

	Gephebase Gene	GepheID
GAL3 (<a +gal3+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+GAL3+"#gephebase-summary-title)	GP00001426	Main curator
	Entry Status	
Published	Prigent	

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=~Physiology~#gephebase-summary-title)		Trait Category
Carbohydrate metabolism (https://www.gephebase.org/search-criteria?/and+Trait=~Carbohydrate metabolism~#gephebase-summary-title)		Trait
Yeast without growth lag because GAL genes not repressed on glucose-galactose medium		Trait State in Taxon A
Yeast with growth lag because GAL genes repressed on glucose-galactose medium		Trait State in Taxon B
		Ancestral State
Taxon A		Taxonomic Status
Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=~Interspecific~#gephebase-summary-title)		
Taxon A		Taxon B
Saccharomyces bayanus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces bayanus~#gephebase-summary-title)	Latin Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=~Saccharomyces cerevisiae~#gephebase-summary-title)
-	Common Name	baker's yeast
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	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; Saccharomyces cerevisiae; Saccharomyces cerevisiae; Saccharomyces cerevisiae
species	Rank	species
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage	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)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
4931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4931)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
No	is Taxon A an Intraspecies?	No

Gal3	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
	Synonyms	P13045 (http://www.uniprot.org/uniprot/P13045)
YDR009W; YD8119.14		GenebankID or UniProtKB
	String	NM_001180317 (https://www.ncbi.nlm.nih.gov/nucore/NM_001180317)
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)		

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, <i>Saccharomyces cerevisiae</i>, but not <i>S. bayanus</i> or other <i>Saccharomyces</i> species, delayed commitment to galactose metabolism until glucose was exhausted. Promoters of seven galactose (GAL) metabolic genes from <i>S. cerevisiae</i>, when introduced together into <i>S. bayanus</i>, 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, <i>S. cerevisiae</i> GAL coding regions gave rise to profound growth defects in the <i>S. bayanus</i> background. In medium containing 2.5% glucose supplemented with galactose, wild-type <i>S. cerevisiae</i> repressed GAL gene expression and had a robust growth advantage relative to <i>S. bayanus</i>; transgenesis of <i>S. cerevisiae</i> GAL promoter alleles or GAL coding regions was sufficient for partial reconstruction of these phenotypes. <i>S. cerevisiae</i> 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