GEPHE SUMMARY

Gephebase Gene

BNA4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BNA4^#gephebase-summary-title)

GepheID

GP00001880

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

Nicotinid acid metabolism (https://www.gephebase.org/search-criteria?/and+Trait=^Nicotinid acid metabolism^#gephebase-summary-title)

Trait State in Taxon A

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 B

Candida glabrata - auxotroph for nicotinic acid

Ancestral State

Taxon A

Taxonomic Status

Interspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Interspecific^#gephebase-summary-title)

Taxon A

Latin Name

Candida albicans (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Candida albicans^#gephebase-summary-title)

Common Name

-

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

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Debaryomycetaceae; Candida/Lodderomyces clade; Candida

Parent

Candida () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1535326)

NCBI Taxonomy ID

5476 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5476)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

[Candida] glabrata (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^[Candida] glabrata^#gephebase-summary-title)

Common Name

-

Synonyms

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; Candidia glabrata

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Nakaseomyces; Nakaseomyces/Candida clade

Parent

Nakaseomyces/Candida clade () - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 600669)

NCBI Taxonomy ID

5478 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5478)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

BNA4

Synonyms

YBL098W; YBL0828

String

4932.YBL098W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YBL098W)

Sequence Similarities

Belongs to the aromatic-ring hydroxylase family. KMO subfamily.

GO - Molecular Function

GO:0071949 : FAD binding (https://www.ebi.ac.uk/QuickGO/term/GO:0071949)

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P38169 (http://www.uniprot.org/uniprot/P38169)

GenebankID or UniProtKB

()

GO:0050660 : flavin adenine dinucleotide binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0050660)
GO:0004502 : kynurenine 3-monooxygenase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004502)
GO:0016174 : NAD(P)H oxidase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0016174)

GO - Biological Process

GO:0034354 : 'de novo' NAD biosynthetic process from tryptophan
(https://www.ebi.ac.uk/QuickGO/term/GO:0034354)
GO:0043420 : anthranilate metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0043420)
GO:0019805 : quinolinate biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0019805)
GO:0006569 : tryptophan catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0006569)
GO:0070189 : kynurenine metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0070189)
GO:0019674 : NAD metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0019674)

GO - Cellular Component

GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0005741 : mitochondrial outer membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005741)

Presumptive Null

Yes (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)

Aberration Type

Deletion (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)

Main Reference

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

Authors

Domergue R; CastaÃ±o I; De Las PeÃ±as A; Zupancic M; Lockatell 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, BNA5, BNA6) (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 nicotinid 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