

**Supplementary table 1** Chrysanthemum yellows phytoplasma (CYP) population in *Arabidopsis thaliana*, *Euscelidius variegatus*, and *Macrosteles quadripunctulatus* (mean CYP cell/100 mg leaf tissue  $\pm$  SEM).

Within rows different letters indicate significant differences (Tukey Test,  $P < 0,05$ ).

Species	dpi/ dpa						H value Kruskal- Wallis
	7	10	14	21	28	35	
<i>A. thaliana</i>	-	2.54E+07 $\pm$ 7.34E+06, a	2.27E+08 $\pm$ 5.29E+07, a	1.45E+09 $\pm$ 2.39E+08, b	1.29E+09 $\pm$ 1.47E+08, b	-	32.036 (df=3; P<0.001)
<i>E. variegatus</i>	2.37E+04 $\pm$ 1.19E+04, a	-	5.42E+05 $\pm$ 1.40E+05, ab	1.34E+06 $\pm$ 3.80E+05, bc	2.10E+06 $\pm$ 3.45E+05, bc	3.90E+06 $\pm$ 1.21E+06, c	28.176 (df=4; P<0.001)
<i>M. quadri- punctulatus</i>	8.53E+03 $\pm$ 2.65E+03, a	-	3.72E+05 $\pm$ 2.12E+05, ab	6.30E+06 $\pm$ 8.84E+05, bc	4.34E+06 $\pm$ 2.28E+06, bc	1.53E+07 $\pm$ 3.88E+06, c	31.087 (df=4; P<0.001)

**Supplementary table 2** Mean expression index (EI) ± SEM and sample size (within brackets) of genes

grouped by functional category, measured at different days post inoculation (dpi) in *Arabidopsis thaliana*

samples. Within rows different letters indicate significant differences (P < 0,05) according to the appropriate all pairwise multiple comparison procedure.

Functional category	Gene name	dpi				H value Kruskal-Wallis	Comparison procedure
		10	14	21	28		
Antigenic membrane proteins	<i>amp</i>	5.68E+03 ± 3.01E+03 (10) a	3.29E+03 ± 1.04E+03 (10) a	5.31E+02 ± 1.80E+02 (10) ab	1.51E+02 ± 2.05E+01 (10) b	19.523 (df=3; P<0.001)	Tukey Test
	<i>imp</i>	5.42E+00 ± 2.71E+00 (10)	6.43E+00 ± 3.52E+00 (10)	1.32E+00 ± 5.05E-01 (10)	6.32E-01 ± 1.36E-01 (10)	5.435 (df=3; P=0.143)	/
Generic transporters	<i>mscL</i>	8.78E+02 ± 3.81E+02 (10) ab	6.55E+02 ± 2.68E+02 (10) a	1.02E+02 ± 4.06E+01 (10) ab	3.30E+01 ± 4.99E+00 (10) b	14.349 (df=3; P=0.002)	Tukey Test
