

GEPHE SUMMARY

AEP2 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=AEP2^#gephebase-summary-title)	Gephebase Gene	GP00000051	GepheID
	Entry Status	Martin	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=Physiology^#gephebase-summary-title)		Trait Category	
Hybrid Incompatibility (F2 sterility) (https://www.gephebase.org/search-criteria?/and+Trait=Hybrid Incompatibility (F2 sterility)^#gephebase-summary-title)		Trait	
Saccharomyces cerevisiae		Trait State in Taxon A	
Saccharomyces bayanus		Trait State in Taxon B	
Data not curated		Ancestral State	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=Domesticated^#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=Saccharomyces cerevisiae^#gephebase-summary-title)		Saccharomyces bayanus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=Saccharomyces bayanus^#gephebase-summary-title)	
Common Name		Common Name	
baker’s yeast		-	
Synonyms		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		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		Rank	
species		species	
Lineage		Lineage	
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Parent		Parent	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	
NCBI Taxonomy ID		NCBI Taxonomy ID	
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)		4931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4931)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No	

GENOTYPIC CHANGE

AEP2		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)	
ATP13; YMR282C; YM8021.08C		P22136 (http://www.uniprot.org/uniprot/P22136)	GenebankID or UniProtKB
4932.YMR282C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YMR282C)		AAA34412 (https://www.ncbi.nlm.nih.gov/nuccore/AAA34412)	
Belongs to the AEP2 family.			
GO - Molecular Function			
GO:0003723 : RNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003723)			
GO - Biological Process			
GO:0070124 : mitochondrial translational initiation (https://www.ebi.ac.uk/QuickGO/term/GO:0070124)			
GO:0006417 : regulation of translation (https://www.ebi.ac.uk/QuickGO/term/GO:0006417)			

GO - Cellular Component

GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)

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

The region between aa 348 and aa 496 plays a critical role. When this region was further dissected in the constructs H-AEP2-bcb and H-AEP2-m3; both failed to restore respiration in the Chromosome 13 line. This result suggests that multiple critical mutations have occurred during the functional diversification of Sc-AEP2 and Sb-AEP2.

Exact causing mutation(s) not determined

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	-	-	-

Main Reference

Incompatibility of nuclear and mitochondrial genomes causes hybrid sterility between two yeast species. (2008) (<https://pubmed.ncbi.nlm.nih.gov/19070577>)

Authors

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Abstract

Hybrids between species are usually unviable or sterile. One possible mechanism causing reproductive isolation is incompatibility between genes from different species. These “speciation” genes are interacting components that cannot function properly when mixed with alleles from other species. To test whether such genes exist in two closely related yeast species, we constructed hybrid lines in which one or two chromosomes were derived from *Saccharomyces bayanus*, and the rest were from *Saccharomyces cerevisiae*. We found that the hybrid line with Chromosome 13 substitution was completely sterile and identified Aep2, a mitochondrial protein encoded on Chromosome 13, to cause the sporulation defect as *S. bayanus* AEP2 is incompatible with *S. cerevisiae* mitochondria. This is caused by the inability of *S. bayanus* Aep2 protein to regulate the translation of the *S. cerevisiae* OLI1 mRNA. We speculate that AEP2 and OLI1 have evolved during the adaptation of *S. bayanus* to nonfermentable carbon sources, thereby driving speciation.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS