

## GEPHE SUMMARY

	Gephebase Gene		GepheID
Lethal Hybrid rescue ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=Lethal+Hybrid+rescue">#https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=Lethal+Hybrid+rescue</a> )		GP00000541	
	Entry Status	Martin	Main curator
Published			

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology">#https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology</a> )			
	Trait		
Hybrid incompatibility (F1 male lethality) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=Hybrid+incompatibility+(F1+male+lethality)#gepbebase-summary-title">#https://www.gephebase.org/search-criteria?/and+Trait=Hybrid+incompatibility+(F1+male+lethality)</a> )			
	Trait State in Taxon A		
<i>Drosophila melanogaster</i>			
	Trait State in Taxon B		
<i>Drosophila simulans</i>			
	Ancestral State		
Data not curated			
	Taxonomic Status		
Interspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Interspecific">#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Interspecific</a> )			
Taxon A		Taxon B	
	Latin Name		Latin Name
<i>Drosophila melanogaster</i> ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Drosophila+melanogaster">#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Drosophila+melanogaster</a> )		<i>Drosophila simulans</i> ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Drosophila+simulans">#https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Drosophila+simulans</a> )	
	Common Name		Common Name
fruit fly		-	
	Synonyms		Synonyms
<i>Sophophora melanogaster</i> ; fruit fly; <i>Drosophila melanogaster</i> Meigen, 1830; <i>Sophophora melanogaster</i> (Meigen, 1830); <i>Drosophila melangaster</i>		-	
	Rank		Rank
species		species	
	Lineage		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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; <i>Drosophila</i> ; <i>Sophophora</i> ; melanogaster group; melanogaster subgroup		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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; <i>Drosophila</i> ; <i>Sophophora</i> ; melanogaster group; melanogaster subgroup	
	Parent		Parent
melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )		melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
7227 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227</a> )		7240 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7240</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB <i>Drosophila melanogaster</i>
Lhr		Q95RV3 ( <a href="http://www.uniprot.org/uniprot/Q95RV3">http://www.uniprot.org/uniprot/Q95RV3</a> )	
	Synonyms		GenebankID or UniProtKB
CG18468; DmelCG18468; HP3; LHR; LHR[[mel]]; mel-Lhr; DmelCG18468		KMY94534 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/KMY94534">https://www.ncbi.nlm.nih.gov/nuccore/KMY94534</a> )	
	String		
7227.FBpp0086073 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0086073">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=7227.FBpp0086073</a> )			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0003677 : DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003677">https://www.ebi.ac.uk/QuickGO/term/GO:0003677</a> )			
	GO - Biological Process		
GO:0000070 : mitotic sister chromatid segregation ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000070">https://www.ebi.ac.uk/QuickGO/term/GO:0000070</a> )			

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](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](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](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](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](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](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