

## GEPHE SUMMARY

|  |                |            |              |
|--|----------------|------------|--------------|
| ERG3 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ERG3^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ERG3^#gephebase-summary-title</a> ) | Gephebase Gene | GP00001745 | GepheID      |
| Published  | Entry Status   | Courtier   | Main curator |

## PHENOTYPIC CHANGE

|  |                              |  |                              |
|--|------------------------------|--|------------------------------|
| Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title</a> )   | Trait Category               |  |                              |
| Xenobiotic resistance (drug) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(drug)^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(drug)^#gephebase-summary-title</a> )   | 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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Experimental+Evolution^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Experimental+Evolution^#gephebase-summary-title</a> )   | Taxonomic Status             |  |                              |
|  | Latin Name                   |  | Latin Name                   |
| Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )   | Common Name                  | Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )   | Common Name                  |
| baker's yeast  | Synonyms                     | 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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae | Rank                         | 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 | Rank                         |
| species  | Lineage                      | species  | Lineage                      |
| cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces   | Parent                       | cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces   | Parent                       |
| Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )   | NCBI Taxonomy ID             | Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930</a> )   | NCBI Taxonomy ID             |
| 4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932</a> )   | is Taxon A an Infrasppecies? | 4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932</a> )   | is Taxon B an Infrasppecies? |
| No   |                              | No   |                              |

## GENOTYPIC CHANGE

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

Ser95Stop C284A in line 23

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