## GEPHE SUMMARY

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

GepheID
GP00001820

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

Common Name
barber pole worm

Synonyms
barber pole worm; red stomach worm; Haemonchus contortus (Rudolphi, 1803)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Strongylida; Trichostrongyloidea; Haemonchidae; Haemonchus

Parent
Haemonchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6288 )

NCBI Taxonomy ID
6289 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6289 )

is Taxon A an Infraspecies?
No

### Taxon B

Latin Name
Haemonchus contortus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Haemonchus contortus^#gephebase-summary-title)

Common Name
barber pole worm

Synonyms
barber pole worm; red stomach worm; Haemonchus contortus (Rudolphi, 1803)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Strongylida; Trichostrongyloidea; Haemonchidae; Haemonchus

Parent
Haemonchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6288 )

NCBI Taxonomy ID
6289 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6289 )

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 )

UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
P02557 (http://www.uniprot.org/uniprot/P02557)

Sequence Similarities
Belongs to the tubulin family.

GenebankID or UniProtKB
()

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

(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

Glu198Ala

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 | Glu | Ala | 198 |

Main Reference

Phenotyping and genotyping of Haemonchus contortus isolates reveals a new putative candidate mutation for benzimidazole resistance in nematodes. (2007)
(https://pubmed.ncbi.nlm.nih.gov/17101226)

Authors

Ghisi M; Kaminsky R; MÃ¤ser P

Abstract

In order to monitor and eventually control the spread of drug-resistant Haemonchus contortus, knowledge of the molecular mechanisms underlying resistance is essential. Here we phenotypically and genotypically characterize three multidrug-resistant H. contortus field isolates from Australia and South Africa. All were significantly less susceptible to thiabendazole than a sensitive reference strain in an in vitro egg-hatch assay. The sensitivity was further reduced in a surviving population after treatment of infected sheep with albendazole. The beta-tubulin genes were amplified from genomic DNA of the H. contortus isolates, cloned, and sequenced. There was a high degree of sequence variation. The known mutation phenylalanine-200 to tyrosine (F200Y) occurred in 60% of the sequences from resistant isolates, but not in the sensitive reference. Interestingly, 90% of the beta-tubulin sequences from resistant isolates lacking tyrosine-200 carried another mutation nearby, glutamate-198 to alanine (E198A). This mutation was not found in the sensitive isolate, nor in sequences from resistant isolates carrying the mutation F200Y. However, the mutation E198A is known from benomyl-resistant isolates of phytopathogenic fungi such as Monilinia fructicola. The finding that alanine-198 correlates with thiabendazole resistance in H. contortus isolates from South Africa and Australia suggests that also in nematodes, the mutation E198A plays a role in benzimidazole resistance. Alanine-198 alleles of beta-tubulin can be detected by PCR-RFLP and we suggest to include this test in future surveys of H. contortus field populations.

Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

2 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^beta-tubulin^/and+Taxon ID=^6289^/or+Gene Gephebase=^beta-tubulin^/and+Taxon ID=^6289^#gephebase-summary-title)

## EXTERNAL LINKS