

GEPHE SUMMARY

	Gephebase Gene		GepheID
PHO5 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~PHO5~#gephebase-summary-title)		GP00000864	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)			
	Trait		
Low-phosphate adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=~Low-phosphate adaptation (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; Saccaromyces 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; Saccaromyces 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)
PHO5		P00635 (http://www.uniprot.org/uniprot/P00635)	
	Synonyms		GenebankID or UniProtKB
YBR093C; YBR0814		V01320 (https://www.ncbi.nlm.nih.gov/nuccore/V01320)	
	String		
4932.YBR093C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YBR093C)			
	Sequence Similarities		
Belongs to the histidine acid phosphatase family.			
	GO - Molecular Function		
GO:0003993 : acid phosphatase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003993)			
GO:0017111 : nucleoside-triphosphatase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0017111)			
GO:0047429 : nucleoside-triphosphate diphosphatase activity			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0047429>)

GO - Biological Process

GO:0016036 : cellular response to phosphate starvation

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016036>)

GO:0006796 : phosphate-containing compound metabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006796>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)

GO:0009277 : fungal-type cell wall (<https://www.ebi.ac.uk/QuickGO/term/GO:0009277>)

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

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

Insertion Size

1-10 kb

Molecular Details of the Mutation

Gene duplication. Out of 8 lines; 2 distinct lines evolved structural variation at PHO5. (Interestingly; one was a deletion and another one was a gene amplification)

Experimental Evidence

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

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

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

1 (<https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^PHO5^/and+Taxon ID=^4932^/or+Gene Gephebase=^PHO5^/and+Taxon ID=^4932^#gephebase-summary-title>)

EXTERNAL LINKS

COMMENTS

Two independent alleles