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## Genomic Studies of Myanmar Rice (*Oryza sativa* L.) Varieties Using DArT and SNP Markers

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### Abstract

Two ultra-high-throughput diversity array technology (DArT) markers (silicoDArT and SNP) were employed to investigate the genetic diversity and population structure of rice (*Oryza sativa* L.) varieties of Myanmar. The study was performed using 117 rice genotypes comprising 112 landraces and 5 improved (control) varieties with 4,064 silicoDArT and 7,643 SNPs derived from DArT platform. Quality control parameters included > 95 % call rate, > 95 % reproducibility, and minor allele frequency (MAF) >0.1 for screening. Polymorphic information content (PIC) values for silicoDArT ranged from 0.02 to 0.5 with an average of 0.37. In the case of SNP markers, PIC values ranged from 0 to 0.5 with an average of 0.41. Genetic variance among the genotypes ranged from 0.001 to 0.954 in silicoDArT and 0 to 0.753 in SNP markers. Genetic relationships among the genotypes were identified utilizing weighted neighbor-joining dendrograms. All the genotypes were grouped into two major clusters with both silicoDArT and SNP markers. Population structure were tested using  $K$  values from 1 to 5, maximum  $\Delta k$  was found at  $K = 2$ , confirming that the structure analysis also revealed two distinct genetic clusters. Analysis of Molecular Variance (AMOVA) with SNP markers showed that within individuals only 4% diversity existed whereas among individuals it was 22%. Maximum diversity has been observed at population level (74%). This study demonstrated that DArT markers are a useful tool for the genomic studies with regard to rice. It will support researchers to identify useful DNA polymorphisms in genes and germplasm of interest and apply that information for rice varietal development and release.

**Keywords:** DArT markers, genetic diversity, Myanmar, rice landraces, SilicoDArT, SNP