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Article

Genome-Wide Characterization of *HSP90* Gene Family in *Malus sieversii* and Their Potential Roles in Response to *Valsa mali* Infection

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Supplementary Materials

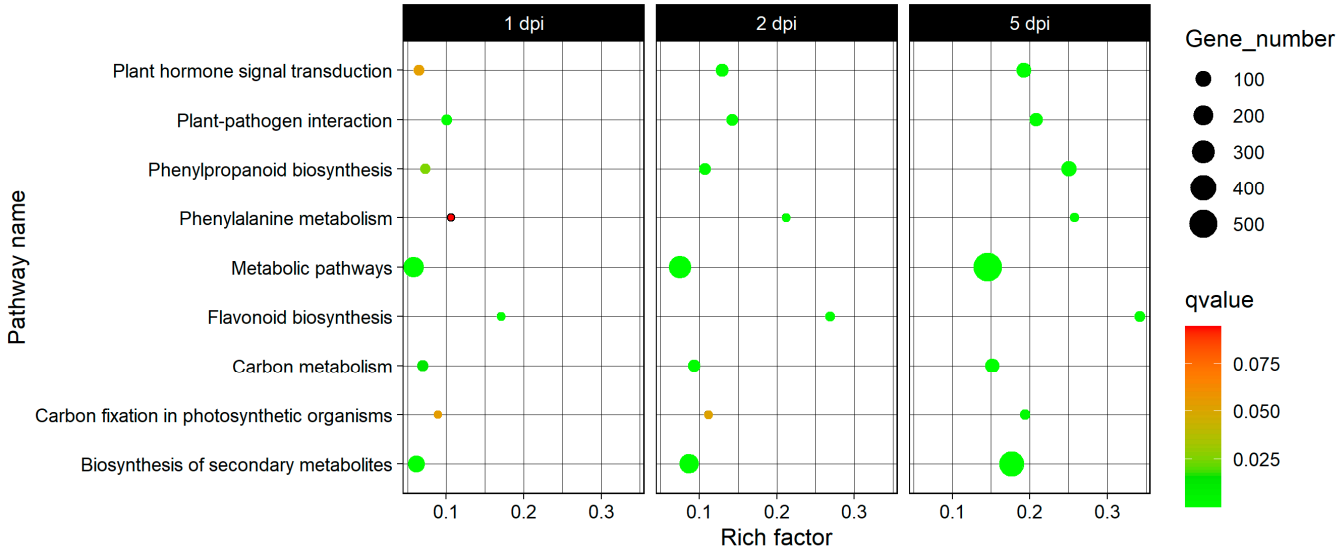


Figure S1. KEGG pathway enrichment analysis of differentially expressed genes response to *V.mali* infection in *M.sieversii*. The horizontal axis represents rich factor and the vertical axis represents pathway name. The size and colour of the bubble represent the amount and significance of differentially expressed genes enriched in a single pathway, respectively. Rich factor represents the ration of input number to the background number in specific pathway.

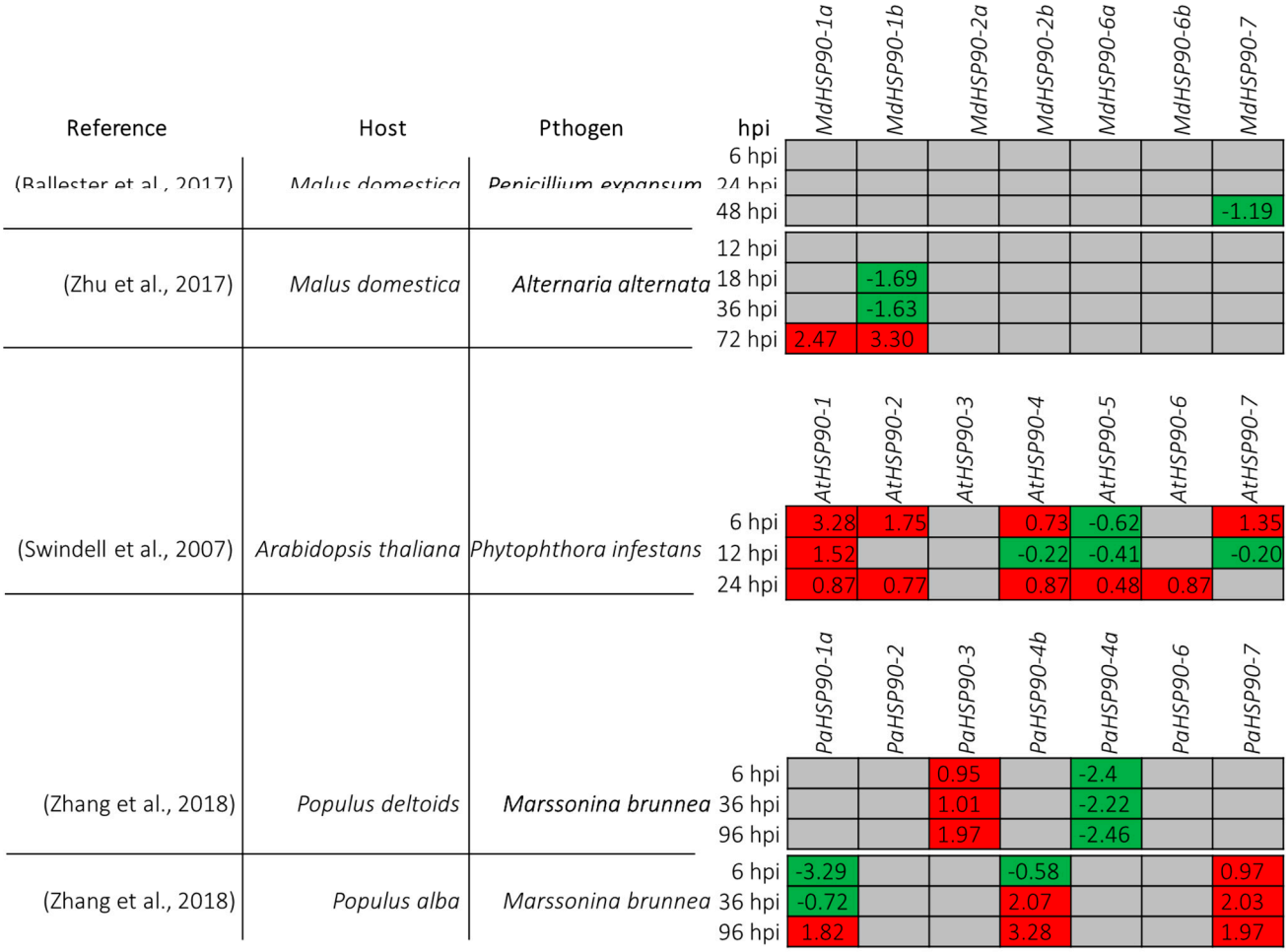


Figure S2. Expression profiles of *HSP90* genes in response to different plant fungal pathogens. Numbers represent foldchange expression of differentially expressed genes (log2 Foldchange>1 or log2 Foldchange<-1, *P*-value<0.05) were presented. Genes up-regulated are highlighted in red and down-regulated genes are highlighted in green. The unchanged or undeected genes are highlighted in grey.

Table S1: List of the qRT-PCR primers of the *MsHSP90* genes.

Gene name	Forward primers	Reverse primers
MsHSP90-1a	TTTCACGGGTAGAGAAGGTT	GAGGACGATGACACTGATTCT
MsHSP90-1b	ACAAGGGATGTCAATGGC	CTTCGTCTTCGTCGTCACT
MsHSP90-2a	GGAGAAAGAGAAGGAAGAGAAGA	AGACAAGCTTCTTGCCCTCGA
MsHSP90-2b	GAACTCAGCGGCTCCTATCT	GTGGACTCATACCGATTGCC
MsHSP90-5	GGCAACTGCTTCTCTGGCTT	AACCTTCCACTTCAATCCGC
MsHSP90-6	GAACTCAGCGGCTCCTATCT	GTGGACTCATACCGATTGCC
MsHSP90-7a	GGCAGTTTGGAGTTGGGTTC	TTTCTGTATCCTCGGCGACT
MsHSP90-7b	GGCAGTTTGGAGTTGGGTTC	TTTCTGTATCCTCGGCGACT