

GEPHE SUMMARY

	Gephebase Gene		GepheID
GAL10 (<a +gal10+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+GAL10+"#gephebase-summary-title)		GP00001428	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
	Trait		
Carbohydrate metabolism (<a +carbohydrate+metabolism+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Saccharomyces bayanus (<a +saccharomyces+bananus+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Saccharomyces+bananus+"#gephebase-summary-title)		Saccharomyces cerevisiae (<a +saccharomyces+cerevisiae+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Saccharomyces+cerevisiae+"#gephebase-summary-title)	
	Common Name		Common Name
-		baker’s yeast	
	Synonyms		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		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		Rank
species		species	
	Lineage		Lineage
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	
	Parent		Parent
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)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4931)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
GAL10		P04397 (http://www.uniprot.org/uniprot/P04397)	
	Synonyms		GenebankID or UniProtKB
YBR019C; YBR0301		K02115 (https://www.ncbi.nlm.nih.gov/nuccore/K02115)	
	String		
4932.YBR019C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YBR019C)			
	Sequence Similarities		
In the N-terminal section; belongs to the NAD(P)-dependent epimerase/dehydratase family.;In the C-terminal section; belongs to the aldose epimerase family.			
	GO - Molecular Function		
GO:0030246 : carbohydrate binding (https://www.ebi.ac.uk/QuickGO/term/GO:0030246)			
GO:0004034 : aldose 1-epimerase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004034)			
GO:0003978 : UDP-glucose 4-epimerase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003978)			

GO - Biological Process

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

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

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

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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, 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 Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

it is unclear if the change is only cis-regulatory