

GEPHE SUMMARY

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)	Gephebase Gene	GP00002522	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

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 Category		
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		
Anopheles stephensi - Sensitive to Pyrethroids	Trait State in Taxon A		
Anopheles stephensi - Resistant to Pyrethroids	Trait State in Taxon B		
Taxon A	Ancestral State		
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)	Taxonomic Status		
	Taxon A	Taxon B	
Anopheles stephensi (<a +anopheles+stephensi+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Anopheles stephensi+"#gephebase-summary-title)	Latin Name	Anopheles stephensi (<a +anopheles+stephensi+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="+Anopheles stephensi+"#gephebase-summary-title)	Latin Name
Asian malaria mosquito	Common Name	Asian malaria mosquito	Common Name
Anopheles mysorensis; Anopheles stephensi mysorensis; Anopheles stephensi var. mysorensis; Neocellia intermedia; Neocellia intermedia Rothwell, 1907; Asian malaria mosquito; Anopheles stephensi Liston, 1901; Anopheles stephensis	Synonyms	Anopheles mysorensis; Anopheles stephensi mysorensis; Anopheles stephensi var. mysorensis; Neocellia intermedia; Neocellia intermedia Rothwell, 1907; Asian malaria mosquito; Anopheles stephensi Liston, 1901; Anopheles stephensis	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Neocellia	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Neocellia	Lineage
Neocellia () - (Rank: clade) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=44535)	Parent	Neocellia () - (Rank: clade) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=44535)	Parent
30069 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=30069)	NCBI Taxonomy ID	30069 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=30069)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

para	Generic Gene Name	P35500 (http://www.uniprot.org/uniprot/P35500)	UniProtKB Drosophila melanogaster
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	Synonyms	()	GenebankID or UniProtKB
7227.FBpp0303597 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303597)	String		
Belongs to the sodium channel (TC 1.A.1.10) family. Para subfamily.	Sequence Similarities		
GO:0005509 : calcium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005509)	GO - Molecular Function		
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>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title>)

Aberration Type

SNP (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^SNP^#gephebase-summary-title>)

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

L1014S

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title>)

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Leu	Ser	1014

Main Reference

Status of insecticide resistance and its biochemical and molecular mechanisms in *Anopheles stephensi* (Diptera: Culicidae) from Afghanistan. (2019)

(<https://pubmed.ncbi.nlm.nih.gov/31349836>)

Authors

Safi NHZ; Ahmadi AA; Nahzat S; Warusavithana S; Safi N; Valadan R; Shemshadian A; Sharifi M; Enayati A; Hemingway J

Abstract

Insecticide resistance of *Anopheles stephensi*, the main malaria vector in eastern Afghanistan, has been reported previously. This study describes the biochemical and molecular mechanisms of resistance to facilitate effective vector control and insecticide resistance management.

Mosquito larvae were collected from the provinces of Kunar, Laghman and Nangarhar from 2014 to 2017. The susceptibility of the reared 3-4 days old adults was tested with deltamethrin 0.05%, bendiocarb 0.1%, malathion 5%, permethrin 0.75% and DDT 4%. Cytochrome P450 content and general esterase, glutathione S-transferase (GST) and acetylcholinesterase (AChE) activities were measured in the three field populations and the results were compared with those of the laboratory susceptible *An. stephensi* Beech strain. Two separate allele-specific PCR assays were used to identify L1014, L1014F and L1014S mutations in the voltage gated sodium channel gene of *An. stephensi*. Probit analysis, ANOVA and Hardy-Weinberg equilibrium were used to analyse bioassay, biochemical assay and gene frequency data respectively.

The population of *An. stephensi* from Kunar was susceptible to bendiocarb, apart from this, all populations were resistant to all the other insecticides tested. The differences between all values for cytochrome P450s, general esterases, GSTs and AChE inhibition rates in the Kunar, Laghman and Nangarhar populations were statistically significant when compared to the Beech strain, excluding GST activities between Kunar and Beech due to the high standard deviation in Kunar. The three different sodium channel alleles [L1014 (wild type), L1014F (kdr west) and L1014S (kdr east)] were all segregated in the Afghan populations. The frequencies of kdr east mutation were 22.9%, 32.7% and 35% in Kunar, Laghman and Nangarhar populations respectively. Kdr west was at the lowest frequency of 4.44%.

Resistance to different groups of insecticides in the field populations of *An. stephensi* from Kunar, Laghman and Nangarhar Provinces of Afghanistan is caused by a range of metabolic and site insensitivity mechanisms, including esterases, cytochrome P450s and GSTs combined with AChE and sodium channel target site insensitivity. The intensity and frequency of these mechanisms are increasing in these populations, calling for urgent reorientation of vector control programmes and implementation of insecticide resistance management strategies.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^30069^/or+Gene Gephebase=^para \(kdr\)^/and+Taxon ID=^30069^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^30069^/or+Gene Gephebase=^para (kdr)^/and+Taxon ID=^30069^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@Parallelism