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Cloning and characterization of the *SERK1* gene in triploid Pingyi Tiancha [*Malus hupehensis* (Pamp.) Rehd. var. *pingyiensis* Jiang] and a tetraploid hybrid strain

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ABSTRACT. This study aims to explore the roles of somatic embryogenesis receptor-like kinase (*SERK*) in *Malus hupehensis* (Pingyi Tiancha). The full-length sequences of *SERK1* in triploid Pingyi Tiancha (3n) and a tetraploid hybrid strain 33# (4n) were cloned, sequenced, and designated as *MhSERK1* and *MhdSERK1*, respectively. Multiple alignments of amino acid sequences were conducted to identify similarity between *MhSERK1* and *MhdSERK1* and *SERK* sequences in other species, and a neighbor-joining phylogenetic tree was constructed to elucidate their phylogenetic relations. Expression levels of *MhSERK1* and *MhdSERK1* in different tissues and developmental stages were investigated using quantitative real-time PCR. The coding sequence lengths of *MhSERK1* and *MhdSERK1* were 1899 bp (encoding 632 amino acids) and 1881 bp (encoding 626 amino acids), respectively. Sequence analysis demonstrated that *MhSERK1* and *MhdSERK1* display high similarity to *SERKs* in other species, with a conserved intron/exon structure that is unique to members of the *SERK*

family. Additionally, the phylogenetic tree showed that *MhSERK1* and *MhdSERK1* clustered with orange *CitSERK* (93%). Furthermore, *MhSERK1* and *MhdSERK1* were mainly expressed in the reproductive organs, in particular the ovary. Their expression levels were highest in young flowers and they differed among different tissues and organs. Our results suggest that *MhSERK1* and *MhdSERK1* are related to plant reproduction, and that *MhSERK1* is related to apomixis in triploid Pingyi Tiancha.

Key words: *Malus*; Apomixis; Somatic embryogenesis receptor-like kinase; Expression analysis

