

Mining for Polymorphic Sites in Rice Salinity Tolerance Gene HKT1;5 for Molecular Marker Development

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With a 389 Mbp genome, rice (*Oryza sativa* L.) has a well curated genome assembly. Genome assemblies have enabled pre-breeders to design and develop intragenic molecular markers targeting specific genes. The High-Affinity Cation Transporter (HKT1;5, Os01g0307500) is a gene mapped to the Saltol-region in rice chromosome 1, and it is known to convey tolerance to salinity through its involvement in Na⁺ or/and K⁺ transport. To identify genomic variations in the coding sequence (CDS) of HKT1;5, and to define genomic haplotypes, a 1,668bp CDS from 2,406 rice accessions were retrieved from 3000 Rice Genomes Project sequence repository at the Rice SNP-Seek Database. The retrieved sequences were aligned using Clustal Omega v1.2.0 using UGENE v1.28.1 with manual editing. In the alignment, eight single nucleotide polymorphisms (SNP) with more than 5% occurrence among the panel of accessions were identified. Based on seven SNPs at the exon 1 and one SNP at exon 2, 22 genomic haplotypes (nine confirmed haplotypes (representing at least 1% of the accessions) and 13 putative haplotypes (representing less than 1% of the accessions)) were defined using DnaSP v6. These eight SNP sites in the HKT1;5 CDS are potential sites to develop intragenic molecular markers to evaluate their suitability for diagnostic detection of salinity tolerance in rice.

Keywords: HKT 1;5, marker-assisted selection, Na⁺ transporter, salinity tolerance, Saltol