GEPHE SUMMARY

Gephebase Gene

MEP2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^MEP2^#gephebase-summary-title)

GepheID

GP00000651

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

Salt tolerance (experimental evolution; low ammonium) (https://www.gephebase.org/search-criteria?/and+Trait=^Salt tolerance (experimental evolution; low ammonium)^#gephebase-summary-title)

Trait State in Taxon A

Saccharomyces cerevisiae

Trait State in Taxon B

Saccharomyces uvarum

Ancestral State

Data not curated

Taxonomic Status

Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Experimental Evolution^#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?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Saccharomyces bayanus var. uvarum; Saccharomyces globosus; Saccharomyces bayanus var. uvarum (Beij.) G.I. Naumov; Saccharomyces globosus Osterw., 1924; Saccharomyces uvarum Beij. 1898; BCRC:21964; BCRC:21970; CBS 395; CBS 424; CBS:395; CBS:424; CCRC 21964; CCRC 21970; CCRC:21964; CCRC:21970; CLIB 250; CLIB 251; CLIB:250; CLIB:251; DBVPG 6115; DBVPG 6179; DBVPG:6115; DBVPG:6179; DSM 70547; DSM:70547; IFO 0254; IFO 0615; IFO 10557; IFO 11025; IFO:0254; IFO:0615; IFO:10557; IFO:11025; IGC 4567; IGC 4568; IGC:4567; IGC:4568; NCYC 509; NCYC:509; NRRL Y-12645; NRRL Y-12663; NRRL Y-17034; NRRL:Y:12645; NRRL:Y:12663; NRRL:Y:17034

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

230603 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 230603)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

MEP2

Synonyms

AMT2; YNL142W; N1207; N1820

String

4932.YNL142W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YNL142W)

Sequence Similarities

Belongs to the ammonia transporter channel (TC 1.A.11.2) family.

GO - Molecular Function

GO:0008519 : ammonium transmembrane transporter activity

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P41948 (http://www.uniprot.org/uniprot/P41948)

GenebankID or UniProtKB

CAA96025 (https://www.ncbi.nlm.nih.gov/nuccore/CAA96025)

(https://www.ebi.ac.uk/QuickGO/term/GO:0008519)

GO - Biological Process

GO:0007124 : pseudohyphal growth (https://www.ebi.ac.uk/QuickGO/term/GO:0007124)
GO:0015696 : ammonium transport (https://www.ebi.ac.uk/QuickGO/term/GO:0015696)
GO:0019740 : nitrogen utilization (https://www.ebi.ac.uk/QuickGO/term/GO:0019740)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)

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

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

Molecular Details of the Mutation

Chimeric gene in diploid hybrids formed by recombination between the parental alleles

Experimental Evidence

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

Main Reference

Recurrent rearrangement during adaptive evolution in an interspecific yeast hybrid suggests a model for rapid introgression. (2013) (https://pubmed.ncbi.nlm.nih.gov/23555283)

Authors

Dunn B; Paulish T; Stanbery A; Piotrowski J; Koniges G; Kroll E; Louis EJ; Liti G; Sherlock G; Rosenzweig F

Abstract

Genome rearrangements are associated with eukaryotic evolutionary processes ranging from tumorigenesis to speciation. Rearrangements are especially common following interspecific hybridization, and some of these could be expected to have strong selective value. To test this expectation we created de novo interspecific yeast hybrids between two diverged but largely syntenic Saccharomyces species, S. cerevisiae and S. uvarum, then experimentally evolved them under continuous ammonium limitation. We discovered that a characteristic interspecific genome rearrangement arose multiple times in independently evolved populations. We uncovered nine different breakpoints, all occurring in a narrow ~1-kb region of chromosome 14, and all producing an "interspecific fusion junction" within the MEP2 gene coding sequence, such that the 5′ portion derives from S. cerevisiae and the 3′ portion derives from S. uvarum. In most cases the rearrangements altered both chromosomes, resulting in what can be considered to be an introgression of a several-kb region of S. uvarum into an otherwise intact S. cerevisiae chromosome 14, while the homeologous S. uvarum chromosome 14 experienced an interspecific reciprocal translocation at the same breakpoint within MEP2, yielding a chimaeric chromosome; these events result in the presence in the cell of two MEP2 fusion genes having identical breakpoints. Given that MEP2 encodes for a high-affinity ammonium permease, that MEP2 fusion genes arise repeatedly under ammonium-limitation, and that three independent evolved isolates carrying MEP2 fusion genes are each more fit than their common ancestor, the novel MEP2 fusion genes are very likely adaptive under ammonium limitation. Our results suggest that, when homoploid hybrids form, the admixture of two genomes enables swift and otherwise unavailable evolutionary innovations. Furthermore, the architecture of the MEP2 rearrangement suggests a model for rapid introgression, a phenomenon seen in numerous eukaryotic phyla, that does not require repeated backcrossing to one of the parental species.

Additional References

RELATED GEPHE

Related Genes

4 (CYC8, ENA1-2-5 cluster, PMA1, TRK1) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Salt tolerance/or+Taxon ID=^230603^/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Introgression