

GEPHE SUMMARY

ERG3 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ERG3^#gephebase-summary-title)	Gephebase Gene	GP00001754	GepheID
Published	Entry Status	Courtier	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)	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; Saccharomyces 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=4930)	Parent	Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	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

ERG3	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P32353 (http://www.uniprot.org/uniprot/P32353)	
PSO6; SYR1; YLR056W; L2150	Synonyms	X94607 (https://www.ncbi.nlm.nih.gov/nuccore/X94607)	GenebankID or UniProtKB
4932.YLR056W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YLR056W)	String		
Belongs to the sterol desaturase family.	Sequence Similarities		
GO:0005506 : iron ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005506)	GO - Molecular Function		
GO:0000248 : C-5 sterol desaturase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000248)			
GO:0006696 : ergosterol biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006696)	GO - Biological Process		

GO:0016126 : sterol biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016126>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005788 : endoplasmic reticulum lumen
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005788>)

GO:0005789 : endoplasmic reticulum membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005789>)

Presumptive Null

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))

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

Gly300Arg G898C in line 32

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	-	-	-
Amino-acid	-	-	-

Main Reference

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

Authors

Gerstein AC; Lo DS; Otto SP

Abstract

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.

Additional References

RELATED GEPHE

Related Genes

15 (APJ1, ERG5, 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 Haplotypes

14 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~ERG3^/and+Taxon ID=~4932^/or+Gene Gephebase=~ERG3^/and+Taxon ID=~4932^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=~ERG3^/and+Taxon+ID=~4932^/or+Gene+Gephebase=~ERG3^/and+Taxon+ID=~4932^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

@GxE - 11 unique mutations in ERG3 in 14 independently-evolved lines