

GEPHE SUMMARY

Gephebase Gene		GepheID
fiz (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~fiz~#gephebase-summary-title)	GP00002017	
Entry Status	Courtier	Main curator
Published		

PHENOTYPIC CHANGE

Trait Category			
Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Morphology~#gephebase-summary-title)		Trait	
Body size (https://www.gephebase.org/search-criteria?/and+Trait=~Body+size~#gephebase-summary-title)		Trait State in Taxon A	
Drosophila melanogaster		Trait State in Taxon B	
Drosophila melanogaster		Ancestral State	
Taxon A		Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)			
Taxon A		Taxon B	
Drosophila melanogaster		Drosophila melanogaster	
(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)	
Common Name		Common Name	
fruit fly		fruit fly	
Synonyms		Synonyms	
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster		Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	
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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; 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; Acalyptratae; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	
Parent		Parent	
melanogaster subgroup () - (Rank: species subgroup)		melanogaster subgroup () - (Rank: species subgroup)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
7227		7227	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster	
fiz		Q9VY04 (http://www.uniprot.org/uniprot/Q9VY04)	
Synonyms		GenebankID or UniProtKB	
CG9509; Dm GMCbeta2; Dmel\CG9509; DmeL_CG9509		()	
String			
7227.FBpp0073795			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0073795)			
Sequence Similarities			
Belongs to the GMC oxidoreductase family.			
GO - Molecular Function			
GO:0016491 : oxidoreductase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016491)			
GO:0050660 : flavin adenine dinucleotide binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050660)			
GO:0016614 : oxidoreductase activity, acting on CH-OH group of donors			

GO:0007498 : mesoderm development

(<https://www.ebi.ac.uk/QuickGO/term/GO:0007498>)

GO:0045455 : ecdysteroid metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0045455>)

Mutation #1

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

C>G at position 67 within a 1.2 kb enhancer upstream of the CG9509 gene

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title>)

Main Reference

Functional characterization of adaptive variation within a cis-regulatory element influencing Drosophila melanogaster growth. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29324742>)

Authors

Glaser-Schmitt A; Parsch J

Abstract

Gene expression variation is a major contributor to phenotypic diversity within species and is thought to play an important role in adaptation. However, examples of adaptive regulatory polymorphism are rare, especially those that have been characterized at both the molecular genetic level and the organismal level. In this study, we perform a functional analysis of the Drosophila melanogaster CG9509 enhancer, a cis-regulatory element that shows evidence of adaptive evolution in populations outside the species’ ancestral range in sub-Saharan Africa. Using site-directed mutagenesis and transgenic reporter gene assays, we determined that 3 single nucleotide polymorphisms are responsible for the difference in CG9509 expression that is observed between sub-Saharan African and cosmopolitan populations. Interestingly, while 2 of these variants appear to have been the targets of a selective sweep outside of sub-Saharan Africa, the variant with the largest effect on expression remains polymorphic in cosmopolitan populations, suggesting it may be subject to a different mode of selection. To elucidate the function of CG9509, we performed a series of functional and tolerance assays on flies in which CG9509 expression was disrupted. We found that CG9509 plays a role in larval growth and influences adult body and wing size, as well as wing loading. Furthermore, variation in several of these traits was associated with variation within the CG9509 enhancer. The effect on growth appears to result from a modulation of active ecdysone levels and expression of growth factors. Taken together, our findings suggest that selection acted on 3 sites within the CG9509 enhancer to increase CG9509 expression and, as a result, reduce wing loading as D. melanogaster expanded out of sub-Saharan Africa.

