

GEPHE SUMMARY

	Gephebase Gene	GephelD
beta-tubulin (ben-1) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^beta-tubulin (ben-1)^#gephebase-summary-title)	GP00001848	
	Entry Status	Main curator
Published	Courtier	

PHENOTYPIC CHANGE

	Trait Category		
	Trait		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)			
Xenobiotic resistance (benzimidazole) (https://www.gephebase.org/search-criteria?/and+Trait=^Xenobiotic+resistance+(benzimidazole)^#gephebase-summary-title)	Trait State in Taxon A		
sensitive			
resistant	Trait State in Taxon B		
Taxon A	Ancestral State		
	Taxonomic Status		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)			
Taxon A	Latin Name	Taxon B	Latin Name
Caenorhabditis elegans (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Caenorhabditis+elegans^#gephebase-summary-title)		Caenorhabditis elegans (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Caenorhabditis+elegans^#gephebase-summary-title)	
-	Common Name	-	Common Name
roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900	Synonyms	roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis	Lineage
Caenorhabditis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237)	Parent	Caenorhabditis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237)	Parent
6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239)	NCBI Taxonomy ID	6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
		ED3012	Taxon B Description

GENOTYPIC CHANGE

	Generic Gene Name		
TUB2		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c) P02557 (http://www.uniprot.org/uniprot/P02557)	GenebankID or UniProtKB
ARM10; SHE8; YFL037W	Synonyms		
4932.YFL037W (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 4932.YFL037W)	String	0	
Belongs to the tubulin family.	Sequence Similarities		
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 - Molecular Function		
GO:0007010 : cytoskeleton organization	GO - Biological Process		

(<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

Yes ([https://www.gephebase.org/search-criteria?/and+Presumptive Null=%27Yes%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive%20Null=%27Yes%27#gephebase-summary-title))

Molecular Type

Coding ([https://www.gephebase.org/search-criteria?/and+Molecular Type=%27Coding%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular%20Type=%27Coding%27#gephebase-summary-title))

Aberration Type

Deletion ([https://www.gephebase.org/search-criteria?/and+Aberration Type=%27Deletion%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration%20Type=%27Deletion%27#gephebase-summary-title))

Deletion Size

1-9 bp

Molecular Details of the Mutation

Del_3540300_3540301 â€“ 1bp deletion in coding exon 2

Experimental Evidence

Association Mapping ([https://www.gephebase.org/search-criteria?/and+Experimental Evidence=%27Association Mapping%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/and+Experimental%20Evidence=%27Association%20Mapping%27#gephebase-summary-title))

Main Reference

Extreme allelic heterogeneity at a *Caenorhabditis elegans* beta-tubulin locus explains natural resistance to benzimidazoles. (2018) (<https://pubmed.ncbi.nlm.nih.gov/30372484>)

Authors

Hahnel SR; Zdraljevic S; Rodriguez BC; Zhao Y; McGrath PT; Andersen EC

Abstract

Benzimidazoles (BZ) are essential components of the limited chemotherapeutic arsenal available to control the global burden of parasitic nematodes. The emerging threat of BZ resistance among multiple nematode species necessitates the development of novel strategies to identify genetic and molecular mechanisms underlying this resistance. All detection of parasitic helminth resistance to BZ is focused on the genotyping of three variant sites in the orthologs of the β -tubulin gene found to confer resistance in the free-living nematode *Caenorhabditis elegans*. Because of the limitations of laboratory and field experiments in parasitic nematodes, it is difficult to look beyond these three sites to identify additional mechanisms that might contribute to BZ resistance in the field. Here, we took an unbiased genome-wide mapping approach in the free-living nematode species *C. elegans* to identify the genetic underpinnings of natural resistance to the commonly used BZ, albendazole (ABZ). We found a wide range of natural variation in ABZ resistance in natural *C. elegans* populations. In agreement with known mechanisms of BZ resistance in parasites, we found that a majority of the variation in ABZ resistance among wild *C. elegans* strains is caused by variation in the β -tubulin gene *ben-1*. This result shows empirically that resistance to ABZ naturally exists and segregates within the *C. elegans* population, suggesting that selection in natural niches could enrich for resistant alleles. We identified 25 distinct *ben-1* alleles that are segregating at low frequencies within the *C. elegans* population, including many novel molecular variants. Population genetic analyses indicate that *ben-1* variation arose multiple times during the evolutionary history of *C. elegans* and provide evidence that these alleles likely occurred recently because of local selective pressures. Additionally, we find purifying selection at all five β -tubulin genes, despite predicted loss-of-function variants in *ben-1*, indicating that BZ resistance in natural niches is a stronger selective pressure than loss of one β -tubulin gene. Furthermore, we used genome-editing to show that the most common parasitic nematode β -tubulin allele that confers BZ resistance, F200Y, confers resistance in *C. elegans*. Importantly, we identified a novel genomic region that is correlated with ABZ resistance in the *C. elegans* population but independent of *ben-1* and the other β -tubulin loci, suggesting that there are multiple mechanisms underlying BZ resistance. Taken together, our results establish a population-level resource of nematode natural diversity as an important model for the study of mechanisms that give rise to BZ resistance.

Additional References

RELATED GEPHE

3 (acetyl-CoA carboxylase (ACC), GLC-1, str-217) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=%276239%27/and+Trait=%27Xenobiotic resistance%27/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon%20ID=%276239%27/and+Trait=%27Xenobiotic%20resistance%27/and+groupHaplotypes=true#gephebase-summary-title))

Related Genes

26 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=%27beta-tubulin \(ben-1\)%27/and+Taxon ID=%276239%27/or+Gene Gephebase=%27beta-tubulin \(ben-1\)%27/and+Taxon ID=%276239%27#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene%20Gephebase=%27beta-tubulin%20(ben-1)%27/and+Taxon%20ID=%276239%27/or+Gene%20Gephebase=%27beta-tubulin%20(ben-1)%27/and+Taxon%20ID=%276239%27#gephebase-summary-title))

Related Haplotypes

EXTERNAL LINKS

COMMENTS