

GEPHE SUMMARY

PHGPx (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~PHGPx~#gephebase-summary-title)	Gephebase Gene	GP00001405	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)	Trait Category		
Xenobiotic resistance (gemcitabine ; female fertility) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic+resistance+(gemcitabine+;+female+fertility)~#gephebase-summary-title)	Trait		
Drosophila melanogaster more sensitive to gemcitabine	Trait State in Taxon A		
Drosophila melanogaster less sensitive to gemcitabine	Trait State in Taxon B		
Unknown	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)	Latin Name	Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Drosophila+melanogaster~#gephebase-summary-title)	Latin Name
fruit fly	Common Name	fruit fly	Common Name
Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms	Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster	Synonyms
species	Rank	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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	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; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent	melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351)	Parent
7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID	7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

PHGPx	Generic Gene Name	UniProtKB Drosophila melanogaster
anon-WO025745.17; CG12013; Dmel\CG12013; DmGPx; DmPHGPx; Gpx; GPx; GTPx; Gtpx-1; GTPx-1; PGTPx; phGpx; Tpx1; Dmel_CG12013	Synonyms	GenebankID or UniProtKB
-	String	38413 (https://www.ncbi.nlm.nih.gov/nucore/38413)
Belongs to the glutathione peroxidase family.	Sequence Similarities	
GO:0004601 : peroxidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004601)	GO - Molecular Function	
GO:0004602 : glutathione peroxidase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004602)	GO - Biological Process	

GO:0006979 : response to oxidative stress
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006979>)
GO:0006982 : response to lipid hydroperoxide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006982>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0012505 : endomembrane system
(<https://www.ebi.ac.uk/QuickGO/term/GO:0012505>)

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

Presumptive Null

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

Molecular Type

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

Aberration Type

unknown

Molecular Details of the Mutation

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

Experimental Evidence

Using *Drosophila melanogaster* to identify chemotherapy toxicity genes. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25236447>)

Main Reference

King EG; Kislukhin G; Walters KN; Long AD

Authors

The severity of the toxic side effects of chemotherapy shows a great deal of interindividual variability, and much of this variation is likely genetically based. Simple DNA tests predictive of toxic side effects could revolutionize the way chemotherapy is carried out. Due to the challenges in identifying polymorphisms that affect toxicity in humans, we use *Drosophila* fecundity following oral exposure to carboplatin, gemcitabine and mitomycin C as a model system to identify naturally occurring DNA variants predictive of toxicity. We use the *Drosophila* Synthetic Population Resource (DSPR), a panel of recombinant inbred lines derived from a multiparent advanced intercross, to map quantitative trait loci affecting chemotoxicity. We identify two QTL each for carboplatin and gemcitabine toxicity and none for mitomycin. One QTL is associated with fly orthologs of a priori human carboplatin candidate genes ABCC2 and MSH2, and a second QTL is associated with fly orthologs of human gemcitabine candidate genes RRM2 and RRM2B. The third, a carboplatin QTL, is associated with a posteriori human orthologs from solute carrier family 7A, INPP4A&B, and NALCN. The fourth, a gemcitabine QTL that also affects methotrexate toxicity, is associated with human ortholog GPx4. Mapped QTL each explain a significant fraction of variation in toxicity, yet individual SNPs and transposable elements in the candidate gene regions fail to singly explain QTL peaks. Furthermore, estimates of founder haplotype effects are consistent with genes harboring several segregating functional alleles. We find little evidence for nonsynonymous SNPs explaining mapped QTL; thus it seems likely that standing variation in toxicity is due to regulatory alleles.

Abstract

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Additional References

RELATED GEPHE

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, kin of irre (kire), para (kdr), 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 Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS