

Supplementary information

The effect of insecticide synergist treatment on genome-wide gene expression in a polyphagous pest

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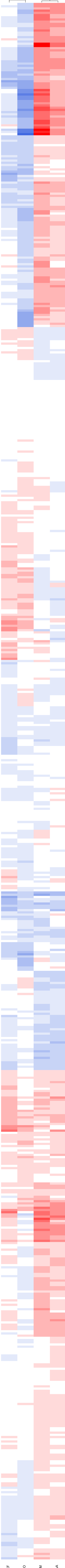
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tetur32g01950
tetur22g00570
tetur01g12650
tetur02g09660
tetur03g08660
tetur09g04370
tetur13g00160
tetur29g13280
tetur15g03610
tetur11g01940
tetur36g00460
tetur15g02270
tetur09g04800
tetur19g01540
tetur09g01320
tetur04g08350
tetur19g01970
tetur01g12770
tetur04g05170
tetur49g00160
tetur03g04900
tetur08g04900
tetur29g02720
tetur11g05920
tetur29g01820
tetur04g08600
tetur04g01460
tetur01g01260
tetur03g03990
tetur08g01710
tetur03g08200
tetur10g00950
tetur06g04280
tetur24g01340
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Supplementary Table S1 - Number of strand-specific paired-end Illumina reads and their mapping rates against the *T. urticae* annotation for all treatments (CON, DEF, DEM, CsA, PBO and FORM).

Supplementary Table S2 - Differentially expressed genes (absolute fold change (FC) ≥ 1.5 and Benjamini-Hochberg adjusted p-value < 0.05) between adult *T. urticae* females of the JP-R strain treated with PBO compared to adult *T. urticae* females treated with formulation only.

Supplementary Table S3 - Differentially expressed genes (absolute fold change (FC) ≥ 1.5 and Benjamini-Hochberg adjusted p-value < 0.05) between adult *T. urticae* females of the JP-R strain treated with DEF compared to adult *T. urticae* females treated with formulation only.

Supplementary Table S4 - Differentially expressed genes (absolute fold change (FC) ≥ 1.5 and Benjamini-Hochberg adjusted p-value < 0.05) between adult *T. urticae* females of the JP-R strain treated with DEM compared to adult *T. urticae* females treated with formulation only.

Supplementary Table S5 - Differentially expressed genes (absolute fold change (FC) ≥ 1.5 and Benjamini-Hochberg adjusted p-value < 0.05) between adult *T. urticae* females of the JP-R strain treated with CsA compared to adult *T. urticae* females treated with formulation only.

Supplementary Table S6 - Differentially expressed Major Facilitator Superfamily (MFS) genes (absolute fold change (FC) ≥ 1.5 and Benjamini-Hochberg adjusted p-value < 0.05) between adult *T. urticae* females of the JP-R strain treated with CsA compared to adult *T. urticae* females treated with formulation only.

Supplementary Table S7 - *T. urticae* genes coding for transcription factors with an absolute fold change ≥ 1.25 in both the PBO and DEF treatment and with an opposite direction of fold change compared to the CsA and DEM treatment.

Supplementary Table S8 - Primers used in this study.

Primer	Sequence (5'-3')	Tm(°C)	Reference	Description
tetur06g04520_F	AAATACCGAGGTCGGACGTA	59.45	(1)	Cytochrome P450 - CYP392A16
tetur06g04520_R	AAGCACTTTTCAATCTGGTCAC	59.69	(1)	
tetur13g04550_F	CTGGCAAGCCAATGCTTTA	59.96	(1)	Intradiol ring-cleavage dioxygenase
tetur13g04550_R	ACCTCTGAGGAATCTTTCACCA	60.11	(1)	
tetur01g02650_F	CCGTCAATGTGTTAATTCAGCA	58.58	This study	Immunoglobulin E-set
tetur01g02650_R	TGTACGGAGACAGTTGGGTT	58.58	This study	
tetur09g06670_F	ATTTGATCATGGAAGTGTGGT	58.04	This study	Protein midA homolog; mitochondrial precursor
tetur09g06670_R	CCAGTGCATCATTGAGAGAAGT	58.39	This study	
tetur03g00830_F	TTGCCTGGTGGTGGTGAA	58.99	(2)	Cytochrome P450 - CYP392A12
tetur03g00830_R	ATGGTACTCTTCCAAGACCGATA	59.04	(2)	
tetur03g00970_F	TTGTTCAATTTAGCCAAGGTGTT	57.39	(2)	Cytochrome P450 - CYP392A11
tetur03g00970_R	CCACTTGGTTGCTTCTCTC	57.37	(2)	
tetur11g05010-20_F	CAGTGCCAAGGAAAATGCTG	57.93	This study	Hypothetical protein
tetur11g05010-20_R	TGCGAACAATCAGTCCCAG	57.77	This study	
tetur40g00030_F	GTTACATGATTGGCGGAGTAGT	58.21	This study	Major facilitator superfamily transporter
tetur40g00030_R	GCATAGATTGGATTGAATGTGGTG	58.47	This study	
tetur08g06890_F	TGGATTATTGGGTGCTTTGACT	57.95	This study	Solute carrier family 17
tetur08g06890_R	GCAAAGTACCAATGAGATAAAATACAG	57.28	This study	
tetur08g06870_F	GTGGACTATTGGCTGCTTTATGT	59.05	This study	

Primer	Sequence (5'-3')	Tm(°C)	Reference	Description
tetur08g06870_R	TGATAACGAGTTGAAAAGTGCCT	58.61	This study	Sodium-dependent phosphate transporter
tetur06g01700_F	CTAATGATTCACGACCATGACACT	58.89	This study	Glycoside hydrolase
tetur06g01700_R	CAGCTCATCATAATAGTGACCGAA	58.47	This study	
RP49_F	CTTCAAGCGGCATCAGAGC	62.19	(1)	Ribosomal protein 49
RP49_R	CGCATCTGACCCCTTGA ACTTC	62.09	(1)	
UBQ_F	GTCTCCGTGGTGGAAATGC	58.11	(3)	Ubiquitin C
UBQ_R	TTGGATTTGGCTTTCACG	54.50	(3)	

- (1) Dermauw, W. *et al.* A link between host plant adaptation and pesticide resistance in the polyphagous spider mite *Tetranychus urticae*. *Proc. Natl. Acad. Sci. U. S. A.* **110**, E113-22 (2013).
- (2) Khalighi, M. *et al.* Molecular analysis of cyenopyrafen resistance in the two-spotted spider mite *Tetranychus urticae*. *Pest Manag. Sci.* **72**, 103–112 (2015).
- (3) Demaeght, P. *et al.* Molecular analysis of resistance to acaricidal spirocyclic tetronic acids in *Tetranychus urticae*: CYP392E10 metabolizes spirodiclofen, but not its corresponding enol. *Insect Biochem. Mol. Biol.* **43**, 544–554 (2013).