GEPHE SUMMARY

Gephebase Gene

resistance to dieldrin (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^resistance to dieldrin^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00002557

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Xenobiotic resistance (insecticide) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic resistance (insecticide)^#gephebase-summary-title)

Trait State in Taxon A

Anopheles funestus

Trait State in Taxon B

Anopheles funestus - resistant

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Anopheles funestus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles funestus^#gephebase-summary-title)

Common Name

African malaria mosquito

Synonyms

African malaria mosquito; Anopheles funestus Giles, 1900

Rank

species

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; Anophelinae; Anopheles; Cellia; Myzomyia; funestus group; funestus subgroup

Parent

funestus subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62323)

NCBI Taxonomy ID

62324 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62324)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Anopheles funestus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Anopheles funestus^#gephebase-summary-title)

Common Name

African malaria mosquito

Synonyms

African malaria mosquito; Anopheles funestus Giles, 1900

Rank

species

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; Anophelinae; Anopheles; Cellia; Myzomyia; funestus group; funestus subgroup

Parent

funestus subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62323)

NCBI Taxonomy ID

62324 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62324)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

Rdl

Synonyms

CG10537; CT29555; Dmel\CG10537; DmRdl; DmRDL; gaba; GABA; GABA-R; GABAr; GABA[[A]]; GABA[[A]] receptor; GABA[[A]]-R; GABA[[A]]R; LCCH1; Rd1; rdl; RDL

String

7227.FBpp0305970 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0305970)

Sequence Similarities

Belongs to the ligand-gated ion channel (TC 1.A.9) family. Gamma-aminobutyric acid receptor (TC 1.A.9.5) subfamily.

GO - Molecular Function

GO:0004890 : GABA-A receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004890)

GO:0022851 : GABA-gated chloride ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0022851)

UniProtKB Drosophila melanogaster

P25123 (http://www.uniprot.org/uniprot/P25123)

GenebankID or UniProtKB

()

GO:0030594 : neurotransmitter receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0030594)

GO - Biological Process

GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0007268 : chemical synaptic transmission
(https://www.ebi.ac.uk/QuickGO/term/GO:0007268)
GO:0034220 : ion transmembrane transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0034220)
GO:0042493 : response to drug (https://www.ebi.ac.uk/QuickGO/term/GO:0042493)
GO:0050877 : nervous system process
(https://www.ebi.ac.uk/QuickGO/term/GO:0050877)
GO:0042391 : regulation of membrane potential
(https://www.ebi.ac.uk/QuickGO/term/GO:0042391)
GO:0006811 : ion transport (https://www.ebi.ac.uk/QuickGO/term/GO:0006811)
GO:0042048 : olfactory behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0042048)
GO:0030431 : sleep (https://www.ebi.ac.uk/QuickGO/term/GO:0030431)
GO:0009612 : response to mechanical stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009612)
GO:0002121 : inter-male aggressive behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0002121)
GO:0050805 : negative regulation of synaptic transmission
(https://www.ebi.ac.uk/QuickGO/term/GO:0050805)
GO:0042749 : regulation of circadian sleep/wake cycle
(https://www.ebi.ac.uk/QuickGO/term/GO:0042749)
GO:0090328 : regulation of olfactory learning
(https://www.ebi.ac.uk/QuickGO/term/GO:0090328)

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:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0030054 : cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0030054)
GO:0030425 : dendrite (https://www.ebi.ac.uk/QuickGO/term/GO:0030425)
GO:0043005 : neuron projection (https://www.ebi.ac.uk/QuickGO/term/GO:0043005)
GO:0030424 : axon (https://www.ebi.ac.uk/QuickGO/term/GO:0030424)
GO:0045211 : postsynaptic membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0045211)
GO:0045202 : synapse (https://www.ebi.ac.uk/QuickGO/term/GO:0045202)
GO:0034707 : chloride channel complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0034707)
GO:0032589 : neuron projection membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0032589)
GO:0032809 : neuronal cell body membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0032809)

Mutation #1

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

A296S = A301S + V327I = V332I

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	-	-	-

Main Reference

Identification and distribution of a GABA receptor mutation conferring dieldrin resistance in the malaria vector Anopheles funestus in Africa. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21501685)

Authors

Wondji CS; Dabire RK; Tukur Z; Irving H; Djouaka R; Morgan JC

Abstract

Growing problems of pyrethroid resistance in Anopheles funestus have intensified efforts to identify alternative insecticides. Many agrochemicals target the GABA receptors, but cross-resistance from dieldrin resistance may preclude their introduction. Dieldrin resistance was detected in An. funestus populations from West (Burkina Faso) and central (Cameroon) Africa, but populations from East (Uganda) and Southern Africa (Mozambique and Malawi) were fully susceptible to this insecticide. Partial sequencing of the dieldrin target site, the Î³-aminobutyric acid (GABA) receptor, identified two amino acid substitutions, A296S and V327I. The A296S mutation has been associated with dieldrin resistance in other species. The V327I mutations was detected in the resistant sample from Burkina Faso and Cameroon and consistently associated with the A296S substitution. The full-length of the An. funestus

GABA-receptor gene, amplified by RT-PCR, generated a sequence of 1674Â bp encoding 557 amino acid of the protein in An. funestus with 98% similarity to that of Anopheles gambiae. Two diagnostic assays were developed to genotype the A296S mutation (pyrosequencing and PCR-RFLP), and use of these assays revealed high frequency of the resistant allele in Burkina Faso (60%) and Cameroon (82%), moderate level in Benin (16%) while low frequency or absence of the mutation was observed respectively in Uganda (7.5%) or 0% in Malawi and Mozambique. The distribution of the Rdl(R) mutation in An. funestus populations in Africa suggests extensive barriers to gene flow between populations from different regions.

Additional References

Mutation #2

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

A296S = A301S + V327I = V332I

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	-	-	-

Main Reference

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Authors

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Abstract

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Additional References

RELATED GEPHE

Related Genes

3 (CYP6P9 cluster (CYP6P9a and CYP6P9b), CYP6P9; CYP6P4 cluster, GSTe) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^62324^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS