

GEPHE SUMMARY

	Gephebase Gene	GephelD
ENA1-2-5 cluster (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ENA1-2-5 cluster">#gephebase-summary-title)	GP00000265	
	Entry Status	Main curator
Published	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	
Data not curated	Taxonomic Status	
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#gephebase-summary-title)		
Taxon A		Taxon B
	Latin Name	Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	
baker's yeast	Common Name	Common Name
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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Synonyms	Synonyms
	Rank	Rank
species	Lineage	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	Parent	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	NCBI Taxonomy ID	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

ENA1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P13587 (http://www.uniprot.org/uniprot/P13587)
HOR6; PMR2; PMR2A; YDR040C; YD6888.02C	Synonyms	GenebankID or UniProtKB Z54075 (https://www.ncbi.nlm.nih.gov/nuccore/Z54075)
4932.YDR040C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YDR040C)	String	
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IID subfamily. GO - Molecular Function	Sequence Similarities	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) GO:0008556 : potassium-transporting ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008556) GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism (https://www.ebi.ac.uk/QuickGO/term/GO:0008553) GO:0008554 : sodium-exporting ATPase activity, phosphorylative mechanism	GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) GO:0008556 : potassium-transporting ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008556) GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism (https://www.ebi.ac.uk/QuickGO/term/GO:0008553) GO:0008554 : sodium-exporting ATPase activity, phosphorylative mechanism	

GO:0055085 : transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)

GO:0006813 : potassium ion transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)

GO:0009651 : response to salt stress (<https://www.ebi.ac.uk/QuickGO/term/GO:0009651>)

GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)

GO:0042149 : cellular response to glucose starvation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042149>)

GO:0006972 : hyperosmotic response

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006972>)

GO:0009268 : response to pH (<https://www.ebi.ac.uk/QuickGO/term/GO:0009268>)

GO - Cellular Component

GO:0016021 : integral component of membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title>)

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Gene+Amplification^#gephebase-summary-title>)

Aberration Type

Complex Change (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Complex+Change^#gephebase-summary-title>)

Molecular Details of the Mutation

uncharacterized expansion

Experimental Evidence

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

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; Parreira 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

4 (CYC8, 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

1 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^ENA1-2-5+cluster^/and+Taxon+ID=^4932^/or+Gene+Gephebase=^ENA1-2-5+cluster^/and+Taxon+ID=^4932^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

Cluster of paralogous genes ; Expansion is highly repeatable