

Gephebase Gene		GepheID
PGRP-LC (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=*PGRP-LC^#gephebase-summary-title)	GP00000861	Main curator
Entry Status		Martin
Published		

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)		Trait Category	
Pathogen resistance (https://www.gephebase.org/search-criteria?/and+Trait=~Pathogen+resistance^#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+Taxonomic+Status=~Intraspecific^#gephebase-summary-title)		Taxonomic Status	
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)	
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)	
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 Intraspecies?		is Taxon B an Intraspecies?	
No		No	

UniProtKB Drosophila melanogaster	Generic Gene Name
Q9GNK5 (http://www.uniprot.org/uniprot/Q9GNK5)	PGRP-LC
GenebankID or UniProtKB	Synonyms
AE014296 (https://www.ncbi.nlm.nih.gov/nucore/AE014296)	(PGRP)-LC; CG4432; Dm PGRP-LC; Dmel\CG4432; ird7; pgrp lc; pgrp-lc; Pgrp-LC; PGRP-LCa; PGRP-LCx; PGRP-LC; tot
	String
	7227.FBpp0088492 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0088492)
	Sequence Similarities
	Belongs to the N-acetylmuramoyl-L-alanine amidase 2 family.
	GO - Molecular Function
	GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)
	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

polymorphism in genes near the top of the immune system signaling cascade can have a disproportionate effect on organismal phenotype due to the amplification of minor effects through the cascade.

Additional References

RELATED GEPHE

Related Genes

15 (18-wheeler, CG8492, Dipteracin, Drosomycin-like 5, Ge-1, GGBP1, GGBP2, Immune deficiency, Lectin-24A, pastel, 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