

## Genome-wide analysis of terpene synthase gene family to explore candidate genes related to disease resistance in *Prunus persica*

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### Abstract

In plants, a family of terpene synthases (TPSs) is responsible for the biosynthesis of terpenes and contributes to species-specific diversity of volatile organic compounds, which play essential roles in fitness of plants. However, little is known about the TPS gene family in peach and/or nectarine (*Prunus persica* L.). In this study, we identified 40 *PpTPS* genes in peach genome v2.0. Although these *PpTPS*s could be clustered into five classes, they distribute in several gene clusters of three chromosomes, share conserved exon-intron organizations, and code similar protein motifs. Thirty-five *PpTPS*s, especially *PpTPS2*, *PpTPS23*, *PpTPS17*, *PpTPS18*, and *PpTPS19*, altered their transcript levels after inoculation with *Botryosphaeria dothidea*, a cause of peach gummosis, compared to the mock treatments, which might further affect the contents of 133 terpenoids at 48 hours and/or 84 hours post inoculations in the current-year shoots of ‘Huyou018’, a highly susceptible nectarine cultivar. Moreover, about fifteen *PpTPS*s, such as *PpTPS1*, *PpTPS2*, *PpTPS3*, and *PpTPS5*, showed distinct expression patterns during fruit development and ripening in two peach cultivars, yellow-fleshed ‘Jinchun’ and white-fleshed ‘Hikawa Hakuho’. Among them, the transcription level of chloroplast-localized *PpTPS3* was obviously related to the content of linalool in fruit pulps. In addition, elevated concentrations (0.1 g/L to 1.0 g/L) of linalool showed antifungal activities in PDA medium. These results improve our understanding of peach *PpTPS* genes and their potential roles in defense responses against pathogens.

**Keywords:** peach (*Prunus persica* L.), terpene synthase genes, gummosis disease, terpenoids, linalool

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