	<i>mdlB</i>	3.20E+01 ± 1.36E+01 (10) ab	2.13E+01 ± 7.08E+00 (10) a	3.36E+00 ± 1.34E+00 (10) ab	1.14E+00 ± 1.61E-01 (10) b	15.078 (df=3; P=0.002)	Tukey Test
	<i>oppC</i>	1.24E+01 ± 5.35E+00 (10) a	4.76E+00 ± 1.84E+00 (10) a	2.27E-01 ± 7.52E-02 (10) b	6.58E-02 ± 6.91E-03 (10) b	27.642 (df=3; P<0.001)	Tukey Test
	<i>ftsY</i>	1.36E+01 ± 6.10E+00 (10) a	8.21E+00 ± 3.13E+00 (10) a	1.11E+00 ± 4.06E-01 (10) ab	3.06E-01 ± 4.51E-02 (10) b	19.032 (df=3; P<0.001)	Tukey Test
Specific transporters	<i>artI</i>	7.02E+00 ± 3.12E+00 (9) a	2.76E+00 ± 1.00E+00 (10) a	3.96E-01 ± 1.33E-01 (10) ab	1.16E-01 ± 1.32E-02 (9) b	20.394 (df=3; P<0.001)	Dunn's Method
	<i>zntA</i>	1.21E+01 ± 5.29E+00 (10) a	9.16E+00 ± 4.10E+00 (9) a	9.07E-01 ± 2.75E-01 (10) ab	2.53E-01 ± 5.77E-02 (10) b	20.605 (df=3; P<0.001)	Dunn's Method
Secreted proteins	<i>SAP54</i>	1.27E+02 ± 6.09E+01 (10) a	5.96E+01 ± 2.29E+01 (10) a	4.65E+00 ± 2.10E+00 (10) b	8.31E-01 ± 1.77E-01 (10) b	24.006 (df=3; P<0.001)	Tukey Test
	<i>SAP67</i>	4.12E+00 ± 1.80E+00 (10) ab	2.08E+00 ± 9.19E-01 (10) a	1.75E-01 ± 7.32E-02 (10) bc	5.03E-02 ± 1.20E-02 (10) c	18.795 (df=3; P<0.001)	Tukey Test
	<i>SAP68</i>	2.33E+00 ± 9.80E-01 (10) ab	1.29E+00 ± 4.63E-01 (10) a	1.25E-01 ± 5.47E-02 (10) bc	3.05E-02 ± 5.74E-03 (10) c	21.224 (df=3; P<0.001)	Tukey Test
	<i>tengu</i>	2.243E+03 ± 9.47E+02 (10) ab	1.702E+03 ± 7.67E+02 (10) a	4.168E+02 ± 1.48E+02 (9) ab	9.443E+01 ± 1.57E+01 (10) b	12.981 (df=3; P=0.005)	Dunn's Method
Phospholipid metabolism	<i>pgsA</i>	3.06E+00 ± 1.48E+00 (10) ab	2.05E+00 ± 6.48E-01 (10) a	3.37E-01 ± 1.57E-01 (10) b	1.06E-01 ± 1.66E-02 (10) b	13.989 (df=3; P=0.003)	Tukey Test
30S ribosomal subunit	<i>rpsU</i>	1.30E+01 ± 5.71E+00 (10) a	9.94E+00 ± 3.74E+00 (10) a	1.67E+00 ± 5.26E-01 (10) ab	5.05E-01 ± 7.99E-02 (10) b	19.848 (df=3; P<0.001)	Tukey Test

