

# EVALUATING THE COWPEA DEHYDRATION STRESS TOLERANCE BASED ON INOSITOL AND RAPHINOSIS PATHWAYS

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## Abstract

Plants evolved to survive in environments that often impose adverse conditions, such as abiotic and biotic stresses. They developed several survival mechanisms that enable the detection of environmental changes, as well as induction of specific responses to imposed stress conditions. Cowpea is one of the most important food and forage legumes in north- and northeastern Brazilian regions and its ability to survive under environmental pressure make it an ideal crop model to study the molecular mechanisms of drought tolerance. In this context, the identification and characterization of inositol (Ins) and raphinosis (RFO) pathways genes was carried out for cowpea in their transcriptome by computational methods. The cowpea transcriptome was assembled from 453 millions of reads, resulting in more than 185,000 non-redundant transcripts, which include transcriptional variants, splicing products. Using seed sequences obtained from the Kyoto Encyclopedia of Genes and Genomes (KEGG) Pathway database 1.119 transcripts were obtained, 521 related to inositol pathway and 598 transcripts associated with raphinosis pathway. It was possible identify 31 KO numbers associated with the raffinose pathway, whereas 29 KO numbers were related to the Inositol pathway. Among all 1.119 transcripts, 468 gene ontology terms were obtained (238 for Ins and 230 for RFO), being reallocated with different enzymatic/metabolic activities that its members perform. For the RFO pathway, the most important biological processes comprise the metabolism of carbohydrates, galactose and raffinose, whereas for Ins we found phosphatidylinositol phosphorylation, lipid catabolism and inositol biosynthesis. Our data pointed out the importance of Ins and RFO availability for cowpea under dehydration, where many cellular processes require many members of both pathways, especially plants which use free Ins to synthesize essential compounds, including those involved in hormonal regulation and stress tolerance.

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