GEPHE SUMMARY

Gephebase Gene

RnrS (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^RnrS^#gephebase-summary-title)

GepheID

GP00001404

Entry Status

Published

Main curator

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)

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+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank

species

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

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Drosophila melanogaster (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gephebase-summary-title)

Common Name

fruit fly

Synonyms

Sophophora melanogaster; fruit fly; Drosophila melanogaster Meigen, 1830; Sophophora melanogaster (Meigen, 1830); Drosophila melangaster

Rank

species

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

Parent

melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)

NCBI Taxonomy ID

7227 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7227)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

RnrS

Synonyms

anon-WO0118547.148; CG8975; Dmel\CG8975; DmRNR2; dRNR2; rnr2; Rnr2; RNR2; rnrS; Rnrs; RNrS; RNRS

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

UniProtKB Drosophila melanogaster

P48592 (http://www.uniprot.org/uniprot/P48592)

GenebankID or UniProtKB

AY051936 (https://www.ncbi.nlm.nih.gov/nuccore/AY051936)

acceptor (https://www.ebi.ac.uk/QuickGO/term/GO:0004748)

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; Kislukhin 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