

# Identification and expression analysis of abscisic acid signal transduction genes during peach fruit ripening

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## Abstract

To characterize transcriptional regulation of the abscisic acid (ABA) signal transduction pathway during peach fruit early development and ripening, genes encoding the core components of the pathway, including 7 *PpPYR* (ABA receptor), 10 *PpPP2C* (type 2C protein phosphatase), and 7 *PpSnRK2* (subfamily 2 of SNF1-related kinases), were identified from the peach (*Prunus persica*) reference genome. *PpPYRs*, *PpPP2Cs*, and *PpSnRK2s* from peach were putative homologous to proteins from tomato and *Arabidopsis*. Phylogenetic analysis showed that *PpPYRs* and *PpSnRK2s* were clustered into three subfamilies/subclasses. Transcript profile indicated that *PpPYR2*, *PpPYR6*, and *PpPYR7* expression decreased sharply while ABA concentration increased during peach fruit ripening. Expression of *PpPP2C4*, *PpPP2C9*, and *PpPP2C10* increased along with ABA concentration during fruit ripening. Expression of *PpSnRK2.4* and *PpSnRK2.6* also increased together with ABA concentration during fruit ripening. Furthermore, *PpPP2C10* could interact with *PpSnRK2.6* was determined by Yeast two-hybrid and BiFC analyses. The results will improve our understanding of ABA signal transduction genes in peach and lay the foundation for further exploring the mechanisms underlying peach fruit ripening.