

TPD3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^TPD3~#gephebase-summary-title)	Gephebase Gene	GP00001499	GepheID
Published	Entry Status	Prigent	Main curator

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)		Trait Category	
Cell size (https://www.gephebase.org/search-criteria?/and+Trait=~Cell+size~#gephebase-summary-title)		Trait	
Budding yeast Y55 laboratory strain from wine (France)		Trait State in Taxon A	
Budding yeast evolved clones in 15% glucose 48h condition		Trait State in Taxon B	
Taxon A		Ancestral State	
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Experimental+Evolution~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae~#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=~Saccharomyces+cerevisiae~#gephebase-summary-title)	
baker’s yeast		baker’s yeast	
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		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	
species		species	
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
NCBI Taxonomy ID 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		NCBI Taxonomy ID 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
Budding yeast Y55 laboratory strain from wine (France)		Budding yeast evolved clones in 15% glucose 48h condition	

TPD3	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)
	Synonyms	P31383 (http://www.uniprot.org/uniprot/P31383)
FUN32; YAL016W		GenebankID or UniProtKB
	String	M98389.1 (https://www.ncbi.nlm.nih.gov/nuccore/M98389.1)
4932.YAL016W (http://string-db.org/newstring_cgj/show_network_section.pl?identifier=4932.YAL016W)	Sequence Similarities	
Belongs to the phosphatase 2A regulatory subunit A family.		
GO:0019888 : protein phosphatase regulator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0019888)	GO - Molecular Function	
GO:0006417 : regulation of translation	GO - Biological Process	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006417>)
GO:0007094 : mitotic spindle assembly checkpoint
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007094>)
GO:0006470 : protein dephosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006470>)

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:0043332 : mating projection tip (<https://www.ebi.ac.uk/QuickGO/term/GO:0043332>)
GO:0005935 : cellular bud neck (<https://www.ebi.ac.uk/QuickGO/term/GO:0005935>)
GO:0005934 : cellular bud tip (<https://www.ebi.ac.uk/QuickGO/term/GO:0005934>)
GO:0000159 : protein phosphatase type 2A complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000159>)
GO:0005816 : spindle pole body (<https://www.ebi.ac.uk/QuickGO/term/GO:0005816>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes^#gephebase-summary-title))

Molecular Type

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

C>T p.Q557* heterozygous nonsense mutation which may cause the larger cell size

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping^#gephebase-summary-title](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; Kvitek DJ; Nidelet T; Martin J; Legrand J; Dillmann C; Bourgaïs 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

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Tpd3p is a regulatory subunit of protein phosphatase 2A (PP2A) and is required for transcription by RNA pol III which when mutated results in larger cell size as well as a general decrease in resistance to stress

