

# GEPHE SUMMARY

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

## PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=^Physiology^#gephebase-summary-title)	Trait Category
Xenobiotic resistance (methylmercury ; development) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(methylmercury+;+development)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(methylmercury+;+development)^#gephebase-summary-title</a> )	Trait
Drosophila melanogaster DGRP lines less tolerant to MeHg derived from the Raleigh (US) population	Trait State in Taxon A
Drosophila melanogaster DGRP lines more tolerant to MeHg derived from the Raleigh (US) population	Trait State in Taxon B
Unknown	Ancestral State
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status=^Intraspecific^#gephebase-summary-title)	Taxonomic Status

### Taxon A

Drosophila melanogaster ( <a href="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</a> )	Latin Name
fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms
species	Rank
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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
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> )	Parent
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> )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?

### Taxon B

Drosophila melanogaster ( <a href="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</a> )	Latin Name
fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms
species	Rank
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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
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> )	Parent
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> )	NCBI Taxonomy ID
No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

kirre	Generic Gene Name	UniProtKB Drosophila melanogaster Q9N9Y9 ( <a href="http://www.uniprot.org/uniprot/Q9N9Y9">http://www.uniprot.org/uniprot/Q9N9Y9</a> )
duf; CG3653	Synonyms	GenebankID or UniProtKB AF196553 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AF196553">https://www.ncbi.nlm.nih.gov/nuccore/AF196553</a> )
-	String	
-	Sequence Similarities	
GO:0050839 : cell adhesion molecule binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0050839">https://www.ebi.ac.uk/QuickGO/term/GO:0050839</a> )	GO - Molecular Function	
		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; Vorojeikina 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