Table S1. Primers used for qPCR, cloning and RNAi

Experiments	GenBank No. or Gene ID.	Genes	Primer names and sequences (5′-3′)	Product length (bp)
qPCR	tetur01g00650	*TcCYP4G*	F: AAGAGGGTTTGCGACTTTGC R: ATTTCGTGGTCCAGCTGAGA	242
	KY084264	*TcCHIT*	F: TTCTTCTCGGTGATCTCGGG R: TGGGATTGGCTGGAGGAA	163
	tetur07g01030	*TcCPR*	F: ACTCAGTTACCAGCTCCACC R: TGAAGCTGGTTGAGGAGGAG	219
	tetur03g08510	*TcCHS*	F: TGTTGGTCGGAGCTATGGTT R: CGGTACCAACAAAGACAGCC	186
	FJ608659	*RPS18*	F:AACGACTCCATGCATCCTGA R:TGCCTATTCAAGAACCAAAGTGGG	99
cloning	MW816148	*TcCPR*	F: ATGAATTGGATAACTTTCATT R: TTAACGATCACGATAAACTGG	2391
RNAi	KY084264	*TcCHIT10*	F:taatacgactcactatagggTCGACCAATACTCAGCGTCA R:taatacgactcactatagggCGATAAACTGGAGCGGCTTG	191
	ACY56286	*GFP*	F:taatacgactcactatagggTCGGCGGCAATCCTGATCAA R:taatacgactcactatagggTCACAGGGTAAAATTCAGCA	476
heterologous expression	tetur07g01030	*TcCPR*	F:CGCGGATCCGCGATGAATTGGATAACTTTC R:TCCCCCGGGGGTTAACGATCACGATAAAC	2414

Table S2. The complete sequence information of CPR gene of *T. cinnabarinus*

Gene	Accession number	Coding sequence (bp)	Deduced amino acid	Calculated molecular (kDa)	Isoelectric point
TcCPR	MW816148	2391	797	89.73	8.12

Table S3. Sequences and relevant information for phylogenetic analysis of *TcCPR*.

Genes	GenBank No. or Gene ID.	Species	Class
TcCPR	*Tetranychus cinnabarinus*	MW816148	Arachnida
TuCPR	*Tetranychus urticae*	tetur07g01030	Arachnida
PtCPR	*Parasteatoda tepidariorum*	XP_015930112.1	Arachnida
IrCPR	*Ixodes ricinus*	P84252	Arachnida
AbCPR	*Argiope bruennichi*	KAF8766829.1	Arachnida
AdCPR	*Araneus diadematu*	P80519	Arachnida
MoCPR	*Metaseiulus occidentalis*	XP_003737070.1	Arachnida
LdCPR	*Leptotrombidium deliense*	RWS30154.1	Arachnida
RmCPR	*Rhipicephalus microplus*	XP_037285625.1	Arachnida
AvCPR	*Araneus ventricosus*	GBM78335.1	Arachnida
RsCPR	*Rhipicephalus sanguineus*	XP_037509318.1	Arachnida
TcaCPR	*Tribolium castaneum*	XP_968674.1	Insecta
AgCPR	*Anoplophora glabripennis*	XP_018572821.1	Insecta
LdCPR	*Leptinotarsa decemlineata*	XP_023012035.1	Insecta
DvCPR	*Diabrotica virgifera*	XP_028140893.1	Insecta

Table S4. The total thermodynamic parameters of the interaction between GO and CPR protein.

T (°C)	N (bases/complex)	K_a×10^6 (M^{-1})	△H (cal/mol)	△S (cal/mol)	△G (cal/mol)
25	0.87 ± 0.02	1.492 ± 0.28	-635.22 ± 39.16	17.23	-5772.34

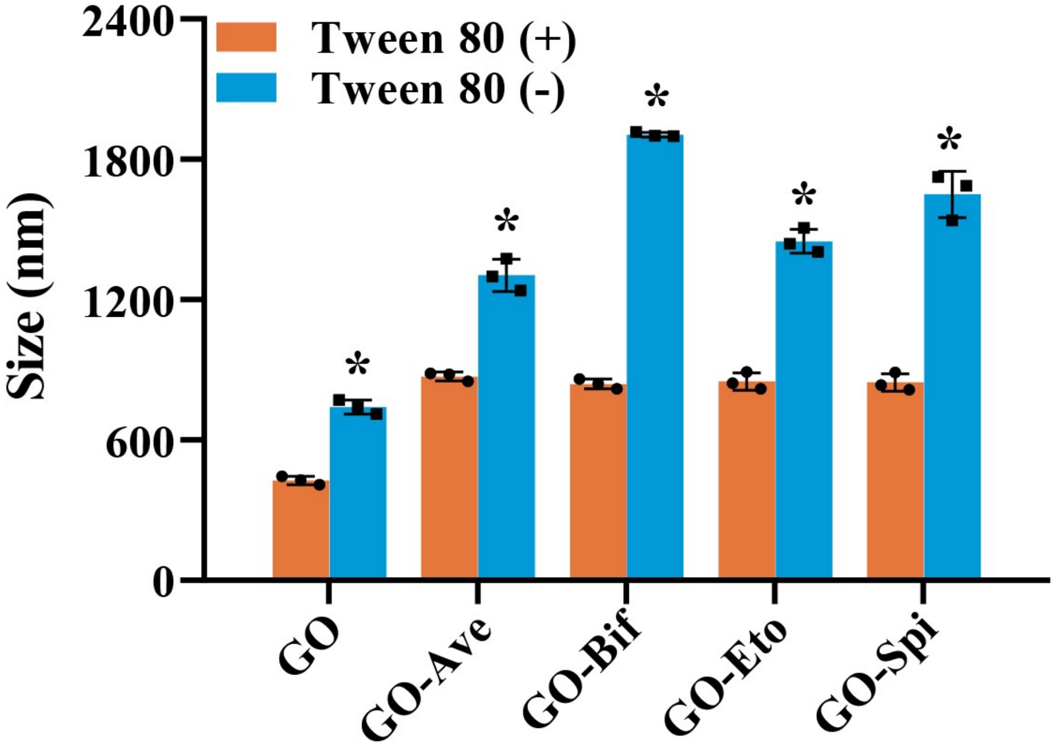

Fig. S1. The Tween 80 modified (+) and unmodified (-) hydrodynamic size of GO, GO-Ave, GO-Bif, GO-Eto and GO-Spi. Error bars represent the standard error of the calculated mean based on three biological replicates. An asterisk (*) on the error bar indicates a significant difference between the treatment and group CK according to t-tests, $*P < 0.0001$.

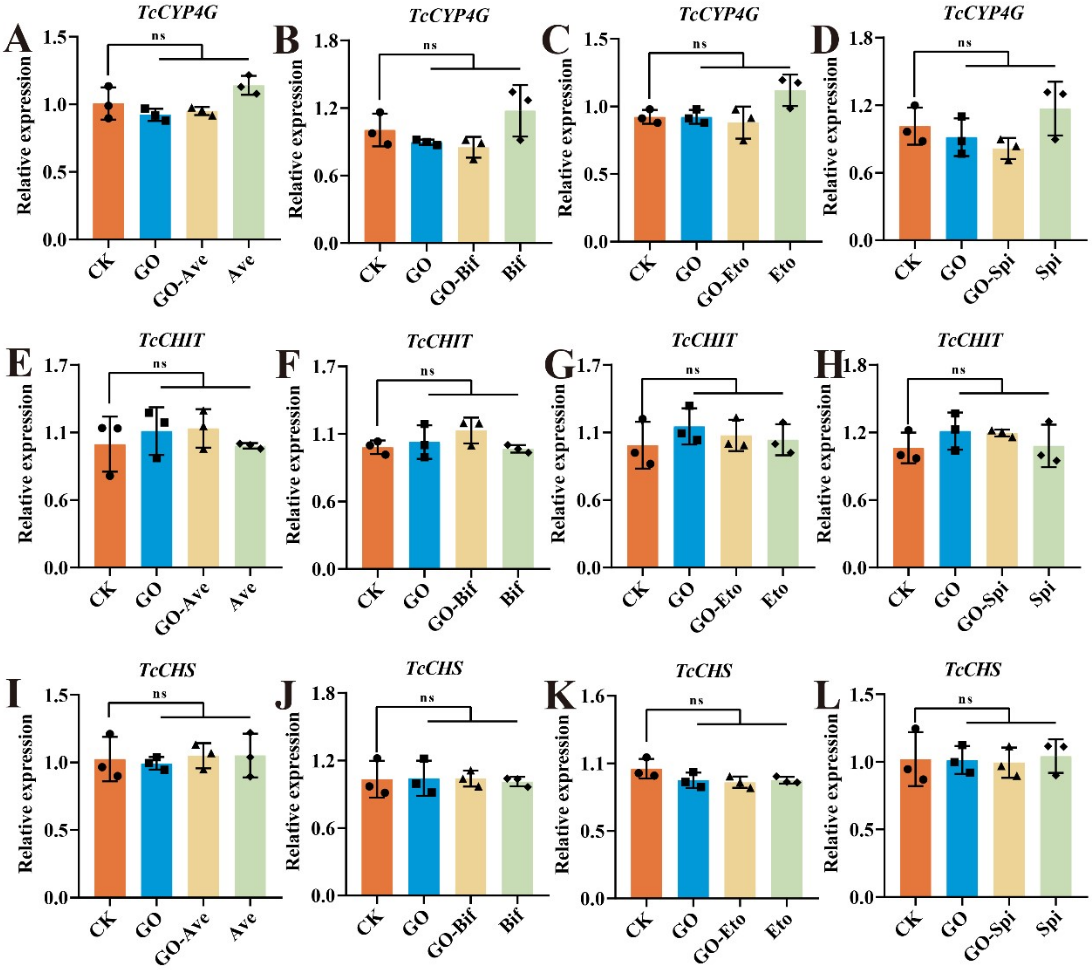

Fig. S2. Expression profiles of *TcCYP4G*, *TcCHIT*, and *TcCHS* transcripts after treatment at the adult stage for 24 h in *T. cinnabarinus*. Relative expression of the *TcCYP4G* of *T. cinnabarinus* exposed to (A) GO, Ave and GO-Ave, (B) GO, Bif and GO-Bif, (C) GO, Eto and GO-Eto and (D) GO, Spi and GO-Spi, the *TcCHIT* of *T. cinnabarinus* exposed to (E) GO, Ave and GO-Ave, (F) GO, Bif and GO-Bif, (G) GO, Eto and GO-Eto and (H) GO, Spi and GO-Spi, and the *TcCHS* of *T. cinnabarinus* exposed to (I) GO, Ave and GO-Ave, (J) GO, Bif and GO-Bif, (K) GO, Eto and GO-Eto and (L) GO, Spi and GO-Spi in 0.1% (v/v) Tween-80 and 2% (v/v) acetone were analyzed using qPCR, respectively. *T. cinnabarinus* were exposed to 0.9 μg/L (LC_{50} value of GO-Ave) of GO, Ave and GO-Ave, 0.769 mg/L (the LC_{50} value of GO-Bif) of GO, Bif and GO-Bif, 0.072 mg/L (the LC_{50} value of GO-Eto) of GO, Eto and GO-Eto, and 70.730 mg/L (the LC_{50} value of GO-Spi) of GO, Spi and GO-Spi. Water containing 0.1% (v/v) Tween-80 and 2% (v/v) acetone was used as the control treatment (CK). Error bars represent the standard error of the calculated mean based on three biological replicates. ns, not significant. *RPS18* was used as the reference gene.