

Transcriptome analysis reveals the responsive pathways and genes to potassium (K⁺) deficiency in grapes

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Grapevine is sensitive to potassium (K⁺) deficiency, while its underlying responsive mechanisms are unknown. In this study, RNA-sequencing (RNA-seq) was performed with samples of roots and shoots collected under K⁺ deficiency and normal conditions, and numerous differentially expressed genes (DEGs) induced by K⁺ deficiency were identified, including some ion transporter genes, ethylene-responsive transcription factor (ERF) genes, and cell wall biosynthesis-related genes. In roots, genes (especially *ERF*) involving in ethylene signal and cell wall biosynthesis pathway were upregulated and downregulated, respectively; and in shoots, genes involving in ethylene signal and photosynthesis pathway were upregulated and downregulated, suggesting that ethylene signal was activated, while photosynthesis and cell wall biosynthesis were suppressed under K⁺ deficiency treatment. One K⁺ transporter gene of HAK family, *VvHAK5*, was further identified and cloned. *VvHAK5* was specifically expressed in grape roots, and could be significantly induced by K⁺ deficiency treatment. *VvHAK5* protein was localized in cytomembrane, and could transport K⁺ as revealed by the yeast system assay. Taken together, this study demonstrated the responsive pathways (like ethylene signal, ion homeostasis, and other metabolic pathways) and the key genes (like K⁺ transporter *VvHAK5*) to K⁺ deficiency in grapes.