

## GEPHE SUMMARY

**Gephebase Gene**  
ERG3

**Entry Status**  
Published

**GepheID**  
GP00001745

**Main curator**  
Courtier

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Xenobiotic resistance (drug)

**Trait State in Taxon A**  
Saccharomyces cerevisiae - experimentally evolved resistance to nystation fungicide

**Trait State in Taxon B**  
Saccharomyces cerevisiae - experimentally evolved resistance to nystation fungicide

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Experimental Evolution

### Taxon A

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon A an Intraspecies?**  
No

### Taxon B

**Latin Name**  
*Saccharomyces cerevisiae*

**Common Name**  
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; Saccaromyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

**Rank**  
species

**Lineage**  
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces

**Parent**  
Saccharomyces () - (Rank: genus)

**NCBI Taxonomy ID**  
4932

**is Taxon B an Intraspecies?**  
No

## GENOTYPIC CHANGE

**Generic Gene Name**  
ERG3

**Synonyms**  
PSO6; SYR1; YLR056W; L2150

**String**  
4932.YLR056W

**Sequence Similarities**  
Belongs to the sterol desaturase family.

**GO - Molecular Function**  
GO:0005506 : iron ion binding  
GO:0000248 : C-5 sterol desaturase activity

**GO - Biological Process**  
GO:0006696 : ergosterol biosynthetic process  
GO:0016126 : sterol biosynthetic process

**GO - Cellular Component**  
GO:0016021 : integral component of membrane  
GO:0005788 : endoplasmic reticulum lumen

**UniProtKB** Saccharomyces cerevisiae (strain ATCC 204508 / S288c)  
P32353

**GenebankID or UniProtKB**  
X94607

GO:0005789 : endoplasmic reticulum membrane

**Presumptive Null**

Yes

**Molecular Type**

Coding

**Aberration Type**

SNP

**SNP Coding Change**

Nonsense

**Molecular Details of the Mutation**

Ser95Stop C284A in line 23

**Experimental Evidence**

Association Mapping

	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)

**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)

**Related Haplotypes**

14

**EXTERNAL LINKS**

**COMMENTS**

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