

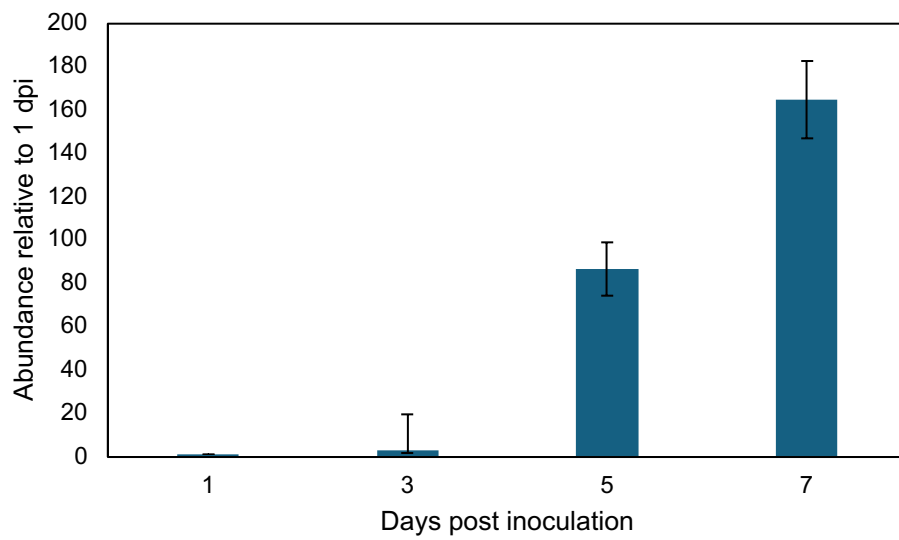


Figure S1. Relative fungal load of samples across time post inoculation determined by qPCR. *Sclerotinia sclerotiorum* 18S rDNA was used as a target for qPCR. Error bars correspond to standard error.

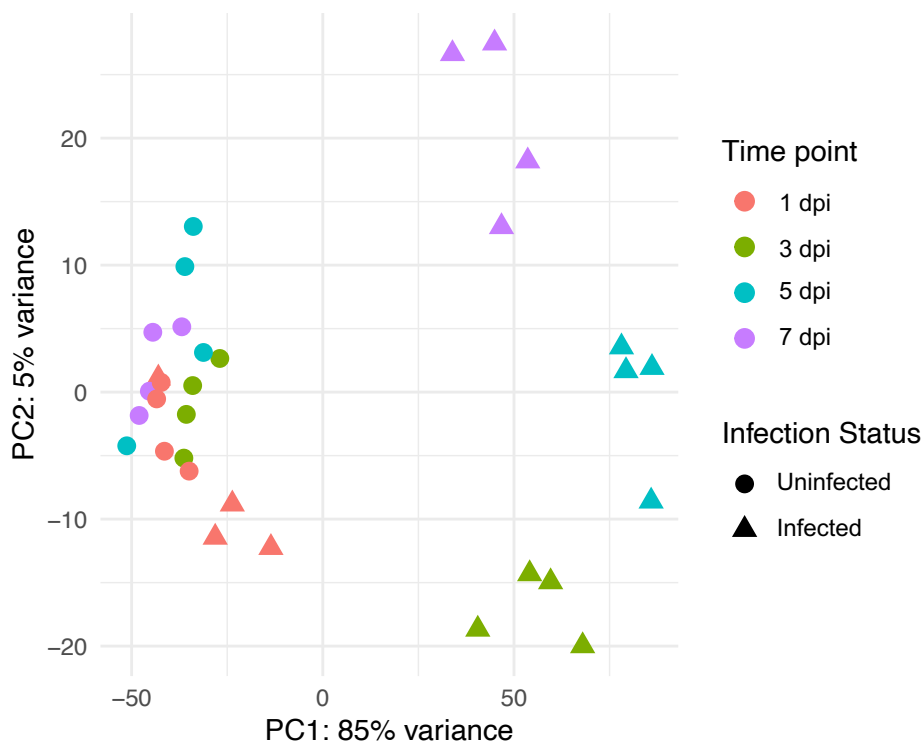


Figure S2. Principal component analysis (PCA) of *C. sativa* in the presence and absence of *S. sclerotiorum* across a seven-day infection period. Circles correspond to uninfected tissues, while triangles correspond to infected tissues. Colour corresponds to timepoint. PCA generated considering the top 1000 most variable genes. dpi = days post inoculation.

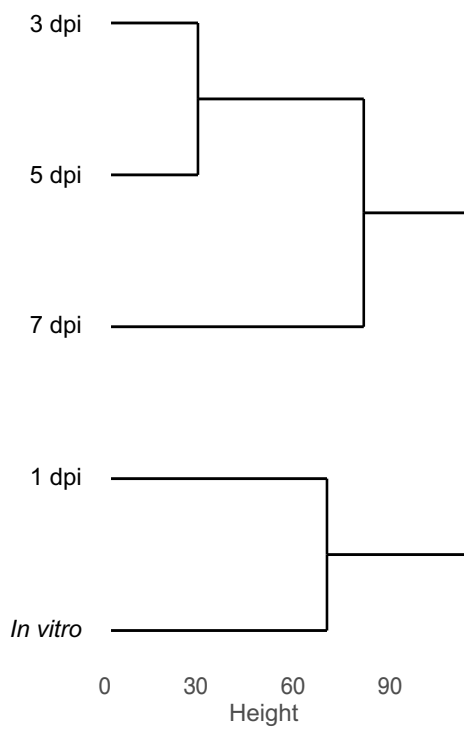


Figure S3. Hierarchical clustering of the top 1000 most variable genes of *S. sclerotiorum* grown *in vitro* or *in planta* during infection of *C. sativa*. Height corresponds to distance between clusters as computed by Euclidian distance. dpi = days post inoculation.

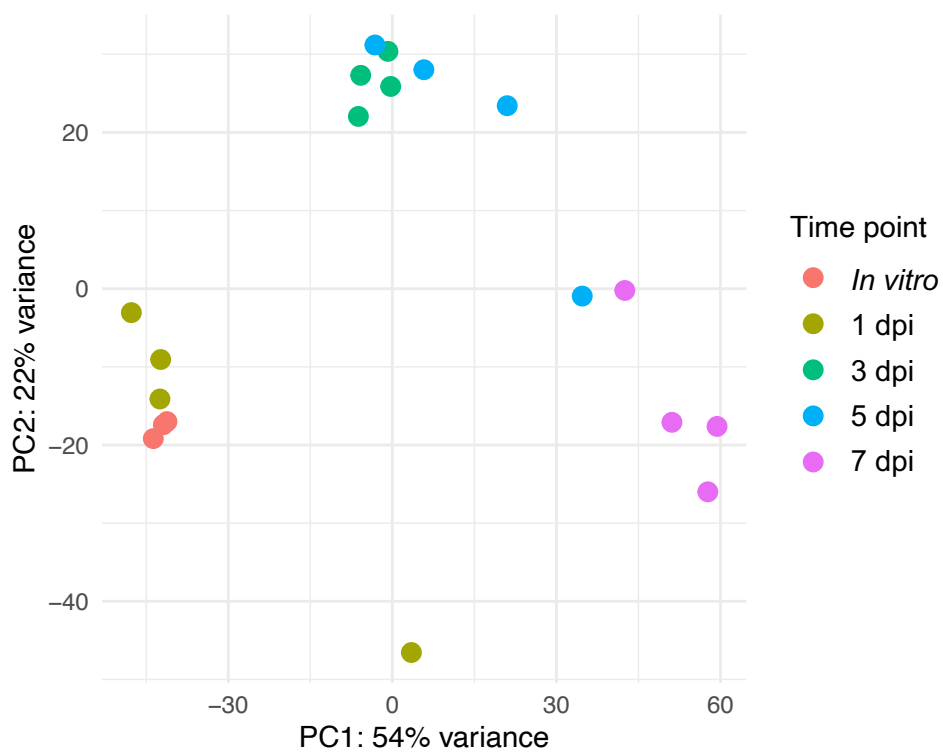


Figure S4. Principal component analysis (PCA) of *S. sclerotiorum* grown *in vitro* or *in planta* during a seven-day infection of *C. sativa*. Colour corresponds to timepoint, while red corresponds to *in vitro* grown *S. sclerotiorum*. PCA generated considering the top 500 most variable genes. dpi = days post inoculation.

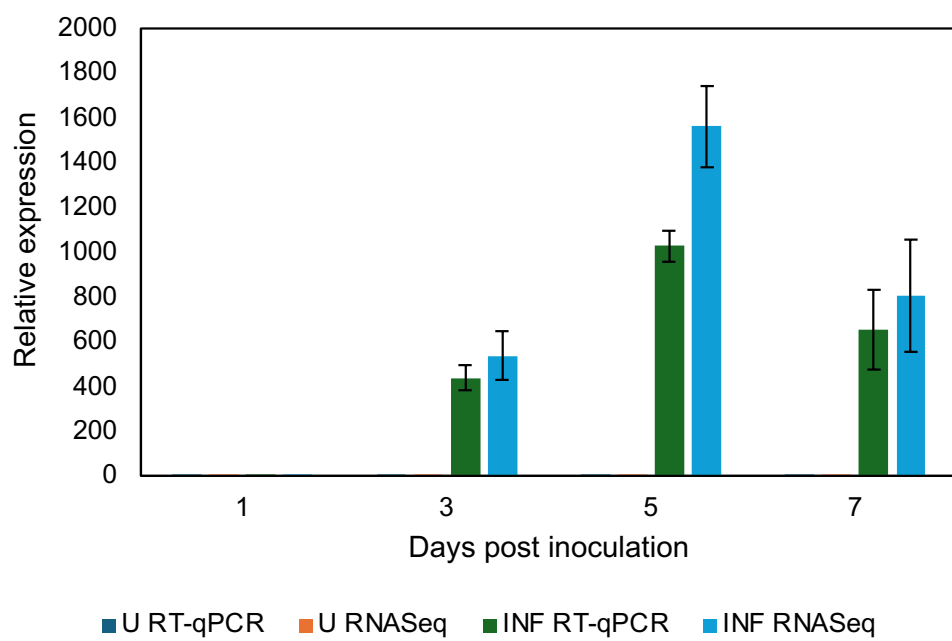


Figure S5. Comparison of relative expression levels of *PATHOGENESIS RELATED PROTEIN 1* resulting from RT-qPCR and RNA sequencing across time post inoculation with *Sclerotinia sclerotiorum*. U corresponds to uninfected samples (dark blue and orange), while INF corresponds to samples that had been inoculated with *S. sclerotiorum* (green and light blue). Bars correspond to standard error.

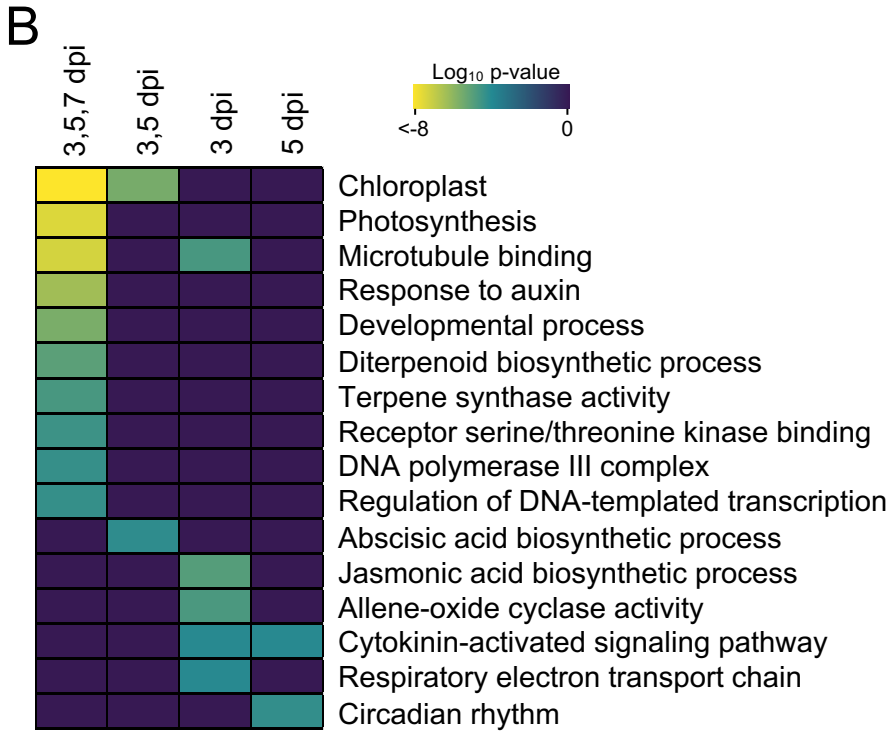
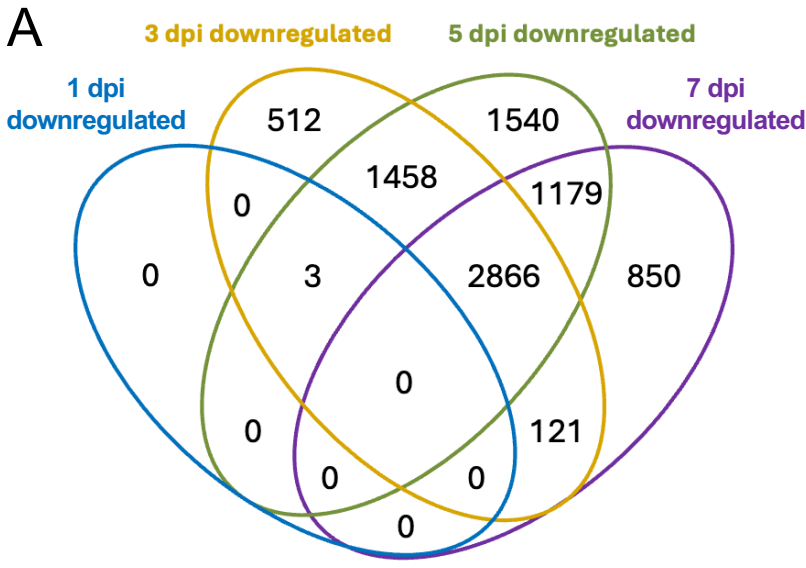


Figure S6. Differential gene expression analysis of down-regulated genes in *C. sativa* infected with *S. sclerotiorum* across a seven-day infection period. (A) Venn diagram of significantly downregulated differentially expressed gene sets (FDR<0.05) in response to infection. (B) Heatmap of significantly enriched GO terms (FDR <0.01) resulting from timepoint-specific and shared subsets. A brighter yellow colour indicates greater statistical significance. dpi = days post inoculation.

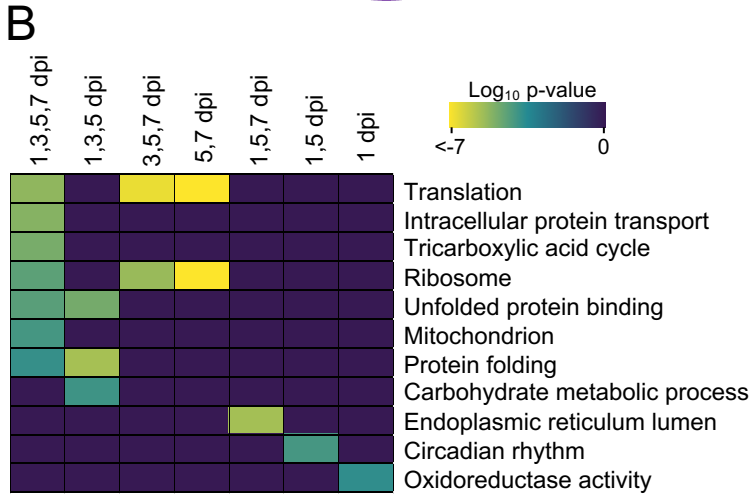
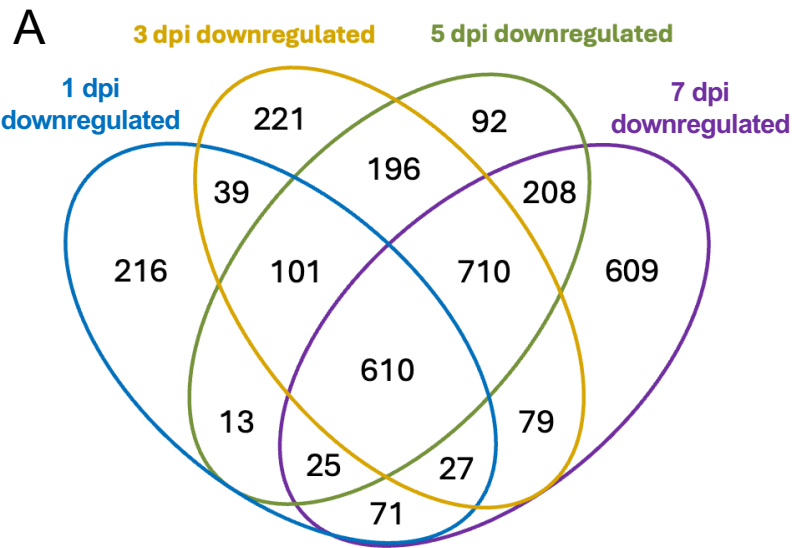


Figure S7. Differential gene expression analysis of significantly downregulated gene sets of *S. sclerotiorum* infection of *C. sativa* across a seven-day infection period. (A) Venn diagram of significantly downregulated differentially expressed gene sets (FDR<0.05) in response to infection. (B) Heatmap of significantly enriched GO terms (FDR <0.01) resulting from timepoint-specific and shared subsets. A brighter yellow colour indicates greater statistical significance. dpi = days post inoculation.

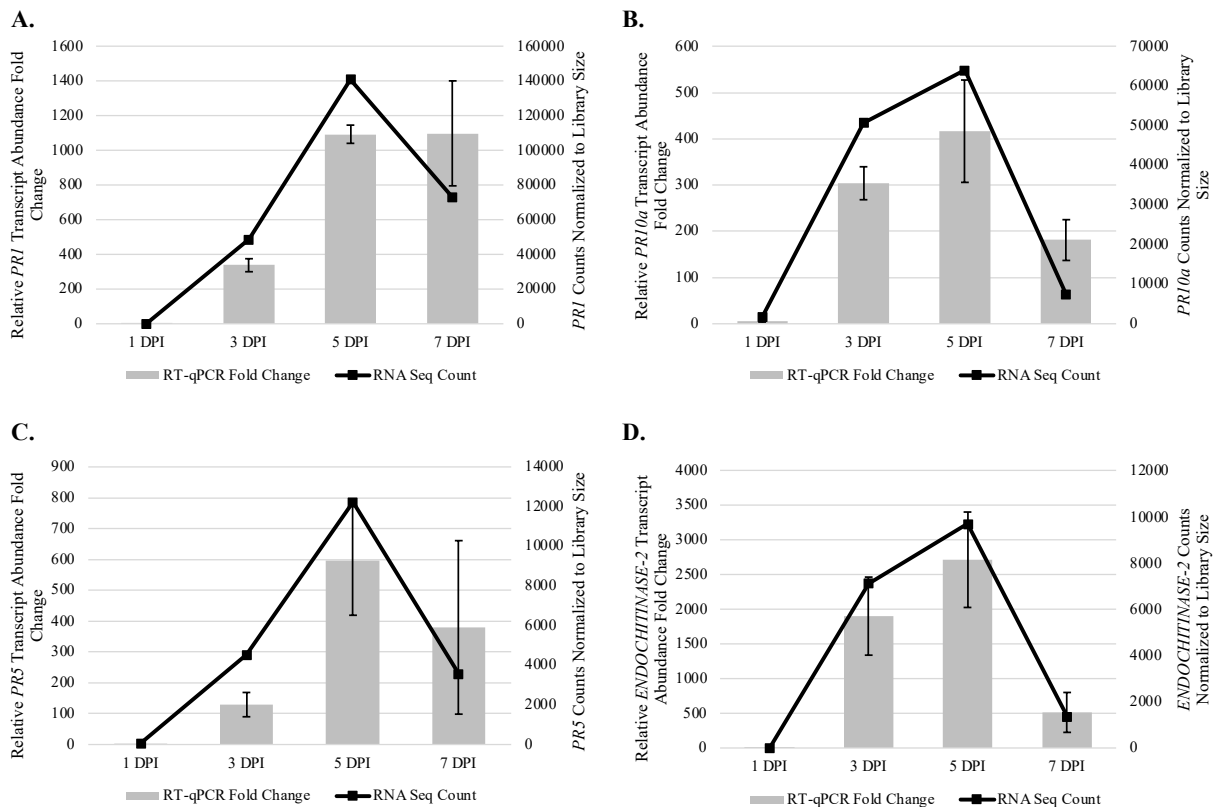


Figure S8. RT-qPCR validation of four representative *C. sativa* genes. A) *PATHOGENESIS RELATED PROTEIN 1 (PR-1; LOC115704466)*. B) *PATHOGENESIS-RELATED PROTEIN STH-2 (PR-10a; LOC115722015)*. C) *THAUMATIN-LIKE PROTEIN 1B (PR-5; LOC115710654)*. D) *ENDOCHITINASE 2 (LOC115705823)*. *ADENINE PHOSPHO-RIOSYLTRANSFERASE 1 (APT1)* was used as the housekeeping control. Target transcript relative abundance was calculated using the $\Delta\Delta CT$ method with four biological replicates quantified per timepoint. Error bars represent standard error. RNA sequencing gene counts were normalized to library size. Data were scored at 1, 3, 5, and 7 days post inoculation (dpi). A complete list of primers sequences used in these experiments is found in Table S1.

Supplementary Table S1. Primer sequences, target information, and efficiencies of primers used in qPCR and RT-qPCR.

Species	Gene name/identifier	Sequence (5'-3')	Efficiency
<i>S. sclerotiorum</i>	18S rDNA	F: AGCCGATGGAAGTTTGAGGC R: CTCGTTGGCTCTGTCAAGTGT	104.8 %
	<i>PATHOGENESIS-RELATED PROTEIN-1</i> LOC115704466	F: TTCGTCTTGGGTGTGCTAAG R: ATCATATGGTCTCTGGCCATTC	102.4 %
	<i>TIP41-LIKE PROTEIN</i> LOC115703022	F: GGCACCCAAAGAGCCTATTCT R: CCCATTATCTGCAAGTTCATCT	109.2 %
	<i>ADENINE-PHOSPHORIBOSYLTRANSFERASE-1</i> LOC115713640	F: TTGCAACTGGAGGAACCTTGT R: CATCCACTCCAACACGTTCAA	97.8 %
<i>C. sativa</i>	<i>PATHOGENESIS-RELATED PROTEIN-STH-2 (PR-10a)</i> LOC115722015	F: ACTTCACTCAAGCTAGTCAGTTC R: ACCCAATGGATCTCCTTCAATC	98.9 %
	<i>THAUMATIN-LIKE PROTEIN-1B (PR-5)</i> LOC115710654	F: GCAACGGTGGTACTGGAAA R: CATTGCTGACGTCGTAGTAGTC	100.8 %
	<i>ENDOCHITINASE-2</i> LOC115705823	F: GGTGGGATCGAATGTGGTATAG R: CGAACGACCTCTGGTTGTAA	100.5 %