GEPHE SUMMARY

Gephebase Gene

Allantoin permease DAL4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Allantoin permease DAL4^#gephebase-summary-title)

Entry Status

Published

GephеID

GP00001503

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Nitrogen use (growth rate on allantoin) (https://www.gephebase.org/search-criteria?/and+Trait=^Nitrogen use (growth rate on allantoin)^#gephebase-summary-title)

Trait State in Taxon A

Budding yeast

Trait State in Taxon B

Budding yeast West African DBVPG6044 (WA)

Ancestral State

Taxon A

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

Common Name

baker's yeast

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

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

Parent

Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Budding yeast (wild strains - see article)

Taxon B

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

Common Name

baker's yeast

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

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

Parent

Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Budding yeast West African DBVPG6044 (WA)

GENOTYPIC CHANGE

Generic Gene Name

DAL4

Synonyms

YIR028W

String

4932.YIR028W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YIR028W)

Sequence Similarities

Belongs to the purine-cytosine permease (2.A.39) family.

GO - Molecular Function

GO:0005274 : allantoin:proton symporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005274)
GO:0015205 : nucleobase transmembrane transporter activity (https://www.ebi.ac.uk/QuickGO/term/GO:0015205)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) Q04895 (http://www.uniprot.org/uniprot/Q04895)

GenebankID or UniProtKB

()

GO - Biological Process

GO:0000256 : allantoin catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0000256)
GO:0015720 : allantoin transport (https://www.ebi.ac.uk/QuickGO/term/GO:0015720)
GO:0006144 : purine nucleobase metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006144)

GO - Cellular Component

GO:0016021 : integral component of membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)

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

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

Indel Size

1-9 bp

Molecular Details of the Mutation

c.1201delA a single nucleotide frameshifting insertion (deletion?)

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

Ibstedt 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 (Allantoinase DAL1, 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