

GEPHE SUMMARY

Tehao (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~Tehao~#gephebase-summary-title)	Gephebase Gene	GP00001115	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait Category	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogenresistance~#gephebase-summary-title)		Trait	
Drosophila melanogaster		Trait State in Taxon A	
Drosophila melanogaster		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Intraspecific~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Drosophilamelanogaster~#gephebase-summary-title)		Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Drosophilamelanogaster~#gephebase-summary-title)	
fruit fly		fruit fly	
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	
species		species	
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	
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)	
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)	
No		No	
is Taxon A an Infraspecies?		is Taxon B an Infraspecies?	

GENOTYPIC CHANGE

Tehao		Generic Gene Name		UniProtKB Drosophila melanogaster Q9VJX9 (http://www.uniprot.org/uniprot/Q9VJX9)	
toll; CG7121; CT22017; Dmel\CG7121; dTLR5; dToll5; tehao; Tho; Tl-5; Toll 5; Toll-5; Dmel_CG7121		Synonyms		GenebankID or UniProtKB AE014134 (https://www.ncbi.nlm.nih.gov/nucore/AE014134)	
7227.FBpp0080080 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0080080)		String			
		Sequence Similarities			
		GO - Molecular Function			
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)					
GO:0015026 : coreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015026)					
GO:0005121 : Toll binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005121)					

GO - Biological Process

GO:0045087 : innate immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045087>)
GO:0006954 : inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0006967 : positive regulation of antifungal peptide biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006967>)
GO:0002807 : positive regulation of antimicrobial peptide biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002807>)
GO:0008063 : Toll signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008063>)
GO:0002224 : toll-like receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002224>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)

	Presumptive Null
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=">https://www.gephebase.org/search-criteria?/and+Presumptive Null="+Unknown+"#gephebase-summary-title)	
	Molecular Type
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type="+Unknown+"#gephebase-summary-title)	
	Aberration Type
Unknown (<a +unknown+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Aberration Type=">https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown+"#gephebase-summary-title)	
	Molecular Details of the Mutation
unknown	
	Experimental Evidence
Candidate Gene (<a +candidate="" gene+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=">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 (18-wheeler, CG8492, Diptericin, Drosomycin-like 5, Ge-1, GNBP1, GNBP2, Immune deficiency, Lectin-24A, pastrel, PGRP-LC, ref(2)P, SR-CII, Ubiquitin conjugating enzyme E2H (Ubc-E2H), CHKov1) (<a +7227+"and+trait="Pathogen" and+grouphaplotypes='true#gephebase-summary-title"' href="https://www.gephebase.org/search-criteria?/or+Taxon ID=" resistance="">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