

Genetic Relationships of Selected Traditional and Newly Improved Sri Lankan Rice Germplasm

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Rice (*Oryza sativa* L.) germplasm of Sri Lanka consists of many traditional accessions (TAs) and newly improved varieties (NIVs). However, the genetic relationships between these rice accessions/varieties are not fully understood. In the current study, the genetic relationships of a panel of 64 Sri Lankan rice accessions/varieties (representing 24 TAs and 40 NIVs) were deduced using a Bayesian approach and a hierarchical cluster analysis, with 12 unlinked molecular markers representing all rice chromosomes. The Bayesian genetic assignment analysis was conducted in Structure v2.3.4, adopting an admixture model and the optimum most probable number of ancestral clusters (K) were derived based on the log-likelihood values in Structure Harvester v0.6.93. (K = 2; group-1 and group-2). Of the two genetically distinct groups recovered ($\geq 95\%$ assignment probability), group 1 corresponded to 90% of the NIVs and group 2 to 79% of the TAs in the study panel. The remaining NIVs (10%) and TAs (21%) shared alleles indicating possible historical genetic admixture. The resulted two genetically isolated gene pools are indicative that the contribution of TAs in the development of NIVs has been at a minimum. Based on the hierarchical cluster analysis adopting Ward's method as the algorithm with squared Euclidian distance as the interval, two clusters (cluster 1 and cluster 2) were defined at the fifth rescaled distance cluster combine. The NIVs formed cluster-1, with the exception of Bg 357, At 311 and Bg 94-1, which were clustered with TAs in the cluster-2. Of the TAs, only *Kalu baala wee* clustered with NIVs in the cluster-1. The study clearly reflects a genetic separation in the gene pools of TAs and NIVs, warranting the need to further characterize the Sri Lankan TAs for the better use of their desirable gene alleles in future rice breeding programs.

Keywords: Bayesian genetic assignment, Genetic admixture, Hierarchical cluster analysis, *Oryza sativa*

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