GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00000228

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Drosophila simulans

Trait State in Taxon B

Drosophila simulans - resistant to Providencia rettgeri (Gram- bacteria)

Ancestral State

Data not curated

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

-

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

-

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Diptera; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

DptA

Synonyms

143443_at; CG12763; Dep; DIM 27; dip; Dip; dipt; Dipt; DIPT; diptA; DiptA; Dit; Dmel\CG12763; dpt; Dpt; DPT

String

7227.FBpp0085802 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0085802)

Sequence Similarities

Belongs to the attacin/sarcotoxin-2 family.

GO - Molecular Function

-

GO - Biological Process

GO:0019731 : antibacterial humoral response (https://www.ebi.ac.uk/QuickGO/term/GO:0019731)

UniProtKB Drosophila melanogaster

P24492 (http://www.uniprot.org/uniprot/P24492)

GenebankID or UniProtKB

KU200261 (https://www.ncbi.nlm.nih.gov/nuccore/KU200261)

GO:0045087 : innate immune response
(https://www.ebi.ac.uk/QuickGO/term/GO:0045087)
GO:0009617 : response to bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0009617)
GO:0042742 : defense response to bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0042742)
GO:0050829 : defense response to Gram-negative bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0050829)
GO:0050830 : defense response to Gram-positive bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0050830)
GO:0045089 : positive regulation of innate immune response
(https://www.ebi.ac.uk/QuickGO/term/GO:0045089)
GO:0055093 : response to hyperoxia (https://www.ebi.ac.uk/QuickGO/term/GO:0055093)

GO - Cellular Component

GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)

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

Ser>Arg (AGC>AGG)

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

Convergent Balancing Selection on an Antimicrobial Peptide in Drosophila. (2016) (https://pubmed.ncbi.nlm.nih.gov/26776733)

Authors

Unckless RL; Howick VM; Lazzaro BP

Abstract

Genes of the immune system often evolve rapidly and adaptively, presumably driven by antagonistic interactions with pathogens [1-4]. Those genes encoding secreted antimicrobial peptides (AMPs), however, have failed to exhibit conventional signatures of strong adaptive evolution, especially in arthropods (e.g., [5, 6]) and often segregate for null alleles and gene deletions [3, 4, 7, 8]. Furthermore, quantitative genetic studies have failed to associate naturally occurring polymorphism in AMP genes with variation in resistance to infection [9-11]. Both the lack of signatures of positive selection in AMPs and lack of association between genotype and immune phenotypes have yielded an interpretation that AMP genes evolve under relaxed evolutionary constraint, with enough functional redundancy that variation in, or even loss of, any particular peptide would have little effect on overall resistance [12, 13]. In stark contrast to the current paradigm, we identified a naturally occurring amino acid polymorphism in the AMP Diptericin that is highly predictive of resistance to bacterial infection in Drosophila melanogaster [13]. The identical amino acid polymorphism arose in parallel in the sister species D.Â simulans, by independent mutation with equivalent phenotypic effect. Convergent substitutions at the same amino acid residue have evolved at least five times across the Drosophila genus. We hypothesize that the alternative alleles are maintained by balancing selection through context-dependent or fluctuating selection. This pattern of evolution appears to be common in AMPs but is invisible to conventional screens for adaptive evolution that are predicated on elevated rates of amino acid divergence.

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Additional References

The potential for adaptive maintenance of diversity in insect antimicrobial peptides. (2016) (https://pubmed.ncbi.nlm.nih.gov/27160594)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@BalancingSelection ; Parallelism ; Tandem dulication and paralogous gene conversion ; similar pattern of evolution for another antimicrobial-peptide: attacin