

GEPHE SUMMARY

PGRP-LC (#gephebase-summary-title)	Gephebase Gene	GP00000861	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

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

GENOTYPIC CHANGE

PGRP-LC	Generic Gene Name	UniProtKB Drosophila melanogaster
(PGRP)-LC; CG4432; Dm PGRP-LC; Dmel\CG4432; ird7; pgrp lc; pgrp-lc; Pgrp-LC; PGRP-LCa; PGRP-LCx; PGRPLC; tot	Synonyms	GenebankID or UniProtKB
7227.FBpp0088492 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0088492)	String	AE014296 (https://www.ncbi.nlm.nih.gov/nuccore/AE014296)
Belongs to the N-acetyl muramoyl-L-alanine amidase 2 family.	Sequence Similarities	
GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)	GO - Molecular Function	
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		

GO:0042834 : peptidoglycan binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042834>)
GO:0008329 : signaling pattern recognition receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008329>)
GO:0001875 : lipopolysaccharide receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001875>)
GO:0008745 : N-acetylMuramoyl-L-alanine amidase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008745>)
GO:0016019 : peptidoglycan receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016019>)

GO - Biological Process

GO:0019731 : antibacterial humoral response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019731>)
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:0009617 : response to bacterium (<https://www.ebi.ac.uk/QuickGO/term/GO:0009617>)
GO:0051607 : defense response to virus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051607>)
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:0019730 : antimicrobial humoral response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019730>)
GO:0061057 : peptidoglycan recognition protein signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061057>)
GO:0006963 : positive regulation of antibacterial peptide biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006963>)
GO:0006964 : positive regulation of biosynthetic process of antibacterial peptides active against Gram-negative bacteria (<https://www.ebi.ac.uk/QuickGO/term/GO:0006964>)
GO:0032827 : negative regulation of natural killer cell differentiation involved in immune response (<https://www.ebi.ac.uk/QuickGO/term/GO:0032827>)
GO:0006909 : phagocytosis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006909>)
GO:0061059 : positive regulation of peptidoglycan recognition protein signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061059>)
GO:0002920 : regulation of humoral immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002920>)
GO:0035007 : regulation of melanization defense response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035007>)
GO:0048167 : regulation of synaptic plasticity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048167>)

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>)
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)
GO:0016327 : apicolateral plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016327>)
GO:0098793 : presynapse (<https://www.ebi.ac.uk/QuickGO/term/GO:0098793>)
GO:0044214 : spanning component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0044214>)

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

Genotype and gene expression associations with immune function in Drosophila. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20066029>)

Authors

Sackton TB; Lazzaro BP; Clark AG

Abstract

It is now well established that natural populations of *Drosophila melanogaster* harbor substantial genetic variation associated with physiological measures of immune function. In no case, however, have intermediate measures of immune function, such as transcriptional activity of immune-related genes, been tested as mediators of phenotypic variation in immunity. In this study, we measured bacterial load sustained after infection of *D. melanogaster* with *Serratia marcescens*, *Providencia rettgeri*, *Enterococcus faecalis*, and *Lactococcus lactis* in a panel of 94 third-chromosome substitution lines. We also measured transcriptional levels of 329 immune-related genes eight hours after infection with *E. faecalis* and *S. marcescens* in lines from the phenotypic tails of the test panel. We genotyped the substitution lines at 137 polymorphic markers distributed across 25 genes in order to test for statistical associations among genotype, bacterial load, and transcriptional dynamics. We find that genetic polymorphisms in the pathogen recognition genes (and particularly in PGRP-LC, GNBP1, and GNBP2) are most significantly associated with variation in bacterial load. We also find that overall transcriptional induction of effector proteins is a significant predictor of bacterial load after infection with *E. faecalis*, and that a marker upstream of the recognition gene PGRP-SD is statistically associated with variation in both bacterial load and transcriptional induction of effector proteins. These results show that

RELATED GEPHE

Related Genes
15 (18-wheeler, CG8492, Diptericin, Drosomycin-like 5, Ge-1, GNBP1, GNBP2, Immune deficiency, Lectin-24A, pastrel, ref(2)P, SR-CII, Tehao, Ubiquitin conjugating enzyme E2H (Ubc-E2H), CHKov1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=%7227%20and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title>)
Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS