

GEPHE SUMMARY

BMH1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~BMH1~#gephebase-summary-title)	Gephebase Gene	GP00001490	GepheID
	Entry Status	Prigent	Main curator
	Published		

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait Category	
Growth rate (time to diauxic shift) (https://www.gephebase.org/search-criteria?/and+Trait=~Growth rate (time to diauxic shift)~#gephebase-summary-title)		Trait	
Budding yeast Y55 laboratory strain from wine (France)		Trait State in Taxon A	
Budding yeast evolved clone in 1% glucose 96h condition with decreased growth rate during fermentation (R ferm) and increased time to diauxic shift (T shift)		Trait State in Taxon B	
Taxon A		Ancestral State	
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~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)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces cerevisiae~#gephebase-summary-title)	
baker’s yeast		baker’s yeast	
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	
species		species	
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	
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)	
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)	
Yes		Yes	
Budding yeast Y55 laboratory strain from wine (France)		Budding yeast evolved clone in 1% glucose 96h condition with decreased growth rate during fermentation (R ferm) and increased time to diauxic shift (T shift)	

GENOTYPIC CHANGE

BMH1		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)	
APR6; YER177W		P29311 (http://www.uniprot.org/uniprot/P29311)	
4932.YER177W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YER177W)		X66206.1 (https://www.ncbi.nlm.nih.gov/nuccore/X66206.1)	
Belongs to the 14-3-3 family.			
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

Yes ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes))

Molecular Type

Coding ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding))

Aberration Type

SNP ([#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP))

SNP Coding Change

Nonsense

Molecular Details of the Mutation

A>T p.K217* (2 times independently). Truncated protein will lack the final helix of the C-terminus as well as a glutamine repeat known to be involved in protein/protein interactions

Experimental Evidence

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

	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; Bourgaïs 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

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.