

GEPHE SUMMARY

ERG3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^ERG3^#gephebase-summary-title)	Gephebase Gene	GP00001749	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^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	Taxonomic Status	Taxon B	
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Experimental Evolution^#gephebase-summary-title)			
	Latin Name		Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)	
baker’s yeast	Common Name	baker’s yeast	Common Name
	Synonyms		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		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	
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
	Parent		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)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)	
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		GenebankID or UniProtKB
4932.YLR056W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YLR056W)	String	X94607 (https://www.ncbi.nlm.nih.gov/nucleotide/X94607)	
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

Nonsense

Molecular Details of the Mutation

Trp205Stop G615A in line 27

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