

GEPHE SUMMARY

<p>BMH1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=~BMH1^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001495</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)</p> <p>Growth rate (time to diauxic shift) (https://www.gephebase.org/search-criteria?/and+Trait=~Growth+rate+(time+to+diauxic+shift)^#gephebase-summary-title)</p> <p>Budding yeast UWOPS83-787.3 isolated from <i>Opuntia stricta</i> fruit (Bahamas)</p> <p>Budding yeast evolved clone in 1% 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)</p> <p>Taxon A</p> <p>Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Experimental+Evolution^#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Taxon B</p>	<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology^#gephebase-summary-title)</p> <p>Growth rate (time to diauxic shift) (https://www.gephebase.org/search-criteria?/and+Trait=~Growth+rate+(time+to+diauxic+shift)^#gephebase-summary-title)</p> <p>Budding yeast UWOPS83-787.3 isolated from <i>Opuntia stricta</i> fruit (Bahamas)</p> <p>Budding yeast evolved clone in 1% 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)</p> <p>Taxon A</p> <p>Taxon B</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p> <p>Taxon A Description</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p> <p>Taxon B Description</p>
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GENOTYPIC CHANGE

<p>BMH1</p> <p>APR6; YER177W</p> <p>4932.YER177W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YER177W)</p> <p>Belongs to the 14-3-3 family.</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)</p> <p>P29311 (http://www.uniprot.org/uniprot/P29311)</p> <p>X66206.1 (https://www.ncbi.nlm.nih.gov/nucore/X66206.1)</p>	<p>GenebankID or UniProtKB</p>
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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

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

G>T p.G174V homozygous functionally disruptive 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)

Experimental Evidence

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

	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; Kvitck 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

6 (Allantoin permease DAL4, Allantoinase DAL1, Proline specific permease PUT4, Aquaporin (AQY1), Aquaporin (AQY2), IRA2) (<https://www.gephebase.org/search-criteria?or+Taxon ID=%5E4932%5E/and+Trait=Growth rate/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

10 (<https://www.gephebase.org/search-criteria?or+Gene Gephebase=%5EBMH1%5E/and+Taxon ID=%5E4932%5E/or+Gene Gephebase=%5EBMH1%5E/and+Taxon ID=%5E4932%5E#gephebase-summary-title>)

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.