

GEPHE SUMMARY

<p>COX18 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+COX18+Gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001708</p> <p>Noor</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category+Physiology+Gephebase-summary-title)</p> <p>Low-glucose adaptation (experimental evolution) (https://www.gephebase.org/search-criteria?/and+Trait+Low-glucose+adaptation+(experimental+evolution)+Gephebase-summary-title)</p> <p>Saccharomyces cerevisiae</p> <p>Saccharomyces cerevisiae</p> <p>Taxon A</p> <p>Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status+Experimental+Evolution+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 cerevisiae (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; Saccharomyces cerevisiae; Saccharomyces 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=4932)</p> <p>NCBI Taxonomy ID</p> <p>4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)</p> <p>is Taxon A an Intraspecies?</p> <p>No</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Saccharomyces cerevisiae (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; Saccharomyces cerevisiae; Saccharomyces 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=4932)</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>COX18</p> <p>OXA2; YGR062C; G4532</p> <p>4932.YGR062C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YGR062C)</p> <p>Belongs to the OXA1/ALB3/YidC family.</p> <p>GO:0032977 : membrane insertase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0032977)</p> <p>GO:0032979 : protein insertion into mitochondrial inner membrane from matrix side (https://www.ebi.ac.uk/QuickGO/term/GO:0032979)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p> <p>GO - Biological Process</p>	<p>UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P53239 (http://www.uniprot.org/uniprot/P53239)</p> <p>0</p> <p>GenebankID or UniProtKB</p>
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GO:0031305 : integral component of mitochondrial inner membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0031305>)

Presumptive Null

No ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No~#gephebase-summary-title](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](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](https://www.gephebase.org/search-criteria?/and+Aberration+Type=~SNP~#gephebase-summary-title))

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Leu59His (T>A at position 617107 according to Table 1) - CTY to CAY position 617107

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	617107
Amino-acid	Leu	His	59

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 (HXT6/7, IRA1, 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](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