

## GEPHE SUMMARY

Diptericin ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase=Diptericin">#gephebase-summary-title)	Gephebase Gene GP00000227	GephelD
	Entry Status Martin	Main curator
Published		

## PHENOTYPIC CHANGE

Trait Category		Trait	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=Physiology">#gephebase-summary-title)			
Pathogen resistance (bacteria) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Criteria?/and+Trait=^Pathogen resistance (bacteria)^#gephebase-summary-title)		Trait State in Taxon A	
Drosophila melanogaster		Trait State in Taxon B	
Drosophila melanogaster		Ancestral State	
Data not curated		Taxonomic Status	
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status=Intraspecific">#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Drosophila melanogaster ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title</a> )		Drosophila melanogaster ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title</a> )	
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melanogaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melanogaster	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; Ephydriodea; 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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )	Parent	melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )	Parent
7227 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227</a> )	NCBI Taxonomy ID	7227 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227</a> )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

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

(<https://www.ebi.ac.uk/QuickGO/term/GO:0019731>)  
 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>AGA)

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

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

The complex contributions of genetics and nutrition to immunity in *Drosophila melanogaster*. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25764027>)

Main Reference

Unckless RL; Rottschaefer SM; Lazzaro BP

Authors

Both malnutrition and undernutrition can lead to compromised immune defense in a diversity of animals, and “nutritional immunology” has been suggested as a means of understanding immunity and determining strategies for fighting infection. The genetic basis for the effects of diet on immunity, however, has been largely unknown. In the present study, we have conducted genome-wide association mapping in *Drosophila melanogaster* to identify the genetic basis for individual variation in resistance, and for variation in immunological sensitivity to diet (genotype-by-environment interaction, or GxE). *D. melanogaster* were reared for several generations on either high-glucose or low-glucose diets and then infected with *Providencia rettgeri*, a natural bacterial pathogen of *D. melanogaster*. Systemic pathogen load was measured at the peak of infection intensity, and several indicators of nutritional status were taken from uninfected flies reared on each diet. We find that dietary glucose level significantly alters the quality of immune defense, with elevated dietary glucose resulting in higher pathogen loads. The quality of immune defense is genetically variable within the sampled population, and we find genetic variation for immunological sensitivity to dietary glucose (genotype-by-diet interaction). Immune defense was genetically correlated with indicators of metabolic status in flies reared on the high-glucose diet, and we identified multiple genes that explain variation in immune defense, including several that have not been previously implicated in immune response but which are confirmed to alter pathogen load after RNAi knockdown. Our findings emphasize the importance of dietary composition to immune defense and reveal genes outside the conventional “immune system” that can be important in determining susceptibility to infection. Functional variation in these genes is segregating in a natural population, providing the substrate for evolutionary response to pathogen pressure in the context of nutritional environment.

Abstract

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

Additional References

## RELATED GEPHE

Related Genes  
 15 (18-wheeler, CG8492, Drosomycin-like 5, Ge-1, GNBP1, GNBP2, Immune deficiency, Lectin-24A, pastrel, PGRP-LC, ref(2)P, SR-CII, Tehao, Ubiquitin conjugating enzyme E2H (Ubc-E2H), CHKov1) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^7227^/and+Trait=Pathogen+resistance/and+groupHaplotypes=true#gephebase-summary-title>)  
 Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

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

