GEPHE SUMMARY

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

GepheID
GP00000541

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
Lhr

Synonyms
CG18468; Dmel\CG18468; HP3; LHR; LHR[[mel]]; mel-Lhr; Dmel_CG18468

String
7227.FBpp0086073 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0086073)

Sequence Similarities
-

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

GO - Biological Process
GO:0000070 : mitotic sister chromatid segregation (https://www.ebi.ac.uk/QuickGO/term/GO:0000070)

UniProtKB Drosophila melanogaster
Q95RV3 (http://www.uniprot.org/uniprot/Q95RV3)

GenebankID or UniProtKB
KMY94534 (https://www.ncbi.nlm.nih.gov/nuccore/KMY94534)

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:0070868 : heterochromatin organization involved in chromatin silencing
(https://www.ebi.ac.uk/QuickGO/term/GO:0070868)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
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:0035012 : polytene chromosome, telomeric region
(https://www.ebi.ac.uk/QuickGO/term/GO:0035012)
GO:0010369 : chromocenter (https://www.ebi.ac.uk/QuickGO/term/GO:0010369)

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

Coding divergence in a conserved stretch of 10 C-terminal amino-acids

Experimental Evidence

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

Main Reference

An indel polymorphism in the hybrid incompatibility gene lethal hybrid rescue of Drosophila is functionally relevant. (2012) (https://pubmed.ncbi.nlm.nih.gov/22865735)

Authors

Maheshwari S; Barbash DA

Abstract

Hybrid incompatibility (HI) genes are frequently observed to be rapidly evolving under selection. This observation has led to the attractive conjecture that selection-derived protein-sequence divergence is culpable for incompatibilities in hybrids. The Drosophila simulans HI gene Lethal hybrid rescue (Lhr) is an intriguing case, because despite having experienced rapid sequence evolution, its HI properties are a shared function inherited from the ancestral state. Using an unusual D. simulans Lhr hybrid rescue allele, Lhr(2), we here identify a conserved stretch of 10 amino acids in the C terminus of LHR that is critical for causing hybrid incompatibility. Altering these 10 amino acids weakens or abolishes the ability of Lhr to suppress the hybrid rescue alleles Lhr(1) or Hmr(1), respectively. Besides single-amino-acid substitutions, Lhr orthologs differ by a 16-aa indel polymorphism, with the ancestral deletion state fixed in D. melanogaster and the derived insertion state at very high frequency in D. simulans. Lhr(2) is a rare D. simulans allele that has the ancestral deletion state of the 16-aa polymorphism. Through a series of transgenic constructs we demonstrate that the ancestral deletion state contributes to the rescue activity of Lhr(2). This indel is thus a polymorphism that can affect the HI function of Lhr.

Additional References

RELATED GEPHE

Related Genes

6 (gfzf, Hybrid male rescue, JYalpha, 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

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^Lethal Hybrid rescue^/and+Taxon ID=^7227^/or+Gene Gephebase=^Lethal Hybrid rescue^/and+Taxon ID=^7240^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS