Physiological analysis and transcriptome comparison of two muskmelon (*Cucumis melo* L.) cultivars in response to salt stress

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**ABSTRACT.** Melon (*Cucumis melo* L.) is an important vegetable crop that ranks second in salt tolerance among the Cucurbitaceae. Previous studies on the two muskmelon cultivars ‘Bing XueCui’ (BXC) and ‘Yu Lu’ (YL) revealed that they had different characteristics under salt stress, but the molecular basis underlying their different physiological responses is unclear. Here, we combined a physiological study with a genome-wide transcriptome analysis to understand the molecular basis of genetic variation that responds to salt stress in the melon. BXC performed better under salt stress than YL in terms of biomass and photosynthetic characteristics, because it exhibited less reduction in transpiration rate, net photosynthesis rate, and stomatal conductance under 150-mM NaCl stress than YL. A transcriptome comparison of the
leaves of the cultivars revealed that 1171 genes responded to salt stress in BXC while 1487 genes were identified as salt-stress-responsive in YL. A real-time polymerase chain reaction analysis of 12 of the responsive genes revealed that there was a strong, positive correlation with RNA sequencing data. The genes were involved in several pathways, including photosynthesis, the biosynthesis of secondary metabolites, metabolism, and plant hormone signal transduction, and their expression levels differed between the two cultivars in response to salt stress. This study provides a molecular perspective of two melon cultivars in response to salt stress, and its results could be used to investigate the complex molecular mechanisms underlying salt tolerance in the melon.

**Key words:** Melon (*Cucumis melo* L.); RNA sequencing; Salt stress; Physiological analysis; Transcriptome comparison