

GEPHE SUMMARY

	Gephebase Gene	GepheID
kin of irre (kire) (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~kin of irre (kire)^#gephebase-summary-title)	GP00001398	
	Entry Status	Prigent
Published		Main curator

PHENOTYPIC CHANGE

	Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)		
	Trait	
Xenobiotic resistance (methylmercury ; development) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic resistance (methylmercury ; development)^#gephebase-summary-title)		
	Trait State in Taxon A	
Drosophila melanogaster DGRP lines less tolerant to MeHg derived from the Raleigh (US) population		
	Trait State in Taxon B	
Drosophila melanogaster DGRP lines more tolerant to MeHg derived from the Raleigh (US) population		
	Ancestral State	
Unknown		
	Taxonomic Status	
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?
No		No

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
kirre		Q9N9Y9 (http://www.uniprot.org/uniprot/Q9N9Y9)
	Synonyms	GenebankID or UniProtKB
duf: CG3653		AF196553 (https://www.ncbi.nlm.nih.gov/nucleotide/AF196553)
	String	
-		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0050839 : cell adhesion molecule binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050839)		
	GO - Biological Process	

GO:0007156 : homophilic cell adhesion via plasma membrane adhesion molecules
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007156>)
GO:0007520 : myoblast fusion (<https://www.ebi.ac.uk/QuickGO/term/GO:0007520>)
GO:0001745 : compound eye morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001745>)
GO:0007523 : larval visceral muscle development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007523>)
GO:0036058 : filtration diaphragm assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0036058>)
GO:0061321 : garland nephrocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061321>)
GO:0007157 : heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007157>)
GO:0036059 : nephrocyte diaphragm assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0036059>)
GO:0097206 : nephrocyte filtration (<https://www.ebi.ac.uk/QuickGO/term/GO:0097206>)
GO:1901739 : regulation of myoblast fusion
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901739>)
GO:0016202 : regulation of striated muscle tissue development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016202>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
GO:0005912 : adherens junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0005912>)
GO:0005917 : nephrocyte diaphragm
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005917>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#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

unknown

Experimental Evidence

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

Main Reference

Genome-wide association analysis of tolerance to methylmercury toxicity in Drosophila implicates myogenic and neuromuscular developmental pathways. (2014)
(<https://pubmed.ncbi.nlm.nih.gov/25360876>)

Authors

Montgomery SL; Vorobjikina D; Huang W; Mackay TF; Anholt RR; Rand MD

Abstract

Methylmercury (MeHg) is a persistent environmental toxin present in seafood that can compromise the developing nervous system in humans. The effects of MeHg toxicity varies among individuals, despite similar levels of exposure, indicating that genetic differences contribute to MeHg susceptibility. To examine how genetic variation impacts MeHg tolerance, we assessed developmental tolerance to MeHg using the sequenced, inbred lines of the Drosophila melanogaster Genetic Reference Panel (DGRP). We found significant genetic variation in the effects of MeHg on development, measured by eclosion rate, giving a broad sense heritability of 0.86. To investigate the influence of dietary factors, we measured MeHg toxicity with caffeine supplementation in the DGRP lines. We found that caffeine counteracts the deleterious effects of MeHg in the majority of lines, and there is significant genetic variance in the magnitude of this effect, with a broad sense heritability of 0.80. We performed genome-wide association (GWA) analysis for both traits, and identified candidate genes that fall into several gene ontology categories, with enrichment for genes involved in muscle and neuromuscular development. Overexpression of glutamate-cysteine ligase, a MeHg protective enzyme, in a muscle-specific manner leads to a robust rescue of eclosion of flies reared on MeHg food. Conversely, mutations in kirre, a pivotal myogenic gene identified in our GWA analyses, modulate tolerance to MeHg during development in accordance with kirre expression levels. Finally, we observe disruptions of indirect flight muscle morphogenesis in MeHg-exposed pupae. Since the pathways for muscle development are evolutionarily conserved, it is likely that the effects of MeHg observed in Drosophila can be generalized across phyla, implicating muscle as an additional hitherto unrecognized target for MeHg toxicity. Furthermore, our observations that caffeine can ameliorate the toxic effects of MeHg show that nutritional factors and dietary manipulations may offer protection against the deleterious effects of MeHg exposure.

Additional References

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), GSS (glutathione synthetase), GSTE1-E10 cluster, 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

fonctionaly verified by the use of mutants