

Alternative splicing: peeling another layer of cold stress response in plants

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Cold stress is one of the major abiotic stresses that limits the productivity and geographical distribution of food crops, especially of non-cold acclimatizing crops like tomato whose productivity is severely affected. Alternative splicing, a post transcriptional modification of mRNA, is responsible for providing functional diversity to proteins originating from the same gene. It has been reported that cold stress in plants leads to an increased number of differentially alternatively spliced (DAS) genes which acts as another layer of stress response in addition to the differential expression (DE) of genes. Previously, our group collected RNA-seq data from a time-series experiment on tomato (*Solanum lycopersicum*) which involved subjecting the plants to 4°C cold stress and sampling at 14 time points from 5 mins to 120 mins. Now, we analyzed this data using multiple bioinformatics tools like rMATS and Stringtie which can report de novo splice variants. The results from these tools were merged and filtered using custom parameters to get a DAS gene list. Then this gene list was passed on to functional annotation and GO term enrichment analysis. It was found that a significant number of genes were localized in chloroplast and were involved in photosynthesis. Next, we plan to integrate this DAS gene list with DE gene list and gene regulatory network to find out genes that play a major role in cold stress response in tomato as well as other related species.