

GEPHE SUMMARY

	Gephebase Gene	GepheID
GAL1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="GAL1">#gephebase-summary-title)	GP00000385	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology">#gephebase-summary-title)	Trait
Carbohydrate metabolism (galactose) (https://www.gephebase.org/search-criteria?/and+Trait=^Carbohydrate+metabolism+(galactose)^#gephebase-summary-title)	Trait State in Taxon A
Kluyveromyces lactis	Trait State in Taxon B
Saccharomyces cerevisiae	Ancestral State
Data not curated	Taxonomic Status
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Intergeneric or Higher">#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Kluyveromyces lactis (#gephebase-summary-title)		Saccharomyces cerevisiae (#gephebase-summary-title)	
-	Common Name	baker's yeast	Common Name
Kluyveromyces drosophilicola; Kluyveromyces lactis var. drosophilicola; Kluyveromyces lactis var. lactis; Kluyveromyces marxianus lactis; Kluyveromyces marxianus var. drosophilicola; Kluyveromyces marxianus var. lactis; ATCC 56498; ATCC:56498; CBS 2105; CBS 683; CBS:2105; CBS:683; NRRL Y-8278; NRRL Y-8279; NRRL:Y-8278; NRRL:Y-8279	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; Sccharomyces cerevisiae	
species	Rank	species	Rank
cellular organisms; Eukaryota; Opistokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Kluyveromyces	Lineage	cellular organisms; Eukaryota; Opistokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Lineage
Kluyveromyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4910)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID
28985 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=28985)	NCBI Taxonomy ID	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon B an Infraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37)
GAL1		
KLLA0F08393g	Synonyms	P09608 (http://www.uniprot.org/uniprot/P09608)
284590.XP_455461.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=284590.XP_455461.1)	String	GenebankID or UniProtKB CAA84962 (https://www.ncbi.nlm.nih.gov/nuccore/CAA84962)
Belongs to the GHMP kinase family. GalK subfamily.	Sequence Similarities	
	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 - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title>)

Molecular Type

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

Aberration Type

Complex Change (<https://www.gephebase.org/search-criteria/?and+Aberration+Type=%Complex+Change%#gephebase-summary-title>)

Molecular Details of the Mutation

Helical phasing of GAL4 elements in promoter region following duplication

Experimental Evidence

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

Main Reference

Gene duplication and the adaptive evolution of a classic genetic switch. (2007) (<https://pubmed.ncbi.nlm.nih.gov/17928853>)

Authors

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Abstract

How gene duplication and divergence contribute to genetic novelty and adaptation has been of intense interest, but experimental evidence has been limited. The genetic switch controlling the yeast galactose use pathway includes two paralogous genes in *Saccharomyces cerevisiae* that encode a co-inducer (GAL3) and a galactokinase (GAL1). These paralogues arose from a single bifunctional ancestral gene as is still present in *Kluyveromyces lactis*. To determine which evolutionary processes shaped the evolution of the two paralogues, here we assess the effects of precise replacement of coding and non-coding sequences on organismal fitness. We suggest that duplication of the ancestral bifunctional gene allowed for the resolution of an adaptive conflict between the transcriptional regulation of the two gene functions. After duplication, previously disfavoured binding site configurations evolved that divided the regulation of the ancestral gene into two specialized genes, one of which ultimately became one of the most tightly regulated genes in the genome.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Duplication