**Supplementary table 3** Mean expression index (EI) ± SEM and sample size (within brackets) of genes grouped by functional category, measured in *Euscelidius variegatus* individuals sampled at different days post acquisition (dpa). Within rows different letters indicate significant differences (P < 0,05) according to the all pairwise multiple comparison procedure (Dunn's Method).

Functional category	Gene name	dpa					H value Kruskal-Wallis
		7	14	21	28	35	
Antigenic membrane proteins	<i>amp</i>	6.66E+02 ±	7.34E+02 ±	4.22E+02 ±	4.59E+02 ±	1.76E+02 ±	4.807
		3.36E+02 (8)	4.47E+02 (8)	1.77E+02 (8)	1.60E+02 (8)	3.27E+01 (8)	(df=4; P=0.308)
	<i>imp</i>	3.70E+00 ±	2.17E+00 ±	1.53E+00 ±	2.31E+00 ±	1.12E+00 ±	4.080
		1.65E+00 (6)	1.11E+00 (8)	6.10E-01 (8)	6.11E-01 (8)	1.74E-01 (8)	(df=4; P=0.395)
Generic transporters	<i>mScL</i>	1.52E+01 ±	2.72E+01 ±	1.98E+01 ±	1.86E+01 ±	6.11E+00 ±	7.475
		7.71E+00 (7)	1.59E+01 (8)	6.81E+00 (8)	4.82E+00 (8)	7.99E-01 (8)	(df=4; P=0.113)
	<i>mdlB</i>	2.61E+00 ±	3.20E+00 ±	2.22E+00 ±	2.47E+00 ±	1.15E+00 ±	5.064
		9.84E-01 (6)	1.42E+00 (8)	8.78E-01 (8)	5.67E-01 (8)	1.98E-01 (8)	(df=4; P=0.281)
	<i>oppC</i>	9.19E-01 ±	6.25E-01 ±	5.39E-01 ±	7.63E-01 ±	3.81E-01 ±	4.367
		3.05E-01 (6)	2.92E-01 (8)	2.34E-01 (8)	2.00E-01 (8)	1.00E-01 (8)	(df=4; P=0.359)
<i>ftsY</i>	2.14E+00 ±	1.71E+00 ±	9.46E-01 ±	1.25E+00 ±	6.43E-01 ±	9.012	
	6.39E-01 (4)	8.53E-01 (8)	4.36E-01 (8)	1.98E-01 (8)	1.70E-01 (8)	(df=4; P=0.061)	
Specific transporters	<i>artI</i>	1.10E-01 ±	4.14E-02 ±	4.26E-02 ±	1.08E-01 ±	2.05E-01 ±	9.857
		7.08E-02 (6)	1.81E-02 (7)	2.94E-02 (8)	3.66E-02 (8)	4.05E-02 (8)	(df=4; P=0.043)
	<i>zntA</i>	2.23E+00 ±	2.23E+00 ±	1.73E+00 ±	1.29E+00 ±	6.66E-01 ±	10.733
		6.32E-01 (5) a	4.71E-01 (8) a	5.42E-01 (8) ab	3.69E-01 (8) ab	1.42E-01 (8) b	(df=4; P=0.030)
Secreted proteins	<i>SAP54</i>	3.12E+01 ±	1.25E+01 ±	4.53E+00 ±	4.67E+00 ±	2.08E+00 ±	10.723
		1.67E+01 (7) a	5.24E+00 (8) ab	2.01E+00 (8) ab	1.83E+00 (8) ab	3.74E-01 (8) b	(df=4; P=0.030)
	<i>SAP67</i>	3.02E+00 ±	1.95E+00 ±	1.18E+00 ±	1.23E+00 ±	6.11E-01 ±	6.669
		1.45E+00 (4)	8.60E-01 (8)	4.93E-01 (7)	2.75E-01 (8)	1.10E-01 (8)	(df=4; P=0.154)
	<i>SAP68</i>	2.79E+00 ±	1.45E+00 ±	8.50E-01 ±	9.08E-01 ±	4.77E-01 ±	8.409
		1.11E+00 (5)	5.00E-01 (8)	3.73E-01 (8)	2.54E-01 (8)	7.63E-02 (8)	(df=4; P=0.078)
<i>tengu</i>	2.12E+02 ±	1.75E+02 ±	7.08E+01 ±	7.74E+01 ±	2.91E+01 ±	8.850	
	1.14E+02 (8)	8.70E+01 (8)	2.81E+01 (8)	2.97E+01 (8)	4.42E+00 (8)	(df=4; P=0.065)	
Phospholipid metabolism	<i>pgsA</i>	1.68E+00 ±	2.45E+00 ±	1.90E+00 ±	1.16E+00 ±	5.09E-01 ±	13.763
		5.18E-01 (5) ab	8.70E-01 (8) a	6.52E-01 (8) ab	2.99E-01 (8) ab	1.04E-01 (8) b	(df=4; P=0.008)
30S ribosomal subunit	<i>rpsU</i>	4.38E+00 ±	2.40E+00 ±	2.91E+00 ±	4.07E+00 ±	2.26E+00 ±	7.476
		1.00E+00 (6)	9.90E-01 (8)	1.10E+00 (8)	1.06E+00 (8)	4.12E-01 (8)	(df=4; P=0.113)

**Supplementary table 4** Mean expression index (EI) ± SEM and sample size (within brackets) of genes grouped by functional category, measured in *Macrosteles quadripunctulatus* individuals sampled at different days post acquisition (dpa). Within rows different letters indicate significant differences (P < 0,05) according to the appropriate all pairwise multiple comparison procedure.

Functional category	Gene name	dpa					H value Kruskal-Wallis	Comparison procedure
		7	14	21	28	35		
Antigenic membrane proteins	<i>amp</i>	2.62E+02 ± 4.32E+01 (8) a	1.84E+02 ± 4.02E+01 (8) ab	5.80E+01 ± 1.17E+01 (8) abc	5.84E+01 ± 3.35E+01 (8) bc	1.55E+01 ± 6.44E+00 (8) c	23.621 (df=4; P<0.001)	Tukey Test
	<i>imp</i>	6.19E-01 ± 1.37E-01 (8) a	2.99E-01 ± 6.99E-02 (8) ab	1.61E-01 ± 3.40E-02 (8) abc	1.49E-01 ± 8.82E-02 (8) bc	5.26E-02 ± 1.84E-02 (8) c	23.373 (df=4; P<0.001)	Tukey Test
Generic transporters	<i>mscL</i>	1.15E+01 ± 3.91E+00 (7) ab	1.84E+01 ± 3.47E+00 (8) a	8.86E+00 ± 1.71E+00 (8) abc	3.29E+00 ± 1.10E+00 (8) bc	1.60E+00 ± 2.81E-01 (8) c	22.239 (df=4; P<0.001)	Dunn's Method
	<i>mdlB</i>	9.17E-01 ± 2.08E-01 (8) a	5.90E-01 ± 1.28E-01 (8) ab	2.23E-01 ± 5.11E-02 (8) abc	3.36E-01 ± 2.10E-01 (8) b	9.67E-02 ± 3.57E-02 (8) c	21.205 (df=4; P<0.001)	Tukey Test
	<i>oppC</i>	1.23E-01 ± 2.72E-02 (8) a	7.25E-02 ± 1.67E-02 (8) ab	5.15E-02 ± 1.79E-02 (8) ab	1.17E-01 ± 6.74E-02 (8) ab	2.88E-02 ± 1.06E-02 (8) b	11.965 (df=4; P=0.018)	Tukey Test
	<i>ftsY</i>	3.96E-01 ± 7.93E-02 (7) a	2.44E-01 ± 5.08E-02 (8) a	1.10E-01 ± 2.45E-02 (8) ab	1.85E-01 ± 1.16E-01 (8) ab	5.43E-02 ± 2.23E-02 (8) b	20.076 (df=4; P<0.001)	Dunn's Method
Specific transporters	<i>artI</i>	9.17E-02 ± 2.27E-02 (8) a	3.39E-02 ± 6.74E-03 (8) ab	2.30E-02 ± 1.17E-02 (8) ab	6.14E-02 ± 3.01E-02 (8) ab	1.82E-02 ± 6.70E-03 (8) b	10.248 (df=4; P=0.036)	Tukey Test
	<i>zntA</i>	1.53E-01 ± 2.58E-02 (7) a	8.54E-02 ± 1.35E-02 (8) ab	2.53E-02 ± 5.64E-03 (8) b	6.51E-02 ± 3.37E-02 (8) abc	1.43E-02 ± 4.65E-03 (8) c	23.546 (df=4; P<0.001)	Dunn's Method
Secreted proteins	<i>SAP54</i>	3.88E+00 ± 8.71E-01 (8) a	1.67E+00 ± 3.92E-01 (8) ab	5.10E-01 ± 1.20E-01 (8) bc	6.09E-01 ± 3.35E-01 (8) bc	2.26E-01 ± 9.39E-02 (8) c	26.385 (df=4; P<0.001)	Tukey Test
	<i>SAP67</i>	7.70E-01 ± 2.35E-01 (6) a	1.35E-01 ± 2.59E-02 (8) ab	5.07E-02 ± 1.17E-02 (8) bc	1.24E-01 ± 5.79E-02 (7) abc	2.32E-02 ± 4.74E-03 (7) c	23.463 (df=4; P<0.001)	Dunn's Method
	<i>SAP68</i>	4.24E-01 ± 1.87E-01 (8) a	4.63E-02 ± 8.96E-03 (8) ab	2.82E-02 ± 6.17E-03 (8) b	4.88E-02 ± 2.87E-02 (7) b	9.92E-03 ± 2.59E-03 (8) b	23.675 (df=4; P<0.001)	Dunn's Method
	<i>tengu</i>	8.61E+01 ± 3.78E+01 (8) a	3.01E+01 ± 7.03E+00 (8) ab	1.04E+01 ± 2.97E+00 (8) abc	8.46E+00 ± 4.79E+00 (8) bc	2.83E+00 ± 1.02E+00 (8) c	26.766 (df=4; P<0.001)	Tukey Test
General metabolism	<i>pgsA</i>	7.52E-01 ± 1.61E-01 (7) a	3.31E-01 ± 5.83E-02 (8) ab	1.10E-01 ± 2.10E-02 (8) abc	1.11E-01 ± 7.46E-02 (8) bc	2.22E-02 ± 7.03E-03 (8) c	28.649 (df=4; P<0.001)	Dunn's Method
	<i>rpsU</i>	2.19E+00 ± 3.96E-01 (8) a	7.58E-01 ± 1.26E-01 (8) ab	3.39E-01 ± 7.33E-02 (8) b	9.01E-01 ± 4.95E-01 (8) ab	3.54E-01 ± 1.43E-01 (8) b	20.149 (df=4; P<0.001)	Tukey Test

**Supplementary Table 5** Mean expression index (EI)  $\pm$  SEM and sample size (within brackets) of genes grouped by functional category, measured in *Arabidopsis thaliana*, *Euscelidius variegatus* and *Macrosteles quadripunctulatus* sampled at the first two dates (10 and 14 days post inoculation and 7 and 14 days post acquisition for plant and insect samples, respectively). Within rows different letters indicate significant differences ( $P < 0,05$ ) according to the all pairwise multiple comparison procedure (Dunn's Method).

