

GEPHE SUMMARY

Gephebase Gene
Diptericin

Entry Status
Published

GepheID
GP00000228

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Pathogen resistance (bacteria)

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

	Taxon A	Taxon B
Latin Name	<i>Drosophila simulans</i>	<i>Drosophila simulans</i>
Common Name	-	-
Synonyms	-	-
Rank	species	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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup
Parent	melanogaster subgroup () - (Rank: species subgroup)	melanogaster subgroup () - (Rank: species subgroup)
NCBI Taxonomy ID	7240	7240
is Taxon A an Intraspecies?	No	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

Sequence Similarities
Belongs to the attacin/sarcotoxin-2 family.

GO - Molecular Function
-

GO - Biological Process
GO:0019731 : antibacterial humoral response
GO:0045087 : innate immune response
GO:0009617 : response to bacterium
GO:0042742 : defense response to bacterium
GO:0050829 : defense response to Gram-negative bacterium

UniProtKB Drosophila melanogaster
P24492

GenebankID or UniProtKB
KU200261

GO:0050830 : defense response to Gram-positive bacterium
GO:0045089 : positive regulation of innate immune response
GO:0055093 : response to hyperoxia

GO - Cellular Component
GO:0005615 : extracellular space

Presumptive Null
No

Molecular Type
Coding

Aberration Type
SNP

SNP Coding Change
Nonsynonymous

Molecular Details of the Mutation
Ser>Arg (AGC>AGG)

Experimental Evidence
Candidate Gene

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference
[Convergent Balancing Selection on an Antimicrobial Peptide in Drosophila. \(2016\)](#)

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. 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. \(2016\)](#)

RELATED GEPHE

Related Genes
No matches found.
Related Haplotypes
No matches found.

EXTERNAL LINKS

COMMENTS

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

