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沙漠植物 *Solenostemma argel* 中特异器官的转录组和代谢组学整合分析揭示盐胁迫响应机制

ORGAN-SPECIFIC INTEGRATED *DE NOVO* TRANSCRIPTOME AND METABOLOME ANALYSES OF *Solenostemma argel* DESERT PLANTS REVEAL POTENTIAL RESPONSE MECHANISMS TO SALINITY STRESS

研 究 生：
CANDIDATE：　HASAN AHMAD HASAN AHMAD

学　　号：
STUDENT NO.：2016304060008

专　　业：　生物化学与分子生物学
MAJOR：　BIOCHEMISTRY AND MOLECULAR BIOLOGY

导　　师：　罗杰　教授
SUPERVISOR：　PROFESSOR LUO JIE

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Organ-specific integrated *de novo* transcriptome and metabolome analyses of *Solenostemma argel* desert plants reveal potential response mechanisms to salinity stress

博士研究生： **HASAN AHMAD HASAN AHMAD**

学　　号： **2016304060008**

指 导 教 师： 罗　杰　　教授

指 导 小 组： 赵　毓　　教授

李兴旺　　教授

练兴明　　教授

欧阳亦聃　教授

专业：生物化学与分子生物学　究方向：植物代谢分子生物学

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Abstract

Climate change significantly increased the problem of soil salinity and its potential adverse effects on plant growth and productivity. Transcriptomic and metabolomic changes in plants during exposure to salinity stress reveal the potential mechanism behind salinity stress tolerance. *Solenostemma argel* (Delile) Hayne is a desert plant that survives harsh environmental conditions with several vital medicinal properties. However, response mechanisms by *S.argel* plants adaptation to salt stress are poorly understood. In the current study, we applied omics approach to explore how this plant adapts to salinity stress by integrating transcriptomic and metabolomics changes in roots and leaves of *S. argel* plants under soil salinity stress. *De novo* assembly of transcriptome produced 57,796 unigenes represented by 165,147 transcripts/isoforms with 37.93% and 38.46% GC contents, respectively. All assembled unigenes were functionally annotated in at least one of Uniprot, eggNOG, GO, and KEGG databases. A total of 730 DEGs were identified in roots of *S. argel* under salinity stress of them 396 and 334 were up- and down-regulated. In leaves, 927 DEGs were identified (601 and 326 up- and down-regulated). Different GO and KEGG pathway enrichment analysis revealed several defense-related biological pathways such as response to osmotic and oxidative stress, MAPK signaling and plant hormonal signal transduction pathways were among potential mechanisms involved in *S. argel* plants tolerance to salinity. The auxin and ABA signaling pathways were up-regulated in roots and leaves, while ethylene and salicylate signaling pathways were up-regulated in leaves, which are important pathways that mediate salinity signals, regulate plant growth and build a defence system for salt stress tolerance. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) was used to detect metabolite variations of *S. argel* leaves and roots under control and salinity stress. Forty-five and fifty-six critical metabolites showed changes in levels in stressed roots and leaves, respectively; there were 20 metabolites in common between roots and leaves. Overall, both ornithine, quercetin, tricetin, sinapic acid, spermidine, hydroxybenzoic acid derivatives, trehalose and sucrose were changed dramatically, which might improve antioxidant ability and osmotic adjustment of *S. argel* plants. Interestingly, gene expression levels positively correlated with metabolites levels in some pathways. The current study's findings provide insights into salinity response mechanisms in desert plants and might help metabolic engineering research efforts to enhance abiotic stress tolerance of strategic crops.

Keywords: Transcriptomics; metabolomics; hormones; salinity stress; *S. argel.*