

GEPHE SUMMARY

ERG3 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~ERG3~#gephebase-summary-title)	Gephebase Gene	GP00001753	GepheID
	Entry Status	Courtier	Main curator
	Published		

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	
Taxon A		Ancestral State	
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Experimental Evolution~#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
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		baker’s yeast	
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		species	
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)	
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		No	

GENOTYPIC CHANGE

ERG3		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)	
PSO6; SYR1; YLR056W; L2150		P32353 (http://www.uniprot.org/uniprot/P32353)	
4932.YLR056W (http://string-db.org/newstring.cgi/show_network_section.pl?identifier= 4932.YLR056W)		X94607 (https://www.ncbi.nlm.nih.gov/nucleotide/X94607)	
Belongs to the sterol desaturase family.		GenebankID or UniProtKB	
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 - Biological Process	
GO:0006696 : ergosterol biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006696)			

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

Tyr299Stop C897A in line 31

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~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~4932~#gephebase-summary-title))

Related Haplotypes

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

EXTERNAL LINKS

COMMENTS

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