GEPHE SUMMARY

Gephebase Gene

BMH1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BMH1^#gephebase-summary-title)

GepheID

GP00001498

Entry Status

Published

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

Growth rate (time to diauxic shift) (https://www.gephebase.org/search-criteria?/and+Trait=^Growth rate (time to diauxic shift)^#gephebase-summary-title)

Trait State in Taxon A

Budding yeast UWOPS83-787.3 isolated from Opuntia stricta fruit (Bahamas)

Trait State in Taxon B

Budding yeast evolved clone in 15% glucose 48h condition with decreased average growth rate during fermentation (R ferm) increased time to diauxic shift (T shift) and growth rate during respiration (R resp)

Ancestral State

Taxon A

Taxonomic Status

Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#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

Budding yeast UWOPS83-787.3 isolated from Opuntia stricta fruit (Bahamas)

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

Budding yeast evolved clone in 15% glucose 48h condition with decreased average growth rate during fermentation (R ferm) increased time to diauxic shift (T shift) and growth rate during respiration (R resp)

GENOTYPIC CHANGE

Generic Gene Name

BMH1

Synonyms

APR6; YER177W

String

4932.YER177W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YER177W)

Sequence Similarities

Belongs to the 14-3-3 family.

GO - Molecular Function

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P29311 (http://www.uniprot.org/uniprot/P29311)

GenebankID or UniProtKB

X66206.1 (https://www.ncbi.nlm.nih.gov/nuccore/X66206.1)

GO:0001102 : RNA polymerase II activating transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001102)
GO:0019904 : protein domain specific binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0019904)
GO:0003688 : DNA replication origin binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0003688)
GO:0050815 : phosphoserine residue binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0050815)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0007265 : Ras protein signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0007265)
GO:0007124 : pseudohyphal growth (https://www.ebi.ac.uk/QuickGO/term/GO:0007124)
GO:0030437 : ascospore formation (https://www.ebi.ac.uk/QuickGO/term/GO:0030437)
GO:0070842 : aggresome assembly (https://www.ebi.ac.uk/QuickGO/term/GO:0070842)
GO:0000077 : DNA damage checkpoint
(https://www.ebi.ac.uk/QuickGO/term/GO:0000077)
GO:0034221 : fungal-type cell wall chitin biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0034221)
GO:0005977 : glycogen metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0005977)
GO:0031578 : mitotic spindle orientation checkpoint
(https://www.ebi.ac.uk/QuickGO/term/GO:0031578)
GO:1904667 : negative regulation of ubiquitin protein ligase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:1904667)
GO:0001402 : signal transduction involved in filamentous growth
(https://www.ebi.ac.uk/QuickGO/term/GO:0001402)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0010494 : cytoplasmic stress granule
(https://www.ebi.ac.uk/QuickGO/term/GO:0010494)

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

G>A p.G55D located inside the groove where Bmh1p is expected to interact with other proteins as predicted by docking with arbitrary peptides and with two known Bmh1 protein partners (Serine/threonine-protein phosphatase PP1-2 and Heat shock protein Ssb1)

Experimental Evidence

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

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

Main Reference

Phenotypic and genotypic convergences are influenced by historical contingency and environment in yeast. (2014) (https://pubmed.ncbi.nlm.nih.gov/24164389)

Authors

Spor A; Kvitek DJ; Nidelet T; Martin J; Legrand J; Dillmann C; Bourgais A; de Vienne D; Sherlock G; Sicard D

Abstract

Different organisms have independently and recurrently evolved similar phenotypic traits at different points throughout history. This phenotypic convergence may be caused by genotypic convergence and in addition, constrained by historical contingency. To investigate how convergence may be driven by selection in a particular environment and constrained by history, we analyzed nine life-history traits and four metabolic traits during an experimental evolution of six yeast strains in four different environments. In each of the environments, the population converged toward a different multivariate phenotype. However, the evolution of most traits, including fitness components, was constrained by history. Phenotypic convergence was partly associated with the selection of mutations in genes involved in the same pathway. By further investigating the convergence in one gene, BMH1, mutated in 20% of the evolved populations, we show that both the history and the environment influenced the types of mutations (missense/nonsense), their location within the gene itself, as well as their effects on multiple traits. However, these effects could not be easily predicted from ancestors' phylogeny or past selection. Combined, our data highlight the role of pleiotropy and epistasis in shaping a rugged fitness landscape.

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Additional References

RELATED GEPHE

Related Genes

6 (Allantoin permease DAL4, Allantoinase DAL1, Proline specific permease PUT4, Aquaporin (AQY1), Aquaporin (AQY2), IRA2) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Growth rate/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

10 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^BMH1^/and+Taxon ID=^4932^/or+Gene Gephebase=^BMH1^/and+Taxon ID=^4932^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

Bmh1p functions in nutrient signaling and mitotic cell cycle. Bmh1 has an impact on the reproduction rate in fermentation and respiration the length of fermentation (until the diauxic shift) and on cell size. Which traits controlled by Bmh1p have been selected for in this experiment remains to be studied. Mutations are observed in other genes that may also be causative.