

GEPHE SUMMARY

	Gephebase Gene		GepheID
beta-tubulin (ben-1) (https://www.gephebase.org/search-criteria?/and+Gene)		GP00001849	
Gephebase="beta-tubulin (ben-1)"#gephebase-summary-title)			Main curator
	Entry Status	Courtier	
Published			

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	Taxon B	
	Latin Name		Latin Name
Caenorhabditis elegans		Caenorhabditis elegans	
(<a caenorhabditis+elegans"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Caenorhabditis elegans"#gephebase-summary-title)		(<a caenorhabditis+elegans"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms="Caenorhabditis elegans"#gephebase-summary-title)	
	Common Name		Common Name
-		-	
	Synonyms		Synonyms
roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900		roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900	
	Rank		Rank
species		species	
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis		cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis	
	Parent		Parent
Caenorhabditis () - (Rank: genus)		Caenorhabditis () - (Rank: genus)	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6237)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6237)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
6239		6239	
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6239)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6239)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		Yes	
			Taxon B Description
		MY518	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Saccharomyces cerevisiae (strain ATCC 204508 / S288c)
TUB2		P02557 (http://www.uniprot.org/uniprot/P02557)	
	Synonyms		GenebankID or UniProtKB
ARM10; SHE8; YFL037W		0	
	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:000525 : GTP binding (https://www.ebi.ac.uk/QuickGO/term/GO:000525)			
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

Yes (<https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes^#gephebase-summary-title>)

Molecular Type

Coding (<https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title>)

Aberration Type

Inversion (<https://www.gephebase.org/search-criteria?/and+Aberration Type=~Inversion^#gephebase-summary-title>)

Inversion Size

-

Molecular Details of the Mutation

Inv_3540316_3543965 â€” 3649bp inversion â€” the text indicates that there is â€œca 1kb inversion that spans exon 1 and the promoter regionâ€” but the nucleotide numbers in the supplemental table indicates that 3.6kb are disrupted. Steffen Hahnel comment: we don't know the exact size of this large structural variation. I estimated conservatively from the BAM files that a region of 3649 bp is messed up in this strain compared to wildtype including one or more inversions. The largest inversion is around 1 kb. If one wants to be sure about size and location you would need to amplify this region by PCR

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Association Mapping^#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

Related Genes

3 (acetyl-CoA carboxylase (ACC), GLC-1, str-217) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~6239^/and+Trait=Xenobiotic resistance/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

26 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~beta-tubulin \(ben-1\)^/and+Taxon ID=~6239^/or+Gene Gephebase=~beta-tubulin \(ben-1\)^/and+Taxon ID=~6239^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene Gephebase=~beta-tubulin (ben-1)^/and+Taxon ID=~6239^/or+Gene Gephebase=~beta-tubulin (ben-1)^/and+Taxon ID=~6239^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS