GEPHE SUMMARY

Gephebase Gene
GNBP1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^GNBP1^#gephebase-summary-title)

GepheID
GP00000408

Entry Status
Published

Main curator
Martin

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

Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank
species

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

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name
fruit fly

Synonyms
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank
species

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

Parent
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
GNBP1

Synonyms
CG6895; DGNBP-1; DGNBP1; Dmel\CG6895; GNBP; GNBP 1; GNBP-1

String
7227.FBpp0074817 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0074817)

Sequence Similarities
Belongs to the insect beta-1,3-glucan binding protein family.

GO - Molecular Function
GO:0001872 : (1->3)-beta-D-glucan binding (https://www.ebi.ac.uk/QuickGO/term/GO:0001872)
GO:0004553 : hydrolase activity, hydrolyzing O-glycosyl compounds (https://www.ebi.ac.uk/QuickGO/term/GO:0004553)

UniProtKB Drosophila melanogaster
Q9NHB0 (http://www.uniprot.org/uniprot/Q9NHB0)

GenebankID or UniProtKB
AE014296 (https://www.ncbi.nlm.nih.gov/nuccore/AE014296)

GO:0001530 : lipopolysaccharide binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001530)
GO:0042834 : peptidoglycan binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0042834)
GO:0030247 : polysaccharide binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0030247)
GO:0008329 : signaling pattern recognition receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0008329)

GO - Biological Process

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:0005975 : carbohydrate metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0005975)
GO:0045088 : regulation of innate immune response
(https://www.ebi.ac.uk/QuickGO/term/GO:0045088)
GO:0050830 : defense response to Gram-positive bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0050830)
GO:0002758 : innate immune response-activating signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0002758)
GO:0002221 : pattern recognition receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0002221)
GO:0009253 : peptidoglycan catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0009253)
GO:0045752 : positive regulation of Toll signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0045752)

GO - Cellular Component

GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0009986 : cell surface (https://www.ebi.ac.uk/QuickGO/term/GO:0009986)
GO:0046658 : anchored component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0046658)

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, Diptericin, Drosomycin-like 5, Ge-1, GNBP2, 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