GEPHE SUMMARY

Gephebase Gene
MRS1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MRS1^#gephebase-summary-title)

GepheID
GP00000678

Entry Status
Published

Main curator
Martin

PHENOTYPIC CHANGE

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

Trait
F2 lethality (https://www.gephebase.org/search-criteria?/and+Trait=^F2 lethality^#gephebase-summary-title)

Trait State in Taxon A
Saccharomyces cerevisiae

Trait State in Taxon B
Saccharomyces bayanus

Ancestral State
Taxon A

Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A #1

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

Common Name
-

Synonyms
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

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
27291 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27291)

is Taxon A an Infraspecies?
No

Taxon A #2

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

Common Name
-

Synonyms
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

Rank
species

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

Parent

Taxon B

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

Common Name
baker's yeast

Synonyms
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

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
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon B an Infraspecies?
No

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 Infraspecies?

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 Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

MRS1

Synonyms

PET157; YIR021W

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)

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

GenebankID or UniProtKB

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

Mutation #1

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

Nonsynonymous

Molecular Details of the Mutation

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

Experimental Evidence

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

	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

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

Nonsynonymous

Molecular Details of the Mutation

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

Experimental Evidence

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

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

Main Reference

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

Authors

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Additional References

Mutation #3

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

Nonsynonymous

Molecular Details of the Mutation

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

Experimental Evidence

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

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

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

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Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect