

GEPHE SUMMARY

SUL1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=SUL1^#gephebase-summary-title)	Gephebase Gene	GP00001083	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=Physiology^#gephebase-summary-title)	Trait Category		
Low-sulfate adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=Low-sulfate+adaptation+(experimental+evolution)^#gephebase-summary-title)	Trait		
Saccharomyces cerevisiae	Trait State in Taxon A		
Saccharomyces cerevisiae	Trait State in Taxon B		
Data not curated	Ancestral State		
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Experimental+Evolution^#gephebase-summary-title)	Taxonomic Status		
	Taxon A		Taxon B
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Saccharomyces+cerevisiae^#gephebase-summary-title)	Latin Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Saccharomyces+cerevisiae^#gephebase-summary-title)	Latin Name
baker's yeast	Common Name	baker's yeast	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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	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	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	Parent
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

SUL1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P38359 (http://www.uniprot.org/uniprot/P38359)	GenebankID or UniProtKB
SFP2; YBR294W; YBR2110	Synonyms	Z36163 (https://www.ncbi.nlm.nih.gov/nuccore/Z36163)	
4932.YBR294W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YBR294W)	String		
Belongs to the SLC26A/SulP transporter (TC 2.A.53) family.	Sequence Similarities		
GO:0015301 : anion:anion antiporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015301)	GO - Molecular Function		
GO:0008271 : secondary active sulfate transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008271)			
GO:0015116 : sulfate transmembrane transporter activity			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0015116>)

GO - Biological Process

GO:0055085 : transmembrane transport

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

GO:0008272 : sulfate transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0008272>)

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](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=))

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

out of 16 lines; 15 distinct SUL1 amplification alleles evolved. Copy number ranged from 2 to 16 ; Amplicon size ranged from 2.5kb to 40kb

Experimental Evidence

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

Main Reference

The repertoire and dynamics of evolutionary adaptations to controlled nutrient-limited environments in yeast. (2008) (<https://pubmed.ncbi.nlm.nih.gov/19079573>)

Authors

Gresham D; Desai MM; Tucker CM; Jenq HT; Pai DA; Ward A; DeSevo CG; Botstein D; Dunham MJ

Abstract

The experimental evolution of laboratory populations of microbes provides an opportunity to observe the evolutionary dynamics of adaptation in real time. Until very recently, however, such studies have been limited by our inability to systematically find mutations in evolved organisms. We overcome this limitation by using a variety of DNA microarray-based techniques to characterize genetic changes -- including point mutations, structural changes, and insertion variation -- that resulted from the experimental adaptation of 24 haploid and diploid cultures of *Saccharomyces cerevisiae* to growth in either glucose, sulfate, or phosphate-limited chemostats for approximately 200 generations. We identified frequent genomic amplifications and rearrangements as well as novel retrotransposition events associated with adaptation. Global nucleotide variation detection in ten clonal isolates identified 32 point mutations. On the basis of mutation frequencies, we infer that these mutations and the subsequent dynamics of adaptation are determined by the batch phase of growth prior to initiation of the continuous phase in the chemostat. We relate these genotypic changes to phenotypic outcomes, namely global patterns of gene expression, and to increases in fitness by 5-50%. We found that the spectrum of available mutations in glucose- or phosphate-limited environments combined with the batch phase population dynamics early in our experiments allowed several distinct genotypic and phenotypic evolutionary pathways in response to these nutrient limitations. By contrast, sulfate-limited populations were much more constrained in both genotypic and phenotypic outcomes. Thus, the reproducibility of evolution varies with specific selective pressures, reflecting the constraints inherent in the system-level organization of metabolic processes in the cell. We were able to relate some of the observed adaptive mutations (e.g., transporter gene amplifications) to known features of the relevant metabolic pathways, but many of the mutations pointed to genes not previously associated with the relevant physiology. Thus, in addition to answering basic mechanistic questions about evolutionary mechanisms, our work suggests that experimental evolution can also shed light on the function and regulation of individual metabolic pathways.

Additional References

Whole-genome sequencing of a laboratory-evolved yeast strain. (2010) (<https://pubmed.ncbi.nlm.nih.gov/20128923>)

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS