

Title: Comparative transcriptome and metabolome analysis reveal key regulatory defense networks and genes involved in enhanced salt tolerance of *Actinidia* (kiwifruit)

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Abstract

The *Actinidia* (kiwifruit) is an emerging fruit plant that is severely affected by salt stress in northern China. Plants have evolved several signaling network mechanisms to cope with the detrimental effects of salt stress. To date, no reported work is available on metabolic and molecular mechanisms involved in kiwifruit salt tolerance. Therefore, the present study was aimed to decipher intricate adaptive responses of two contrasting salt tolerance kiwifruit species *Actinidia valvata* [ZMH (an important genotype), hereafter referred to as R] and *Actinidia deliciosa* ['Hayward' (an important green-fleshed cultivar), hereafter referred to as H] under 0.4% (w/w) salt stress for time courses of 0, 12, 24, and 72 hours (hereafter referred to as h) by combined transcriptome and metabolome analysis. Data revealed that kiwifruit displayed specific enrichment of differentially expressed genes (DEGs) under salt stress. Interestingly, roots of R plants showed a differential expression pattern for up-regulated genes. The KEGG pathway analysis revealed the enrichment of DEGs related to plant hormone signal transduction, glycine metabolism, serine and threonine metabolism, glutathione metabolism, and pyruvate metabolism in the roots of R under salt stress. The WGCNA resulted in the identification of five candidate genes related to glycine betaine (GB), pyruvate, total soluble sugars (TSS), and glutathione biosynthesis in kiwifruit. An integrated study of transcriptome and metabolome identified several genes encoding metabolites involved in pyruvate metabolism. Furthermore, several genes encoding transcription factors were mainly induced in R under salt stress. Functional validation results for overexpression of a candidate gene betaine aldehyde dehydrogenase (*AvBADH*, R_transcript_80484) from R showed significantly improved salt tolerance in *A. thaliana* (hereafter referred to as *At*) and *A. chinensis* ['Hongyang' (an important red-fleshed cultivar), hereafter referred to as *Ac*] transgenic plants than in WT plants. All in all, salt stress tolerance in kiwifruit roots is an intricate regulatory mechanism that consists of several genes encoding specific metabolites.

Funding

This study was funded by Agricultural Science and Technology Innovation Program of the Chinese Academy of Agricultural Science (CAAS-ASTIP-2021-ZFRI), the China Agriculture Research System of MOF and MARA (CARS-26), Yunnan Science and Technology Program (202205AF150043), Sichuan Science and Technology Program (2021YFN0060), and Yangtze River Kiwifruit Industry Technology Research Center (CJZX20210110).