GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00000227

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 melanogaster

Trait State in Taxon B

Drosophila melanogaster

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

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

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

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

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

UniProtKB Drosophila melanogaster

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

GenebankID or UniProtKB

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

(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	-	-	-

Main Reference

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

Authors

Unckless RL; Rottschaefer SM; Lazzaro BP

Abstract

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.

Additional References

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

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