

## GEPHE SUMMARY

	Gephebase Gene	GephelD
BMH1 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase=^BMH1">#gephebase-summary-title)	GP00001489	Main curator
Published	Entry Status	Prigent

## PHENOTYPIC CHANGE

Trait Category		Trait	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=^Physiology^#gephebase-summary-title)			
Growth rate (time to diauxic shift) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Criteria=^Growth rate (time to diauxic shift)^#gephebase-summary-title)		Trait State in Taxon A	
Budding yeast Y55 laboratory strain from wine (France)		Trait State in Taxon B	
Budding yeast evolved clone in 1% glucose 48h condition with decreased growth rate during fermentation (R ferm ) and increased time to diauxic shift (T shift )		Ancestral State	
Taxon A			Taxonomic Status
Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )	Latin Name	Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )	Latin Name
baker's yeast	Common Name	baker's yeast	Common Name
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvvarum 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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Synonyms	Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces uvvarum 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; Saccharomyces 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) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )	Parent	Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )	Parent
4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932</a> )	NCBI Taxonomy ID	4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932</a> )	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Budding yeast Y55 laboratory strain from wine (France)	Taxon A Description	Budding yeast evolved clone in 1% glucose 48h condition with decreased growth rate during fermentation (R ferm ) and increased time to diauxic shift (T shift )	Taxon B Description

## GENOTYPIC CHANGE

BMH1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P29311 ( <a href="http://www.uniprot.org/uniprot/P29311">http://www.uniprot.org/uniprot/P29311</a> )
APR6; YER177W	Synonyms	GenebankID or UniProtKB X66206.1 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/X66206.1">https://www.ncbi.nlm.nih.gov/nuccore/X66206.1</a> )
4932.YER177W ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YER177W">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YER177W</a> )	String	
Belongs to the 14-3-3 family.	Sequence Similarities	
GO:0001102 : RNA polymerase II activating transcription factor binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0001102">https://www.ebi.ac.uk/QuickGO/term/GO:0001102</a> )	GO - Molecular Function	

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

G>T p.E214\*. 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; 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) ([#gephebase-summary-title](https://www.gephebase.org/search-criteria/?or+Taxon+ID=^4932+and+Trait=Growth+rate+and+groupHaplotypes=true))

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.