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Alternative Splicing Events of Stress Responsive Genes in Arabidopsis and Rice Universal Stress Protein Domains



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Short Abstract: We have combined alternative splicing information from Gramene and Alternative Splicing in Plants (ASIP) databases for genes of Arabidopsis and Rice encoding the Universal Stress Protein (USP) domain. Majority of USP genes generate transcript diversity using intron retention. Gene categories based on alternative splicing events represent targets for trait improvement.

Long Abstract:

Genes encoding proteins that contain the UspA domain (IPR006016) and/or the Usp domain (IPR006015) are described as members of the Universal Stress Protein (USP) family. USP genes are known to provide plants with the ability to respond to environmental stresses such as nutrient starvation, drought, high salinity, extreme temperatures and exposure to toxic chemicals. Despite their importance in plant survival USP genes have not been extensively characterized. Transcript diversity produced by alternative splicing events can contribute to the functional complexity and ability of plants to adapt to environmental stress. In order to compare the alternative splicing events between the USP genes of Arabidopsis thaliana and Oryza sativa (rice), we have used a high-throughput binary integration strategy to combine alternative splicing information from Gramene (<http://www.gramene.org/>) and Alternative Splicing in Plants (<http://www.plantgdb.org/ASIP>) databases. Database queries with the InterPro USP domains as the search filter via the GrameneMart tool revealed 60 and 40 USP genes in Arabidopsis and Rice respectively. We constructed 6-digit binary signatures for 4707 Arabidopsis and 6555 Rice genes in ASIP encoding the presence or absence of the following alternative splicing events: Alternative Donor, Alternative Acceptor, Alternative Position Both Site, Exon Skipping, Intron Retention and Possibly Non-Independent. Integrating the list of USP genes for each plant species from Gramene with the list of alternative spliced genes in the ASIP database revealed 16 Arabidopsis USP genes compared to 11 rice USP genes. These alternative spliced genes classified into 7 of the 64 possible binary categories with majority predicted to undergo intron retention. Our classification could help accelerate the characterization of USP genes as useful targets for engineering crop plant varieties tolerant to unfavorable environmental conditions and thus address food security in the world.