

## **INSIGHT INTO THE GENE EXPRESSION PROFILE OF FOUR CASSAVA (*MANIHOT ESCULENTA*) GENOTYPES OVER THE SEASONAL TRANSITION**

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Cassava (*Manihot esculenta*) is ranked among the world's most important root crops. Its starchy roots are a major source of affordable dietary energy for millions of people in the subtropics area which is rapidly increasing in population. Cassava can grow under adverse conditions, and this resilience makes it an excellent crop in the face of climate change. Therefore, understanding the genetic and molecular basis underlying this trait is of great interest and essential to developing effective and durable sustainable production.

Cassava is a perennial plant cultivated in an annual cycle. It is normally planted in the tropical rainy season and continues constantly growing during the dry and the beginning of the subsequent rainy seasons of the year thereby getting exposed to stresses related to changes in temperature, and water deficiency/ excess before harvest.

This study investigated the molecular basis of field-grown cassava adaptation to the seasonal transitions by comparing gene expression profiles over four time points of four genotypes with different genetic and adaptation characteristics. We identified seasonally-regulated differentially expressed genes whose expression levels were reverted upon transition from rainy-dry to dry-rainy seasons.

We associated Gene Ontology (GO) terms and mapped with the help of KEGG differentially expressed genes into pathways. These analyses revealed the

enrichment of processes typical of stress responses to heat, dehydration, salt, oxidation, nutrient metabolism, and hormone flux activation, among others. Transcription factor (TF) enrichment analysis revealed a typical stress response regulation due to the presence of significantly represented TF target binding motifs in the differentially expressed gene sets. The genes with the target motifs were allied with the respective transcription regulation processes of the enriched factors.

This study identified several genes and processes associated with stress responses during the seasonal transition. Further studies will confirm the function of these genes and their potential use as targets for biotechnological applications and breeding programs. Comparative analysis of gene expression in other plant species will expand the knowledge for effective application in drought and flood stress management of Tropical and Mediterranean crops to reduce future yield gap.