

GEPHE SUMMARY

| | | | |
|---|----------------|------------|--------------|
| RIM15 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+RIM15+gephebase-summary-title) | Gephebase Gene | GP00000989 | GepheID |
| Published | Entry Status | Martin | Main curator |

PHENOTYPIC CHANGE

| | | | |
|--|-----------------------------|---|-----------------------------|
| Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+gephebase-summary-title) | Trait Category | | |
| Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait+Low-glucose+adaptation+(experimental+evolution)+gephebase-summary-title) | Trait | | |
| Saccharomyces cerevisiae | Trait State in Taxon A | | |
| Saccharomyces cerevisiae | Trait State in Taxon B | | |
| Taxon A | Ancestral State | | |
| Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Experimental+Evolution+gephebase-summary-title) | Taxonomic Status | | |
| | Taxon A | | Taxon B |
| Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Saccharomyces+cerevisiae+gephebase-summary-title) | Latin Name | Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms+Saccharomyces+cerevisiae+gephebase-summary-title) | Latin Name |
| baker's yeast | Common Name | baker's yeast | Common Name |
| 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 | 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 | Synonyms |
| species | Rank | species | Rank |
| cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces | Lineage | cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces | Lineage |
| Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932) | Parent | Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932) | Parent |
| 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932) | NCBI Taxonomy ID | 4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932) | NCBI Taxonomy ID |
| No | is Taxon A an Intraspecies? | No | is Taxon B an Intraspecies? |

GENOTYPIC CHANGE

| | | | |
|--|-------------------------|--|-------------------------|
| RIM15 | Generic Gene Name | UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P43565 (http://www.uniprot.org/uniprot/P43565) | GenebankID or UniProtKB |
| TAK1; YFL033C | Synonyms | D50617 (https://www.ncbi.nlm.nih.gov/nuccore/D50617) | |
| 4932.YFL033C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YFL033C) | String | | |
| Belongs to the protein kinase superfamily. Ser/Thr protein kinase family. | Sequence Similarities | | |
| GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) | GO - Molecular Function | | |
| GO:0004674 : protein serine/threonine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004674) | | | |
| GO:0004672 : protein kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004672) | GO - Biological Process | | |

GO:0045944 : positive regulation of transcription by RNA polymerase II
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
 GO:0006468 : protein phosphorylation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
 GO:0000160 : phosphorelay signal transduction system
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000160)
 GO:0018105 : peptidyl-serine phosphorylation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0018105)
 GO:0046777 : protein autophosphorylation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0046777)
 GO:0034605 : cellular response to heat
 (https://www.ebi.ac.uk/QuickGO/term/GO:0034605)
 GO:0035556 : intracellular signal transduction
 (https://www.ebi.ac.uk/QuickGO/term/GO:0035556)
 GO:0009267 : cellular response to starvation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0009267)
 GO:0001324 : age-dependent response to oxidative stress involved in chronological cell aging
 (https://www.ebi.ac.uk/QuickGO/term/GO:0001324)
 GO:0006995 : cellular response to nitrogen starvation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0006995)
 GO:0010508 : positive regulation of autophagy
 (https://www.ebi.ac.uk/QuickGO/term/GO:0010508)
 GO:1903452 : positive regulation of G1 to G0 transition
 (https://www.ebi.ac.uk/QuickGO/term/GO:1903452)
 GO:1901992 : positive regulation of mitotic cell cycle phase transition
 (https://www.ebi.ac.uk/QuickGO/term/GO:1901992)
 GO:0061406 : positive regulation of transcription from RNA polymerase II promoter in response to glucose starvation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0061406)
 GO:0061408 : positive regulation of transcription from RNA polymerase II promoter in response to heat stress
 (https://www.ebi.ac.uk/QuickGO/term/GO:0061408)
 GO:0051039 : positive regulation of transcription involved in meiotic cell cycle
 (https://www.ebi.ac.uk/QuickGO/term/GO:0051039)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
 GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Coding^#gephebase-summary-title)

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

1-9 bp

Molecular Details of the Mutation

1bp deletion resulting in premature stop codon

Experimental Evidence

Association Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Association Mapping^#gephebase-summary-title)

Main Reference

Molecular characterization of clonal interference during adaptive evolution in asexual populations of *Saccharomyces cerevisiae*. (2008) (https://pubmed.ncbi.nlm.nih.gov/19029899)

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) (https://pubmed.ncbi.nlm.nih.gov/21552329)

RELATED GEPHE

Related Genes

12 (COX18, HXT6/7, IRA1, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RAS2, SLY41, TAF5) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Low-glucose adaptation/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

