

## GEPHE SUMMARY

**Gephebase Gene**  
Aquaporin (AQY1)

**Entry Status**  
Published

**GepheID**  
GP00001873

**Main curator**  
Courtier

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Growth rate (environment-dependent)

**Trait State in Taxon A**  
freeze-thawâ€™tolerant

**Trait State in Taxon B**  
freeze-thawâ€™sensitive and higher growth rate in sugar-rich medium

**Ancestral State**  
Taxon A

**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**

-

### 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**

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## GENOTYPIC CHANGE

**Generic Gene Name**  
AQP1

**Synonyms**

CO; CHIP28; AQP-CHIP

**String**

9606.ENSP00000311165

**Sequence Similarities**

Belongs to the MIP/aquaporin (TC 1.A.8) family.

**GO - Molecular Function**

GO:0042802 : identical protein binding

GO:0015079 : potassium ion transmembrane transporter activity

GO:0015250 : water channel activity

GO:0008519 : ammonium transmembrane transporter activity

GO:0022857 : transmembrane transporter activity

GO:0035379 : carbon dioxide transmembrane transporter activity

**UniProtKB Homo sapiens**

P29972

**GenebankID or UniProtKB**

GO:0015168 : glycerol transmembrane transporter activity  
GO:0005223 : intracellular cGMP-activated cation channel activity  
GO:0030184 : nitric oxide transmembrane transporter activity  
GO:0005267 : potassium channel activity  
GO:0005372 : water transmembrane transporter activity

#### GO - Biological Process

GO:0043066 : negative regulation of apoptotic process  
GO:0019934 : cGMP-mediated signaling  
GO:0006813 : potassium ion transport  
GO:0071260 : cellular response to mechanical stimulus  
GO:0042493 : response to drug  
GO:0071280 : cellular response to copper ion  
GO:0003091 : renal water homeostasis  
GO:0071456 : cellular response to hypoxia  
GO:0006833 : water transport  
GO:0006972 : hyperosmotic response  
GO:0071300 : cellular response to retinoic acid  
GO:0042476 : odontogenesis  
GO:0070301 : cellular response to hydrogen peroxide  
GO:0071732 : cellular response to nitric oxide  
GO:0015701 : bicarbonate transport  
GO:0030185 : nitric oxide transport  
GO:0045766 : positive regulation of angiogenesis  
GO:0043154 : negative regulation of cysteine-type endopeptidase activity involved in apoptotic process  
GO:0048146 : positive regulation of fibroblast proliferation  
GO:0071320 : cellular response to cAMP  
GO:0015696 : ammonium transport  
GO:0071549 : cellular response to dexamethasone stimulus  
GO:0030950 : establishment or maintenance of actin cytoskeleton polarity  
GO:0034644 : cellular response to UV  
GO:0030157 : pancreatic juice secretion  
GO:0035378 : carbon dioxide transmembrane transport  
GO:0015670 : carbon dioxide transport  
GO:0006884 : cell volume homeostasis  
GO:0019725 : cellular homeostasis  
GO:0071474 : cellular hyperosmotic response  
GO:0071241 : cellular response to inorganic substance  
GO:0071288 : cellular response to mercury ion  
GO:0071472 : cellular response to salt stress  
GO:0033326 : cerebrospinal fluid secretion  
GO:0015793 : glycerol transport  
GO:0021670 : lateral ventricle development  
GO:0085018 : maintenance of symbiont-containing vacuole by host  
GO:0050891 : multicellular organismal water homeostasis  
GO:0046878 : positive regulation of saliva secretion  
GO:0003097 : renal water transport  
GO:0035377 : transepithelial water transport

#### GO - Cellular Component

GO:0016021 : integral component of membrane  
GO:0005886 : plasma membrane  
GO:0016324 : apical plasma membrane  
GO:0005737 : cytoplasm  
GO:0070062 : extracellular exosome  
GO:0005887 : integral component of plasma membrane  
GO:0005634 : nucleus  
GO:0016323 : basolateral plasma membrane  
GO:0031965 : nuclear membrane  
GO:0045177 : apical part of cell  
GO:0009925 : basal plasma membrane  
GO:0005903 : brush border  
GO:0042383 : sarcolemma  
GO:0031526 : brush border membrane  
GO:0020003 : symbiont-containing vacuole

#### Presumptive Null

Yes

#### Molecular Type

Coding

#### Aberration Type

Deletion

#### Deletion Size

-

#### Molecular Details of the Mutation

aquaporin yeast 1 gene on chromosome 12 - A881 deletion renders AQY1 inactive - size of the deletion not indicated in the paper - GenBank accession numbers for AQY1 and AQY2: GQ848552-74 and GQ870433-54

#### Experimental Evidence

Candidate Gene

#### Main Reference

Incipient balancing selection through adaptive loss of aquaporins in natural *Saccharomyces cerevisiae* populations. (2010)

#### Authors

Will JL; Kim HS; Clarke J; Painter JC; Fay JC; Gasch AP

#### Abstract

A major goal in evolutionary biology is to understand how adaptive evolution has influenced natural variation, but identifying loci subject to positive selection has been a challenge. Here we present the adaptive loss of a pair of paralogous genes in specific *Saccharomyces cerevisiae* subpopulations. We mapped natural variation in freeze-thaw tolerance to two water transporters, AQY1 and AQY2, previously implicated in freeze-thaw survival. However, whereas freeze-thaw-tolerant strains harbor functional aquaporin genes, the set of sensitive strains lost aquaporin function at least 6 independent times. Several genomic signatures at AQY1 and/or AQY2 reveal low variation surrounding these loci within strains of the same haplotype, but high variation between strain groups. This is consistent with recent adaptive loss of aquaporins in subgroups of strains, leading to incipient balancing selection. We show that, although aquaporins are critical for surviving freeze-thaw stress, loss of both genes provides a major fitness advantage on high-sugar substrates common to many strains' natural niche. Strikingly, strains with non-functional alleles have also lost the ancestral requirement for aquaporins during spore formation. Thus, the antagonistic effect of aquaporin function-providing an advantage in freeze-thaw tolerance but a fitness defect for growth in high-sugar environments-contributes to the maintenance of both functional and nonfunctional alleles in *S. cerevisiae*. This work also shows that gene loss through multiple missense and nonsense mutations, hallmarks of pseudogenization presumed to emerge after loss of constraint, can arise through positive selection.

#### Additional References

[Aquaporins in \*Saccharomyces\*. Genetic and functional distinctions between laboratory and wild-type strains. \(1998\)](#)

## RELATED GEPHE

#### Related Genes

6 ([Allantoin permease DAL4](#), [Allantoinase DAL1](#), [Proline specific permease PUT4](#), [Aquaporin \(AQY2\)](#), [BMH1](#), [IRA2](#))

#### Related Haplotypes

2

## EXTERNAL LINKS

## COMMENTS

The paralogs AQY1 and AQY2 may have arisen in the whole-genome duplication (WGD) event in the *Saccharomyces* lineage since all post-WGD species all have two aquaporins whereas most pre-WGD species have a single ortholog (Dana Wohlbach and A.P.G., unpublished).