

GEPHE SUMMARY

MRS1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~MRS1~#gephebase-summary-title)	Gephebase Gene	GP00000678	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)	Trait Category	
	Trait	
	F2 lethality (https://www.gephebase.org/search-criteria?/and+Trait=~F2lethality~#gephebase-summary-title)	
Saccharomyces cerevisiae	Trait State in Taxon A	
	Trait State in Taxon B	
	Saccharomyces bayanus	
Taxon A	Ancestral State	
	Taxonomic Status	
	Interspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Interspecific~#gephebase-summary-title)	

Taxon A #1	
Saccharomyces paradoxus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces paradoxus~#gephebase-summary-title)	Latin Name
	Common Name
	-
AS 2.2401; AS:2.2401; BCRC:22587; CBS 432; CBS:432; CCRC 22587; CCRC:22587; CLIB 228; CLIB:228; DBVPG 6411; DBVPG:6411; IFO 10609; IFO:10609; IGC 4570; IGC:4570; MUCL 31498; MUCL:31498; NCYC 2600; NCYC:2600; NRRL Y-17217; NRRL:Y:17217; PYCC 4570; PYCC:4570	Synonyms
	Rank
	species
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
	Parent
	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
27291 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27291)	NCBI Taxonomy ID
	is Taxon A an Intraspecies?
	No

Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces cerevisiae~#gephebase-summary-title)	Latin Name
	Common Name
	baker’s yeast
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvarum var. melibiosus; baker’s yeast; S. cerevisiae; brewer’s yeast; ATCC 18824; ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Synonyms
	Rank
	species
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
	Parent
	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID
	is Taxon B an Intraspecies?
	No

Taxon A #2	
Saccharomyces bayanus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces bayanus~#gephebase-summary-title)	Latin Name
	Common Name
	-
Saccharomyces bayanus var. bayanus; BCRC:21960; CBS 380; CBS:380; CCRC 21960; CCRC:21960; CLIB 181; CLIB:181; DBVPG 6171; DBVPG:6171; DSM 70412; DSM:70412; IFO 11022; IFO 1127; IFO:11022; IFO:1127; IGC 4456; IGC:4456; JCM 7258; JCM:7258; NCYC 2578; NCYC:2578; NRRL Y-12624; NRRL:Y:12624	Synonyms
	Rank
	species
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
	Parent

Saccharomyces () - (Rank: genus)
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930>)

NCBI Taxonomy ID

4931
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931>)

is Taxon A an Intraspecies?

No

Taxon A #3

Latin Name

Saccharomyces kudriavzevii
(<https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+^Saccharomyces+kudriavzevii^#gephebase-summary-title>)

Common Name

-

Synonyms

Saccharomyces kudriavzevii G.I. Naumov, S.A. James, E.S. Naumova, E.J. Louis & I.N. Roberts, 2000; AS 2.2408; AS:2.2408; ATCC MYA-4449; ATCC:MYA:4449; CBS 8840; CBS:8840; IFO 1802; IFO 1802-2D; IFO:1802; IFO:1802-2D; MUCL 46198; MUCL:46198; NCYC 2889; NCYC:2889

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

Parent

Saccharomyces () - (Rank: genus)
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930>)

NCBI Taxonomy ID

114524
(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=114524>)

is Taxon A an Intraspecies?

No

GENOTYPIC CHANGE

MRS1

Generic Gene Name

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P07266 (<http://www.uniprot.org/uniprot/P07266>)

GenebankID or UniProtKB

PET157; YIR021W

Synonyms

CAA86181 (<https://www.ncbi.nlm.nih.gov/nuccore/CAA86181>)

String

4932.YIR021W
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YIR021W)

Sequence Similarities

-

GO - Molecular Function

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

GO:0004520 : endodeoxyribonuclease activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004520>)

GO:0000402 : crossed form four-way junction DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000402>)

GO:0070336 : flap-structured DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070336>)

GO:0000403 : Y-form DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000403>)

GO - Biological Process

GO:0006397 : mRNA processing (<https://www.ebi.ac.uk/QuickGO/term/GO:0006397>)

GO:0000372 : Group I intron splicing
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000372>)

GO:0000002 : mitochondrial genome maintenance
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000002>)

GO:0000963 : mitochondrial RNA processing
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000963>)

GO - Cellular Component

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>)

GO:1990904 : ribonucleoprotein complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990904>)

Mutation #1

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

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

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

Nonsynonymous

3 non-synonymous changes: Sc to Sp: T201A, V211A, and M227I

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title))

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Thr	Ala	201

Main Reference

Multiple molecular mechanisms cause reproductive isolation between three yeast species. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20652018>)

Authors

Chou JY; Hung YS; Lin KH; Lee HY; Leu JY

Abstract

Nuclear-mitochondrial conflict (cytonuclear incompatibility) is a specific form of Dobzhansky-Muller incompatibility previously shown to cause reproductive isolation in two yeast species. Here, we identified two new incompatible genes, MRS1 and AIM22, through a systematic study of F2 hybrid sterility caused by cytonuclear incompatibility in three closely related *Saccharomyces* species (*S. cerevisiae*, *S. paradoxus*, and *S. bayanus*). MRS1 is a nuclear gene product required for splicing specific introns in the mitochondrial COX1, and Aim22 is a ligase encoded in the nucleus that is required for mitochondrial protein lipoylation. By comparing different species, our result suggests that the functional changes in MRS1 are a result of coevolution with changes in the COX1 introns. Further molecular analyses demonstrate that three nonsynonymous mutations are responsible for the functional differences of MRS1 between these species. Functional complementation assays to determine when these incompatible genes altered their functions show a strong correlation between the sequence-based phylogeny and the evolution of cytonuclear incompatibility. Our results suggest that nuclear-mitochondrial incompatibility may represent a general mechanism of reproductive isolation during yeast evolution.

Additional References

Mutation #2

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

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

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

Nonsynonymous

3 non-synonymous changes: Sc to Sp: T201A, V211A, and M227I

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Linkage+Mapping~#gephebase-summary-title))

Presumptive Null

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Val	Ala	211

Main Reference

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Additional References

Mutation #3

Presumptive Null

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

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

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

Nonsynonymous

3 non-synonymous changes: Sc to Sp: T201A, V211A, and M227I

Linkage Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=`Linkage Mapping`#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=))

Molecular Type

Aberration Type

SNP Coding Change

Molecular Details of the Mutation

Experimental Evidence

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Met	Ile	227

Multiple molecular mechanisms cause reproductive isolation between three yeast species. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20652018>)

Chou JY; Hung YS; Lin KH; Lee HY; Leu JY

Main Reference

Authors

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Additional References

RELATED GEPHE

No matches found.

No matches found.

Related Genes

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect