

## GEPHE SUMMARY

### Gephebase Gene

FLO1

### Entry Status

Published

### GepheID

GP00000342

### Main curator

Martin

## PHENOTYPIC CHANGE

### Trait Category

Physiology

### Trait

Cell separation

### Trait State in Taxon A

*Saccharomyces cerevisiae* EM93 (feral S288c) - flocculating

### Trait State in Taxon B

*Saccharomyces cerevisiae* S288c - non-flocculating

### 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; *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?

Yes

#### Taxon A Description

*Saccharomyces cerevisiae* EM93 (feral S288c) - flocculating

### 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*

#### 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* S288c - non-flocculating

## GENOTYPIC CHANGE

### Generic Gene Name

FLO1

### Synonyms

FLO2; FLO4; FLO8; YAR050W

### String

4932.YAR050W

### Sequence Similarities

Belongs to the flocculin family.

### GO - Molecular Function

GO:0005537 : mannose binding

### GO - Biological Process

GO:0071361 : cellular response to ethanol

GO:0034605 : cellular response to heat

GO:0070301 : cellular response to hydrogen peroxide

GO:0036281 : coflocculation

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

P32768

### GenebankID or UniProtKB

EF670005

GO:0000128 : flocculation  
GO:0000501 : flocculation via cell wall protein-carbohydrate interaction

**GO - Cellular Component**

GO:0005886 : plasma membrane  
GO:0005576 : extracellular region  
GO:0031225 : anchored component of membrane  
GO:0009277 : fungal-type cell wall

**Presumptive Null**

No

**Molecular Type**

Other

**Aberration Type**

Unknown

**Molecular Details of the Mutation**

both coding and non-coding divergence ; polyQ variation

**Experimental Evidence**

**Candidate Gene**

**Main Reference**

FLO1 is a variable green beard gene that drives biofilm-like cooperation in budding yeast. (2008)

**Authors**

Smukalla S; Caldara M; Pochet N; Beauvais A; Guadagnini S; Yan C; Vincos MD; Jansen A; Prevost MC; Latg   JP; Fink GR; Foster KR; Verstrepen KJ

**Abstract**

The budding yeast, *Saccharomyces cerevisiae*, has emerged as an archetype of eukaryotic cell biology. Here we show that *S. cerevisiae* is also a model for the evolution of cooperative behavior by revisiting flocculation, a self-adherence phenotype lacking in most laboratory strains. Expression of the gene FLO1 in the laboratory strain S288C restores flocculation, an altered physiological state, reminiscent of bacterial biofilms. Flocculation protects the FLO1 expressing cells from multiple stresses, including antimicrobials and ethanol. Furthermore, FLO1(+) cells avoid exploitation by nonexpressing flo1 cells by self/non-self recognition: FLO1(+) cells preferentially stick to one another, regardless of genetic relatedness across the rest of the genome. Flocculation, therefore, is driven by one of a few known "green beard genes," which direct cooperation toward other carriers of the same gene. Moreover, FLO1 is highly variable among strains both in expression and in sequence, suggesting that flocculation in *S. cerevisiae* is a dynamic, rapidly evolving social trait.

**Additional References**

Intragenic tandem repeats generate functional variability. (2005)

**RELATED GEPHE**

**Related Genes**

1 (AMN1)

**Related Haplotypes**

No matches found.

**COMMENTS**