

GEPHE SUMMARY

	Gephebase Gene	GepheID
para (kdr) (<a +para+(kdr)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+para+(kdr)+"#gephebase-summary-title)	GP00000829	
	Entry Status	Martin
Published		Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (insecticide) (<a +xenobiotic+resistance+(insecticide)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Xenobiotic+resistance+(insecticide)+"#gephebase-summary-title)			
	Trait State in Taxon A		
Culex pipiens			
	Trait State in Taxon B		
Culex pipiens - resistant - allele 2			
	Ancestral State		
Taxon A			
	Taxonomic Status		
Intraspecific (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
		Taxon B	
	Latin Name		Latin Name
Culex pipiens (<a +culex+pipiens+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Culex+pipiens+"#gephebase-summary-title)		Culex pipiens (<a +culex+pipiens+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Culex+pipiens+"#gephebase-summary-title)	
	Common Name		Common Name
northern house mosquito		northern house mosquito	
	Synonyms		Synonyms
Culex agilis; Culex autogenicus; Culex azoriensis; Culex bicolor; Culex bifurcatus; Culex calcitrans; Culex calloti; Culex comitatus; Culex consobrinus; Culex dipseticus; Culex disjunctus; Culex doliorum; Culex domesticus; Culex erectus; Culex fasciatus; Culex haematophagus; Culex longefurcatus; Culex luteus; Culex marginalis; Culex melanorhinus; Culex meridionalis; Culex osakaensis; Culex pallipes; Culex phytophagus; Culex quasimodestus; Culex rufinus; Culex rufus; Culex sternopunctatus; Culex thoracicus; Culex torridus; Culex trifurcatus; Culex unistriatus; Culex varioannulatus; northern house mosquito; Culex pipiens Linnaeus, 1758		Culex agilis; Culex autogenicus; Culex azoriensis; Culex bicolor; Culex bifurcatus; Culex calcitrans; Culex calloti; Culex comitatus; Culex consobrinus; Culex dipseticus; Culex disjunctus; Culex doliorum; Culex domesticus; Culex erectus; Culex fasciatus; Culex haematophagus; Culex longefurcatus; Culex luteus; Culex marginalis; Culex melanorhinus; Culex meridionalis; Culex osakaensis; Culex pallipes; Culex phytophagus; Culex quasimodestus; Culex rufinus; Culex rufus; Culex sternopunctatus; Culex thoracicus; Culex torridus; Culex trifurcatus; Culex unistriatus; Culex varioannulatus; northern house mosquito; Culex pipiens Linnaeus, 1758	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Culicinae; Culicini; Culex; Culex; Culex pipiens complex		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Culicinae; Culicini; Culex; Culex; Culex pipiens complex	
	Parent		Parent
Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105)		Culex pipiens complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=518105)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7175 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7175)		7175 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7175)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
para	P35500 (http://www.uniprot.org/uniprot/P35500)	
	Synonyms	GenebankID or UniProtKB
bas; bss; CG9907; Dmel\CG9907; DmNav; DmNav1; DmNa[[v]]; DmNa[[V]]; DmNa[[v]]1; l(1)14Da; l(1)ESH548; lincRNA.S9469; Nav1; Ocd; olfD; par; sbl; sbl-1; Shu; Shudderer	AAS89995 (https://www.ncbi.nlm.nih.gov/nuccore/AAS89995)	
	String	
7227.FBpp0303597 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597)		
	Sequence Similarities	
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.		

GO - Molecular Function

GO:0005509 : calcium ion binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005509>)
GO:0005244 : voltage-gated ion channel activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005244>)
GO:0005248 : voltage-gated sodium channel activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005248>)
GO:0005272 : sodium channel activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005272>)

GO - Biological Process

GO:0045433 : male courtship behavior, veined wing generated song production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045433>)
GO:0001666 : response to hypoxia (<https://www.ebi.ac.uk/QuickGO/term/GO:0001666>)
GO:0009612 : response to mechanical stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009612>)
GO:0034765 : regulation of ion transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034765>)
GO:0035725 : sodium ion transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035725>)
GO:0007638 : mechanosensory behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007638>)
GO:0060078 : regulation of postsynaptic membrane potential
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060078>)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0001518 : voltage-gated sodium channel complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001518>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
L1014S	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title)	Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Molecular ecology of pyrethroid knockdown resistance in <i>Culex pipiens pallens</i> mosquitoes. (2010) (https://pubmed.ncbi.nlm.nih.gov/20657783)	Main Reference
Chen L; Zhong D; Zhang D; Shi L; Zhou G; Gong M; Zhou H; Sun Y; Ma L; He J; Hong S; Zhou D; Xiong C; Chen C; Zou P; Zhu C; Yan G	Authors
Pyrethroid insecticides have been extensively used in China and worldwide for public health pest control. Accurate resistance monitoring is essential to guide the rational use of insecticides and resistance management. Here we examined the nucleotide diversity of the para-sodium channel gene, which confers knockdown resistance (kdr) in <i>Culex pipiens pallens</i> mosquitoes in China. The sequence analysis of the para-sodium channel gene identified L1014F and L1014S mutations. We developed and validated allele-specific PCR and the real-time TaqMan methods for resistance diagnosis. The real-time TaqMan method is more superior to the allele-specific PCR method as evidenced by higher amplification rate and better sensitivity and specificity. Significant positive correlation between kdr allele frequency and bioassay-based resistance phenotype demonstrates that the frequency of L1014F and L1014S mutations in the kdr gene can be used as a molecular marker for deltamethrin resistance monitoring in natural <i>Cx. pipiens pallens</i> populations in the East China region. The laboratory selection experiment found that L1014F mutation frequency, but not L1014S mutation, responded to deltamethrin selection, suggesting that the L1014F mutation is the key mutation conferring resistance to deltamethrin. High L1014F mutation frequency detected in six populations of <i>Cx. pipiens pallens</i> suggests high prevalence of pyrethroid resistance in Eastern China, calling for further surveys to map the resistance in China and for investigating alternative mosquito control strategies.	Abstract
	Additional References

RELATED GEPHE

5 (Acetylcholinesterase (Ace-1), Cpm1, esterase A8 and B8, esterase B4, esterase B5) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~7175^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)	Related Genes
2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~para (kdr)^/and+Taxon ID=~7175^/or+Gene Gephebase=~para (kdr)^/and+Taxon ID=~7175^#gephebase-summary-title)	Related Haplotypes

EXTERNAL LINKS

COMMENTS