GEPHE SUMMARY

Gephebase Gene

tyrosyl-tRNA synthetase (mt-TyrRS) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^tyrosyl-tRNA synthetase (mt-TyrRS)^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001972

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Hybrid incompatibility (F1 hybrid viability; F1 hybrid sterility) (https://www.gephebase.org/search-criteria?/and+Trait=^Hybrid incompatibility (F1 hybrid viability; F1 hybrid sterility)^#gephebase-summary-title)

Trait State in Taxon A

Drosophila melanogaster - WT allele

Trait State in Taxon B

Drosophila melanogaster - OreR allele

Ancestral State

Taxon A

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

TyrRS-m

Synonyms

Aatm; Aats-tyr-m; anon-EST:fe1E12; CG16912; Dmel\CG16912

String

7227.FBpp0072334 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0072334)

Sequence Similarities

Belongs to the class-I aminoacyl-tRNA synthetase family.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0003723 : RNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003723)

UniProtKB Drosophila melanogaster

Q9W107 (http://www.uniprot.org/uniprot/Q9W107)

GenebankID or UniProtKB

()

GO:0004831 : tyrosine-tRNA ligase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004831)

GO - Biological Process

GO:0070184 : mitochondrial tyrosyl-tRNA aminoacylation (https://www.ebi.ac.uk/QuickGO/term/GO:0070184)
GO:0043039 : tRNA aminoacylation (https://www.ebi.ac.uk/QuickGO/term/GO:0043039)
GO:0006437 : tyrosyl-tRNA aminoacylation (https://www.ebi.ac.uk/QuickGO/term/GO:0006437)

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0005759 : mitochondrial matrix (https://www.ebi.ac.uk/QuickGO/term/GO:0005759)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

SNP Coding Change

-

Molecular Details of the Mutation

C to T mutation at the base of the anticodon stem, so that G:C becomes G:U in the folded mRNA (see Fig. 1 of Hoekstra et al 2013)

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

An Incompatibility between a mitochondrial tRNA and its nuclear-encoded tRNA synthetase compromises development and fitness in Drosophila. (2013) (https://pubmed.ncbi.nlm.nih.gov/23382693)

Authors

Meiklejohn CD; Holmbeck MA; Siddiq MA; Abt DN; Rand DM; Montooth KL

Abstract

Mitochondrial transcription, translation, and respiration require interactions between genes encoded in two distinct genomes, generating the potential for mutations in nuclear and mitochondrial genomes to interact epistatically and cause incompatibilities that decrease fitness. Mitochondrial-nuclear epistasis for fitness has been documented within and between populations and species of diverse taxa, but rarely has the genetic or mechanistic basis of these mitochondrial-nuclear interactions been elucidated, limiting our understanding of which genes harbor variants causing mitochondrial-nuclear disruption and of the pathways and processes that are impacted by mitochondrial-nuclear coevolution. Here we identify an amino acid polymorphism in the Drosophila melanogaster nuclear-encoded mitochondrial tyrosyl-tRNA synthetase that interacts epistatically with a polymorphism in the D. simulans mitochondrial-encoded tRNA(Tyr) to significantly delay development, compromise bristle formation, and decrease fecundity. The incompatible genotype specifically decreases the activities of oxidative phosphorylation complexes I, III, and IV that contain mitochondrial-encoded subunits. Combined with the identity of the interacting alleles, this pattern indicates that mitochondrial protein translation is affected by this interaction. Our findings suggest that interactions between mitochondrial tRNAs and their nuclear-encoded tRNA synthetases may be targets of compensatory molecular evolution. Human mitochondrial diseases are often genetically complex and variable in penetrance, and the mitochondrial-nuclear interaction we document provides a plausible mechanism to explain this complexity.

Additional References

Pleiotropic effects of a mitochondrial-nuclear incompatibility depend upon the accelerating effect of temperature in Drosophila. (2013) (https://pubmed.ncbi.nlm.nih.gov/24026098)

RELATED GEPHE

Related Genes

6 (gfzf, Hybrid male rescue, JYalpha, Lethal Hybrid rescue, Nup160, Nup96) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7227^/and+Trait=Hybrid incompatibility/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Hybrid incompatibility between D. simulans and D. melanogaster. Nuclear encoded gene. @Epistasis - The hybrid slow development phenotype can only be found when the D. simulans w501 allele of the mitochondrial tyrosine tRNA gene is found in presence of the D. melanogaster OreR allele of the nuclear-encoded mt-TyrRS that aminoacylates this mitochondrial tRNA.- @GxE The defective and slow development of hybrids is amplified at higher temperature. - http://flybase.org/reports/FBal0282670.html