

GEPHE SUMMARY

ABCb4 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ABCb4^#gephebase-summary-title)	Gephebase Gene	GP00002607	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category		
Xenobiotic resistance (insecticide) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(insecticide)^#gephebase-summary-title)	Trait		
Aedes aegypti	Trait State in Taxon A		
Aedes aegypti - resistant strain from the Caribbean	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Aedes aegypti (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Aedes+aegypti^#gephebase-summary-title)	Latin Name	Aedes aegypti (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Aedes+aegypti^#gephebase-summary-title)	Latin Name
yellow fever mosquito	Common Name	yellow fever mosquito	Common Name
Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)	Synonyms	Stegomyia aegypti; yellow fever mosquito; Aedes aegypti (Linnaeus, 1762)	Synonyms
species	Rank	species	Rank
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; Aedini; Aedes; Stegomyia	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; Aedini; Aedes; Stegomyia	Lineage
Stegomyia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541)	Parent	Stegomyia () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=53541)	Parent
7159 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159)	NCBI Taxonomy ID	7159 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7159)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

Abcb4	Generic Gene Name	P21440 (http://www.uniprot.org/uniprot/P21440)	UniProtKB Mus musculus
Mdr2; Pgy2; Pgy-2; mdr-2	Synonyms	()	GenebankID or UniProtKB
10090.ENSMUSP00000003717 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000003717)	String		
Belongs to the ABC transporter superfamily. ABCB family. Multidrug resistance exporter (TC 3.A.1.201) subfamily.	Sequence Similarities		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)	GO - Molecular Function		
GO:0042626 : ATPase activity, coupled to transmembrane movement of substances (https://www.ebi.ac.uk/QuickGO/term/GO:0042626)			
GO:0008525 : phosphatidylcholine transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008525)			
GO:0090554 : phosphatidylcholine-translocating ATPase activity			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0090554>)

GO - Biological Process

- GO:0032782 : bile acid secretion (<https://www.ebi.ac.uk/QuickGO/term/GO:0032782>)
- GO:1903413 : cellular response to bile acid (<https://www.ebi.ac.uk/QuickGO/term/GO:1903413>)
- GO:0055088 : lipid homeostasis (<https://www.ebi.ac.uk/QuickGO/term/GO:0055088>)
- GO:0045332 : phospholipid translocation (<https://www.ebi.ac.uk/QuickGO/term/GO:0045332>)
- GO:0032376 : positive regulation of cholesterol transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0032376>)
- GO:0061092 : positive regulation of phospholipid translocation (<https://www.ebi.ac.uk/QuickGO/term/GO:0061092>)
- GO:2001140 : positive regulation of phospholipid transport (<https://www.ebi.ac.uk/QuickGO/term/GO:2001140>)
- GO:1901557 : response to fenofibrate (<https://www.ebi.ac.uk/QuickGO/term/GO:1901557>)

GO - Cellular Component

- GO:0016021 : integral component of membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
- GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
- GO:0015629 : actin cytoskeleton (<https://www.ebi.ac.uk/QuickGO/term/GO:0015629>)
- GO:0016324 : apical plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016324>)
- GO:0030136 : clathrin-coated vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0030136>)
- GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
- GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
- GO:0005925 : focal adhesion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005925>)
- GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
- GO:0046581 : intercellular canalculus (<https://www.ebi.ac.uk/QuickGO/term/GO:0046581>)
- GO:0016020 : membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0016020>)
- GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)
- GO:0005654 : nucleoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005654>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~No~#gephebase-summary-title))

Molecular Type

Gene Amplification ([https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Amplification~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type=~Gene+Amplification~#gephebase-summary-title))

Aberration Type

Insertion ([https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~Insertion~#gephebase-summary-title))

Insertion Size

unknown

Molecular Details of the Mutation

ABCB4 gene amplified about 6â€”7 times

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene~#gephebase-summary-title))

Main Reference

Gene amplification, ABC transporters and cytochrome P450s: unraveling the molecular basis of pyrethroid resistance in the dengue vector, *Aedes aegypti*. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22720108>)

Authors

Bariami V; Jones CM; Poupardin R; Vontas J; Ranson H

Abstract

Pyrethroid insecticides are widely utilized in dengue control. However, the major vector, *Aedes aegypti*, is becoming increasingly resistant to these insecticides and this is impacting on the efficacy of control measures. The near complete transcriptome of two pyrethroid resistant populations from the Caribbean was examined to explore the molecular basis of this resistance.

Two previously described target site mutations, 1016I and 1534C were detected in pyrethroid resistant populations from Grand Cayman and Cuba. In addition between two and five per cent of the *Ae. aegypti* transcriptome was differentially expressed in the resistant populations compared to a laboratory susceptible population. Approximately 20 per cent of the genes over-expressed in resistant mosquitoes were up-regulated in both Caribbean populations (107 genes). Genes with putative monooxygenase activity were significantly over represented in the up-regulated subset, including five CYP9 P450 genes. Quantitative PCR was used to confirm the higher transcript levels of multiple cytochrome P450 genes from the CYP9J family and an ATP binding cassette transporter. Over expression of two genes, CYP9J26 and ABCB4, is due, at least in part, to gene amplification.

These results, and those from other studies, strongly suggest that increases in the amount of the CYP9J cytochrome P450s are an important mechanism of pyrethroid resistance in *Ae. aegypti*. The genetic redundancy resulting from the expansion of this gene family makes it unlikely that a single gene or mutation responsible for pyrethroid resistance will be identified in this mosquito species. However, the results from this study do pave the way for the development of new pyrethroid synergists and improved resistance diagnostics. The role of copy number polymorphisms in detoxification and transporter genes in providing protection against insecticide exposure requires further investigation.

Additional References

RELATED GEPHE

Related Genes

4 (CYP9J26, CYP9M6, para (kdr), resistance to dieldrin) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~7159~/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~7159~/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS