Genome-wide identification of phospholipase C related to chilling injury in peach fruit

Ke Wang, Ya-li Li and Shuqi Chen

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Abstract

Phospholipase C (PLC) responsible for acyl editing of phospholipids plays crucial roles in chilling sensitive plants and flesh fruit, which is prone to physiological disorders caused by chilling stress, collectively termed chilling injury. Up to now, genes encoding PLC in *Prunus persica* genome (PpPLC) and characteristics closely related to chilling injury remain elusive. In this study, a total of 10 *PpPLCs* were identified and divided into two subclasses, with equal number of phosphatidylinositol-specific PLC (*PpPI-PLCs*) and non-specific PLC (*PpNPCs*). Compared with *PpNPCs*, *PpPI-PLCs* show the differences in the number and the organization of exons and introns, as well as multiple splice variants. Meanwhile, the subclasses share two motifs enriched with lysine and proline. Furthermore, the *PpPLCs* consistently displayed two distinct transcriptional responses to four treatments conferring chilling tolerance in peach fruit, with the upregulation of *PpPI-PLCs* such as *PpPI-PLC4.1/4.2* and the down-regulation of *PpNPCs* except to *PpNPC1*, which is located at the plasma membrane. The results will facilitate deciphering the functions of the PLC in plants and flesh fruit when they undergo chilling injury.