

Plasma membrane ATPase 1 (https://www.gephebase.org/search-criteria?/and+Gene)	Gephebase Gene	GP00001300	GepheID
Gephebase="Plasma membrane ATPase 1"#gephebase-summary-title)			Main curator
Published	Entry Status	Arnoult	

Trait Category		Trait		Trait State in Taxon A		Trait State in Taxon B		Ancestral State		Taxonomic Status	
Physiology (#gephebase-summary-title)		Metal tolerance (copper) (https://www.gephebase.org/search-criteria?/and+Trait=~Metal tolerance (copper))		Saccharomyces cerevisiae		Saccharomyces cerevisiae - after 14 days of growth in high Copper environment. 34 lines		Taxon A		Experimental Evolution (#gephebase-summary-title)	
Taxon A		Taxon B		Latin Name		Latin Name		Common Name		Common Name	
Saccharomyces cerevisiae (#gephebase-summary-title)		Saccharomyces cerevisiae (#gephebase-summary-title)		baker's yeast		baker's yeast		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; Saccharomyes 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; Saccharomyes cerevisiae; Sccharomyces cerevisiae		Rank		Rank		Lineage		Lineage	
species		species		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)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)		NCBI Taxonomy ID		NCBI Taxonomy ID		4932		4932	
(is Taxon A an Intraspecies?)		(is Taxon B an Intraspecies?)		No		No		(is Taxon A an Intraspecies?)		(is Taxon B an Intraspecies?)	

PMA1	Generic Gene Name	UniProtKB <i>Saccharomyces cerevisiae</i> (strain ATCC 204508 / <i>S288c</i>)
KT110; YGL008C	Synonyms	P05030 (http://www.uniprot.org/uniprot/P05030)
4932.YGL008C	String	852876 (https://www.ncbi.nlm.nih.gov/nucore/852876)
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YGL008C)	Sequence Similarities	GenebankID or UniProtKB
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIIA subfamily.		
GO - Molecular Function		
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](https://www.gephebase.org/search-criteria?/and+Presumptive Null=))

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

A>T (Phe > Ile) @ position 1831

Experimental Evidence

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

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

Main Reference

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

Authors

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

Abstract

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

Related Genes

5 (MAM3, metallothionein CUP1, 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](https://www.gephebase.org/search-criteria?/or+Taxon ID=))

Related Haplotypes

2 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase="+Plasma membrane ATPase 1"/and+Taxon ID="+4932"/or+Gene Gephebase="+Plasma membrane ATPase 1"/and+Taxon ID="+4932"#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=))

EXTERNAL LINKS

COMMENTS

in line CBM16

