

GEPHE SUMMARY

Gephebase Gene
BMH1

Entry Status
Published

GepheID
GP00001489

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 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
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 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; 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 1% glucose 48h 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

Yes

Molecular Type

Coding

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

	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.