Additional References

Mutation #2

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

G>T at position 1063 within a 1.2 kb enhancer upstream of the CG9509 gene

Experimental Evidence

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title>)

Main Reference

Functional characterization of adaptive variation within a cis-regulatory element influencing Drosophila melanogaster growth. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29324742>)

Authors

Glaser-Schmitt A; Parsch J

Abstract

Gene expression variation is a major contributor to phenotypic diversity within species and is thought to play an important role in adaptation. However, examples of adaptive regulatory polymorphism are rare, especially those that have been characterized at both the molecular genetic level and the organismal level. In this study, we perform a functional analysis of the Drosophila melanogaster CG9509 enhancer, a cis-regulatory element that shows evidence of adaptive evolution in populations outside the species’ ancestral range in sub-Saharan Africa. Using site-directed mutagenesis and transgenic reporter gene assays, we determined that 3 single nucleotide polymorphisms are responsible for the difference in CG9509 expression that is observed between sub-Saharan African and cosmopolitan populations. Interestingly, while 2 of these variants appear to have been the targets of a selective sweep outside of sub-Saharan Africa, the variant with the largest effect on expression remains polymorphic in cosmopolitan populations, suggesting it may be subject to a different mode of selection. To elucidate the function of CG9509, we performed a series of functional and tolerance assays on flies in which CG9509 expression was disrupted. We found that CG9509 plays a role in larval growth and influences adult body and wing size, as well as wing loading. Furthermore, variation in several of these traits was associated with variation within the CG9509 enhancer. The effect on growth appears to result from a modulation of active ecdysone levels and expression of growth factors. Taken together, our findings suggest that selection acted on 3 sites within the CG9509 enhancer to increase CG9509 expression and, as a result, reduce wing loading as D. melanogaster expanded out of sub-Saharan Africa.

Additional References

Mutation #3

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title>)

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

C>A at position 1174 within a 1.2 kb enhancer upstream of the CG9509 gene

Candidate Gene (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title>)

Experimental Evidence

Main Reference

Functional characterization of adaptive variation within a cis-regulatory element influencing Drosophila melanogaster growth. (2018) (<https://pubmed.ncbi.nlm.nih.gov/29324742>)

Authors

Glaser-Schmitt A; Parsch J

Abstract

Gene expression variation is a major contributor to phenotypic diversity within species and is thought to play an important role in adaptation. However, examples of adaptive regulatory polymorphism are rare, especially those that have been characterized at both the molecular genetic level and the organismal level. In this study, we perform a functional analysis of the Drosophila melanogaster CG9509 enhancer, a cis-regulatory element that shows evidence of adaptive evolution in populations outside the species' ancestral range in sub-Saharan Africa. Using site-directed mutagenesis and transgenic reporter gene assays, we determined that 3 single nucleotide polymorphisms are responsible for the difference in CG9509 expression that is observed between sub-Saharan African and cosmopolitan populations. Interestingly, while 2 of these variants appear to have been the targets of a selective sweep outside of sub-Saharan Africa, the variant with the largest effect on expression remains polymorphic in cosmopolitan populations, suggesting it may be subject to a different mode of selection. To elucidate the function of CG9509, we performed a series of functional and tolerance assays on flies in which CG9509 expression was disrupted. We found that CG9509 plays a role in larval growth and influences adult body and wing size, as well as wing loading. Furthermore, variation in several of these traits was associated with variation within the CG9509 enhancer. The effect on growth appears to result from a modulation of active ecdysone levels and expression of growth factors. Taken together, our findings suggest that selection acted on 3 sites within the CG9509 enhancer to increase CG9509 expression and, as a result, reduce wing loading as D. melanogaster expanded out of sub-Saharan Africa.

Additional References

RELATED GEPHE

2 (foxo, lnr) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~7227~/and+Trait=Body size/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect @Epistasis - Gene identified first due to its expression difference. Adult CG9509 expression is 2â€“3-fold higher in the European populations than in the sub-Saharan populations. A 1.2kb cis-regulatory region upstream of the gene shows evidence of a selective sweep in cosmopolitan populations. CG9509 expression influences larval growth and thus plays a role in determining adult body size and the ratio of body mass to wing area.