

Table S1. Primers used in one or two rounds of PCR amplification

Gene category	Gene Name	PCR round	Hybridization temperature (°C)	Forward primer	Reverse primer
Insecticide target genes	Ace 1	1 st round	66.5	GTATGAACTCCTGTTGACAAGAAGTGGC	GGAATGCCAGCTTTGGGAAGAGGTG
		2 nd round	60.8	TCCTGTTGACAAGAAGTGGCG	ATGCCAGCTTTGGGAAGAGGTG
	Ace 2	1 st round	67.5	CGAATATTTCCAGGCTTCTCCG	ACAAGAGTGGAAGTGGGAGAAGGATTTGG
	nAChR α 1	1 st round	53.7	TCAAGCCACAAGCAATCG	TCCATAACGATCCTCTGATC
		2 nd round	63.5	CCACAAGCAATCGCCGCATC	CGATCCTCTGATCGCAGACGTC
	nAChR α 3	1 st round	70	TTCCACCCACAACGCCAACAG	ATTGCCATTGCCATTGCCATTGCC
		2 nd round	60	CCACAACGCCAACAGGATCATG	ATTGCCATTGCCATTGCCATTGCC
	nAChR β 2	1 st round	43	AGATTATTCCAGCTAGATGTC	GAAATGTAGCGAAGGTACGA
		2 nd round	69.7	AGATGTCCTGGAGCAACCTGTG	GCGAAGGTACGAATTGAGTTCCG
	GluCl iso1	1 st round	57.5	CCACATAGTTCCACCATGCT	ACTTGATAGATGGGTGGGTT
		2 nd round	66.5	ACATAGTTCCACCATGCTGTGGTATG	GATGGGTGGGTTTTGAGATCATAGTC
	GluCl iso2	1 st round	59.2	CCACATAGTTCCACCATGCT	ACTTGATAGATGGGTGGGTT
		2 nd round	63.5	ACATAGTTCCACCATGCTGTGGTATG	GATGGGTGGGTTTTGAGATCATAGTC
	Para F1	1 st round	58.5	CCCATAAACCCACAAACCCCTTC	CACCCAGTTTTTCATGCGTAAGTTC
		2 nd round	63.5	TTGACGTCTTCGACGTCGAGCC	CACCCAGTTTTTCATGCGTAAGTTC
	Para F2	1 st round	66.5	GGATCATCACGATATGATAAGGGACATGGC	GCTAAGCGTATCTTCAATAATCGAGCCAG

	Para F3	1 st round	59.2	GATCTCGAAGAAGAAGAAGGCG	AGCGCGTTTCAGGACGGATC
		2 nd round	70	CTCGAAGAAGAAGAAGGCGAAGAGC	GTTTCAGGACGGATCGAGACGG
	RyR	1 st round	60.8	GGATGACTCGAATTGCAGCCTATACTC	CAGCATCTTCAAACGATTGAGTGAG
Detoxification genes	CCE B	1 st round	59.2	CTGGATCGCTTCGGTTCAAG	GGCAATCCTCGTTTCCATCC
	CCE E	1 st round	60	AGCGAAGAAAATCAGCCGTG	CTTCCGATCTGTTTATTTAAGTTTAC
		2 nd round	62	GAAGAAAATCAGCCGTGTTTCGTAATG	CTGTTTATTTAAGTTTACAATTCGTCAGG
	CYP4G189	1 st round	60	GATCATTCAAGTGGCCTCATTGATAAG	CGATTCTATTCCATTGAGCTAGAAGG
		2 nd round	66.5	CATTCAAGTGGCCTCATTGATAAG	CTATTCCATTGAGCTAGAAGGAGG
	CYP6NP1	1 st round	63.7	ATCATTCCGCCGCATTGAACAGT	CCTGGAATCGAGTCTGGCACTTG
		2 nd round	60	CCGCCGCATTGAACAGTTTAACC	GAATCGAGTCTGGCACTTGG
	CYP6NQ1 N-ter	1 st round	62	GCACTAACTATGTTACTGTGGATTC	CTCGATTCACTTCTCGATCC
		2 nd round	60	GCACTAACTATGTTACTGTGGATTC	GGAGGATACTTCCGCAATGTTTC
	CYP6NQ1 C-ter	1 st round	62.5	TCATAGCGTTCTCGAATTGAATGAG	CGTAGGTACCGGATACTGGATAC
	CYP6NW1	1 st round	63.5	AACCGCGAGACCAATGGATCTCC	GCGCATGCGCACATTTATCCTTTC
	GST D	1 st round	55.6	ACTGCACACGCGTCCATTG	TCCATTTAGAGCACAGAAGTGTAGG
		2 nd round	60	GCACACGCGTCCATTGGAATATC	GAGCACAGAAGTGTAGGTATTATTG
	Control genes	Actin	1 st round	58.5	GCTCTTCCGATCTCCTACAGCAC
EF1alpha		1 st round	66.5	GGGTACAAAGGAGCAATCGGC	GAAAGAGGGAGGAGTCTACAGCTC
GAPDH		1 st round	63.5	CATTAACCTTGCCGTGTCATCAGCC	GTTCTTACAGTGAGTGGGCTTACTGC

Table S2. Primers used in quantitative real-time PCR

Gene Category	Gene Name	Forward Primer	Reverse Primer	Amplicon size (bp)	PCR efficiency (%)
Insecticide target genes	Ace 1	CACGAGGTGGTCAGATGTCT	TGGGGATTTCGAGGATCATGG	86	101
	nAChR α 1	GGATTTTCACGGTGGCTTGT	CTCCGGACCCATCATCATC	144	110
	nAChR α 3	CGGATGGCAATTTTCGAGGTG	CCACGTCTATTTTCGCACGAG	111	98
	nAChR β 2	CACCTTCCTAACAGTTCTCGTT	GAAAGCAAGATGGACACGCA	81	101
Detoxification genes	CCE B	CTGGATCGCTTCGGTTCAAG	GGCAATCCTCGTTTCCATCC	132	105
	CCE E	ATCCTGTGCCCGCCAAAC	CTGGATTCTTAGGAGTGAACAC	150	105
	CYP4G189	TGGAAACGGCTATGGGAGTT	ATGTGGCGGGTATGGAGAAT	100	96
	CYP6NP1	TCCCTGATCCCGAACGTTTC	ACAATTTTCGTGGTCCCTTCGC	104	104
	CYP6NQ1	CCTGTTATCACGCTTCGGAA	TTCTGGACCACGCAACAAAA	132	115
	CYP6NW1	CGTACTCCGCCAATTAACGA	CAGATGTGAACGTGGGTGAC	112	104
	GST D	TGCCGATTGACCTGTACTACT	TGCAGTTTAACGTCCAGGGA	85	110
Control genes	Actin	GGCTGTGCTCTCGTTGTATG	AGTCAGATCACGACCAGCAA	148	103
	EF1 alpha	CAGTGAGAGCTTCGTGATGC	CAGTCGGTTCGAGTTGAAACC	114	103
	GAPDH	TGGTAGAGGTGCTGCTCAAA	ACAGGTACACGGAAAGCCAT	117	101

	<u>Loop A</u>	<u>Loop E</u>	
<i>Forficula auricularia</i> α1	92 WNPEDYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAILHHTGKVVWK	PPAIYKSFCEIDVEYFPFDEQTCFMKFG	172
<i>Forficula auricularia</i> α1 mut	WNPEDYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAILHHTGKVVWK	H PAIYKSFCEIDVEYFPFDEQTCFMKFG	
<i>Drosophila melanogaster</i> α1	WNPDDYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAILHHTGKVVWK	PPAIXKSFCEIDVEYFPFDEQTCFMKFG	
<i>Myzus persicae</i> α1	WEPLEYGGVKELYVPSEHIWLPDIVLYNNADGEYVVTMTKAVLHHSKGVMWT	PPAIFKSSCEIDVRYFPFDQTCFMKFG	
<i>Bombyx mori</i> α1	WNPDDYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAILHHDGKVVWK	PPAIXKSFCEIDVEYFPFDEQTCFMKFG	
<i>Nilaparvata lugens</i> α1	WNPDEYGGVDTLHVPSEHIWLPDIVLYNNADGNYEVTIMTKAILHHTGKVVWK	PPAIXKSFCEIDVEYFPFDEQTCFMKFG	
<i>Drosophila melanogaster</i> α6	WNETEYGGVKDLRITPNKLWKPDLVLMYNSADEGFDGTYHTNIVVKHNGSCLYV	PPGIFKSTCKIDITWFPFDDQHCEMKFG	
<i>Apis mellifera</i> α6	WNESEYGGVKDLRITPNKLWKPDLVLMYNSADEGFDGTYQTNVVVTHNGSCLYV	PPGIFKSTCKIDITWFPFDDQHCDMKFG	
<i>Homo sapiens</i> α6	WDPMEYDGIETLRVPADKIWKPDIVLYNNAVGDFQVEGKTKALLKYNGMITWT	PPAIFKSSCPMDITFFPFDDHQNCSLKF	
	<u>Loop A</u>	<u>Loop E</u>	
<i>Forficula auricularia</i> β2	95 WDPEEYGGVEMLYVPSEHIWLPDIVLYNNADGNYEVTLMTKATLKYNGEVFWK	PPAIYKSSCRINVEYFPFDEQSCMMKFG	175
<i>Forficula Auricularia</i> β2 mut	WDPEEYGRVEMLYVPSEHIWLPDIVLYNNADGNYEVTLMTKATLKYNGEVFWK	PPAIYKSSCRINVEYFPFDEQSCMMKFG	
<i>Drosophila melanogaster</i> β2	WDPEEYGGVEQLYVPSEHIWLPDIVLYNNWDGNYEVTLMTKATLKYTGEVFWEP	PPAIYKSSCEMNVEYFPYDEQICFMKFG	
<i>Diabrotica virgifera</i> v. β2	WDPEEYGGVEMLYVPSEHIWLPDIVLFNNADGNYEVTLMTKATLSYTG	EVWIKPPSIYKSSCEINVQYFPFDEQSCLMKFG	
<i>Homo sapiens</i> β2	WKPEEFDNMKKVRLPSKHIWLPDVVLYNNADGMYEVSFYSNVVSVDGSIFWL	PPAIYKSACKIEVKHFPFDDQQNCTMKFR	

Figure S1: Multiple sequence alignments of part of the N-terminal domain containing loops A and E of insects and human nAChR subunits. The two cysteines of the Cys-loop motif (CX₁₃C) are highlighted in grey, the position of Faα1 P145H and Faβ2 G102R are in bold. Sequences were retrieved from Genbank Dmα1 NP_524481, Mpα1 CAA57476, Bmα1 ABV45511, Nlα1 BBE49554, Dmα6 NP_723494, Apα6 NP_001073564, Hsα6 CAD88994, Dmβ2 NP_524483, Dvβ2 XP028137095, Hsβ2 AAD45422