

GEPHE SUMMARY

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

PHENOTYPIC CHANGE

Trait Category	
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category= [~] 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)	
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
Taxonomic Status	
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status= [~] Intraspecific ^{#gephebase-summary-title})	

Taxon A	Latin Name	Taxon B	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)	
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; Acalyptratae; Ephydrioidea; 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; Acalyptratae; Ephydrioidea; 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 Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

Generic Gene Name	UniProtKB Drosophila melanogaster
RnrS	P48592 (http://www.uniprot.org/uniprot/P48592)
anon-WO0118547.148; CG8975; Dmel\CG8975; DmRNR2; dRNR2; rnr2; Rnr2; RNR2; rnrS; Rnrs; RNrS; RNRS	GenebankID or UniProtKB AY051936 (https://www.ncbi.nlm.nih.gov/nucleotide/AY051936)
7227.FBpp0087152 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0087152)	String
Belongs to the ribonucleoside diphosphate reductase small chain family.	Sequence Similarities
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)	GO - Molecular Function
GO:0004748 : ribonucleoside-diphosphate reductase activity, thioredoxin disulfide as	

GO - Biological Process

GO:0006919 : activation of cysteine-type endopeptidase activity involved in apoptotic

process (<https://www.ebi.ac.uk/QuickGO/term/GO:0006919>)

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>)

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

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

Authors

King EG; Kislyukin G; Walters KN; Long AD

Abstract

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.

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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, 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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS