

GEPHE SUMMARY

	Gephebase Gene	GephelD
tyrosyl-tRNA synthetase (mt-TyrRS) (https://www.gepheebase.org/search-criteria?/and+Gene Gephebase=^tyrosyl-tRNA synthetase (mt-TyrRS)^#gepheebase-summary-title)	GP00001972	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gepheebase.org/search-criteria?/and+Trait Category=^Physiology^#gepheebase-summary-title)	Trait		
Hybrid incompatibility (F1 hybrid viability; F1 hybrid sterility) (https://www.gepheebase.org/search-criteria?/and+Trait=^Hybrid incompatibility (F1 hybrid viability; F1 hybrid sterility)^#gepheebase-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.gepheebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gepheebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Drosophila melanogaster (https://www.gepheebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gepheebase-summary-title)	Common Name	Drosophila melanogaster (https://www.gepheebase.org/search-criteria?/and+Taxon and Synonyms=^Drosophila melanogaster^#gepheebase-summary-title)	Common Name
fruit fly	Synonyms	fruit fly	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	Lineage	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; Ephydriodea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Parent	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; Ephydriodea; 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)		melanogaster subgroup () - (Rank: species subgroup) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32351)	
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
	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
TyrRS-m		
Aatm; Aats-tyr-m; anon-EST:fe1E12; CG16912; Dmel\CG16912	Synonyms	GenebankID or UniProtKB
7227.FBpp0072334 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0072334)	String	
	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)		

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=%27No%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%27No%27#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Coding%27#gephebase-summary-title))

Aberration Type

SNP ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27SNP%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27SNP%27#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=%27Candidate Gene%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Candidate%20Gene%27#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 (gfz, Hybrid male rescue, JYalpha, Lethal Hybrid rescue, Nup160, Nup96) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%277227%27/and+Trait=Hybrid+incompatibility/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%277227%27/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>

