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In Silico Analysis of salt tolerance associated gene OsHKT8 in Sri Lankan rice accessions.

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Rice (*Oryza sativa*) is rated as a salinity sensitive crop since all stages of growth and development could be affected by salinity. Although there are traditional cultivars naturally tolerant to salinity stress they generally lack preferred agronomic characteristics. Therefore, identifying salinity tolerant genes in traditional varieties and incorporating them into agronomically favourable varieties could be a promising approach to produce salinity tolerant rice varieties. Sodium ion transport processes play major roles in the context of salinity stress and tolerance responses. In rice, it is evident that members of HKT (High Affinity K^+ Transporters) gene family of Na^+ and Na^+/K^+ transporters are important for controlling Na^+ accumulation in the cells, thus improving salinity tolerance. The OsHKT8 gene is located on chromosome 1 at the position from 11458956bp to 11463442bp producing a gene 3985bp in size. Using the sequence information of HKT8 of Nipponbare, as the reference rice genome and FL478, as the highest saline tolerant improved rice variety, the rice varieties of Sri Lankan origin reported so far have been compared to detect the genetic diversity of OsHKT8 gene. In this study, HKT8 gene of forty-seven Sri Lankan rice varieties were retrieved from the IRRI (International Rice Research Institute) Database. The retrieved HKT8 gene sequences were aligned using Clustal Omega multiple sequence alignment tool. A total of 117 variants were identified comprising of 95 SNPs and 22 INDELs throughout the gene. There are 3 exons in the HKT8 gene, and highest number of SNPs was present on exome 1, while lowest was on exome 2. The variants were mainly present in non-coding regions of HKT8 and only 21 SNPs and 2 INDELs were present on the coding region. It was shown that Podiwee rice variety has the same SNP variations as that of FL478 with substitutions (T→A, C→T, G→C on exon 1, C→G, G→T on exon 2 and A →C on exon 3). According to the phylogenetic tree drawn based on the presence of SNPs and INDELs in HKT8, varieties were grouped into 3 main clusters. FL478 and Nipponbare were separately sub-clustered with certain varieties, while the traditional salinity tolerant variety, Pokkali, had a separate phylogeny from other selected varieties. The sequence comparison of HKT8 gene across Sri Lankan rice varieties has provided useful information for the plant breeders to utilize the favourable alleles of HKT8 towards salinity tolerance.

Keywords:*Oryza sativa*, Salt tolerance, HKT8

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