Structural Characterization of Salinity-Responsive *OsSWEET15* Allelic Variants in Sri Lankan Traditional Rice Germplasm

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Salinity stress severely constrains rice productivity by disrupting ion homeostasis and metabolic balance. SWEET family sugar transporters regulate sucrose partitioning under abiotic stress, making them important targets for understanding natural adaptation mechanisms. This study investigated molecular variation in *OsSWEET15* across 48 rice accessions to identify sequence-level signatures associated with salinity tolerance in traditional Sri Lankan indica rice varieties. Coding sequences from 48 rice varieties, including the *Nipponbare* reference genome and traditional Sri Lankan indica varieties, were retrieved from International Rice Research Institute (IRRI), 3,000 Rice Genomes Project. They were analysed using MEGA12 software for multiple sequence alignment and phylogenetic reconstruction. Representative varieties — salinity-susceptible *Nipponbare,* moderately tolerant *Godawee*, and salt tolerant *Pachchaperumal* — were selected for comparative analysis. Conserved domain analysis was performed using NCBI CDD, structural analysis using PyMOL, TMHMM was used to predict transmembrane helices, and Protter was used for graphical visualization of membrane topology. Multi-variety alignment of 319 amino acid sequences revealed five distinct substitution patterns clustering phylogenetically: R290H in *Sigardis/Puttunellu/Chandina*, I236T in *Godawee/Pachchaperumal*, P275T in *Samba/Kuruthaseenati*, combined I263T/P275T in *Sudukarayal*, and an N-terminal deletion spanning residues 1–24 in *Murunga. Godawee, Pachchaperumal, Murunga*, and *Samba* clustered with the established salt-tolerant landrace *Pokkali*. Notably, the I236T substitution, replacing hydrophobic isoleucine with polar threonine, occurred exclusively in tolerant varieties. The introduction of threonine may confer greater hydrogen-bonding capacity and potential phosphorylation sites, which could modulate local transporter conformation and improve *OsSWEET15* function under salinity stress. This amino acid change may therefore, enhance structural flexibility at the TM7–cytoplasmic interface, supporting more efficient sugar transport and osmo-protective responses in tolerant genotypes. Conserved domain analysis confirmed preservation of dual MtN3_slv domains and PQ-loop motifs across all varieties with highly significant E-values (10^{-28} to 10^{-3}). TMHMM predicted seven transmembrane helices, positioning residue 236 at the cytoplasmic TM7 interface. PyMOL structural alignment showed a global RMSD of 0.000 Å and a localized RMSD of 0.009 Å at residues 230–240, indicating spatially confined conformational divergence at the mutation site. The I236T substitution in *OsSWEET15* represents a structurally plausible molecular marker of natural salinity adaptation with potential utility for developing salt-resilient rice varieties in affected agricultural regions.

Keywords: *OsSWEET15*, salinity tolerance, i236t substitution, indica rice, phylogenetic clustering