Functional category	Gene name	<i>Arabidopsis thaliana</i>	<i>Euscelidius variegatus</i>	<i>Macrosteles quadripunctulatus</i>	H value Kruskal-Wallis
Immuno-dominant membrane proteins	<i>amp</i>	4.49E+03 $\pm$	7.00E+02 $\pm$	2.23E+02 $\pm$	19.645
		1.58E+03 (20) a	2.70E+02 (16) b	3.02E+01 (16) b	(df=2; <0.001)
	<i>imp</i>	5.92E+00 $\pm$	2.82E+00 $\pm$	4.59E-01 $\pm$	11.304
		2.17E+00 (20) a	9.34E-01 (14) a	8.48E-02 (16) b	(df=2; P=0.004)
Generic transporters	<i>mscL</i>	7.67E+02 $\pm$	2.16E+01 $\pm$	1.52E+01 $\pm$	28.063
		2.28E+02 (20) a	9.07E+00 (15) b	2.67E+00 (15) b	(df=2; P<0.001)
	<i>mdlB</i>	2.66E+01 $\pm$	2.95E+00 $\pm$	7.54E-01 $\pm$	24.166
		7.56E+00 (20) a	8.85E-01 (14) ab	1.25E-01 (16) b	(df=2; P<0.001)
	<i>oppC</i>	8.57E+00 $\pm$	7.51E-01 $\pm$	9.79E-02 $\pm$	24.166
	2.89E+00 (20) a	2.08E-01 (14) a	1.67E-02 (16) b	(df=2; P<0.001)	
Specific transporters	<i>ftsY</i>	1.09E+01 $\pm$	1.86E+00 $\pm$	3.15E-01 $\pm$	22.606
		3.39E+00 (20) a	5.91E-01 (12) a	4.86E-02 (15) b	(df=2; P<0.001)
	<i>artI</i>	4.78E+00 $\pm$	7.30E-02 $\pm$	6.28E-02 $\pm$	31.650
	1.60E+00 (19) a	3.39E-02 (13) b	1.36E-02 (16) b	(df=2; P<0.001)	
Secreted proteins	<i>zntA</i>	1.07E+01 $\pm$	2.23E+00 $\pm$	1.17E-01 $\pm$	30.914
		3.32E+00 (19) a	3.61E-01 (13) a	1.62E-02 (15) b	(df=2; P<0.001)
	<i>SAP54</i>	9.33E+01 $\pm$	2.12E+01 $\pm$	2.77E+00 $\pm$	22.397
		3.26E+01 (20) a	8.33E+00 (15) a	5.43E-01 (16) b	(df=2; P<0.001)
	<i>SAP67</i>	3.10E+00 $\pm$	2.31E+00 $\pm$	4.07E-01 $\pm$	8.709
	1.01E+00 (20) ab	7.26E-01 (12) a	1.30E-01 (14) b	(df=2; P=0.013)	
	<i>SAP68</i>	1.81E+00 $\pm$	1.97E+00 $\pm$	2.35E-01 $\pm$	16.225
		5.41E-01 (20) a	5.32E-01 (13) a	1.03E-01 (16) b	(df=2; P<0.001)
	<i>tengu</i>	1.97E+03 $\pm$	1.94E+02 $\pm$	5.81E+01 $\pm$	22.206
		5.96E+02 (20) a	6.95E+01 (16) b	1.99E+01 (16) b	(df=2; P<0.001)
General metabolism	<i>pgsA</i>	2.56E+00 $\pm$	2.16E+00 $\pm$	5.27E-01 $\pm$	10.260
		7.95E-01 (20) ab	5.64E-01 (13) a	9.63E-02 (15) b	(df=2; P=0.006)
	<i>rpsU</i>	1.15E+01 $\pm$	3.25E+00 $\pm$	1.47E+00 $\pm$	10.282
		3.34E+00 (20) a	7.35E-01 (14) ab	2.73E-01 (16) b	(df=2; P=0.006)