

GEPHE SUMMARY

Diptericin (#gephebase-summary-title)	Gephebase Gene	GP00000228	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

	Trait Category		
Physiology (#gephebase-summary-title)	Trait		
Pathogen resistance (bacteria) (<a and+taxonomicstatus='Intraspecific"' href="https://www.gephebase.org/search-criteria?/and+Trait=Pathogen%20resistance%20(bacteria)#gephebase-summary-title)</td><td>Trait State in Taxon A</td><td></td><td></td></tr> <tr> <td>Drosophila simulans</td><td>Trait State in Taxon B</td><td></td><td></td></tr> <tr> <td>Drosophila simulans - resistant to Providencia rettgeri (Gram- bacteria)</td><td>Ancestral State</td><td></td><td></td></tr> <tr> <td>Data not curated</td><td>Taxonomic Status</td><td></td><td></td></tr> <tr> <td>Intraspecific (#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Drosophila simulans (#gephebase-summary-title)		Drosophila simulans (#gephebase-summary-title)	
-	Common Name	-	Common Name
-	Synonyms	-	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; Brachycera; Muscomorpha; Eremoneura; Cyclorrhapha; Schizophora; Acalyptratae; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	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; Ephydriidae; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240)	NCBI Taxonomy ID	7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

DptA	Generic Gene Name	UniProtKB Drosophila melanogaster
143443_at; CG12763; Dep; DIM 27; dip; Dip; dipt; Dipt; DIPT; diptA; DptA; Dpt; Dmel\CG12763; dpt; Dpt; DPT	Synonyms	P24492 (http://www.uniprot.org/uniprot/P24492)
7227.FBpp0085802 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0085802)	String	GenebankID or UniProtKB
Belongs to the attacin/sarcotoxin-2 family.	Sequence Similarities	KU200261 (https://www.ncbi.nlm.nih.gov/nucleotide/KU200261)
-	GO - Molecular Function	
GO:0019731 : antibacterial humoral response (https://www.ebi.ac.uk/QuickGO/term/GO:0019731)	GO - Biological Process	

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	Presumptive Null
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)	
No (https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%22No%22#gephebase-summary-title)	Molecular Type
Coding (https://www.gephebase.org/search-criteria/?and+Molecular+Type=%22Coding%22#gephebase-summary-title)	Aberration Type
SNP (https://www.gephebase.org/search-criteria/?and+Aberration+Type=%22SNP%22#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=%22Candidate+Gene%22#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. 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.	
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

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

