

GEPHE SUMMARY

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

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

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster	
18w		A1ZBR2 (http://www.uniprot.org/uniprot/A1ZBR2)	
Synonyms		GenebankID or UniProtKB	
18-w; 18-wheeler; 18W; CG8896; CT25100; Dmel\CG8896; l(2)00053; tlr; toll; Toll-2; Dmel_CG8896		AE013599 (https://www.ncbi.nlm.nih.gov/nuccore/AE013599)	
String			
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

	Related Genes
15 (CG8492, Dipteracin, Drosomycin-like 5, Ge-1, GGBP1, GGBP2, 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

