

NAC transcription factors *SNAC4* and *SNAC9* synergistically regulate tomato fruit ripening by affecting expression of genes involved in ethylene and abscisic acid metabolism and signal transduction

Sen Yang, Jiaqian Zhou, Christopher B. Watkins, Caie Wu, Yanchun Feng, Xiaoyang Zhao, Zhaohui Xue and Xiaohong Kou

Postharvest Biology and Technology, Volume 178, August 2021, 111555

Abstract

NAC (NAM, ATF1/2 and CUC2) is a transcription factor that can regulate many physiological and biochemical reactions in plants. Two *NAC* genes, *SNAC4* (NM_001279348.2) and *SNAC9* (NM_001365397.1), with similar secondary structures have been isolated from tomato (*Solanum lycopersicum* L.). The pattern of *SNAC4/9* co-regulation of tomato ripening with abscisic acid (ABA) and ethylene through yeast two-hybrid and bimolecular fluorescence complementation assays has revealed that *SNAC4/9* can interact with genes related to ABA and ethylene (*SAPK3*, *SIPYL9*, *SIAREB1*, *SIACS2* and *SIACO1*) at the protein level. Electrophoretic mobility shift assay and yeast one-hybrid showed that *SNAC4*, but not *SNAC9*, acts directly on the promoter regions of *SAPK3*, *SICYP707A1*, *SIACS8* and *SIACO6* and can activate them. In addition, quantitative real-time PCR analyses of *SNAC4/9*-silenced fruit obtained by virus-induced gene silencing, and phytohormone-treated fruit, confirmed that the interaction genes are regulated by *SNAC4/9* and thereby affect fruit ripening. In summary, we found that *SNAC4/9* can regulate fruit ripening by positively acting on key genes in the synthesis and signal transduction of ABA and ethylene. *SNAC4/9* cooperates with these phytohormones as part of the tomato fruit ripening regulatory network.