

GEPHE SUMMARY

	Gephebase Gene		GepheID
RnrS (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~RnrS^#gephebase-summary-title)		GP00001404	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)			
	Trait		
Xenobiotic resistance (gemcitabine ; female fertility) (https://www.gephebase.org/search-criteria?/and+Trait=~Xenobiotic+resistance+(gemcitabine+;+female+fertility)^#gephebase-summary-title)			
	Trait State in Taxon A		
Drosophila melanogaster more sensitive to gemcitabine			
	Trait State in Taxon B		
Drosophila melanogaster less sensitive to gemcitabine			
	Ancestral State		
Unknown			
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~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
RnrS		P48592 (http://www.uniprot.org/uniprot/P48592)	
	Synonyms		GenebankID or UniProtKB
anon-WO0118547.148; CG8975; Dmel\CG8975; DmRNR2; dRNR2; rnr2; Rnr2; RNR2; rnrS; Rnrs; RNrS; RNRS		AY051936 (https://www.ncbi.nlm.nih.gov/nucore/AY051936)	
	String		
7227.FBpp0087152 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0087152)			
	Sequence Similarities		
Belongs to the ribonucleoside diphosphate reductase small chain family.			
	GO - Molecular Function		
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)			
GO:0004748 : ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as			

acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0004748)	
GO:0006919 : activation of cysteine-type endopeptidase activity involved in apoptotic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006919)	GO - Biological Process
GO:0009263 : deoxyribonucleotide biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0009263)	
GO:0006260 : DNA replication (https://www.ebi.ac.uk/QuickGO/term/GO:0006260)	GO - Cellular Component
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)	
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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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), PHGPx, resistance to dieldrin, 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