

GEPHE SUMMARY

Gephebase Gene		GepheID
SR-CII (<a +sr-cii+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+SR-CII+"#gephebase-summary-title)	GP00001071	
Entry Status		Main curator
Published		

PHENOTYPIC CHANGE

Trait Category			
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)		Trait	
Pathogen resistance (<a +pathogen+resistance+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
Taxon A		Taxon B	
Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Drosophila+melanogaster+"#gephebase-summary-title)		Drosophila melanogaster (<a +drosophila+melanogaster+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">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 simulans
Sr-CII		Q5ELW9 (http://www.uniprot.org/uniprot/Q5ELW9)
Synonyms		GenebankID or UniProtKB
Dsim\GD15238; dsim_GLEANR_15334; GD15238; Sr-CII; SR-CII; Dsim\Sr-CII; Dsimw501_GD15238		AAW79432 (https://www.ncbi.nlm.nih.gov/nuccore/AAW79432)
String		
-		
Sequence Similarities		
-		
GO - Molecular Function		
GO:0030247 : polysaccharide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030247)		
GO:0005044 : scavenger receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005044)		
GO - Biological Process		

GO:0006955 : immune response (https://www.ebi.ac.uk/QuickGO/term/GO:0006955)	
GO - Cellular Component	
GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)	
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)	Experimental Evidence
Genetic variation in Drosophila melanogaster resistance to infection: a comparison across bacteria. (2006) (https://pubmed.ncbi.nlm.nih.gov/16888344)	Main Reference
Lazzaro BP; Sackton TB; Clark AG	Authors
Insects use a generalized immune response to combat bacterial infection. We have previously noted that natural populations of <i>D. melanogaster</i> 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 <i>D. melanogaster</i> lines with <i>Serratia marcescens</i> , the bacterium used in the previous study, and with three additional bacteria that were isolated from the hemolymph of wild-caught <i>D. melanogaster</i> . Two of the new bacteria, <i>Enterococcus faecalis</i> and <i>Lactococcus lactis</i> , are gram positive. The third, <i>Providencia burhodogranaria</i> , is gram negative like <i>S. marcescens</i> . <i>Drosophila</i> 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 <i>Tehao</i> , contributes to phenotypic variation in the suppression of only a subset of the pathogens. Variation in <i>SR-CII</i> and <i>18-wheeler</i> , however, has effects that are more general. Although markers in <i>SR-CII</i> and <i>18-wheeler</i> explain >20% of the phenotypic variation in resistance to <i>L. lactis</i> and <i>E. faecalis</i> , respectively, most of the molecular polymorphisms tested explain <10% of the total variance in bacterial load sustained after infection.	Abstract
	Additional References

RELATED GEPHE

15 (18-wheeler, CG8492, Dipterecin, Drosomycin-like 5, Ge-1, GNBP1, GNBP2, Immune deficiency, Lectin-24A, pastrel, PGRP-LC, ref(2)P, 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
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS