

GEPHE SUMMARY

scd-2 (https://www.gephebase.org/search-criteria/?and+Gene Gephebase=%scd-2%#gephebase-summary-title)	Gephebase Gene	GP00001026	GephelD
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria/?and+Trait Category=%Physiology%#gephebase-summary-title)	Trait Category		
Diapause (https://www.gephebase.org/search-criteria/?and+Trait=%Diapause%#gephebase-summary-title)	Trait		
C. elegans - desert strain	Trait State in Taxon A		
C. elegans - N2	Trait State in Taxon B		
Data not curated	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic Status=%Intraspecific%#gephebase-summary-title)	Taxonomic Status		
Taxon A			Taxon B
Caenorhabditis elegans (https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=%Caenorhabditis elegans%#gephebase-summary-title)	Latin Name		Latin Name
-	Common Name		Common Name
roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900	Synonyms		Synonyms
species	Rank		Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis	Lineage		Lineage
Caenorhabditis () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6237)	Parent		Parent
6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6239)	NCBI Taxonomy ID		NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?		is Taxon B an Infraspecies?
C. elegans - desert strain	Taxon A Description		Taxon B Description
	C. elegans - N2		

GENOTYPIC CHANGE

scd-2	Generic Gene Name	UniProtKB Caenorhabditis elegans
T10H9.2	Synonyms	GenebankID or UniProtKB
6239.T10H9.2 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=6239.T10H9.2)	String	BX284605 (https://www.ncbi.nlm.nih.gov/nuccore/BX284605)
Belongs to the protein kinase superfamily. Tyr protein kinase family. Insulin receptor subfamily.	Sequence Similarities	
GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)	GO - Molecular Function	
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)		
GO:0004714 : transmembrane receptor protein tyrosine kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004714)		

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0043066>)
 GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
 GO:0070374 : positive regulation of ERK1 and ERK2 cascade
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0070374>)
 GO:0006935 : chemotaxis (<https://www.ebi.ac.uk/QuickGO/term/GO:0006935>)
 GO:0009968 : negative regulation of signal transduction
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0009968>)
 GO:0040024 : dauer larval development
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0040024>)
 GO:0007606 : sensory perception of chemical stimulus
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0007606>)
 GO:0050893 : sensory processing (<https://www.ebi.ac.uk/QuickGO/term/GO:0050893>)

GO - Cellular Component

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)
 GO:0005887 : integral component of plasma membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
 GO:0043235 : receptor complex (<https://www.ebi.ac.uk/QuickGO/term/GO:0043235>)

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

Gly985Arg

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

C. elegans anaplastic lymphoma kinase ortholog SCD-2 controls dauer formation by modulating TGF-beta signaling. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18674914>)

Authors

Reiner DJ; Ailion M; Thomas JH; Meyer BJ

Abstract

Different environmental stimuli, including exposure to dauer pheromone, food deprivation, and high temperature, can induce *C. elegans* larvae to enter the dauer stage, a developmentally arrested diapause state. Although molecular and cellular pathways responsible for detecting dauer pheromone and temperature have been defined in part, other sensory inputs are poorly understood, as are the mechanisms by which these diverse sensory inputs are integrated to achieve a consistent developmental outcome.

In this paper, we analyze a wild *C. elegans* strain isolated from a desert oasis. Unlike wild-type laboratory strains, the desert strain fails to respond to dauer pheromone at 25 degrees C, but it does respond at higher temperatures, suggesting a unique adaptation to the hot desert environment. We map this defect in dauer response to a mutation in the *scd-2* gene, which, we show, encodes the nematode anaplastic lymphoma kinase (ALK) homolog, a proto-oncogene receptor tyrosine kinase. *scd-2* acts in a genetic pathway shown here to include the HEN-1 ligand, the RTK adaptor SOC-1, and the MAP kinase SMA-5. The SCD-2 pathway modulates TGF-beta signaling, which mediates the response to dauer pheromone, but SCD-2 might mediate a nonpheromone sensory input, such as food.

Our studies identify a new sensory pathway controlling dauer formation and shed light on ALK signaling, integration of signaling pathways, and adaptation to extreme environmental conditions.

Additional References

RELATED GEPHE

2 (nurf-1, srg-36/37) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^6239^/and+Trait=Diapause/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

Related Genes

EXTERNAL LINKS

COMMENTS

