

GEPHE SUMMARY

	Gephebase Gene	GephelD
ERG6 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase="ERG6">#gephebase-summary-title)	GP00000288	
	Entry Status	Main curator
Published	Martin	

PHENOTYPIC CHANGE

	Trait Category
Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category="Physiology">#gephebase-summary-title)	
Xenobiotic resistance (drug) (https://www.gephebase.org/search-criteria/?and+Trait=Xenobiotic+resistance+(drug) #gephebase-summary-title)	Trait
Saccharomyces cerevisiae - experimentally evolved resistance to nystatin fungicide	Trait State in Taxon A
Saccharomyces cerevisiae - experimentally evolved resistance to nystatin fungicide	Trait State in Taxon B
Saccharomyces cerevisiae - experimentally evolved resistance to nystatin fungicide	Ancestral State
Data not curated	
	Taxonomic Status
Experimental Evolution (https://www.gephebase.org/search-criteria/?and+Taxonomic Status="Experimental Evolution">#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Saccharomyces cerevisiae (#gephebase-summary-title)		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; Saccharomyces 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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	
Rank		Rank	
species	Lineage	species	Lineage
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	
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 Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

erg6	Generic Gene Name	UniProtKB Schizosaccharomyces pombe (strain 972 / ATCC 24843) O14321 (http://www.uniprot.org/uniprot/O14321)
SPBC16E9.05	Synonyms	GenebankID or UniProtKB KZV08836 (https://www.ncbi.nlm.nih.gov/nuccore/KZV08836)
4896.SPBC16E9.05.1 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4896.SPBC16E9.05.1)	String	
	Sequence Similarities	
Belongs to the class I-like SAM-binding methyltransferase superfamily. Erg6/SMT family.		
	GO - Molecular Function	
GO:0003838 : sterol 24-C-methyltransferase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003838)		
GO:0006696 : ergosterol biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006696)	GO - Biological Process	

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

GO:0005783 : endoplasmic reticulum

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005783>)

Presumptive Null

Unknown (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^Unknown^#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Coding^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

7 unique mutations in ERG6 within a total 19 lines ; 4 of these mutations evolved multiple times

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

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, ERG3, ERG5, ERG7, LEU2, PHO84, RAD5, SWS2, TSA2, CIS1, FRM2, GPX2, RTA1, cytochrome b, MKT1) (<https://www.gephebase.org/search-criteria?/or+TaxonID=^4932^/and+Trait=Xenobiotic+resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE