

GEPHE SUMMARY

Gephebase Gene
ASP1

Entry Status
Published

GepheID
GP00000104

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Physiology

Trait
Acetic acid production

Trait State in Taxon A
Saccharomyces cerevisiae - Bo213

Trait State in Taxon B
Saccharomyces cerevisiae - VL1

Ancestral State
Data not curated

Taxonomic Status
Domesticated

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?

Yes

Taxon A Description

Saccharomyces cerevisiae - Bo213

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?

Yes

Taxon B Description

Saccharomyces cerevisiae - VL1

GENOTYPIC CHANGE

Generic Gene Name
APS1

Synonyms

YAP19; YLR170C; L9470.16

String

4932.YLR170C

Sequence Similarities

Belongs to the adaptor complexes small subunit family.

GO - Molecular Function

GO:0030276 : clathrin binding

GO - Biological Process

GO:0006896 : Golgi to vacuole transport

GO:0006886 : intracellular protein transport

GO:0016192 : vesicle-mediated transport

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P35181

GenebankID or UniProtKB

U17246

GO - Cellular Component
GO:0005634 : nucleus
GO:0030121 : AP-1 adaptor complex
GO:0005768 : endosome

Presumptive Null
No

Molecular Type
Coding

Aberration Type
SNP

SNP Coding Change
Nonsynonymous

Molecular Details of the Mutation
Asp142His

Experimental Evidence
Linkage Mapping

| | Taxon A | Taxon B | Position |
|------------|---------|---------|----------|
| Codon | - | - | - |
| Amino-acid | - | - | - |

Main Reference

Single QTL mapping and nucleotide-level resolution of a physiologic trait in wine *Saccharomyces cerevisiae* strains. (2007)

Authors

Marullo P; Aigle M; Bely M; Masneuf-Pomarède I; Durrens P; Dubourdieu D; Yvert G

Abstract

Natural *Saccharomyces cerevisiae* yeast strains exhibit very large genotypic and phenotypic diversity. However, the link between phenotype variation and genetic determinism is still difficult to identify, especially in wild populations. Using genome hybridization on DNA microarrays, it is now possible to identify single-feature polymorphisms among divergent yeast strains. This tool offers the possibility of applying quantitative genetics to wild yeast strains. In this instance, we studied the genetic basis for variations in acetic acid production using progeny derived from two strains from grape must isolates. The trait was quantified during alcoholic fermentation of the two strains and 108 segregants derived from their crossing. A genetic map of 2212 markers was generated using oligonucleotide microarrays, and a major quantitative trait locus (QTL) was mapped with high significance. Further investigations showed that this QTL was due to a nonsynonymous single-nucleotide polymorphism that targeted the catalytic core of asparaginase type I (ASPI) and abolished its activity. This QTL was only effective when asparagine was used as a major nitrogen source. Our results link nitrogen assimilation and CO₂ production rate to acetic acid production, as well as, on a broader scale, illustrating the specific problem of quantitative genetics when working with nonlaboratory microorganisms.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS