GEPHE SUMMARY

Gephebase Gene
CYC8 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^CYC8^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00000195
Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Salt tolerance (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Salt tolerance (experimental evolution)^#gephebase-summary-title)
Trait State in Taxon A
Saccharomyces cerevisiae
Trait State in Taxon B
Saccharomyces cerevisiae
Ancestral State
Taxon A
Taxonomic Status
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#gephebase-summary-title)

Taxon A

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 A an Infraspecies?
No

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

GENOTYPIC CHANGE

Generic Gene Name
CYC8
Synonyms
CRT8; SSN6; YBR112C; YBR0908
String
4932.YBR112C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBR112C)
Sequence Similarities
Belongs to the CYC8/SSN6 family.
GO - Molecular Function
GO:0042826 : histone deacetylase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042826)
GO:0003714 : transcription corepressor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003714)
GO:0003713 : transcription coactivator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003713)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P14922 (http://www.uniprot.org/uniprot/P14922)
GenebankID or UniProtKB
X78993 (https://www.ncbi.nlm.nih.gov/nuccore/X78993)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
GO:0000122 : negative regulation of transcription by RNA polymerase II (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0006338 : chromatin remodeling (https://www.ebi.ac.uk/QuickGO/term/GO:0006338)
GO:0035955 : negative regulation of dipeptide transport by negative regulation of transcription from RNA polymerase II promoter (https://www.ebi.ac.uk/QuickGO/term/GO:0035955)
GO:0016584 : nucleosome positioning (https://www.ebi.ac.uk/QuickGO/term/GO:0016584)
GO:2000531 : regulation of fatty acid biosynthetic process by regulation of transcription from RNA polymerase II promoter (https://www.ebi.ac.uk/QuickGO/term/GO:2000531)
GO:2001020 : regulation of response to DNA damage stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:2001020)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0090568 : nuclear transcriptional repressor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0090568)
GO:0017053 : transcriptional repressor complex (https://www.ebi.ac.uk/QuickGO/term/GO:0017053)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#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

Nonsense

Molecular Details of the Mutation

1bp substitution resulting in premature stop codon

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Determinants of divergent adaptation and Dobzhansky-Muller interaction in experimental yeast populations. (2010) (https://pubmed.ncbi.nlm.nih.gov/20637622)

Authors

Anderson JB; Funt J; Thompson DA; Prabhu S; Socha A; Sirjusingh C; Dettman JR; Parreiras L; Guttman DS; Regev A; Kohn LM

Abstract

Divergent adaptation can be associated with reproductive isolation in speciation [1]. We recently demonstrated the link between divergent adaptation and the onset of reproductive isolation in experimental populations of the yeast Saccharomyces cerevisiae evolved from a single progenitor in either a high-salt or a low-glucose environment [2]. Here, whole-genome resequencing and comparative genome hybridization of representatives of three populations revealed 17 mutations, six of which explained the adaptive increases in mitotic fitness. In two populations evolved in high salt, two different mutations occurred in the proton efflux pump gene PMA1 and the global transcriptional repressor gene CYC8; the ENA genes encoding sodium efflux pumps were overexpressed once through expansion of this gene cluster and once because of mutation in the regulator CYC8. In the population from low glucose, one mutation occurred in MDS3, which modulates growth at high pH, and one in MKT1, a global regulator of mRNAs encoding mitochondrial proteins, the latter recapitulating a naturally occurring variant. A Dobzhansky-Muller (DM) incompatibility between the evolved alleles of PMA1 and MKT1 strongly depressed fitness in the low-glucose environment. This DM interaction is the first reported between experimentally evolved alleles of known genes and shows how reproductive isolation can arise rapidly when divergent selection is strong.

Additional References

Cellular effects and epistasis among three determinants of adaptation in experimental populations of Saccharomyces cerevisiae. (2011) (https://pubmed.ncbi.nlm.nih.gov/21856932)

RELATED GEPHE

Related Genes

4 (ENA1-2-5 cluster, PMA1, TRK1, MEP2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS