GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001818

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

sensitive

Trait State in Taxon B

resistant

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

-

Synonyms

Neurospora crassa Shear & B. O. Dodge 1927

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; sordariomyceta; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora

Parent

Neurospora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5140)

NCBI Taxonomy ID

5141 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5141)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

-

Synonyms

Neurospora crassa Shear & B. O. Dodge 1927

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta; Pezizomycotina; leotiomyceta; sordariomyceta; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora

Parent

Neurospora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5140)

NCBI Taxonomy ID

5141 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 5141)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

TUB2

Synonyms

ARM10; SHE8; YFL037W

String

4932.YFL037W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YFL037W)

Sequence Similarities

Belongs to the tubulin family.

GO - Molecular Function

GO:0005525 : GTP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005525)
GO:0003924 : GTPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003924)
GO:0005200 : structural constituent of cytoskeleton (https://www.ebi.ac.uk/QuickGO/term/GO:0005200)

GO - Biological Process

GO:0007010 : cytoskeleton organization (https://www.ebi.ac.uk/QuickGO/term/GO:0007010)
GO:0000278 : mitotic cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0000278)
GO:0000070 : mitotic sister chromatid segregation

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)

P02557 (http://www.uniprot.org/uniprot/P02557)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0000070)
GO:0007017 : microtubule-based process
(https://www.ebi.ac.uk/QuickGO/term/GO:0007017)
GO:0046677 : response to antibiotic (https://www.ebi.ac.uk/QuickGO/term/GO:0046677)
GO:0000226 : microtubule cytoskeleton organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0000226)
GO:0045143 : homologous chromosome segregation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045143)
GO:0030473 : nuclear migration along microtubule
(https://www.ebi.ac.uk/QuickGO/term/GO:0030473)
GO:0090316 : positive regulation of intracellular protein transport
(https://www.ebi.ac.uk/QuickGO/term/GO:0090316)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005874 : microtubule (https://www.ebi.ac.uk/QuickGO/term/GO:0005874)
GO:0005816 : spindle pole body (https://www.ebi.ac.uk/QuickGO/term/GO:0005816)
GO:0005881 : cytoplasmic microtubule
(https://www.ebi.ac.uk/QuickGO/term/GO:0005881)
GO:0005828 : kinetochore microtubule
(https://www.ebi.ac.uk/QuickGO/term/GO:0005828)
GO:0005880 : nuclear microtubule (https://www.ebi.ac.uk/QuickGO/term/GO:0005880)
GO:0045298 : tubulin complex (https://www.ebi.ac.uk/QuickGO/term/GO:0045298)

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

Phe167Tyr

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Phe	Tyr	167

Main Reference

Cloning and characterization of the gene for beta-tubulin from a benomyl-resistant mutant of Neurospora crassa and its use as a dominant selectable marker. (1986)
(https://pubmed.ncbi.nlm.nih.gov/2946938)

Authors

Orbach MJ; Porro EB; Yanofsky C

Abstract

We cloned the beta-tubulin gene of Neurospora crassa from a benomyl-resistant strain and determined its nucleotide sequence. The gene encodes a 447-residue protein which shows strong homology to other beta-tubulins. The coding region is interrupted by six introns, five of which are within the region coding for the first 54 amino acids of the protein. Intron position comparisons between the N. crassa gene and other fungal beta-tubulin genes reveal considerable positional conservation. The mutation responsible for benomyl resistance was determined; it caused a phenylalanine-to-tyrosine change at position 167. Codon usage in the beta-tubulin gene is biased, as has been observed for other abundantly expressed N. crassa genes such as am and the H3 and H4 histone genes. This bias results in pyrimidines in the third positions of 96% of the codons in codon families in which there is a choice between purines and pyrimidines in this position. Bias is also evident by the absence of 19 of the 61 sense codons. We demonstrated that benomyl resistance is due to the cloned beta-tubulin gene of strain Bml511(r)a and that this gene can be used as a dominant selectable marker in N. crassa transformation.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

In vitro assays have demonstrated that a Tyr residue in position 167 of b-tubulin impeded BZ binding in S. cerevisiae