GEPHE SUMMARY

Gephebase Gene
Ge-1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Ge-1^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00001993

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait
Pathogen resistance (sigma virus) (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen resistance (sigma virus)^#gephebase-summary-title)

Trait State in Taxon A
susceptible

Trait State in Taxon B
resistant

Ancestral State
Taxon A

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
Ge-1

Synonyms
CG6181; dGe-1; Dmel\CG6181; EDC4; GE-1; ref(2)M; Ref(2)Me

String
7227.FBpp0079818 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0079818)

Sequence Similarities
Belongs to the WD repeat EDC4 family.

GO - Molecular Function
-

GO - Biological Process
GO:0050832 : defense response to fungus (https://www.ebi.ac.uk/QuickGO/term/GO:0050832)

UniProtKB Drosophila melanogaster
Q9VKK1 (http://www.uniprot.org/uniprot/Q9VKK1)

GenebankID or UniProtKB
()

GO:0033962 : cytoplasmic mRNA processing body assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0033962)
GO:0035195 : gene silencing by miRNA
(https://www.ebi.ac.uk/QuickGO/term/GO:0035195)
GO:0006402 : mRNA catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006402)
GO:0045451 : pole plasm oskar mRNA localization
(https://www.ebi.ac.uk/QuickGO/term/GO:0045451)

GO - Cellular Component

GO:0000932 : P-body (https://www.ebi.ac.uk/QuickGO/term/GO:0000932)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

10-99 bp

Molecular Details of the Mutation

78bp deletion (2L:11097925 ..11098002 in both Release 5 and Release 6 coordinates) in the fifth exon of Ge-1 which reduces the length of the serine-rich linker region by 26 amino acid residues

Experimental Evidence

Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Linkage Mapping^#gephebase-summary-title)

Main Reference

A Polymorphism in the Processing Body Component Ge-1 Controls Resistance to a Naturally Occurring Rhabdovirus in Drosophila. (2016) (https://pubmed.ncbi.nlm.nih.gov/26799957)

Authors

Cao C; Magwire MM; Bayer F; Jiggins FM

Abstract

Hosts encounter an ever-changing array of pathogens, so there is continual selection for novel ways to resist infection. A powerful way to understand how hosts evolve resistance is to identify the genes that cause variation in susceptibility to infection. Using high-resolution genetic mapping we have identified a naturally occurring polymorphism in a gene called Ge-1 that makes Drosophila melanogaster highly resistant to its natural pathogen Drosophila melanogaster sigma virus (DMelSV). By modifying the sequence of the gene in transgenic flies, we identified a 26 amino acid deletion in the serine-rich linker region of Ge-1 that is causing the resistance. Knocking down the expression of the susceptible allele leads to a decrease in viral titre in infected flies, indicating that Ge-1 is an existing restriction factor whose antiviral effects have been increased by the deletion. Ge-1 plays a central role in RNA degradation and the formation of processing bodies (P bodies). A key effector in antiviral immunity, the RNAi induced silencing complex (RISC), localises to P bodies, but we found that Ge-1-based resistance is not dependent on the small interfering RNA (siRNA) pathway. However, we found that Decapping protein 1 (DCP1) protects flies against sigma virus. This protein interacts with Ge-1 and commits mRNA for degradation by removing the 5′ cap, suggesting that resistance may rely on this RNA degradation pathway. The serine-rich linker domain of Ge-1 has experienced strong selection during the evolution of Drosophila, suggesting that this gene may be under long-term selection by viruses. These findings demonstrate that studying naturally occurring polymorphisms that increase resistance to infections enables us to identify novel forms of antiviral defence, and support a pattern of major effect polymorphisms controlling resistance to viruses in Drosophila.

Additional References

RELATED GEPHE

Related Genes

15 (18-wheeler, CG8492, Diptericin, Drosomycin-like 5, GNBP1, 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

http://flybase.org/reports/FBal0014522