

GEPHE SUMMARY

<p>BNA5 (<a +bna5+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+BNA5+"#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001881</p> <p>Courtier</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)</p> <p>Nicotinid acid metabolism (<a +nicotinid+acid+metabolism+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Nicotinid+acid+metabolism+"#gephebase-summary-title)</p> <p>Candida albicans and Saccharomyces cerevisiae - prototroph for nicotinic acid - can synthesize nicotinic acid mononucleotide (NaMN) from tryptophan via the kynurenine pathway</p> <p>Candida glabrata - auxotroph for nicotinic acid</p> <p>Taxon A</p> <p>Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon A an Intraspecies?</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p>
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GENOTYPIC CHANGE

<p>BNA5</p> <p>YLR231C; L8083.14</p> <p>4932.YLR231C</p> <p>(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=4932.YLR231C)</p> <p>Belongs to the kynureninase family.</p> <p>GO:0030170 : pyridoxal phosphate binding</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)</p> <p>Q05979 (http://www.uniprot.org/uniprot/Q05979)</p> <p>GenebankID or UniProtKB</p> <p>0</p>
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(<https://www.ebi.ac.uk/QuickGO/term/GO:0030170>)
GO:0030429 : kynureninase activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0030429>)
GO - Biological Process

GO:0019441 : tryptophan catabolic process to kynurenine
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019441>)
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:0097053 : L-kynurenine catabolic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097053>)

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; Lockett 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, 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](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