

Supplementary materials

Tables

Table S1. Summary of RNA-Seq datasets generated from whiteflies fed for 0, 2, 6, 12 or 48 h on TYLCV-infected tomato plants.

Sample	Total Raw Reads (M)	Total Clean Reads (M)	Total Mapping (%)	Uniquely Mapping (%)
0 h-1	21.46	21.41	92.04	78.86
0 h-2	21.47	21.41	92.10	77.55
0 h-3	21.46	21.32	92.03	77.99
2 h-1	21.48	21.42	91.60	76.05
2 h-2	21.48	21.42	91.92	77.43
2 h-3	21.49	21.42	92.03	79.63
6 h-1	21.48	21.43	91.94	78.05
6 h-2	21.48	21.42	91.62	76.24
6 h-3	21.48	21.42	91.63	76.76
12 h-1	21.42	21.35	91.11	76.89
12 h-2	21.43	21.36	91.56	79.10
12 h-3	21.41	21.33	91.68	79.28
48 h-1	21.47	21.42	92.03	78.5
48 h-2	21.47	21.42	92.25	79.88
48 h-3	21.49	21.3	91.67	77.05

Table S2. Common DEGs involved in signal transduction in virus-infected whiteflies.

Gene ID	Accession No.	Gene Annotation	log2 (Fold change)			
			0 h vs. 2 h	0 h vs. 6 h	0 h vs. 12 h	0 h vs. 48 h
Bta01475	XP_018896 986.1	uncharacterized protein LOC109030464	-1.55	-1.67	-1.29	-1.57
Bta01655	XP_018906 270.1	rap1 GTPase-activating protein 1 isoform X3	-1.47	-1.21	-1.72	-1.72
Bta02375	XP_018913 743.1	uncharacterized protein LOC109041776	-1.18	-1.19	-1.57	-1.95
Bta02580	XP_018905 067.1	fatty acid synthase	-1.31	-1.12	-2.05	-2.02
Bta03074	XP_018907 085.1	fatty acid synthase	-1.34	-1.20	-1.76	-1.71
Bta04016	XP_018917 600.1	ras-like GTP-binding protein RhoL	-1.12	-1.28	-1.07	-1.24
Bta04099	XP_018907 804.1	acyl-CoA Delta(11) desaturase-like	-1.28	-1.62	-2.37	-3.34
Bta05107	XP_018895 569.1	protein FAM166B-like isoform X2	-1.21	-1.08	-1.15	-1.31
Bta05672	XP_018908 790.1	acyl-CoA desaturase-like	-1.92	-1.26	-1.91	-1.48
Bta06172	XP_018896 161.1	protein sprint	-1.32	-1.18	-1.33	-1.47
Bta06187	XP_018896 237.1	solute carrier family 2, facilitated glucose transporter member 1-like	-1.32	-1.27	-1.35	-1.40
Bta06483	XP_018909 499.1	phospholipase A2-like isoform X1	-3.15	-2.25	-2.16	-3.79
Bta07569	XP_018896 886.1	fatty acid synthase-like	-1.51	-1.31	-2.05	-2.00
Bta08548	XP_018898 043.1	protein decapentaplegic	-1.77	-2.31	-1.48	-1.41
Bta08620	XP_018898 020.1	striated muscle-specific serine/threonine-protein kinase-like	-1.26	-1.34	-1.91	-3.07
Bta09047	XP_018916 310.1	phosphoenolpyruvate carboxykinase [GTP]-like isoform X2	-1.90	-2.26	-2.51	-2.27
Bta09151	XP_018916 388.1	calcium/calmodulin-dependent protein kinase kinase 1 isoform X1	-1.98	-2.10	-2.43	-2.58
Bta09156	XP_018916 405.1	insulin-like peptide receptor	-1.95	-1.50	-1.53	-1.34
Bta09525	XP_002430 571.1	dual specificity protein phosphatase, putative	-1.48	-1.67	-1.96	-2.03
Bta09906	KPJ01710. 1	Nitric oxide synthase-like protein	-1.30	-1.03	-1.21	-1.18
Bta10543	XP_023724 614.1	carnitine O-palmitoyltransferase 1, liver isoform isoform X3	-1.17	-1.22	-1.54	-1.64

Bta11166	XP_018912 277.1	odium-coupled neutral amino acid transporter 9 homolog isoform X1	-1.23	-1.24	-1.51	-1.61
Bta11403	XP_018900 522.1	muscle, skeletal receptor tyrosine protein kinase-like isoform X1	-1.33	-1.13	-1.53	-2.05
Bta11772	XP_022194 226.1	sphingomyelin phosphodiesterase	-1.01	-1.36	-1.20	-1.24
Bta12556	XP_018901 460.1	senecionine N-oxygenase-like	-1.37	-1.17	-1.33	-1.11
Bta12593	XP_018901 501.1	BCL2/adenovirus E1B 19 kDa protein-interacting protein 3 isoform X1	-1.65	-2.00	-2.11	-2.26
Bta15685	XP_018916 054.1	ABC transporter G family member 23-like	-1.36	-1.60	-1.87	-1.92

Figures

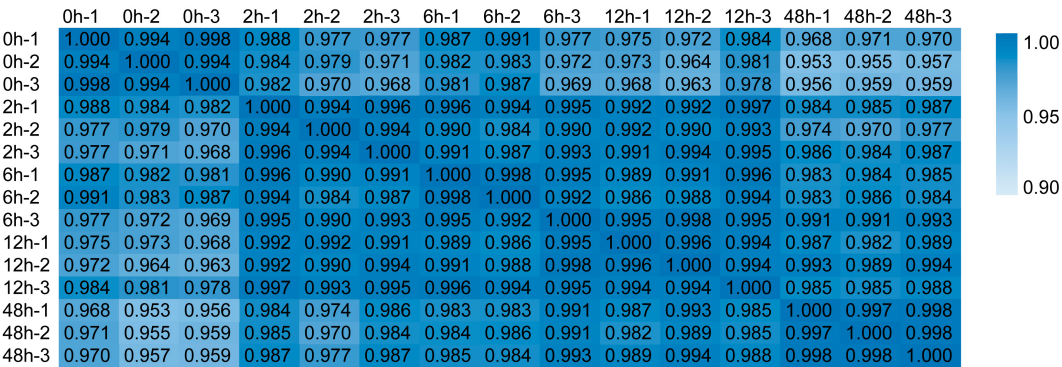


Figure S1. Pearson correlation coefficient of gene expression levels among 15 samples.

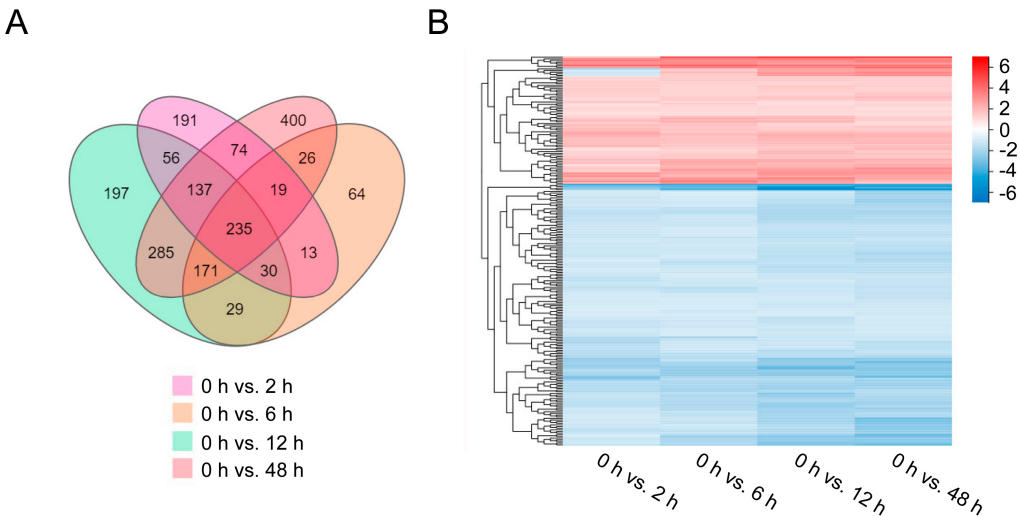


Figure S2. Common DEGs in viruliferous whiteflies. (A) Venn-diagram showing unique and common DEGs in different comparisons of 0 h vs. 2 h, 0 h vs. 6 h, 0 h vs. 12 h and 0 h vs. 48 h. (B) Hierarchical cluster analysis of 235 identified common DEGs.

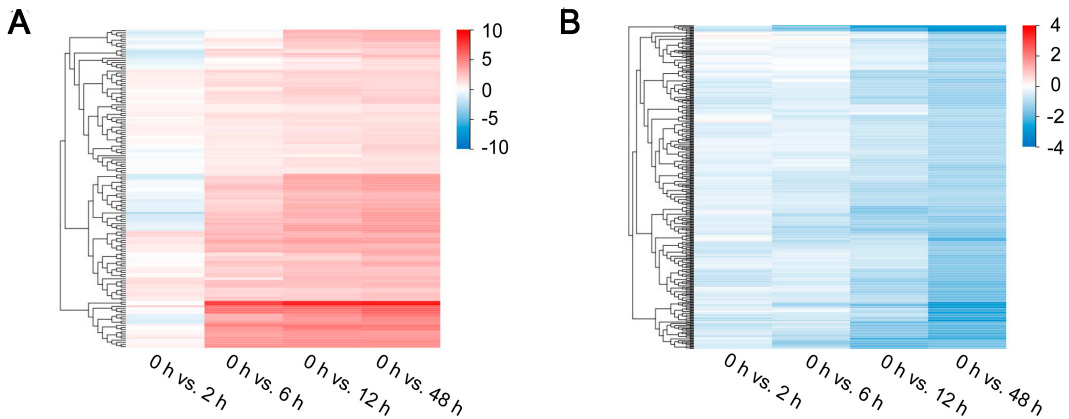


Figure S3. Time-associated gene clusters. For different treatments, genes with similar expression patterns were clustered into different groups. (A) Hierarchical cluster of 127 up-regulated genes. (B) Hierarchical cluster of 355 down-regulated genes.