

GEPHE SUMMARY

Gephebase Gene		GepheID
GSS (glutathione synthetase) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="GSS (glutathione synthetase)"#gephebase-summary-title)	GP00002115	Main curator
Published	Entry Status	Courtier

PHENOTYPIC CHANGE

Trait Category		Trait	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology"#gephebase-summary-title)		Xenobiotic resistance (arsenic) (https://www.gephebase.org/search-criteria?/and+Trait ="Xenobiotic resistance (arsenic)"#gephebase-summary-title)	
Drosophila melanogaster susceptible to arsenic		Drosophila melanogaster resistant to arsenic	
Taxon A		Taxon B	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific"#gephebase-summary-title)		Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intraspecific"#gephebase-summary-title)	
Taxon A		Taxon B	
Latin Name		Latin Name	
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Drosophila melanogaster"#gephebase-summary-title)		Drosophila melanogaster (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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)		7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Taxon A Description		Taxon B Description	
Strain Oregon R; A2; A6 and B3		Strains ISO-1; A1; B2	

GENOTYPIC CHANGE

Generic Gene Name		UniProtKB Drosophila melanogaster
Gss2	Q86B44 (http://www.uniprot.org/uniprot/Q86B44)	GenebankID or UniProtKB
Synonyms		
32495; CG32495; Dmel\CG32495; GS; gss; 6835; CG32497; CG33065; Dmel\CG6835; GSS; Gss1; CG6835; Dmel_CG32495; Dmel_CG6835		()
String		
7227.FBpp0290197 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0290197)		
Sequence Similarities		
Belongs to the eukaryotic GSH synthase family.		
GO - Molecular Function		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		

GO:0042803 : protein homodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042803>)

GO:0000287 : magnesium ion binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000287>)

GO:0043295 : glutathione binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0043295>)

GO:0004363 : glutathione synthase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004363>)

GO - Biological Process

GO:0071722 : detoxification of arsenic-containing substance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071722>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

tandem duplication creating the Gss1/Gss2 gene pair. Associated with increased expression of Gss1.

Experimental Evidence

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

Main Reference

Structural variants exhibit widespread allelic heterogeneity and shape variation in complex traits. (2019) (<https://pubmed.ncbi.nlm.nih.gov/31653862>)

Authors

Chakraborty M; Emerson JJ; Macdonald SJ; Long AD

Abstract

It has been hypothesized that individually-rare hidden structural variants (SVs) could account for a significant fraction of variation in complex traits. Here we identified more than 20,000 euchromatic SVs from 14 *Drosophila melanogaster* genome assemblies, of which ~40% are invisible to high specificity short-read genotyping approaches. SVs are common, with 31.5% of diploid individuals harboring a SV in genes larger than 5kb, and 24% harboring multiple SVs in genes larger than 10kb. SV minor allele frequencies are rarer than amino acid polymorphisms, suggesting that SVs are more deleterious. We show that a number of functionally important genes harbor previously hidden structural variants likely to affect complex phenotypes. Furthermore, SVs are overrepresented in candidate genes associated with quantitative trait loci mapped using the *Drosophila* Synthetic Population Resource. We conclude that SVs are ubiquitous, frequently constitute a heterogeneous allelic series, and can act as rare alleles of large effect.

Additional References

Investigating arsenic susceptibility from a genetic perspective in *Drosophila* reveals a key role for glutathione synthetase. (2009) (<https://pubmed.ncbi.nlm.nih.gov/18779381>)

RELATED GEPHE

Related Genes

19 (Acetylcholinesterase (Ace-2), alcohol dehydrogenase (Adh), Aldehyde dehydrogenase (Aldh), CG11699, Cyp12d1, Cyp28d1, Cyp28d1-Cyp28d2, cyp6d2, cyp6g1, glutamate-gated chloride channel (GluCl), GSTE1-E10 cluster, kin of irre (kire), para (kdr), PHGPx, resistance to dieldrin, RnrS, SOD1, Ugt86Dd, CHKov1) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

There are also insertions of multiple transposable elements at this locus in various lines. This may contribute to differential expression of Gss1 and different responses to arsenic.