

GAL1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~GAL1~#gephebase-summary-title)	Gephebase Gene	GP00001425	GepheID
Published	Entry Status	Prigent	Main curator

Trait Category		Trait		Trait State in Taxon A		Trait State in Taxon B		Ancestral State		Taxonomic Status	
Physiology (#https://www.gephebase.org/search-criteria?/and+Trait+Category=~Physiology)		Carbohydrate metabolism (#https://www.gephebase.org/search-criteria?/and+Trait=~Carbohydrate+metabolism)		Yeast without growth lag because GAL genes not repressed on glucose-galactose medium		Yeast with growth lag because GAL genes repressed on glucose-galactose medium					
Taxon A		Taxon B		Taxon A		Taxon B		Taxon A		Taxon B	
Interspecific (#https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=~Interspecific)		Saccharomyces bayanus (#https://www.gephebase.org/search-criteria?/and+Taxon+Synonyms=~Saccharomyces+bayanus)		Saccharomyces cerevisiae (#https://www.gephebase.org/search-criteria?/and+Taxon+Synonyms=~Saccharomyces+cerevisiae)		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		Saccharomyces cerevisiae var. cerevisiae; 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		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	
-		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		Saccharomyces cerevisiae var. cerevisiae; 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		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		Saccharomyces cerevisiae var. cerevisiae; 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	
species		species		species		species		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		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		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)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
NCBI Taxonomy ID 4931		NCBI Taxonomy ID 4932		NCBI Taxonomy ID 4931		NCBI Taxonomy ID 4932		NCBI Taxonomy ID 4931		NCBI Taxonomy ID 4932	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?		is Taxon A an Intraspecies?		is Taxon B an Intraspecies?		is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
No		No		No		No		No		No	

Gal1	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / S288c)
YBR020W; YBR0302	Synonyms	P04385 (http://www.uniprot.org/uniprot/P04385)
4932.YBR020W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YBR020W)	String	GenebankID or UniProtKB NM_001178368 (https://www.ncbi.nlm.nih.gov/nuccore/NM_001178368)
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:0000411 : positive regulation of transcription by galactose (https://www.ebi.ac.uk/QuickGO/term/GO:0000411)		

GO:0046835 : carbohydrate phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046835>)
GO:0033499 : galactose catabolic process via UDP-galactose
(<https://www.ebi.ac.uk/QuickGO/term/GO:0033499>)

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>)

Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Unknown^#gephebase-summary-title)	Presumptive Null
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)	Experimental Evidence
Polygenic evolution of a sugar specialization trade-off in yeast. (2016) (https://pubmed.ncbi.nlm.nih.gov/26863195)	Main Reference
Roop JI; Chang KC; Brem RB	Authors

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.	Abstract
	Additional References

RELATED GEPHE

3 (GAL10, GAL3, 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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

it is unclear if the change is only cis-regulatory