GEPHE SUMMARY

Gephebase Gene

ref(2)P (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ref(2)P^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001994

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 - O (Oregon) allele

Trait State in Taxon B

resistant - N (Nagoya) allele

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

ref(2)P

Synonyms

CG10360; Dmel\CG10360; dP62; p62; p62/Ref(2)P; p63; ref; ref(2)p; Ref(2)p; Ref(2)P; Ref(2)P/p62; ref(2)Pn; ref(2)Po2; Ref2; ref2p; Ref2p; Ref2P; SQSTM1

String

7227.FBpp0080794 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0080794)

Sequence Similarities

-

GO - Molecular Function

GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0070530 : K63-linked polyubiquitin modification-dependent protein binding

UniProtKB Drosophila melanogaster

P14199 (http://www.uniprot.org/uniprot/P14199)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0070530)
GO:0005080 : protein kinase C binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005080)

GO - Biological Process

GO:0007005 : mitochondrion organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0007005)
GO:0035973 : aggrephagy (https://www.ebi.ac.uk/QuickGO/term/GO:0035973)
GO:0007032 : endosome organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0007032)
GO:0000423 : mitophagy (https://www.ebi.ac.uk/QuickGO/term/GO:0000423)
GO:0061912 : selective autophagy (https://www.ebi.ac.uk/QuickGO/term/GO:0061912)
GO:0030382 : sperm mitochondrion organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0030382)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005776 : autophagosome (https://www.ebi.ac.uk/QuickGO/term/GO:0005776)
GO:0016235 : aggresome (https://www.ebi.ac.uk/QuickGO/term/GO:0016235)
GO:0044753 : amphisome (https://www.ebi.ac.uk/QuickGO/term/GO:0044753)

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

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

Molecular Details of the Mutation

Several differences (SNP and indels) are detected between permissive ref(2)Po and restrictive ref(2)Pn strains. Exact causing mutation(s) unknown.

Experimental Evidence

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

Main Reference

Unusual variability of the Drosophila melanogaster ref(2)P protein which controls the multiplication of sigma rhabdovirus. (1993) (https://pubmed.ncbi.nlm.nih.gov/8462852)

Authors

Dru P; Bras F; DezÃ©lÃ©e S; Gay P; Petitjean AM; Pierre-Deneubourg A; Teninges D; Contamine D

Abstract

The ref(2)P gene of Drosophila melanogaster was identified by the discovery of two alleles, Po and Pp, respectively, permissive and restrictive for sigma rhabdovirus multiplication. A surprising variability of this gene was first noticed by the observation of size differences between the transcripts of permissive and restrictive alleles. In this paper, another restrictive allele, Pn, clearly distinct from Pp, is described: it exhibits a weaker antiviral effect than Pp and differs from Pp by its molecular structure. Five types of alleles were distinguished on the basis of their molecular structure, as revealed by S1 nuclease analysis of 17 D. melanogaster strains; three alleles were permissive and two restrictive. Comparison of the sequences of four haplotypes revealed numerous point mutations, two deletions (21 and 24 bp) and a complex event involving a 3-bp deletion, all affected the coding region. The unusual variability of the ref(2)P locus was confirmed by the high ratio of amino acid replacements to synonymous mutations (7:1), as compared to that of other genes, such as the Adh (2:42). Nevertheless, nucleotide sequence comparison with the Drosophila erecta ref(2)P gene shows that selective pressures are exerted to maintain the existence of a functional protein. The effects of this high variability on the ref(2)P protein are discussed in relation to its specific antiviral properties and to its function in D. melanogaster, where it is required for male fertility.

Additional References

Control of sigma virus multiplication by the ref(2)P gene of Drosophila melanogaster: an in vivo study of the PB1 domain of Ref(2)P. (2007) (https://pubmed.ncbi.nlm.nih.gov/17409092)
Localization of domains within the Drosophila Ref(2)P protein involved in the intracellular control of sigma rhabdovirus multiplication. (1995) (https://pubmed.ncbi.nlm.nih.gov/7769706)

RELATED GEPHE

Related Genes

15 (18-wheeler, CG8492, Diptericin, Drosomycin-like 5, Ge-1, GNBP1, GNBP2, Immune deficiency, Lectin-24A, pastrel, PGRP-LC, 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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^ref(2)P^/and+Taxon ID=^7227^/or+Gene Gephebase=^ref(2)P^/and+Taxon ID=^7227^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

http://flybase.org/reports/FBal0014526.html