

Understanding transcriptional strategy for Inositol pathway in soybean root dehydration stress tolerance

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Throughout the evolutionary process, plants have developed a range of molecular mechanisms to withstand water deficit conditions. Inositol (Ins) is a polyalcohol, a cyclic carbohydrate with six hydroxyl groups one on each of the ring carbons, which has multiple effects on plant metabolism, acting since the production of secondary messengers to the synthesis of osmolytes/antioxidants. Structural genomics and global transcriptome analyses associated to inositol are not available for plants, except regarding genes involved in the metabolism of raffinose in maize. The present work aimed to identify loci linked to Ins metabolism in the soybean genome, besides globally cataloging and analyzing the related transcripts orchestration that acts increasing the pathways efficiency. Using the HT-SuperSAGE experimental data, tags (26 bp) were analyzed to determine unique tags (unitags) and those differentially expressed ($p < 0.05$), while singlets (tags only sequenced once) were excluded from the evaluation. Unitags were annotated by BLASTn against transcripts sequences from Phytozome database (<http://www.phytozome.org/>), anchored in the Phytozome genome, and when the equivalent annotated sequence was an enzyme, the available EC number was recovered. The in silico biochemical pathway analysis involved the Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway database (<http://www.genome.jp/kegg/pathway.html>) applying for the EC numbers in the KEGG Mapper – Search & Color Pathway tool, trying to map the expression levels of genes encoding enzymes. This tool colored EC accessions with green, red, and orange to represent up-regulated (UR), down-regulated (DR) and not significant (n.s.) gene expression, respectively. Considering Inositol Phosphate metabolism, 41 enzymes were identified. From those, 17 green nodes represent enzymes identified in soybean. Anchoring these sequences against the soybean genome, 165 probable non-redundant Ins loci were identified. The significant number of regions related to Ins genes reported in soybean is justified by its highly redundant (polyploid) genome. As expected, most of the unitags did not show significant variation, but the analyzed pathway included differentially expressed unitags. The tolerant accession showed a greater number of UR and DR candidates when compared with the sensitive accession, implying that such accession has a greater plasticity of transcripts responsive to the issued stress, which would allow a better matching (fine tuning) to the new condition. Our data point to the importance of the Ins availability for soybean root cell under dehydration (where many cellular processes require Ins), especially for plants which use free Ins to synthesize essential compounds, including those involved in hormonal regulation and stress tolerance.

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