GEPHE SUMMARY

Gephebase Gene

FLO1 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^FLO1^#gephebase-summary-title)

GepheID

GP00000342

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Cell separation (https://www.gephebase.org/search-criteria?/and+Trait=^Cell separation^#gephebase-summary-title)

Trait State in Taxon A

Saccharomyces cerevisiae EM93 (feral S288c) - floculating

Trait State in Taxon B

Saccharomyces cerevisiae S288c - non-floculating

Ancestral State

Data not curated

Taxonomic Status

Domesticated (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Domesticated^#gephebase-summary-title)

Taxon A

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Saccharomyces cerevisiae EM93 (feral S288c) - floculating

Taxon B

Latin Name

Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Saccharomyces cerevisiae^#gephebase-summary-title)

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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930)

NCBI Taxonomy ID

4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Saccharomyces cerevisiae S288c - non-floculating

GENOTYPIC CHANGE

Generic Gene Name

FLO1

Synonyms

FLO2; FLO4; FLO8; YAR050W

String

4932.YAR050W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YAR050W)

Sequence Similarities

Belongs to the flocculin family.

GO - Molecular Function

GO:0005537 : mannose binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005537)

GO - Biological Process

GO:0071361 : cellular response to ethanol (https://www.ebi.ac.uk/QuickGO/term/GO:0071361)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P32768 (http://www.uniprot.org/uniprot/P32768)

GenebankID or UniProtKB

EF670005 (https://www.ncbi.nlm.nih.gov/nuccore/EF670005)

GO:0034605 : cellular response to heat
(https://www.ebi.ac.uk/QuickGO/term/GO:0034605)
GO:0070301 : cellular response to hydrogen peroxide
(https://www.ebi.ac.uk/QuickGO/term/GO:0070301)
GO:0036281 : coflocculation (https://www.ebi.ac.uk/QuickGO/term/GO:0036281)
GO:0000128 : flocculation (https://www.ebi.ac.uk/QuickGO/term/GO:0000128)
GO:0000501 : flocculation via cell wall protein-carbohydrate interaction
(https://www.ebi.ac.uk/QuickGO/term/GO:0000501)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0031225 : anchored component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0031225)
GO:0009277 : fungal-type cell wall (https://www.ebi.ac.uk/QuickGO/term/GO:0009277)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#gephebase-summary-title)

Molecular Type

Other (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Other^#gephebase-summary-title)

Aberration Type

Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title)

Molecular Details of the Mutation

both coding and non-coding divergence ; polyQ variation

Experimental Evidence

Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=^Candidate Gene^#gephebase-summary-title)

Main Reference

FLO1 is a variable green beard gene that drives biofilm-like cooperation in budding yeast. (2008) (https://pubmed.ncbi.nlm.nih.gov/19013280)

Authors

Smukalla S; Caldara M; Pochet N; Beauvais A; Guadagnini S; Yan C; Vinces MD; Jansen A; Prevost MC; LatgÃ© 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) (https://pubmed.ncbi.nlm.nih.gov/16086015)

RELATED GEPHE

Related Genes

1 (AMN1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Cell separation/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS