

## GEPHE SUMMARY

tyrosyl-tRNA synthetase (mt-TyrRS) ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^tyrosyl-tRNA+synthetase+(mt-TyrRS)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^tyrosyl-tRNA+synthetase+(mt-TyrRS)^#gephebase-summary-title</a> )	Gephebase Gene	GP00001972	GepheID
Published	Entry Status	Courtier	Main curator

## PHENOTYPIC CHANGE

Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title</a> )	Trait Category		
Hybrid incompatibility (F1 hybrid viability; F1 hybrid sterility) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Hybrid+incompatibility+(F1+hybrid+viability;+F1+hybrid+sterility)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Hybrid+incompatibility+(F1+hybrid+viability;+F1+hybrid+sterility)^#gephebase-summary-title</a> )	Trait		
Drosophila melanogaster - WT allele	Trait State in Taxon A		
Drosophila melanogaster - OreR allele	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intraspecific^#gephebase-summary-title</a> )	Taxonomic Status		
	Taxon A		Taxon B
Drosophila melanogaster ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title</a> )	Latin Name	Drosophila melanogaster ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Drosophila+melanogaster^#gephebase-summary-title</a> )	Latin Name
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; Acalyptera; Ephydroidea; 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; Acalyptera; Ephydroidea; Drosophilidae; Drosophilinae; Drosophilini; Drosophila; Sophophora; melanogaster group; melanogaster subgroup	Lineage
melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )	Parent	melanogaster subgroup () - (Rank: species subgroup) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=32351</a> )	Parent
7227 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227</a> )	NCBI Taxonomy ID	7227 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7227</a> )	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

## GENOTYPIC CHANGE

TyrRS-m	Generic Gene Name	Q9W107 ( <a href="http://www.uniprot.org/uniprot/Q9W107">http://www.uniprot.org/uniprot/Q9W107</a> )	UniProtKB Drosophila melanogaster
Aatm; Aats-tyr-m; anon-EST:fe1E12; CG16912; Dmel\CG16912	Synonyms	()	GenebankID or UniProtKB
7227.FBpp0072334 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0072334">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0072334</a> )	String		
Belongs to the class-I aminoacyl-tRNA synthetase family.	Sequence Similarities		
GO:0005524 : ATP binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005524">https://www.ebi.ac.uk/QuickGO/term/GO:0005524</a> )	GO - Molecular Function		
GO:0003723 : RNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0003723">https://www.ebi.ac.uk/QuickGO/term/GO:0003723</a> )			

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 (gzfz, 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/FBa0282670.html>

