial distance showing relatively low differentiation. The cultivars used in this study showed relatively high level of genetic diversity with an average Shanon Index of 0.9441. The information of this research is a valuable source for analyzing genetic diversity, fingerprinting genotypes, determining variety identity, marker assisted breeding, and phylogenetic analysis.

Keywords: SSR markers, genomic DNA, indica rice, traditional rice cultivars in Sri Lanka