

GEPHE SUMMARY

ERG5 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ERG5^#gephebase-summary-title)	Gephebase Gene	GP00000287	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		
Xenobiotic resistance (drug) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(drug)^#gephebase-summary-title)	Trait		
Saccharomyces cerevisiae - experimentally evolved resistance to nystation fungicide	Trait State in Taxon A		
Saccharomyces cerevisiae - experimentally evolved resistance to nystation fungicide	Trait State in Taxon B		
	Ancestral State		
	Taxon A		Taxon B
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Experimental+Evolution^#gephebase-summary-title)	Taxonomic Status		
	Latin Name		Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Common Name	Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title)	Common Name
baker's yeast	Synonyms	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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	Rank	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	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	Parent	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	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 Intraspecies?	4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

ERG5	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P54781 (http://www.uniprot.org/uniprot/P54781)	GenebankID or UniProtKB
CYP61; YMR015C; YM9711.02C	Synonyms	Z49211 (https://www.ncbi.nlm.nih.gov/nuccore/Z49211)	
4932.YMR015C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YMR015C)	String		
Belongs to the cytochrome P450 family.	Sequence Similarities		
	GO - Molecular Function		
GO:0020037 : heme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0020037)			
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)			
GO:0004497 : monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004497)			
GO:0000249 : C-22 sterol desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000249)			

GO - Biological Process

GO:0055114 : oxidation-reduction process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0055114>)
GO:0006696 : ergosterol biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006696>)
GO:0016125 : sterol metabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016125>)

GO - Cellular Component

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

Presumptive Null

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))

Molecular Type

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

Aberration Type

10-99 bp

Deletion Size

60bp deletion

Molecular Details of the Mutation

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))

Experimental Evidence

Parallel genetic changes and nonparallel gene-environment interactions characterize the evolution of drug resistance in yeast. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22714405>)

Main Reference

Gerstein AC; Lo DS; Otto SP

Authors

Beneficial mutations are required for adaptation to novel environments, yet the range of mutational pathways that are available to a population has been poorly characterized, particularly in eukaryotes. We assessed the genetic changes of the first mutations acquired during adaptation to a novel environment (exposure to the fungicide, nystatin) in 35 haploid lines of *Saccharomyces cerevisiae*. Through whole-genome resequencing we found that the genomic scope for adaptation was narrow; all adapted lines acquired a mutation in one of four late-acting genes in the ergosterol biosynthesis pathway, with very few other mutations found. Lines that acquired different ergosterol mutations in the same gene exhibited very similar tolerance to nystatin. All lines were found to have a cost relative to wild type in an unstressful environment; the level of this cost was also strongly correlated with the ergosterol gene bearing the mutation. Interestingly, we uncovered both positive and negative effects on tolerance to other harsh environments for mutations in the different ergosterol genes, indicating that these beneficial mutations have effects that differ in sign among environmental challenges. These results demonstrate that although the genomic target was narrow, different adaptive mutations can lead populations down different evolutionary pathways, with respect to their ability to tolerate (or succumb to) other environmental challenges.

Abstract

Additional References

RELATED GEPHE

15 (APJ1, ERG3, ERG6, ERG7, LEU2, PHO84, RAD5, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~4932^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4932^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title))

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

@GxE