GEPHE SUMMARY

Gephebase Gene

SIR2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^SIR2^#gephebase-summary-title)

GepheID

GP00001054

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

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

Trait State in Taxon A

Saccharomyces cerevisiae - lab strain S288c

Trait State in Taxon B

Saccharomyces cerevisiae - clinical strain YJM145

Ancestral State

Data not curated

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#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 - lab strain S288c

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 - clinical strain YJM145

GENOTYPIC CHANGE

Generic Gene Name

SIR2

Synonyms

MAR1; YDL042C; D2714

String

4932.YDL042C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YDL042C)

Sequence Similarities

Belongs to the sirtuin family. Class I subfamily.

GO - Molecular Function

GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0034739 : histone deacetylase activity (H4-K16 specific) (https://www.ebi.ac.uk/QuickGO/term/GO:0034739)
GO:0070403 : NAD+ binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070403)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P06700 (http://www.uniprot.org/uniprot/P06700)

GenebankID or UniProtKB

Z74090 (https://www.ncbi.nlm.nih.gov/nuccore/Z74090)

GO:0017136 : NAD-dependent histone deacetylase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0017136)
GO:0032041 : NAD-dependent histone deacetylase activity (H3-K14 specific)
(https://www.ebi.ac.uk/QuickGO/term/GO:0032041)
GO:0046969 : NAD-dependent histone deacetylase activity (H3-K9 specific)
(https://www.ebi.ac.uk/QuickGO/term/GO:0046969)
GO:0046970 : NAD-dependent histone deacetylase activity (H4-K16 specific)
(https://www.ebi.ac.uk/QuickGO/term/GO:0046970)
GO:0045129 : NAD-independent histone deacetylase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0045129)

GO - Biological Process

GO:0006325 : chromatin organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0006325)
GO:0034398 : telomere tethering at nuclear periphery
(https://www.ebi.ac.uk/QuickGO/term/GO:0034398)
GO:0001302 : replicative cell aging (https://www.ebi.ac.uk/QuickGO/term/GO:0001302)
GO:0006333 : chromatin assembly or disassembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0006333)
GO:0000183 : chromatin silencing at rDNA
(https://www.ebi.ac.uk/QuickGO/term/GO:0000183)
GO:0030466 : chromatin silencing at silent mating-type cassette
(https://www.ebi.ac.uk/QuickGO/term/GO:0030466)
GO:0006348 : chromatin silencing at telomere
(https://www.ebi.ac.uk/QuickGO/term/GO:0006348)
GO:0001300 : chronological cell aging
(https://www.ebi.ac.uk/QuickGO/term/GO:0001300)
GO:0006303 : double-strand break repair via nonhomologous end joining
(https://www.ebi.ac.uk/QuickGO/term/GO:0006303)
GO:0097695 : establishment of protein-containing complex localization to telomere
(https://www.ebi.ac.uk/QuickGO/term/GO:0097695)
GO:1904524 : negative regulation of DNA amplification
(https://www.ebi.ac.uk/QuickGO/term/GO:1904524)
GO:0045910 : negative regulation of DNA recombination
(https://www.ebi.ac.uk/QuickGO/term/GO:0045910)
GO:0008156 : negative regulation of DNA replication
(https://www.ebi.ac.uk/QuickGO/term/GO:0008156)
GO:0007062 : sister chromatid cohesion
(https://www.ebi.ac.uk/QuickGO/term/GO:0007062)

GO - Cellular Component

GO:0000790 : nuclear chromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000790)
GO:0005730 : nucleolus (https://www.ebi.ac.uk/QuickGO/term/GO:0005730)
GO:0005677 : chromatin silencing complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005677)
GO:0000784 : nuclear chromosome, telomeric region
(https://www.ebi.ac.uk/QuickGO/term/GO:0000784)
GO:0005720 : nuclear heterochromatin
(https://www.ebi.ac.uk/QuickGO/term/GO:0005720)
GO:0031618 : nuclear pericentric heterochromatin
(https://www.ebi.ac.uk/QuickGO/term/GO:0031618)
GO:0005724 : nuclear telomeric heterochromatin
(https://www.ebi.ac.uk/QuickGO/term/GO:0005724)
GO:0030869 : RENT complex (https://www.ebi.ac.uk/QuickGO/term/GO:0030869)
GO:0034967 : Set3 complex (https://www.ebi.ac.uk/QuickGO/term/GO:0034967)

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

1 to 5 amino-acid substitutions

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

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

No matches found.

EXTERNAL LINKS

COMMENTS