

GEPHE SUMMARY

	Gephebase Gene		GepheID
TRK1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~TRK1^#gephebase-summary-title)		GP00001139	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Physiology^#gephebase-summary-title)		Trait	
Salt tolerance (ammonium) (https://www.gephebase.org/search-criteria?/and+Trait=~Salttolerance(ammonium)^#gephebase-summary-title)			
	Trait State in Taxon A		
Saccharomyces cerevisiae - standard strain FY4		Trait State in Taxon B	
Saccharomyces cerevisiae - sake strain K12			
	Ancestral State		
Data not curated		Taxonomic Status	
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated^#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Saccharomycescerevisiae^#gephebase-summary-title)		Saccharomyces cerevisiae (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Saccharomycescerevisiae^#gephebase-summary-title)	
	Common Name		Common Name
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
species		species	
	Lineage		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)		Saccharomyces () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=4930)	
	NCBI Taxonomy ID		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)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Saccharomyces cerevisiae - standard strain FY4		Saccharomyces cerevisiae - sake strain K12	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
NTRK1		P04629 (http://www.uniprot.org/uniprot/P04629)	
	Synonyms		GenebankID or UniProtKB
MTC; TRK; TRK1; TRKA; Trk-A; p140-TrkA		CAA89424 (https://www.ncbi.nlm.nih.gov/nuccore/CAA89424)	
	String		
9606.ENSPO0000431418 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000431418)			
	Sequence Similarities		
Belongs to the protein kinase superfamily. Tyr protein kinase family. Insulin receptor subfamily.			
	GO - Molecular Function		
GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)			

GO:0005524 : ATP binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0005524>)
GO:0042803 : protein homodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042803>)
GO:0004714 : transmembrane receptor protein tyrosine kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004714>)
GO:0004713 : protein tyrosine kinase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0004713>)
GO:0005004 : GPI-linked ephrin receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005004>)
GO:0019900 : kinase binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0019900>)
GO:0048406 : nerve growth factor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048406>)
GO:0010465 : nerve growth factor receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010465>)
GO:0043121 : neurotrophin binding (<https://www.ebi.ac.uk/QuickGO/term/GO:0043121>)
GO:0005166 : neurotrophin p75 receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005166>)
GO:0005030 : neurotrophin receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005030>)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0043524 : negative regulation of neuron apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043524>)
GO:0070374 : positive regulation of ERK1 and ERK2 cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070374>)
GO:0010976 : positive regulation of neuron projection development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010976>)
GO:0046579 : positive regulation of Ras protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046579>)
GO:0008285 : negative regulation of cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008285>)
GO:0051092 : positive regulation of NF-kappaB transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051092>)
GO:0051599 : response to hydrostatic pressure
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051599>)
GO:0006468 : protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006468>)
GO:0043547 : positive regulation of GTPase activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043547>)
GO:0007623 : circadian rhythm (<https://www.ebi.ac.uk/QuickGO/term/GO:0007623>)
GO:0021553 : olfactory nerve development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0021553>)
GO:0009968 : negative regulation of signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009968>)
GO:1990090 : cellular response to nerve growth factor stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:1990090>)
GO:0031175 : neuron projection development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031175>)
GO:0046777 : protein autophosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046777>)
GO:0007568 : aging (<https://www.ebi.ac.uk/QuickGO/term/GO:0007568>)
GO:0001934 : positive regulation of protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001934>)
GO:0007411 : axon guidance (<https://www.ebi.ac.uk/QuickGO/term/GO:0007411>)
GO:0018108 : peptidyl-tyrosine phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018108>)
GO:0051965 : positive regulation of synapse assembly
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051965>)
GO:0007611 : learning or memory (<https://www.ebi.ac.uk/QuickGO/term/GO:0007611>)
GO:0048678 : response to axon injury
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048678>)
GO:0045766 : positive regulation of angiogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045766>)
GO:0030183 : B cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030183>)
GO:0048015 : phosphatidylinositol-mediated signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048015>)
GO:0038083 : peptidyl-tyrosine autophosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038083>)
GO:0009314 : response to radiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0009314>)
GO:0050965 : detection of temperature stimulus involved in sensory perception of pain
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050965>)
GO:0051602 : response to electrical stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051602>)
GO:0031667 : response to nutrient levels
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031667>)
GO:0000186 : activation of MAPKK activity

(<https://www.ebi.ac.uk/QuickGO/term/GO:0000186>)
GO:0060385 : axonogenesis involved in innervation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060385>)
GO:0061368 : behavioral response to formalin induced pain
(<https://www.ebi.ac.uk/QuickGO/term/GO:0061368>)
GO:0071316 : cellular response to nicotine
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071316>)
GO:0050966 : detection of mechanical stimulus involved in sensory perception of pain
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050966>)
GO:0042490 : mechanoreceptor differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042490>)
GO:0038180 : nerve growth factor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0038180>)
GO:0048666 : neuron development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048666>)
GO:0048011 : neurotrophin TRK receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048011>)
GO:0043068 : positive regulation of programmed cell death
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043068>)
GO:0051968 : positive regulation of synaptic transmission, glutamatergic
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051968>)
GO:0010623 : programmed cell death involved in cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010623>)
GO:0060009 : Sertoli cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060009>)
GO:0048485 : sympathetic nervous system development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048485>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
GO:0000139 : Golgi membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0000139>)
GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0043235 : receptor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0043235>)
GO:0032991 : protein-containing complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032991>)
GO:0030425 : dendrite (<https://www.ebi.ac.uk/QuickGO/term/GO:0030425>)
GO:0005769 : early endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005769>)
GO:0043025 : neuronal cell body (<https://www.ebi.ac.uk/QuickGO/term/GO:0043025>)
GO:0010008 : endosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010008>)
GO:0030424 : axon (<https://www.ebi.ac.uk/QuickGO/term/GO:0030424>)
GO:0009986 : cell surface (<https://www.ebi.ac.uk/QuickGO/term/GO:0009986>)
GO:0031901 : early endosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031901>)
GO:0031902 : late endosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031902>)
GO:0005770 : late endosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005770>)

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

Candidate a.a substitutions in K12 : C1143S; H551P; E1190G; Q1227K

Experimental Evidence

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

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

Main Reference

Genetic Basis of Ammonium Toxicity Resistance in a Sake Strain of Yeast: A Mendelian Case. (2013) (<https://pubmed.ncbi.nlm.nih.gov/23550140>)

Authors

Reisser C; Dick C; Kruglyak L; Botstein D; Schacherer J; Hess DC

Abstract

High concentrations of ammonium at physiological concentrations of potassium are toxic for the standard laboratory strain of *Saccharomyces cerevisiae* In the original description of this metabolic phenotype, we focused on the standard laboratory strains of *Saccharomyces* In this study, we screened a large collection of *S. cerevisiae* natural isolates and identified one strain that is resistant to high concentrations of ammonium. This strain, K12, was isolated in sake breweries. When the K12 strain was crossed to the standard laboratory strain (FY4), the resulting tetrads displayed 2:2 segregation of the resistance phenotype, suggesting a single gene trait. Using a bulk segregant analysis strategy, we mapped this trait to a 150-kb region on chromosome X containing the TRK1 gene. This gene encodes a transporter required for high-affinity potassium transport in *S. cerevisiae* Data from reciprocal hemizygosity experiments with TRK1 deletion strains in K12 and BY backgrounds, as well as analysis of the deletion of this gene in the K12 strain, demonstrate that the K12 allele of TRK1 is responsible for ammonium toxicity resistance.

Furthermore, we determined the minimal amount of potassium required for both the K12 and laboratory strain needed for growth. These results demonstrate that the gene encoded by the K12 allele of TRK1 has a greater affinity for potassium than the standard allele of TRK1 found in *Saccharomyces* strains. We hypothesize that this greater-affinity allele of the potassium transporter reduces the flux of ammonium into the yeast cells under conditions of ammonium toxicity. These findings further refine our understanding of ammonium toxicity in yeast and provide an example of using natural variation to understand cellular processes.

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Additional References

RELATED GEPHE

Related Genes

4 (CYC8, ENA1-2-5 cluster, PMA1, MEP2) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^4932^/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS