GEPHE SUMMARY

Gephebase Gene
MKT1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MKT1^#gephebase-summary-title)

GepheID
GP00000662

Entry Status
Published

Main curator
Courtier

PHENOTYPIC CHANGE

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

Trait
Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Low-glucose adaptation (experimental evolution)^#gephebase-summary-title)

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 (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?
Yes

Taxon A Description
Saccharomyces cerevisiae - 30G laboratory strain

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?
Yes

Taxon B Description
Saccharomyces cerevisiae - 30G laboratory strain + experimental evolution regimen

GENOTYPIC CHANGE

Generic Gene Name
MKT1

Synonyms
YNL085W; N2302

String
4932.YNL085W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YNL085W)

Sequence Similarities
-

GO - Molecular Function
GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
GO:0017108 : 5'-flap endonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0017108)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P40850 (http://www.uniprot.org/uniprot/P40850)

GenebankID or UniProtKB
X03534 (https://www.ncbi.nlm.nih.gov/nuccore/X03534)

GO:0051908 : double-stranded DNA 5′-3′ exodeoxyribonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0051908)
GO:0004520 : endodeoxyribonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004520)
GO:0048256 : flap endonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0048256)
GO:0045145 : single-stranded DNA 5′-3′ exodeoxyribonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0045145)

GO - Biological Process

GO:0006974 : cellular response to DNA damage stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:0006974)
GO:0006281 : DNA repair (https://www.ebi.ac.uk/QuickGO/term/GO:0006281)
GO:0044419 : interspecies interaction between organisms (https://www.ebi.ac.uk/QuickGO/term/GO:0044419)

GO - Cellular Component

GO:0034399 : nuclear periphery (https://www.ebi.ac.uk/QuickGO/term/GO:0034399)
GO:0010494 : cytoplasmic stress granule (https://www.ebi.ac.uk/QuickGO/term/GO:0010494)
GO:0000932 : P-body (https://www.ebi.ac.uk/QuickGO/term/GO:0000932)
GO:0005844 : polysome (https://www.ebi.ac.uk/QuickGO/term/GO:0005844)

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

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

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.

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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

12 (COX18, HXT6/7, IRA1, MDS3, MNN4, MTH1, MUK1, RAS1, RAS2, RIM15, SLY41, TAF5) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^MKT1^/and+Taxon ID=^4932^/or+Gene Gephebase=^MKT1^/and+Taxon ID=^4932^#gephebase-summary-title)

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