

Inheritance studies of SSR and ISSR molecular markers and phylogenetic relationship of rice genotypes resistant to tungro virus

ABSTRACT

Multivariate analyses were performed using 13 morphological traits and 13 molecular markers (10 SSRs and three ISSRs) to assess the phylogenetic relationship among tungro resistant genotypes. For morphological traits, the genotypes were grouped into six clusters, according to D2 statistic and Canonical vector analysis. Plant height, days to flowering, days to maturity, panicle length, number of spikelet per panicle, number of unfilled grain per panicle and yield were important contributors to genetic divergence in 14 rice genotypes. Based on Nei's genetic distance for molecular studies, seven clusters were formed among the tungro resistant and susceptible genotypes. Mantel's test revealed a significant correlation ($r = 0.834^*$) between the morphological and molecular data. To develop high yielding tungro resistant varieties based on both morphological and molecular analyses, crosses could be made with susceptible (BR10 and BR11) genotypes with low yielding but highly resistant genotypes, Sonahidemota, Kumragoir, Nakuchimota, Khaiyamota, Khairymota and Kachamota. The chi-square analysis for seven alleles (RM11, RM17, RM20, RM23, RM80, RM108 and RM531) of SSR and five loci (RY1, MR1, MR2, MR4 and GF5) of three ISSR markers in F2 population of cross, BR11 \times Sonahidemota, showed a good fit to the expected segregation ratio (1:2:1) for a single gene model.

Keyword: Tungro resistant genotypes; Genetic diversity; Morphological traits; Molecular markers; Inheritance study