

## **Supplementary material**

**Title:** Molecular mechanisms of *Tetranychus urticae* chemical adaptation in hop fields

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Supplementary Figure 1. The amino acid substitutions response for abamectin resistance in *T. urticae* and the primer design strategy for TuGlu1 and TuGlu3. TM: transmembran region.

Supplementary Figure 2. The 3D structure for *T. urticae* cytochrome *b* showing amino acid substitutions related to bifentazate resistance. The protein tertiary structure of *T. urticae* cytochrome *b* was predicted by using the I-TASSER server (<http://zhanglab.ccmb.med.umich.edu/I-TASSER/>) and then the PDB coordinate file of the highest ranking model was loaded into Chimera (<http://plato.cgl.ucsf.edu/chimera/docs/credits.html>) for molecular visualization and modification.

Supplementary Figure 3. The structure of sodium channel and tested amino acid substitutions in current study. Mutations labelled with white circles denote that these mutations have been examined in *Xenopus* oocytes and the function in pyrethroid resistance had been confirmed. Mutations labelled with black circles stand for having not been investigated in *Xenopus* oocytes.

Fig. S1

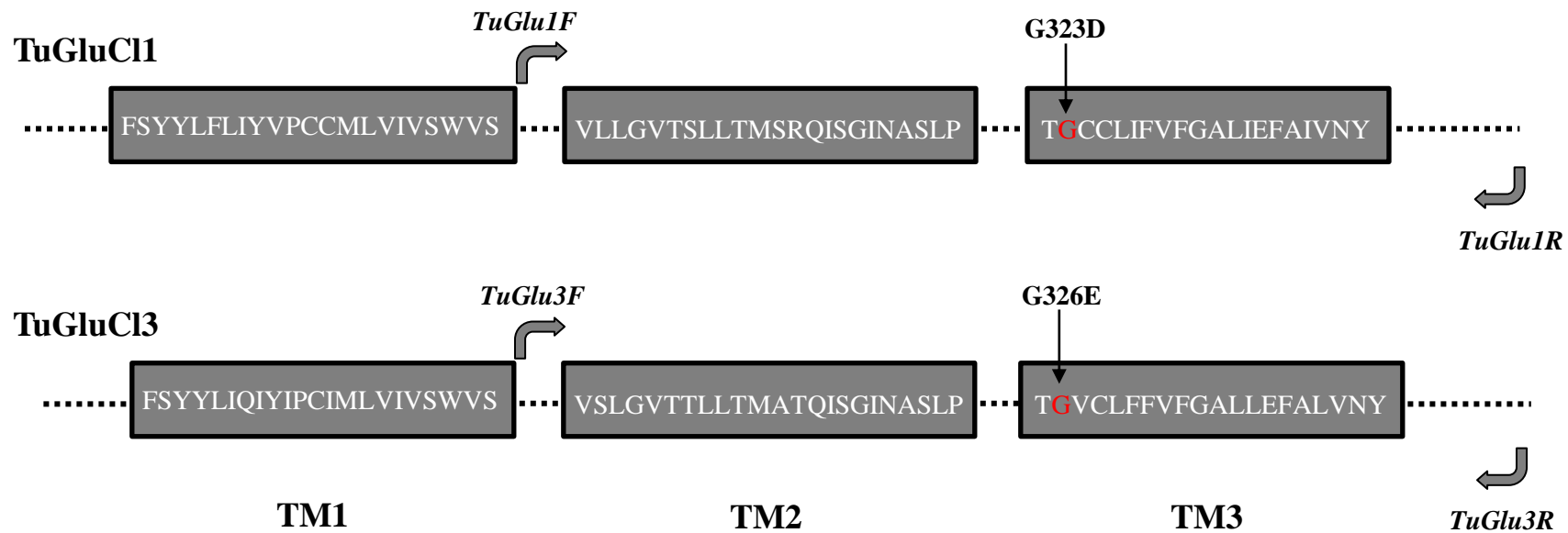


Fig. S2

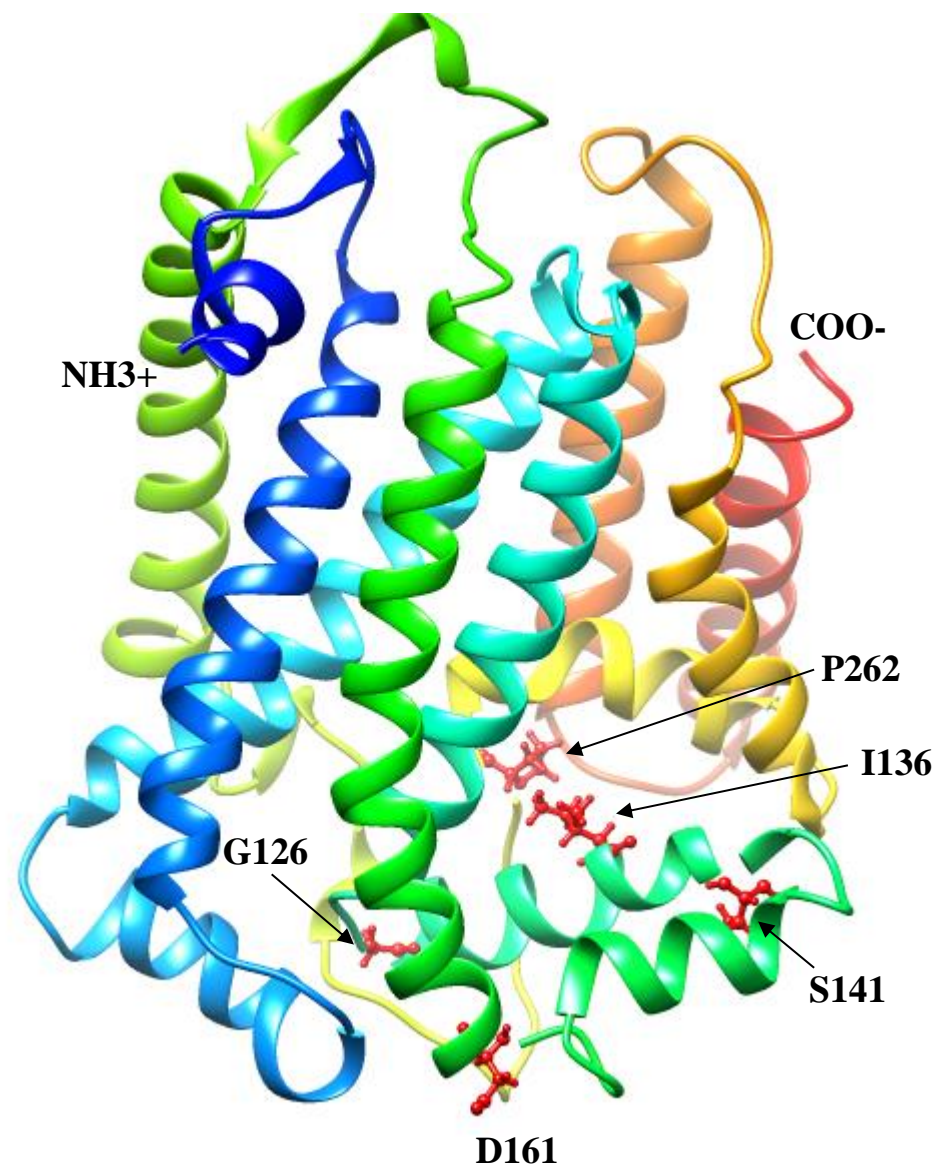
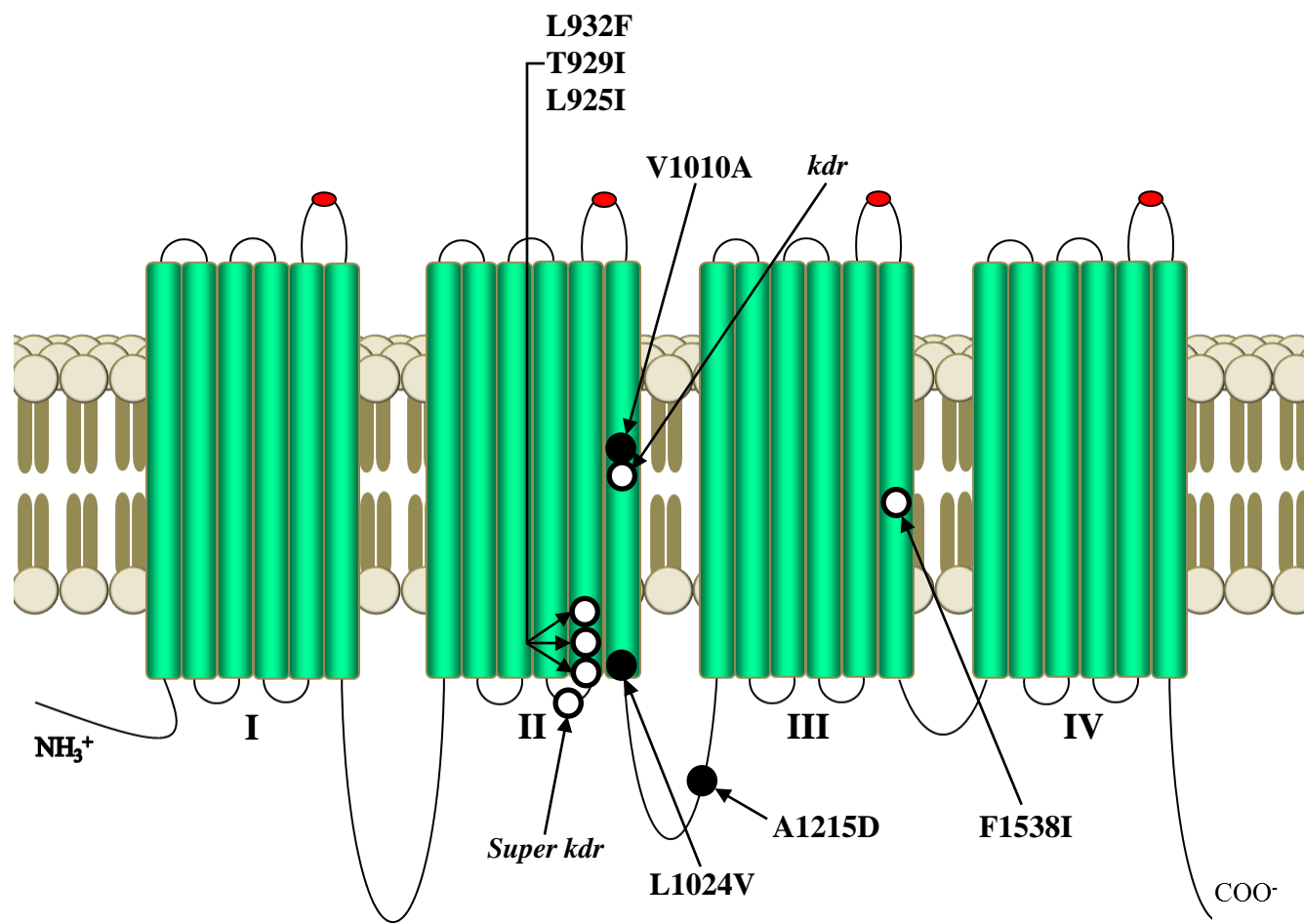


Fig. S3



Supplementary Table S1. Primer information for PCR and qRT-PCR analyses

Primer name	Gene name	Gene ID	Primer sequence (5' → 3')	Amplicon (bp)	Annealing T. (°C)	Reference
KdrIIF1	voltage-gated	JN881331	F: GAAGGTGTTTCGAGGTCTTTTCAG	506	55.4	This study
KdrIIR1	sodium channel		R: AAGCGATCAAAGGCTTCTTGAAG		55.8	
KdrIIF2	voltage-gated	JN881331	F: GTTCGAGGTCTTTTCAGTTTACG	489	53.9	This study
KdrIIR2	sodium channel		R: GGCTTCTTGAAGTTTCTTGGTG		54.4	
KdrII-IIIIF	voltage-gated	JN881331	F: TGCATCTCAATTGTCCAAGG	255	53.0	<i>Pest Manag. Sci.</i> 67:1424-1433
KdrII-IIIR	sodium channel		R: GTTCTTCCAGGCAACATGG		54.3	
KdrIIIF1	voltage-gated	JN881331	F: TGGACAATTATTATGGACCATGC	1,549	53.2	This study
KdrIIIR1	sodium channel		R: ATGATGGCAGCCAATACACC		55.5	
KdrIIIF1	voltage-gated	JN881331	F: TGGACAATTATTATGGACCATGC	259	53.2	This study
KdrIIIR2	sodium channel		R: GTTCTTTGATCCCATCTTTTTCAT		52.3	
TuGlu1F	glutamate-gated	AGN53343	F: TTGGATTGACCCTAACTCAGCAG	266	56.8	<i>Insect Biochem Mol Biol.</i> 42:455-465
TuGlu1R	chloride channel 1		R: TTGCACCAACAATTCCTTGAGG		56.1	
TuGlu3F	glutamate-gated	AFG29908	F: CATTITGGTTGGATCCAAATGCTATTCC	267	57.0	This study
TuGlu3R	chloride channel 3		R: GTTGAACCTTGCTGTTGTTGATTTTCTGCG		59.3	
CytbF1	cytochrome b	EU556749	F: CGGAATAATTTTACAAATAACT	828	51.7	<i>PNAS</i> 105 (16): 5980-5985
CytbR1			R: AATGAAATTTCTGTAAAAGGG		50.4	
CytbF1	cytochrome b	EU556749	F: CGGAATAATTTTACAAATAACT	637	51.7	<i>PNAS</i> 105 (16): 5980-5985
CytbR2			R: TGGTACAGATCGTAGAATTGC		54.6	
TuCYP385C4F	CYP385C4	tetur11g06630	F: CGTAAACGATCGTTCTGGGAAC	105	55.8	This study
TuCYP385C4R			R: TTTCGGTTTAGGTTTCGGTGAAC		55.7	
TuCYP389A1F	CYP389A1	tetur25g02050	F: GTTCCTTCTATTTGGCCATGCG	135	56.8	This study
TuCYP389A1R			R: TGATCCAGATGGCAAAATAAACCCG		57.5	
TuCYP392D8F	CYP392D8	tetur03g05070	F: CTCGATCATTTC AACGTAAGCCC	122	56.0	This study
TuCYP392D8R			R: CATGGGCCAGAAGGGAGTTTAC		57.8	
TuRp49F	ribosomal protein 49	tetur18g03590	F: CTTCAAGCGGCATCAGAGC	105	56.6	This study
TuRp49R			R: CGCATCTGACCCTTGAACCTC		56.0	
TuActinF	actin	tetur03g09480	F: ATGCCATCCTTCGTTTGGATTTGG	111	58.2	This study
TuActinR			R: GGACAATTTCTCGCTCAGCAGTGG		58.2	