

GEPHE SUMMARY

	Gephebase Gene	GephelD
18-wheeler (https://www.gephebase.org/search-criteria?/and+Gene Gephebase^18-wheeler^#gephebase-summary-title)	GP00000001	Main curator
Published	Entry Status	Martin

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category^Physiology^#gephebase-summary-title)	Trait	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen resistance^#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		Taxon B
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms^Drosophila melanogaster^#gephebase-summary-title)	Latin Name	Latin Name
fruit fly	Common Name	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Synonyms
species	Rank	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	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	Parent	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
18w	Synonyms	A1ZBR2 (http://www.uniprot.org/uniprot/A1ZBR2)
18-w; 18-wheeler; 18W; CG8896; CT25100; Dmel\CG8896; l(2)00053; tlr; toll; Toll-2; Dmel_CG8896	String	GenebankID or UniProtKB AE013599 (https://www.ncbi.nlm.nih.gov/nuccore/AE013599)
7227.FBpp0085620 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0085620)	Sequence Similarities	
Belongs to the Toll-like receptor family.	GO - Molecular Function	
GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)	GO - Biological Process	

GO:0009653 : anatomical structure morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009653>)
 GO:0019731 : antibacterial humoral response
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0019731>)
 GO:0003401 : axis elongation (<https://www.ebi.ac.uk/QuickGO/term/GO:0003401>)
 GO:0007155 : cell adhesion (<https://www.ebi.ac.uk/QuickGO/term/GO:0007155>)
 GO:0060026 : convergent extension (<https://www.ebi.ac.uk/QuickGO/term/GO:0060026>)
 GO:0006952 : defense response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006952>)
 GO:0030703 : eggshell formation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030703>)
 GO:0048598 : embryonic morphogenesis
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0048598>)
 GO:0006955 : immune response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006955>)
 GO:0045087 : innate immune response
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
 GO:0007275 : multicellular organism development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0007275>)
 GO:0007297 : ovarian follicle cell migration
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0007297>)
 GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
 GO:0007419 : ventral cord development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0007419>)

GO - Cellular Component

GO:0016021 : integral component of membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
 GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Genetic variation in *Drosophila melanogaster* resistance to infection: a comparison across bacteria. (2006) (<https://pubmed.ncbi.nlm.nih.gov/16888344>)

Authors

Lazzaro BP; Sackton TB; Clark AG

Abstract

Insects use a generalized immune response to combat bacterial infection. We have previously noted that natural populations of *D. melanogaster* harbor substantial genetic variation for antibacterial immunocompetence and that much of this variation can be mapped to genes that are known to play direct roles in immunity. It was not known, however, whether the phenotypic effects of variation in these genes are general across the range of potentially infectious bacteria. To address this question, we have reinfected the same set of *D. melanogaster* lines with *Serratia marcescens*, the bacterium used in the previous study, and with three additional bacteria that were isolated from the hemolymph of wild-caught *D. melanogaster*. Two of the new bacteria, *Enterococcus faecalis* and *Lactococcus lactis*, are gram positive. The third, *Providencia burhodogranaria*, is gram negative like *S. marcescens*. *Drosophila* genotypes vary highly significantly in bacterial load sustained after infection with each of the four bacteria, but mean loads are largely uncorrelated across bacteria. We have tested statistical associations between immunity phenotypes and nucleotide polymorphism in 21 candidate immunity genes. We find that molecular variation in some genes, such as *Tehao*, contributes to phenotypic variation in the suppression of only a subset of the pathogens. Variation in SR-CII and 18-wheeler, however, has effects that are more general. Although markers in SR-CII and 18-wheeler explain >20% of the phenotypic variation in resistance to *L. lactis* and *E. faecalis*, respectively, most of the molecular polymorphisms tested explain <10% of the total variance in bacterial load sustained after infection.

Additional References

RELATED GEPHE

15 (CG8492, Diptericin, 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 Genes

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

