

GEPHE SUMMARY

MAM3 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase="MAM3">#gephebase-summary-title)	Gephebase Gene	GP00001303	GepheID
Published	Entry Status	Arnoult	Main curator

PHENOTYPIC CHANGE

Trait Category	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category="Physiology">#gephebase-summary-title)	Trait
Metal tolerance (copper) (https://www.gephebase.org/search-criteria?/and+Trait=^Metal tolerance (copper)#gephebase-summary-title)	Trait State in Taxon A
Saccharomyces cerevisiae	Trait State in Taxon B
Saccharomyces cerevisiae - after 14 days of growth in high Copper environment. 34 lines	Ancestral State
Taxon A	Taxonomic Status
Experimental Evolution (https://www.gephebase.org/search-criteria?/and+Taxonomic Status="Experimental Evolution">#gephebase-summary-title)	

Taxon A	Latin Name	Taxon B	Latin Name
Saccharomyces cerevisiae (#gephebase-summary-title)		Saccharomyces cerevisiae (#gephebase-summary-title)	
baker's yeast	Common Name	baker's yeast	Common Name
Synonyms		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; Saccharomyces cerevisiae; Sccharomyces cerevisiae		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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	
Rank		Rank	
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces	
Parent		Parent	
Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	NCBI Taxonomy ID	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)		4932 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

PMA1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P05030 (http://www.uniprot.org/uniprot/P05030)	GenebankID or UniProtKB
KTh10; YGL008C	Synonyms	854094 (https://www.ncbi.nlm.nih.gov/nuccore/854094)	
4932.YGL008C (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=4932.YGL008C)	String		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIIA subfamily. GO - Molecular Function	Sequence Similarities		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872) GO:0008553 : proton-exporting ATPase activity, phosphorylative mechanism (https://www.ebi.ac.uk/QuickGO/term/GO:0008553)	GO - Biological Process		
GO:0055085 : transmembrane transport			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0055085>)
 GO:0006885 : regulation of pH (<https://www.ebi.ac.uk/QuickGO/term/GO:0006885>)
 GO:1902906 : proteasome storage granule assembly
 (<https://www.ebi.ac.uk/QuickGO/term/GO:1902906>)
 GO:0120029 : proton export across plasma membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0120029>)
 GO:1902600 : proton transmembrane transport
 (<https://www.ebi.ac.uk/QuickGO/term/GO:1902600>)
 GO:0051453 : regulation of intracellular pH
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0051453>)

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>)
 GO:0045121 : membrane raft (<https://www.ebi.ac.uk/QuickGO/term/GO:0045121>)

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

C>G (Gly > Arg) @ position 250

Experimental Evidence

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

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

Too much of a good thing: the unique and repeated paths toward copper adaptation. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25519894>)

Main Reference

Gerstein AC; Ono J; Lo DS; Campbell ML; Kuzmin A; Otto SP

Authors

Copper is a micronutrient essential for growth due to its role as a cofactor in enzymes involved in respiration, defense against oxidative damage, and iron uptake. Yet too much of a good thing can be lethal, and yeast cells typically do not have tolerance to copper levels much beyond the concentration in their ancestral environment. Here, we report a short-term evolutionary study of *Saccharomyces cerevisiae* exposed to levels of copper sulfate that are inhibitory to the initial strain. We isolated and identified adaptive mutations soon after they arose, reducing the number of neutral mutations, to determine the first genetic steps that yeast take when adapting to copper. We analyzed 34 such strains through whole-genome sequencing and by assaying fitness within different environments; we also isolated a subset of mutations through tetrad analysis of four lines. We identified a multilayered evolutionary response. In total, 57 single base-pair mutations were identified across the 34 lines. In addition, gene amplification of the copper metallothionein protein, CUP1-1, was rampant, as was chromosomal aneuploidy. Four other genes received multiple, independent mutations in different lines (the vacuolar transporter genes VTC1 and VTC4; the plasma membrane H⁺-ATPase PMA1; and MAM3, a protein required for normal mitochondrial morphology). Analyses indicated that mutations in all four genes, as well as CUP1-1 copy number, contributed significantly to explaining variation in copper tolerance. Our study thus finds that evolution takes both common and less trodden pathways toward evolving tolerance to an essential, but highly toxic, micronutrient.

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Additional References

RELATED GEPHE

5 (metallothionein CUP1, Plasma membrane ATPase 1, PMR1, Vacuolar transporter chaperone 1, Vacuolar transporter chaperone 4) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=%4932%/and+Trait=Metal+tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

2 (<https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=%MAM3%/and+Taxon+ID=%4932%/or+Gene+Gephebase=%MAM3%/and+Taxon+ID=%4932%#gephebase-summary-title>)

Related Haplotypes

EXTERNAL LINKS

COMMENTS

in line CBM7

