

**FUNCTIONAL CHARACTERIZATION OF SUGAR
TRANSPORTER GENES IN RICE (*Oryza sativa*
L.)**

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To analyze the function of hexose transporter during rice seed development, we identified the rice hexose transporters (*OsSTP1*, *OsSTP2*, *OsSTP3*, *OsSTP4*) by BLAST searching rice sequence database with the *HvSTP* sequence. To analyze the expression patterns and functions of *OsSTPs*, We performed RT-PCR and yeast complementation experiments. Three of four transporters are expressed in all organs: leaf, root, flower, and seed, particularly seed coat. Sugars, such as sucrose, glucose and fructose, induced the accumulation of transcripts of *OsSTP1*, *OsSTP2* and *OsSTP4* in excised leaves and immature seeds treated with sugars. The level of *OsSTP2* was significantly up-regulated in leaf treated with sucrose. The deduced amino acid sequences are predicted to contain 12 transmembranes. The *OsSTP2* appeared to be most similar to the *HvSTPs* in the analysis of the phylogenetic tree. The *OsSTP1*, *OsSTP2* have been analyzed to have a large central loop, about 360 a.a. The *OsSTP3* is expressed only in the flower specifically pollen, which has been proved by the comparison of the expression of *OsSTP3* in both wild-type and the *UDT1* mutant which does not product the pollen. The result clearly exhibited that the *OsSTP3*s expressed at the 20.5-22 cm panicles of the wild-type but not expressed in the *UDT1* mutant.

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