GEPHE SUMMARY

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

GepheID
GP00001971

Entry Status
Published

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 simulans - WT allele

Trait State in Taxon B
Drosophila simulans - w501 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 simulans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila simulans^#gephebase-summary-title)

Common Name
-

Synonyms
-

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
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon A an Infraspecies?
No

Taxon B

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

Common Name
-

Synonyms
-

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
7240 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7240)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
-

Synonyms
-

String
-

Sequence Similarities
-

GO - Molecular Function
-

GO - Biological Process
-

GO - Cellular Component
-

UniProtKB
()

GenebankID or UniProtKB
()

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

7 (gfzf, Hybrid male rescue, JYalpha, Lethal Hybrid rescue, Nup160, Nup96, Odysseus-site homeobox) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^7240^/and+Trait=Hybrid incompatibility/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@MitochondrialGene Mutation in the "coding" region of gene which encodes an RNA and not a protein. Hybrid incompatibility between D. simulans and D. melanogaster. @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/FBal0282674