

GEPHE SUMMARY

Gephebase Gene		GepheID
peel-1 (<a +peel-1+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">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 (<a +physiology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Physiology+"#gephebase-summary-title)			
Trait			
Hybrid incompatibility (<a +hybrid+incompatibility+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">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 (<a +intraspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Intraspecific+"#gephebase-summary-title)			
Taxon A		Taxon B	
Latin Name		Latin Name	
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)		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)	
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>)

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

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>)

	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 (<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=^peel-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