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Transcriptome Profiling of Differentially Expressed Genes in Cowpea (*Vigna unguiculata* L.) Under Salt Stress

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[Abstract]

Cowpea [*Vigna unguiculata* (L.) Walp] is one of the most important grain legumes that enhance soil fertility and is well-adapted to various abiotic stress. Also, it is cultivated worldwide as a tropical annual crop, and the semi-arid regions are known as the main cowpea-produced regions. However, accumulation of soil salinity induced by low rainfall in these regions is reducing crop yields and quality. In general, plants exposed to soil salinity cause an accumulation of high ion chloride, which leads to the degradation of root and leaf proteins. In this study, we identified candidate genes associated with salinity tolerance through an analysis of differentially expressed genes (DEGs) in four cowpea germplasms with contrasting salinity tolerance. A total of 553,776,035 short reads were obtained using the Illumina Novaseq 6000 platform for RNA-Seq, which were subsequently aligned to the reference genome of cowpea *V. unguiculata* v1.2. A total of 9,806 DEGs were identified between NaCl treatment and control of four cowpea germplasms. Among these DEGs, functions related to salt stress such as calcium transporter and cytochrome-450 family were associated with salt stress. In GO analysis and KEGG analysis, these DEGs were enriched in terms such as the “phosphorylation”, “extracellular region”, and “ion binding”. These RNA-seq results will improve the understanding of the salt tolerance of cowpea and can be used as useful basic data for molecular breeding technology in the future.

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