

## GEPHE SUMMARY

### Gephebase Gene

BMH1

### Entry Status

Published

### GepheID

GP00001491

### Main curator

Prigent

## PHENOTYPIC CHANGE

### Trait Category

Physiology

### Trait

Growth rate (time to diauxic shift)

### Trait State in Taxon A

Budding yeast Y55 laboratory strain from wine (France)

### Trait State in Taxon B

Budding yeast evolved clone in 15% glucose 96h condition with decreased growth rate during fermentation (R ferm ) and increased time to diauxic shift (T shift )

### 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; *Saccharomyces 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 Y55 laboratory strain from wine (France)

## 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; *Saccharomyces 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 96h condition with decreased growth rate during fermentation (R ferm ) and increased time to diauxic shift (T shift )

## 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

GO:0003688 : DNA replication origin binding

GO:0050815 : phosphoserine residue binding

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

P29311

### GenebankID or UniProtKB

X66206.1

#### 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.D101N

#### 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; Kvittek 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

## 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.

