

GEPHE SUMMARY

Gephebase Gene
MKT1

Entry Status
Published

GepheID
GP00000662

Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Low-glucose adaptation (experimental evolution)

Trait State in Taxon A
Saccharomyces cerevisiae - 30G laboratory strain

Trait State in Taxon B
Saccharomyces cerevisiae - experimentally evolved lines

Ancestral State
Taxon A

Taxonomic Status
Experimental Evolution

Taxon A

Latin Name

Saccharomyces cerevisiae

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)

NCBI Taxonomy ID

4932

is Taxon A an Intraspecies?

Yes

Taxon A Description

Saccharomyces cerevisiae - 30G laboratory strain

Taxon B

Latin Name

Saccharomyces cerevisiae

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)

NCBI Taxonomy ID

4932

is Taxon B an Intraspecies?

Yes

Taxon B Description

Saccharomyces cerevisiae - 30G laboratory strain + experimental evolution regimen

GENOTYPIC CHANGE

Generic Gene Name
MKT1

Synonyms

YNL085W; N2302

String

4932.YNL085W

Sequence Similarities

-

GO - Molecular Function

GO:0003677 : DNA binding

GO:0017108 : 5'-flap endonuclease activity

GO:0051908 : double-stranded DNA 5'-3' exodeoxyribonuclease activity

GO:0004520 : endodeoxyribonuclease activity

GO:0048256 : flap endonuclease activity

GO:0045145 : single-stranded DNA 5'-3' exodeoxyribonuclease activity

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P40850

GenebankID or UniProtKB

X03534

GO - Biological Process

GO:0006974 : cellular response to DNA damage stimulus

GO:0006281 : DNA repair

GO:0044419 : interspecies interaction between organisms

GO - Cellular Component

GO:0034399 : nuclear periphery

GO:0010494 : cytoplasmic stress granule

GO:0000932 : P-body

GO:0005844 : polysome

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

D30G (reversion; functionally verified); evolved independently in 3 lines

Experimental Evidence

Association Mapping

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

Main Reference

Determinants of divergent adaptation and Dobzhansky-Muller interaction in experimental yeast populations. (2010)

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.

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Additional References

Cellular effects and epistasis among three determinants of adaptation in experimental populations of *Saccharomyces cerevisiae*. (2011)

RELATED GEPHE

Related Genes

12 (COX18, HXT6/7, IRA1, MDS3, MNN4, MTH1, MUK1, RAS1, RAS2, RIM15, SLY41, TAF5)

Related Haplotypes

1

EXTERNAL LINKS

COMMENTS

@Parallelism. Mutation replicated 3 times by experimental evolution; the reverse mutation (see other *MKT1* entry) has evolved in BY laboratory strains by domestication

