

## GEPHE SUMMARY

**Gephebase Gene**  
MEP2

**Entry Status**  
Published

**GepheID**  
GP00000651

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Salt tolerance (experimental evolution; low ammonium)

**Trait State in Taxon A**  
Saccharomyces cerevisiae

**Trait State in Taxon B**  
Saccharomyces uvarum

**Ancestral State**  
Data not curated

**Taxonomic Status**  
Experimental Evolution

### 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; Saccharomyces cerevisiae; Saccharomyces 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?**

No

### Taxon B

**Latin Name**

*Saccharomyces uvarum*

**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; BCR:21964; BCR: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)

**NCBI Taxonomy ID**

230603

**is Taxon B an Intraspecies?**

No

## GENOTYPIC CHANGE

**Generic Gene Name**  
MEP2

**Synonyms**

AMT2; YNL142W; N1207; N1820

**String**

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

**GO - Biological Process**

GO:0007124 : pseudohyphal growth

GO:0015696 : ammonium transport

**UniProtKB** Saccharomyces cerevisiae (strain ATCC 204508 / S288c)  
P41948

**GenebankID or UniProtKB**

CAA96025

GO:0019740 : nitrogen utilization

GO - Cellular Component

GO:0016021 : integral component of membrane

GO:0005886 : plasma membrane

Presumptive Null

No

Molecular Type

Other

Aberration Type

Complex Change

Molecular Details of the Mutation

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

Experimental Evidence

Association Mapping

Main Reference

Recurrent rearrangement during adaptive evolution in an interspecific yeast hybrid suggests a model for rapid introgression. (2013)

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)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@Introgression