GEPHE SUMMARY

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

GepheID
GP00000495

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
Hybrid incompatibility (F1 male lethality) (https://www.gephebase.org/search-criteria?/and+Trait=^Hybrid incompatibility (F1 male lethality)^#gephebase-summary-title)

Trait State in Taxon A
Drosophila melanogaster

Trait State in Taxon B
Drosophila simulans

Ancestral State
Data not curated

Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#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 simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila simulans^#gephebase-summary-title)

Common Name
-

Synonyms
-

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
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Hmr

Synonyms
BcDNA:LD22117; CG1619; Dmel\CG1619; hmr; HMR; Hmr-mel; Hmr[[mel]]; Dmel_CG1619

String
7227.FBpp0071440 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0071440)

Sequence Similarities
-

GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)

GO - Biological Process
GO:0006355 : regulation of transcription, DNA-templated

UniProtKB Drosophila melanogaster
Q86CW5 (http://www.uniprot.org/uniprot/Q86CW5)

GenebankID or UniProtKB
KMZ09112 (https://www.ncbi.nlm.nih.gov/nuccore/KMZ09112)

(https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
GO:0006351 : transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0006351)
GO:0000070 : mitotic sister chromatid segregation
(https://www.ebi.ac.uk/QuickGO/term/GO:0000070)
GO:0010529 : negative regulation of transposition
(https://www.ebi.ac.uk/QuickGO/term/GO:0010529)
GO:0010528 : regulation of transposition
(https://www.ebi.ac.uk/QuickGO/term/GO:0010528)
GO:0000723 : telomere maintenance
(https://www.ebi.ac.uk/QuickGO/term/GO:0000723)

GO - Cellular Component

GO:0005700 : polytene chromosome
(https://www.ebi.ac.uk/QuickGO/term/GO:0005700)
GO:0000775 : chromosome, centromeric region
(https://www.ebi.ac.uk/QuickGO/term/GO:0000775)
GO:0000792 : heterochromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000792)
GO:0005854 : nascent polypeptide-associated complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005854)
GO:0005730 : nucleolus (https://www.ebi.ac.uk/QuickGO/term/GO:0005730)
GO:0005701 : polytene chromosome chromocenter
(https://www.ebi.ac.uk/QuickGO/term/GO:0005701)
GO:0035012 : polytene chromosome, telomeric region
(https://www.ebi.ac.uk/QuickGO/term/GO:0035012)

Presumptive Null

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

Rapid coding divergence

Experimental Evidence

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

Main Reference

Two Dobzhansky-Muller genes interact to cause hybrid lethality in Drosophila. (2006) (https://pubmed.ncbi.nlm.nih.gov/17124320)

Authors

Brideau NJ; Flores HA; Wang J; Maheshwari S; Wang X; Barbash DA

Abstract

The Dobzhansky-Muller model proposes that hybrid incompatibilities are caused by the interaction between genes that have functionally diverged in the respective hybridizing species. Here, we show that Lethal hybrid rescue (Lhr) has functionally diverged in Drosophila simulans and interacts with Hybrid male rescue (Hmr), which has functionally diverged in D. melanogaster, to cause lethality in F1 hybrid males. LHR localizes to heterochromatic regions of the genome and has diverged extensively in sequence between these species in a manner consistent with positive selection. Rapidly evolving heterochromatic DNA sequences may be driving the evolution of this incompatibility gene.

Additional References

RELATED GEPHE

Related Genes

6 (gfzf, JYalpha, Lethal Hybrid rescue, Nup160, Nup96, tyrosyl-tRNA synthetase (mt-TyrRS)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Hybrid incompatibility/or+Taxon ID=^7240^/and+Trait=Hybrid incompatibility/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

D. melanogaster Hmr1 allele suppresses hybrid male lethality of hybrid sons of crosses between D.melanogaster females and D.mauritiana males. This hybrid rescue is not suppressed if the hybrids also carry Dsim\Hmr+t8.6 or Dmau\Hmr+t9.4. - http://flybase.org/reports/FBal0005499