

	Gephebase Gene	GepheID
Allantoinase DAL1 (<a +allantoinase+dal1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Allantoinase+DAL1+"#gephebase-summary-title)	GP00001502	Main curator
Published	Entry Status	Prigent

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology~#gephebase-summary-title)		Trait Category	
Nitrogen use (growth rate on allantoin) (https://www.gephebase.org/search-criteria?/and+Trait=~Nitrogen+use+(growth+rate+on+allantoin)~#gephebase-summary-title)		Trait	
Budding yeast		Trait State in Taxon A	
Budding yeast West African DBVPG6044 (WA)		Trait State in Taxon B	
Taxon A		Ancestral State	
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Intraspecific~#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; Saccaromyces 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; Saccaromyces 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=4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		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 (wild strains - see article)		Budding yeast West African DBVPG6044 (WA)	

Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
DAL1	P32375 (http://www.uniprot.org/uniprot/P32375)
YIR027C	M69294.1 (https://www.ncbi.nlm.nih.gov/nucore/M69294.1)
4932.YIR027C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YIR027C)	GenebankID or UniProtKB
Sequence Similarities	
Belongs to the metallo-dependent hydrolases superfamily. Allantoinase family.	
GO - Molecular Function	
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)	
GO:0004038 : allantoinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004038)	
GO:0050897 : cobalt ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0050897)	
GO:0016888 : endodeoxyribonuclease activity, producing 5'-phosphomonoesters	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016888>)

GO - Biological Process

GO:0009442 : allantoin assimilation pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009442>)
GO:0006145 : purine nucleobase catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006145>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

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

c.415C>T p.P139S predicted to be strongly detrimental

Experimental Evidence

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

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

Main Reference

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

Authors

Ibstedt S; Stenberg S; BagÅ©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.

Å© The Author 2014. Published by Oxford University Press on behalf of the Society for Molecular Biology and Evolution. All rights reserved. For permissions, please e-mail: journals.permissions@oup.com.

Additional References

RELATED GEPHE

Related Genes

3 (Allantoin permease DAL4, Proline specific permease PUT4, Serine/threonine protein kinase RIM15) (<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

DAL4 and DAL1 encode enzymes catalyzing the first two steps in allantoin uptake and degradation and are arranged back-to-back in an allantoin use gene cluster

