

GEPHE SUMMARY

	Gephebase Gene		GepheID
peel-1 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase+^peel-1*#gephebase-summary-title)		GP00001322	
	Entry Status	Courtier	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology*#gephebase-summary-title)			
	Trait		
Hybrid incompatibility (https://www.gephebase.org/search-criteria?/and+Trait=^Hybrid+incompatibility*#gephebase-summary-title)			
	Trait State in Taxon A		
C. elegans			
	Trait State in Taxon B		
C. elegans - Utah strain EG4348			
	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 (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
-		-	
	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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6237)		Caenorhabditis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6237)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6239)		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
		C. elegans - Utah strain EG4348	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Caenorhabditis elegans
peel-1		G5EGC6 (http://www.uniprot.org/uniprot/G5EGC6)	
	Synonyms		GenebankID or UniProtKB
CELE_Y39G10AR.25; Y39G10AR.25		HQ291556.1 (https://www.ncbi.nlm.nih.gov/nuccore/HQ291556.1)	
	String		
6239.Y39G10AR.25 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=6239.Y39G10AR.25)			
	Sequence Similarities		
-			
	GO - Molecular Function		
-			
	GO - Biological Process		
-			
	GO - Cellular Component		
GO:0016021 : integral component of membrane			

(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

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

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

SNP Coding Change

Nonsense

Molecular Details of the Mutation

G>T - glycine to stop codon at position 57. Total length of wild-type protein is 174 amino acids.

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

A novel sperm-delivered toxin causes late-stage embryo lethality and transmission ratio distortion in *C. elegans*. (2011) (<https://pubmed.ncbi.nlm.nih.gov/21814493>)

Authors

Seidel HS; Ailion M; Li J; van Oudenaarden A; Rockman MV; Kruglyak L

Abstract

The evolutionary fate of an allele ordinarily depends on its contribution to host fitness. Occasionally, however, genetic elements arise that are able to gain a transmission advantage while simultaneously imposing a fitness cost on their hosts. We previously discovered one such element in *C. elegans* that gains a transmission advantage through a combination of paternal-effect killing and zygotic self-rescue. Here we demonstrate that this element is composed of a sperm-delivered toxin, *peel-1*, and an embryo-expressed antidote, *zeel-1*. *peel-1* and *zeel-1* are located adjacent to one another in the genome and co-occur in an insertion/deletion polymorphism. *peel-1* encodes a novel four-pass transmembrane protein that is expressed in sperm and delivered to the embryo via specialized, sperm-specific vesicles. In the absence of *zeel-1*, sperm-delivered PEEL-1 causes lethal defects in muscle and epidermal tissue at the 2-fold stage of embryogenesis. *zeel-1* is expressed transiently in the embryo and encodes a novel six-pass transmembrane domain fused to a domain with sequence similarity to *zyg-11*, a substrate-recognition subunit of an E3 ubiquitin ligase. *zeel-1* appears to have arisen recently, during an expansion of the *zyg-11* family, and the transmembrane domain of *zeel-1* is required and partially sufficient for antidote activity. Although PEEL-1 and ZEEL-1 normally function in embryos, these proteins can act at other stages as well. When expressed ectopically in adults, PEEL-1 kills a variety of cell types, and ectopic expression of ZEEL-1 rescues these effects. Our results demonstrate that the tight physical linkage between two novel transmembrane proteins has facilitated their co-evolution into an element capable of promoting its own transmission to the detriment of organisms carrying it.

Additional References

Widespread genetic incompatibility in *C. elegans* maintained by balancing selection. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18187622>)

RELATED GEPHE

Related Genes

1 (*peel-1/zeel-1*) ([https://www.gephebase.org/search-criteria?/or+Taxon ID=^6239^/and+Trait=Hybrid incompatibility/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=^6239^/and+Trait=Hybrid+incompatibility/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

1 ([https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^peel-1^/and+Taxon ID=^6239^/or+Gene Gephebase=^zeel-1^/and+Taxon ID=^6239^#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Gene+Gephebase=^peel-1^/and+Taxon+ID=^6239^/or+Gene+Gephebase=^zeel-1^/and+Taxon+ID=^6239^#gephebase-summary-title))

EXTERNAL LINKS

COMMENTS

Two other mutations disrupting *peel-1* have been found in wild strains. A 19-kb deletion removing *peel-1* and *zeel-1* genes has also been characterized ; Presumptive Null Mutation