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Unzipping the Stress Response Genes in Moringa oleifera Lam. through Transcriptomics

Authors : Vivian A. Panes, Raymond John S. Rebong, Miel Q. Diaz

Abstract : Moringa oleifera Lam. is known mainly for its high nutritional value and medicinal properties contributing to its popular reputation as a 'miracle plant' in the tropical climates where it usually grows. The main objective of this study is to discover the genes and gene products involved in abiotic stress-induced activity that may impact the M. oleifera Lam. mature seeds as well as their corresponding functions. In this study, RNA-sequencing and de novo transcriptome assembly were performed using two assemblers, Trinity and Oases, which produced 177,417 and 120,818 contigs respectively. These transcripts were then subjected to various bioinformatics tools such as Blast2GO, UniProt, KEGG, and COG for gene annotation and the analysis of relevant metabolic pathways. Furthermore, FPKM analysis was performed to identify gene expression levels. The sequences were filtered according to the 'response to stress' GO term since this study dealt with stress response. Clustered Orthologous Groups (COG) showed that the highest frequencies of stress response gene functions were those of cytoskeleton which make up approximately 14% and 23% of stress-related sequences under Trinity and Oases respectively, recombination, repair and replication at 11% and 14% respectively, carbohydrate transport and metabolism at 23% and 9% respectively and defense mechanisms 16% and 12% respectively. KEGG pathway analysis determined the most abundant stress-response genes in the phenylpropanoid biosynthesis at counts of 187 and 166 pathways for Oases and Trinity respectively, purine metabolism at 123 and 230 pathways, and biosynthesis of antibiotics at 105 and 102. Unique and cumulative GO term counts revealed that majority of the stress response genes belonged to the category of cellular response to stress at cumulative counts of 1,487 to 2,187 for Oases and Trinity respectively, defense response at 754 and 1,255, and response to heat at 213 and 208, response to water deprivation at 229 and 228, and oxidative stress at 508 and 488. Lastly, FPKM was used to determine the levels of expression of each stress response gene. The most upregulated gene encodes for thiamine thiazole synthase chloroplastic-like enzyme which plays a significant role in DNA damage tolerance. Data analysis implies that M. oleifera stress response genes are directed towards the effects of climate change more than other stresses indicating the potential of M. oleifera for cultivation in harsh environments because it is resistant to climate change, pathogens, and foreign invaders.

Keywords : stress response, genes, Moringa oleifera, transcriptomics
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