

GEPHE SUMMARY

	Gephebase Gene		GepheID
Plasma membrane ATPase 1 (https://www.gephebase.org/search-criteria?/and+Gene)		GP00001302	
Gephebase="Plasma membrane ATPase 1"#gephebase-summary-title)			Main curator
Published	Entry Status	Arnout	

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	Taxon B	
	Latin Name		Latin Name
Saccharomyces cerevisiae		Saccharomyces cerevisiae	
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces		(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Saccharomyces	
cerevisiae"#gephebase-summary-title)	Common Name	cerevisiae"#gephebase-summary-title)	Common Name
baker's yeast		baker's yeast	
	Synonyms		Synonyms
Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces		Saccharomyces capensis; Saccharomyces italicus; Saccharomyces oviformis; Saccharomyces	
uvarum var. melibiosus; baker's yeast; S. cerevisiae; brewer's yeast; ATCC 18824;		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;		ATCC:18824; CBS 1171; CBS:1171; NRRL Y-12632; NRRL:Y:12632; Saccharomyces cerevisiae;	
Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae		Saccharomyce cerevisiae; Saccharomyes cerevisiae; Sccharomyces cerevisiae	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta;		cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta;	
Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae;		Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae;	
Saccharomyces		Saccharomyces	
	Parent		Parent
Saccharomyces () - (Rank: genus)		Saccharomyces () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
4932		4932	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4932)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
PMA1		P05030 (http://www.uniprot.org/uniprot/P05030)	
	Synonyms		GenebankID or UniProtKB
KT10; YGL008C		852876 (https://www.ncbi.nlm.nih.gov/nuccore/852876)	
	String		
4932.YGL008C			
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YGL008C)			
	Sequence Similarities		
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

G>T (Ala > Asp) @ position 2204

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 CBM20 and 1 other line

