

## GEPHE SUMMARY

**Gephebase Gene**  
RIM15

**Entry Status**  
Published

**GepheID**  
GP00000989

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Low-glucose adaptation (experimental evolution)

**Trait State in Taxon A**  
Saccharomyces cerevisiae

**Trait State in Taxon B**  
Saccharomyces cerevisiae

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Experimental Evolution

### Taxon A

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
baker's yeast

**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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
baker's yeast

**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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
RIM15

**Synonyms**  
TAK1; YFL033C

**String**  
4932.YFL033C

**Sequence Similarities**  
Belongs to the protein kinase superfamily. Ser/Thr protein kinase family.

**GO - Molecular Function**  
GO:0005524 : ATP binding  
GO:0004674 : protein serine/threonine kinase activity  
GO:0004672 : protein kinase activity

**GO - Biological Process**  
GO:0045944 : positive regulation of transcription by RNA polymerase II  
GO:0006468 : protein phosphorylation  
GO:0000160 : phosphorelay signal transduction system  
GO:0018105 : peptidyl-serine phosphorylation

**UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)**  
P43565

**GenebankID or UniProtKB**  
D50617

GO:0046777 : protein autophosphorylation  
GO:0034605 : cellular response to heat  
GO:0035556 : intracellular signal transduction  
GO:0009267 : cellular response to starvation  
GO:0001324 : age-dependent response to oxidative stress involved in chronological cell aging  
GO:0006995 : cellular response to nitrogen starvation  
GO:0010508 : positive regulation of autophagy  
GO:1903452 : positive regulation of G1 to G0 transition  
GO:1901992 : positive regulation of mitotic cell cycle phase transition  
GO:0061406 : positive regulation of transcription from RNA polymerase II promoter in response to glucose starvation  
GO:0061408 : positive regulation of transcription from RNA polymerase II promoter in response to heat stress  
GO:0051039 : positive regulation of transcription involved in meiotic cell cycle

#### GO - Cellular Component

GO:0005737 : cytoplasm  
GO:0005634 : nucleus

#### Presumptive Null

Yes

#### Molecular Type

Coding

#### Aberration Type

Deletion

#### Deletion Size

1-9 bp

#### Molecular Details of the Mutation

1bp deletion resulting in premature stop codon

#### Experimental Evidence

Association Mapping

#### Main Reference

Molecular characterization of clonal interference during adaptive evolution in asexual populations of *Saccharomyces cerevisiae*. (2008)

#### Authors

Kao KC; Sherlock G

#### Abstract

The classical model of adaptive evolution in an asexual population postulates that each adaptive clone is derived from the one preceding it. However, experimental evidence has suggested more complex dynamics, with theory predicting the fixation probability of a beneficial mutation as dependent on the mutation rate, population size and the mutation's selection coefficient. Clonal interference has been demonstrated in viruses and bacteria but not in a eukaryote, and a detailed molecular characterization is lacking. Here we use three different fluorescent markers to visualize the dynamics of asexually evolving yeast populations. For each adaptive clone within one of our evolving populations, we identified the underlying mutations, monitored their population frequencies and used microarrays to characterize changes in the transcriptome. These results represent the most detailed molecular characterization of experimental evolution to date and provide direct experimental evidence supporting both the clonal interference and the multiple mutation models.

#### Additional References

Reciprocal sign epistasis between frequently experimentally evolved adaptive mutations causes a rugged fitness landscape. (2011)

## RELATED GEPHE

#### Related Genes

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RAS2, SLY41, TAF5)

#### Related Haplotypes

No matches found.

## COMMENTS