

GEPHE SUMMARY

	Gephebase Gene	GepheID
Serine/threonine protein kinase RIM15 (#Gephebase-summary-title)	GP00001500	
	Prigent	Main curator
Published	Entry Status	

PHENOTYPIC CHANGE

	Trait Category		
Physiology (#Gephebase-summary-title)	Trait		
Nitrogen use (growth efficiency) (#Gephebase-summary-title)	Trait State in Taxon A		
Budding yeast	Trait State in Taxon B		
Budding yeast European DBVPG6765 (E) from wine	Ancestral State		
Taxon A	Taxonomic Status		
Intraspecific (#Gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Saccharomyces cerevisiae (#Gephebase-summary-title)	Common Name		Common Name
baker's yeast	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; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Rank		Rank
species	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent		Parent
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID		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	Taxon A Description		Taxon B Description
Budding yeast (wild strains - see article)			Budding yeast European DBVPG6765 (E) from wine

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
RIM15	Synonyms	P43565 (http://www.uniprot.org/uniprot/P43565)
TAK1; YFL033C	String	U83459.1 (https://www.ncbi.nlm.nih.gov/nuccore/U83459.1)
4932.YFL033C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YFL033C)	Sequence Similarities	
Belongs to the protein kinase superfamily. Ser/Thr protein kinase family.	GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0004674 : protein serine/threonine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004674)		

GO:0004672 : protein kinase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0004672>)
GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0006468 : protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006468>)
GO:0000160 : phosphorelay signal transduction system
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000160>)
GO:0018105 : peptidyl-serine phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018105>)
GO:0046777 : protein autophosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046777>)
GO:0034605 : cellular response to heat
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034605>)
GO:0035556 : intracellular signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035556>)
GO:0009267 : cellular response to starvation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009267>)
GO:0001324 : age-dependent response to oxidative stress involved in chronological cell aging (<https://www.ebi.ac.uk/QuickGO/term/GO:0001324>)
GO:0006995 : cellular response to nitrogen starvation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006995>)
GO:0010508 : positive regulation of autophagy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010508>)
GO:1903452 : positive regulation of G1 to G0 transition
(<https://www.ebi.ac.uk/QuickGO/term/GO:1903452>)
GO:1901992 : positive regulation of mitotic cell cycle phase transition
(<https://www.ebi.ac.uk/QuickGO/term/GO:1901992>)
GO:0061406 : positive regulation of transcription from RNA polymerase II promoter in response to glucose starvation (<https://www.ebi.ac.uk/QuickGO/term/GO:0061406>)
GO:0061408 : positive regulation of transcription from RNA polymerase II promoter in response to heat stress (<https://www.ebi.ac.uk/QuickGO/term/GO:0061408>)
GO:0051039 : positive regulation of transcription involved in meiotic cell cycle
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051039>)

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>)

Presumptive Null

Yes (<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>)

Aberration Type

Insertion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Insertion~#gephebase-summary-title>)

Insertion Size

1-9 bp

Molecular Details of the Mutation

2 bp insertion 459_460insCA shifting the reading frame to cause an early stop codon (null allele)

Experimental Evidence

Linkage Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title>)

Main Reference

Concerted evolution of life stage performances signals recent selection on yeast nitrogen use. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25349282>)

Authors

Ilbstedt S; Stenberg S; BagÃ©s S; Gjuvsland AB; Salinas F; Kourtchenko O; Samy JK; Blomberg A; Omholt SW; Liti G; Beltran G; Warringer J

Abstract

Exposing natural selection driving phenotypic and genotypic adaptive differentiation is an extraordinary challenge. Given that an organism’s life stages are exposed to the same environmental variations, we reasoned that fitness components, such as the lag, rate, and efficiency of growth, directly reflecting performance in these life stages, should often be selected in concert. We therefore conjectured that correlations between fitness components over natural isolates, in a particular environmental context, would constitute a robust signal of recent selection. Critically, this test for selection requires fitness components to be determined by different genetic loci. To explore our conjecture, we exhaustively evaluated the lag, rate, and efficiency of asexual population growth of natural isolates of the model yeast *Saccharomyces cerevisiae* in a large variety of nitrogen-limited environments. Overall, fitness components were well correlated under nitrogen restriction. Yeast isolates were further crossed in all pairwise combinations and coinheritance of each fitness component and genetic markers were traced. Trait variations tended to map to quantitative trait loci (QTL) that were private to a single fitness component. We further traced QTLs down to single-nucleotide resolution and uncovered loss-of-function mutations in RIM15, PUT4, DAL1, and DAL4 as the genetic basis for nitrogen source use variations. Effects of SNPs were unique for a single fitness component, strongly arguing against pleiotropy between lag, rate, and efficiency of reproduction under nitrogen restriction. The strong correlations between life stage performances that cannot be explained by pleiotropy compellingly support adaptive differentiation of yeast nitrogen source use and suggest a generic approach for detecting selection.

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Additional References

RELATED GEPHE

Related Genes

3 (Allantoin permease DAL4, Allantoinase DAL1, Proline specific permease PUT4) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932~/and+Trait=Nitrogen use/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

RIM15 encodes a poorly understood protein kinase known to control stationary phase entry and sporulation efficiency