

GEPHE SUMMARY

BNA6 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=BNA6#gephebase-summary-title)	Gephebase Gene	GP00001882	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=Physiology#gephebase-summary-title)	Trait Category		
Nicotinid acid metabolism (https://www.gephebase.org/search-criteria?/and+Trait=Nicotinid acid metabolism#gephebase-summary-title)	Trait		
Candida albicans and Saccharomyces cerevisiae - prototroph for nicotinic acid - can synthesize nicotinic acid mononucleotide (NaMN) from tryptophan via the kynurenine pathway	Trait State in Taxon A		
Candida glabrata - auxotroph for nicotinic acid	Trait State in Taxon B		
Taxon A	Ancestral State		
Interspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=Interspecific#gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Candida albicans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=Candida albicans#gephebase-summary-title)	Latin Name	[Candida] glabrata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=[Candida] glabrata#gephebase-summary-title)	Latin Name
-	Common Name	-	Common Name
	Synonyms		Synonyms
Candida stellatoidea; Candida stellatoidea type I; ATCC 11006; ATCC 18804; ATCC 20308; ATCC:11006; ATCC:18804; ATCC:20308; BCC 5390; BCC:5390; BCRC 20512; BCRC:20512; CBS 562; CBS:562; CCRC 20512; CCRC:20512; CECT 1002; CECT:1002; IFO 1385; IFO:1385; JCM 1537; JCM 1542; JCM:1537; JCM:1542; KCTC 7270; KCTC:7270; MUCL 29800; MUCL:29800; NBIMCC 72; NBIMCC:72; NBRC 1385; NBRC:1385; NCAIM Y.00971; NCYC 597; NCYC:597; NRRL Y-12983; NRRL:Y:12983; PYCC 3436; PYCC:3436; UAMH 8765; UAMH:8765; Candida albican	Rank	Candida glabrata; Cryptococcus glabratus; Torulopsis glabrata; Cryptococcus glabratus H.W. Anderson, 1917; ATCC 2001; ATCC:2001; BCRC:20586; CBS 138; CBS:138; CCRC 20586; CCRC:20586; DBVPG 3828; DBVPG:3828; IFO 0622; IFO:0622; JCM 3761; JCM:3761; KCTC 1714; KCTC:1714; NCPF 3309; NCPF:3309; NRRL Y-1417; NRRL Y-65; NRRL:Y:1417; NRRL:Y:65; Candida glabrata	Rank
species	Lineage	species	Lineage
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Debaryomycetaceae; Candida/Lodderomyces clade; Candida	Parent	cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Nakaseomyces; Nakaseomyces/Candida clade	Parent
Candida () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1535326)	NCBI Taxonomy ID	Nakaseomyces/Candida clade () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=600669)	NCBI Taxonomy ID
5476 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5476)	is Taxon A an Intraspecies?	5478 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=5478)	is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

BNA6	Generic Gene Name	UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
QPT1; YFR047C	Synonyms	P43619 (http://www.uniprot.org/uniprot/P43619)
4932.YFR047C (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YFR047C)	String	()
Belongs to the NadC/ModD family.	Sequence Similarities	
GO:0004514 : nicotinate-nucleotide diphosphorylase (carboxylating) activity	GO - Molecular Function	

(<https://www.ebi.ac.uk/QuickGO/term/GO:0004514>)

GO - Biological Process

GO:0034354 : 'de novo' NAD biosynthetic process from tryptophan

(<https://www.ebi.ac.uk/QuickGO/term/GO:0034354>)

GO:0009435 : NAD biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009435>)

GO:0034213 : quinolinate catabolic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0034213>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null=~Yes~#gephebase-summary-title))

Molecular Type

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

Aberration Type

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

Deletion Size

unknown

Molecular Details of the Mutation

Size of the deletion not mentioned in the paper

Experimental Evidence

Candidate Gene ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene~#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=~Candidate+Gene~#gephebase-summary-title))

Main Reference

Nicotinic acid limitation regulates silencing of *Candida* adhesins during UTI. (2005) (<https://pubmed.ncbi.nlm.nih.gov/15774723>)

Authors

Domergue R; Castaño I; De Las Peñas A; Zupancic M; Locketell V; Hebel JR; Johnson D; Cormack BP

Abstract

The adherence of *Candida glabrata* to host cells is mediated, at least in part, by the EPA genes, a family of adhesins encoded at subtelomeric loci, where they are subject to transcriptional silencing. We show that normally silent EPA genes are expressed during murine urinary tract infection (UTI) and that the inducing signal is the limitation of nicotinic acid (NA), a precursor of nicotinamide adenine dinucleotide (NAD⁺). *C. glabrata* is an NA auxotroph, and NA-induced EPA expression is likely the result of a reduction in NAD⁺ availability for the NAD⁺-dependent histone deacetylase Sir2p. The adaptation of *C. glabrata* to the host, therefore, involves a loss of metabolic capacity and exploitation of the resulting auxotrophy to signal a particular host environment.

Additional References

RELATED GEPHE

Related Genes

4 (BNA1, BNA2, BNA4, BNA5) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=~5476~/and+Trait=Nicotinid acid metabolism/or+Taxon ID=~5478~/and+Trait=Nicotinid acid metabolism/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=~5476~/and+Trait=Nicotinid+acid+metabolism/or+Taxon+ID=~5478~/and+Trait=Nicotinid+acid+metabolism/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Loss of four de novo biosynthesis of nicotinic acid (BNA) genes (all except BNA3 were lost) is associated with increased pathogenicity: the nicotinic acid present in the urinary tract activates expression of epithelial adhesion (EPA) genes in *C. glabrata*; thus activating adherence to host cells within the renal system. @& UniprotKB not fetched