CHARACTERIZATION AND HORMONAL REGULATION OF KNOX GENES IN PEACH (PRUNUS PERSICA [L.] BATSCH)

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The knotted-like homeobox genes (KNOX) are known to play fundamental roles in the regulation of plant development and morphogenesis. They have been clustered into two classes according to homeodomain similarities and gene expression patterns. The class I KNOX genes such as KN1, STM, and KNAT1 are expressed mainly in the shoot apical meristems, whereas messages of class II members are abundant in several tissues. Moreover, complex interactions between hormones and KNOX genes have emerged in the determination of meristem identity, organ differentiation and development. So far, the role and function of KNOX genes have been poorly investigated in peach, a model for fruit tree species. Using tissue specific RT-PCR and based on the conservation of functional domains, we attempted to clone and characterize new members from both classes at the structural and expression levels. To elucidate any possible relation to hormones, KNOX transcripts were monitored in response to the exogenous supply of distinct phyto-hormones.