

GEPHE SUMMARY

<p>GAL4 (<a +gal4+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+GAL4+"#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001427</p> <p>Prigent</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>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)</p> <p>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)</p> <p>Yeast without growth lag because GAL genes not repressed on glucose-galactose medium</p> <p>Yeast with growth lag because GAL genes repressed on glucose-galactose medium</p> <p>Taxon A</p> <p>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)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>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)</p> <p>-</p> <p>Synonyms</p> <p>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</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces</p> <p>Parent</p> <p>Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)</p> <p>NCBI Taxonomy ID</p> <p>4931 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4931)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>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)</p> <p>Common Name</p> <p>baker's yeast</p> <p>Synonyms</p> <p>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; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces</p> <p>Parent</p> <p>Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)</p> <p>NCBI Taxonomy ID</p> <p>4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)</p> <p>is Taxon B an Intraspecies?</p> <p>No</p>
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GENOTYPIC CHANGE

<p>GAL4</p> <p>GAL81; YPL248C</p> <p>4932.YPL248C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YPL248C)</p> <p>-</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P04386 (http://www.uniprot.org/uniprot/P04386)</p> <p>GenebankID or UniProtKB NM_001184062 (https://www.ncbi.nlm.nih.gov/nuccore/NM_001184062)</p> <p>GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)</p> <p>GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)</p> <p>GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)</p> <p>GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA</p>
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polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000978>)
GO:0001085 : RNA polymerase II transcription factor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001085>)

GO - Biological Process

GO:0006351 : transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006351>)
GO:0006012 : galactose metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006012>)
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: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, GAL3) (<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