

GEPHE SUMMARY

| | | |
|---|----------------|--------------|
| | Gephebase Gene | GephelD |
| Acetylcholinesterase (Ace-1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Acetylcholinesterase (Ace-1)^#gephebase-summary-title) | GP00001373 | Main curator |
| Published | Entry Status | Prigent |

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 gambiae Mosquitoes- Acerduplikis ; resistant to OP and CX insecticides ; slightly lower viability than wildtype | Trait State in Taxon B |
| Anopheles gambiae Mosquitoes- AcerKisR3 ; more resistant to OP and CX insecticides ; much lower viability and fertility than wildtype | Ancestral State |

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

| Taxon A | Latin Name |
|--|-------------|
| Anopheles gambiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Anopheles+gambiae^#gephebase-summary-title) | |
| African malaria mosquito | Common Name |
| Anopheles gambiae S; African malaria mosquito; Anopheles gambiae Giles, 1902; Anopheles gambia | Synonyms |
| species | Rank |

| | |
|--|------------------|
| | Lineage |
| cellular organisms; Eukaryota; Opistokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Nematocera; Culicomorpha; Culicoidea; Culicidae; Anophelinae; Anopheles; Cellia; Pyretophorus; gambiae species complex | |
| gambiae species complex () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 44542) | Parent |
| 7165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7165) | NCBI Taxonomy ID |

| | |
|---|---|
| is Taxon A an Infraspecies? | Taxon A Description |
| Yes | Anopheles gambiae Mosquitoes- Acerduplikis ; resistant to OP and CX insecticides ; slightly lower viability than wildtype |
| 7165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7165) | NCBI Taxonomy ID |

| | |
|---|---|
| is Taxon B an Infraspecies? | Taxon B Description |
| Yes | Anopheles gambiae Mosquitoes- AcerKisR3 ; more resistant to OP and CX insecticides ; much lower viability and fertility than wildtype |
| 7165 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7165) | NCBI Taxonomy ID |

GENOTYPIC CHANGE

| | | |
|---|-----------------------|--|
| | Generic Gene Name | UniProtKB Drosophila melanogaster |
| Ace | Synonyms | P07140 (http://www.uniprot.org/uniprot/P07140) |
| AcChE; ace; ACE; ace-2;ache; AchE; AChE; CG17907; CHE; dAChE; dmAChE; DmAChE; Dmel\CG17907; Dm_ace; FBgn0000024; l(3)26; l(3)87Ed | String | GenebankID or UniProtKB |
| 7227.FBpp0289713 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0289713) | Sequence Similarities | 0 |
| Belongs to the type-B carboxylesterase/lipase family. | | |

GO:0042803 : protein homodimerization activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042803>)

GO:0003990 : acetylcholinesterase activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0003990>)

GO:0004104 : cholinesterase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0004104>)

GO:0043199 : sulfate binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0043199>)

GO - Biological Process

GO:0006581 : acetylcholine catabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006581>)

GO:0001507 : acetylcholine catabolic process in synaptic cleft

(<https://www.ebi.ac.uk/QuickGO/term/GO:0001507>)

GO:0007268 : chemical synaptic transmission

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007268>)

GO:0042426 : choline catabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042426>)

GO:0042331 : phototaxis (<https://www.ebi.ac.uk/QuickGO/term/GO:0042331>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

GO:0031225 : anchored component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0031225>)

GO:0030054 : cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0030054>)

GO:0043083 : synaptic cleft (<https://www.ebi.ac.uk/QuickGO/term/GO:0043083>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

100-1000 kb

Molecular Details of the Mutation

Strict tandem 3 times duplication of 203kb encompassing 12 genes with partial internal deletion of 97kb in the third copy - ace1 homogeneous gene duplications (all 3 copies S119 resistant)

Experimental Evidence

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

Main Reference

The ace-1 Locus Is Amplified in All Resistant Anopheles gambiae Mosquitoes: Fitness Consequences of Homogeneous and Heterogeneous Duplications. (2016)

(<https://pubmed.ncbi.nlm.nih.gov/27918584/>)

Authors

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Abstract

Gene copy-number variations are widespread in natural populations, but investigating their phenotypic consequences requires contemporary duplications under selection. Such duplications have been found at the ace-1 locus (encoding the organophosphate and carbamate insecticides' target) in the mosquito *Anopheles gambiae* (the major malaria vector); recent studies have revealed their intriguing complexity, consistent with the involvement of various numbers and types (susceptible or resistant to insecticide) of copies. We used an integrative approach, from genome to phenotype level, to investigate the influence of duplication architecture and gene-dosage on mosquito fitness. We found that both heterogeneous (i.e., one susceptible and one resistant ace-1 copy) and homogeneous (i.e., identical resistant copies) duplications segregated in field populations. The number of copies in homogeneous duplications was variable and positively correlated with acetylcholinesterase activity and resistance level. Determining the genomic structure of the duplicated region revealed that, in both types of duplication, ace-1 and 11 other genes formed tandem 203kb amplicons. We developed a diagnostic test for duplications, which showed that ace-1 was amplified in all 173 resistant mosquitoes analyzed (field-collected in several African countries), in heterogeneous or homogeneous duplications. Each type was associated with different fitness trade-offs: heterogeneous duplications conferred an intermediate phenotype (lower resistance and fitness costs), whereas homogeneous duplications tended to increase both resistance and fitness cost, in a complex manner. The type of duplication selected seemed thus to depend on the intensity and distribution of selection pressures. This versatility of trade-offs available through gene duplication highlights the importance of large mutation events in adaptation to environmental variation. This impressive adaptability could have a major impact on vector control in Africa.

Additional References

RELATED GEPHE

Related Genes

3 (para (kdr), resistance to dieldrin, SAP-2) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7165^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true))

Related Haplotypes

3 ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^Acetylcholinesterase+(Ace-1)^/and+Taxon+ID=^7165^/or+Gene+Gephebase=^Acetylcholinesterase+(Ace-1)^/and+Taxon+ID=^7165^))

EXTERNAL LINKS

COMMENTS

@GxE - This triplication probably does not derived from the S/R duplication

