

## GEPHE SUMMARY

TPD3 ( <a href="https://www.gephebase.org/search-criteria/?and+Gene+Gephebase=%TPD3%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Gene Gephebase=%TPD3%#gephebase-summary-title</a> )	Gephebase Gene	GP00001499	GepheID
Published	Entry Status	Prigent	Main curator

## PHENOTYPIC CHANGE

Trait Category			
Physiology ( <a href="https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait+Category=%Physiology%#gephebase-summary-title</a> )	Trait		
Cell size ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=%Cell+size%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=%Cell+size%#gephebase-summary-title</a> )	Trait State in Taxon A		
Budding yeast Y55 laboratory strain from wine (France)	Trait State in Taxon B		
Budding yeast evolved clones in 15% glucose 48h condition	Ancestral State		
Taxon A	Taxonomic Status		
Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Saccharomyces+cerevisiae%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Saccharomyces+cerevisiae%#gephebase-summary-title</a> )	Latin Name	Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Saccharomyces+cerevisiae%#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=%Saccharomyces+cerevisiae%#gephebase-summary-title</a> )	Latin Name
baker's yeast	Common Name	baker's yeast	Common Name
Synonyms		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; Saccharomyces 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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyces cerevisiae; Sccharomyces cerevisiae	
Rank	Rank		
species	Lineage	species	Lineage
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	
Parent		Parent	
Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930</a> )	NCBI Taxonomy ID	Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930</a> )	NCBI Taxonomy ID
4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932</a> )		4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932</a> )	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Budding yeast Y55 laboratory strain from wine (France)	Taxon A Description	Budding yeast evolved clones in 15% glucose 48h condition	Taxon B Description

## GENOTYPIC CHANGE

TPD3	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P31383 ( <a href="http://www.uniprot.org/uniprot/P31383">http://www.uniprot.org/uniprot/P31383</a> )	GenebankID or UniProtKB
FUN32; YAL016W	Synonyms	M98389.1 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/M98389.1">https://www.ncbi.nlm.nih.gov/nuccore/M98389.1</a> )	
4932.YAL016W ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YAL016W">http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YAL016W</a> )	String		
Belongs to the phosphatase 2A regulatory subunit A family.	Sequence Similarities		
GO:0019888 : protein phosphatase regulator activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0019888">https://www.ebi.ac.uk/QuickGO/term/GO:0019888</a> )	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 ([#gephebase-summary-title\)](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Yes)

Molecular Type

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

Aberration Type

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

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

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

Phenotypic and genotypic convergences are influenced by historical contingency and environment in yeast. (2014) (<https://pubmed.ncbi.nlm.nih.gov/24164389>)

Main Reference

Spor A; Kvitek DJ; Nidelet T; Martin J; Legrand J; Dillmann C; Bourgais A; de Vienne D; Sherlock G; Sicard D

Authors

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

No matches found.

Related Haplotypes

No matches found.

## 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

