

GEPHE SUMMARY

Gephebase Gene
ERG3

Entry Status
Published

GepheID
GP00001751

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; Saccharomyces 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; Saccharomyces cerevisiae; Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae

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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

Trp219Stop G656A in line 29

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

COMMENTS

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