GEPHE SUMMARY

Gephebase Gene
GAL3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^GAL3^#gephebase-summary-title)

GepheID
GP00001426

Entry Status
Published

Main curator
Prigent

PHENOTYPIC CHANGE

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

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

Trait State in Taxon A
Yeast without growth lag because GAL genes not repressed on glucose-galactose medium

Trait State in Taxon B
Yeast with growth lag because GAL genes repressed on glucose-galactose medium

Ancestral State
Taxon A

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

Taxon A

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

Common Name
-

Synonyms
Saccharomyces bayanus var. bayanus; BCRC:21960; CBS 380; CBS:380; CCRC 21960; CCRC:21960; CLIB 181; CLIB:181; DBVPG 6171; DBVPG:6171; DSM 70412; DSM:70412; IFO 11022; IFO 1127; IFO:11022; IFO:1127; IGC 4456; IGC:4456; JCM 7258; JCM:7258; NCYC 2578; NCYC:2578; NRRL Y-12624; NRRL:Y:12624

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
4931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4931)

is Taxon A an Infraspecies?
No

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?
No

GENOTYPIC CHANGE

Generic Gene Name
GAL3

Synonyms
YDR009W; YD8119.14

String
4932.YDR009W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YDR009W)

Sequence Similarities
Belongs to the GHMP kinase family. GalK subfamily.

GO - Molecular Function
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0004335 : galactokinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004335)
GO:0005534 : galactose binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005534)

GO - Biological Process
GO:0006012 : galactose metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006012)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P13045 (http://www.uniprot.org/uniprot/P13045)

GenebankID or UniProtKB
NM_001180317 (https://www.ncbi.nlm.nih.gov/nuccore/NM_001180317)

GO:0033499 : galactose catabolic process via UDP-galactose (https://www.ebi.ac.uk/QuickGO/term/GO:0033499)
GO:0045185 : maintenance of protein location (https://www.ebi.ac.uk/QuickGO/term/GO:0045185)
GO:0000435 : positive regulation of transcription from RNA polymerase II promoter by galactose (https://www.ebi.ac.uk/QuickGO/term/GO:0000435)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

Polygenic evolution of a sugar specialization trade-off in yeast. (2016) (https://pubmed.ncbi.nlm.nih.gov/26863195)

Authors

Roop JI; Chang KC; Brem RB

Abstract

The evolution of novel traits can involve many mutations scattered throughout the genome. Detecting and validating such a suite of alleles, particularly if they arose long ago, remains a key challenge in evolutionary genetics. Here we dissect an evolutionary trade-off of unprecedented genetic complexity between long-diverged species. When cultured in 1% glucose medium supplemented with galactose, Saccharomyces cerevisiae, but not S. bayanus or other Saccharomyces species, delayed commitment to galactose metabolism until glucose was exhausted. Promoters of seven galactose (GAL) metabolic genes from S. cerevisiae, when introduced together into S. bayanus, largely recapitulated the delay phenotype in 1% glucose-galactose medium, and most had partial effects when tested in isolation. Variation in GAL coding regions also contributed to the delay when tested individually in 1% glucose-galactose medium. When combined, S. cerevisiae GAL coding regions gave rise to profound growth defects in the S. bayanus background. In medium containing 2.5% glucose supplemented with galactose, wild-type S. cerevisiae repressed GAL gene expression and had a robust growth advantage relative to S. bayanus; transgenesis of S. cerevisiae GAL promoter alleles or GAL coding regions was sufficient for partial reconstruction of these phenotypes. S. cerevisiae GAL genes thus encode a regulatory program of slow induction and avid repression, and a fitness detriment during the glucose-galactose transition but a benefit when glucose is in excess. Together, these results make clear that genetic mapping of complex phenotypes is within reach, even in deeply diverged species.

Additional References

RELATED GEPHE

Related Genes

3 (GAL1, GAL10, GAL4) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4931^/and+Trait=Carbohydrate metabolism/or+Taxon ID=^4932^/and+Trait=Carbohydrate metabolism/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

it is unclear if the change is only cis-regulatory