

## GEPHE SUMMARY

	Gephebase Gene	GephelD
metallothionein CUP1 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase=^metallothionein CUP1^#gephebase-summary-title)	GP00001289	Main curator
Published	Entry Status	Arnoult

## PHENOTYPIC CHANGE

	Trait Category	
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category=^Physiology^#gephebase-summary-title)		Trait
Metal tolerance (copper) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Metal">https://www.gephebase.org/search-criteria?/and+Trait=^Metal</a> 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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status=^Experimental Evolution^#gephebase-summary-title)		

Taxon A	Latin Name	Taxon B	Latin Name
Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )	Common Name	Saccharomyces cerevisiae ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Saccharomyces+cerevisiae^#gephebase-summary-title</a> )	Common Name
baker's yeast	Synonyms	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; Saccharomyces cerevisiae; Sccharomyces cerevisiae	Rank	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
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	
Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930</a> )	Parent	Saccharomyces () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4930</a> )	Parent
4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932</a> )	NCBI Taxonomy ID	4932 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 4932</a> )	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

## GENOTYPIC CHANGE

CUP1-1	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) PoCX80 ( <a href="http://www.uniprot.org/uniprot/PoCX80">http://www.uniprot.org/uniprot/PoCX80</a> )
CUP1; MTH1; YHR053C	Synonyms	GenebankID or UniProtKB 856452 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/856452">https://www.ncbi.nlm.nih.gov/nuccore/856452</a> )
4932.YHR055C ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YHR055C">http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YHR055C</a> )	String	
Belongs to the metallothionein superfamily. Type 12 family.	Sequence Similarities	
GO:0016209 : antioxidant activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016209">https://www.ebi.ac.uk/QuickGO/term/GO:0016209</a> ) GO:0005507 : copper ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005507">https://www.ebi.ac.uk/QuickGO/term/GO:0005507</a> ) GO:0046870 : cadmium ion binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0046870">https://www.ebi.ac.uk/QuickGO/term/GO:0046870</a> ) GO:0004784 : superoxide dismutase activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0004784">https://www.ebi.ac.uk/QuickGO/term/GO:0004784</a> )	GO - Molecular Function	
		GO - Biological Process

GO:0071585 : detoxification of cadmium ion  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071585>)  
GO:0010273 : detoxification of copper ion  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010273>)  
GO:0046688 : response to copper ion  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046688>)  
GO:0019430 : removal of superoxide radicals  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019430>)

#### GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria/?and+Presumptive+Null=%No%#gephebase-summary-title>)

Molecular Type

Gene Amplification (<https://www.gephebase.org/search-criteria/?and+Molecular+Type=%Gene+Amplification%#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

Gene duplication

Experimental Evidence

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

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

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

24 over 34 lines