

## GEPHE SUMMARY

**Gephebase Gene**  
BMH1

**Entry Status**  
Published

**GepheID**  
GP00001498

**Main curator**  
Prigent

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Growth rate (time to diauxic shift)

**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

### Taxon A

**Latin Name**  
*Saccharomyces cerevisiae*

**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)

**NCBI Taxonomy ID**  
4932

**is Taxon A an Intraspecies?**  
Yes

**Taxon A Description**  
Budding yeast UWOPS83-787.3 isolated from *Opuntia stricta* fruit (Bahamas)

### Taxon B

**Latin Name**  
*Saccharomyces cerevisiae*

**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)

**NCBI Taxonomy ID**  
4932

**is Taxon B an Intraspecies?**  
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

**Sequence Similarities**  
Belongs to the 14-3-3 family.

**GO - Molecular Function**  
GO:0001102 : RNA polymerase II activating transcription factor binding  
GO:0019904 : protein domain specific binding

**UniProtKB** Saccharomyces cerevisiae (strain ATCC 204508 / S288c)  
P29311

**GenebankID or UniProtKB**  
X66206.1

GO:0003688 : DNA replication origin binding

GO:0050815 : phosphoserine residue binding

#### GO - Biological Process

GO:0043066 : negative regulation of apoptotic process

GO:0000122 : negative regulation of transcription by RNA polymerase II

GO:0007265 : Ras protein signal transduction

GO:0007124 : pseudohyphal growth

GO:0030437 : ascospore formation

GO:0070842 : aggresome assembly

GO:0000077 : DNA damage checkpoint

GO:0034221 : fungal-type cell wall chitin biosynthetic process

GO:0005977 : glycogen metabolic process

GO:0031578 : mitotic spindle orientation checkpoint

GO:1904667 : negative regulation of ubiquitin protein ligase activity

GO:0001402 : signal transduction involved in filamentous growth

#### GO - Cellular Component

GO:0005737 : cytoplasm

GO:0005634 : nucleus

GO:0010494 : cytoplasmic stress granule

#### Presumptive Null

No

#### Molecular Type

Coding

#### Aberration Type

SNP

#### 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

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

#### Main Reference

Phenotypic and genotypic convergences are influenced by historical contingency and environment in yeast. (2014)

#### Authors

Spor A; Kvitek DJ; Nidelet T; Martin J; Legrand J; Dillmann C; Bourgeois 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)

#### Related Haplotypes

10

## 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.