GEPHE SUMMARY

Gephebase Gene
IRA1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^IRA1^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001709
Main curator
Noor

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait=^Low-glucose adaptation (experimental evolution)^#gephebase-summary-title)
Trait State in Taxon A
Saccharomyces cerevisiae
Trait State in Taxon B
Saccharomyces cerevisiae
Ancestral State
Taxon A
Taxonomic Status
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#gephebase-summary-title)

Taxon A

Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)
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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)
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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)
NCBI Taxonomy ID
4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)
is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
IRA1
Synonyms
GLC1; PPD1; YBR140C; YBR1016
String
4932.YBR140C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBR140C)
Sequence Similarities
-
GO - Molecular Function
GO:0005096 : GTPase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005096)
GO - Biological Process
GO:0043547 : positive regulation of GTPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0043547)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P18963 (http://www.uniprot.org/uniprot/P18963)
GenebankID or UniProtKB
()

GO:0007193 : adenylate cyclase-inhibiting G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007193)
GO:0046580 : negative regulation of Ras protein signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0046580)
GO:0045761 : regulation of adenylate cyclase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0045761)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0016020 : membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0016020)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Arg1583Lys (G>A at position 521875 according to Table 1) - AGR to AAR position 521875

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Arg	Lys	1583

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, MDS3, MKT1, MNN4, MTH1, MUK1, RAS1, RAS2, RIM15, 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

COMMENTS