

GEPHE SUMMARY

	Gephebase Gene		GepheID
ENA1-2-5 cluster (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^ENA1-2-5 cluster^#gephebase-summary-title)		GP00000265	
	Entry Status	Martin	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^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+TaxonomicStatus=^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)	
	Common Name		Common Name
baker’s yeast		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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae		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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
	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)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
ENA1		P13587 (http://www.uniprot.org/uniprot/P13587)	
	Synonyms		GenebankID or UniProtKB
HOR6; PMR2; PMR2A; YDR040C; YD6888.02C		Z54075 (https://www.ncbi.nlm.nih.gov/nuccore/Z54075)	
	String		
4932.YDR040C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YDR040C)			
	Sequence Similarities		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IID subfamily.			
	GO - Molecular Function		
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			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008554>)

GO - Biological Process

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; 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 <i>Saccharomyces cerevisiae</i> 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 <i>Saccharomyces cerevisiae</i> . (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