GEPHE SUMMARY

Gephebase Gene

BUL2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BUL2^#gephebase-summary-title)

GepheID

GP00000166

Entry Status

Published

Main curator

Martin

PHENOTYPIC CHANGE

Trait #1

Trait Category

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

Trait

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

Trait State in Taxon A

Saccharomyces cerevisiae - lab strain

Trait State in Taxon B

Saccharomyces cerevisiae - vineyard strain

Trait #2

Trait Category

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

Trait

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

Trait State in Taxon A

-

Trait State in Taxon B

-

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 - lab strain

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 - vineyard strain

GENOTYPIC CHANGE

Generic Gene Name

BUL2

Synonyms

YML111W; YM8339.08

String

4932.YML111W
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YML111W)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

Q03758 (http://www.uniprot.org/uniprot/Q03758)

GenebankID or UniProtKB

Z49210 (https://www.ncbi.nlm.nih.gov/nuccore/Z49210)

Sequence Similarities

Belongs to the BUL1 family.

GO - Molecular Function

GO:0034450 : ubiquitin-ubiquitin ligase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0034450)

GO - Biological Process

GO:0006513 : protein monoubiquitination
(https://www.ebi.ac.uk/QuickGO/term/GO:0006513)
GO:0000209 : protein polyubiquitination
(https://www.ebi.ac.uk/QuickGO/term/GO:0000209)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0000151 : ubiquitin ligase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0000151)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Leu883Phe

Experimental Evidence

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

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

Main Reference

Natural polymorphism in BUL2 links cellular amino acid availability with chronological aging and telomere maintenance in yeast. (2011) (https://pubmed.ncbi.nlm.nih.gov/21901113)

Authors

Kwan EX; Foss E; Kruglyak L; Bedalov A

Abstract

Aging and longevity are considered to be highly complex genetic traits. In order to gain insight into aging as a polygenic trait, we employed an outbred Saccharomyces cerevisiae model, generated by crossing a vineyard strain RM11 and a laboratory strain S288c, to identify quantitative trait loci that control chronological lifespan. Among the major loci that regulate chronological lifespan in this cross, one genetic linkage was found to be congruent with a previously mapped locus that controls telomere length variation. We found that a single nucleotide polymorphism in BUL2, encoding a component of an ubiquitin ligase complex involved in trafficking of amino acid permeases, controls chronological lifespan and telomere length as well as amino acid uptake. Cellular amino acid availability changes conferred by the BUL2 polymorphism alter telomere length by modulating activity of a transcription factor Gln3. Among the GLN3 transcriptional targets relevant to this phenotype, we identified Wtm1, whose upregulation promotes nuclear retention of ribonucleotide reductase (RNR) components and inhibits the assembly of the RNR enzyme complex during S-phase. Inhibition of RNR is one of the mechanisms by which Gln3 modulates telomere length. Identification of a polymorphism in BUL2 in this outbred yeast population revealed a link among cellular amino acid availability, chronological lifespan, and telomere length control.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS