

GEPHE SUMMARY

	Gephebase Gene		GepheID
scd-2 (<a +scd-2+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+scd-2+"#gephebase-summary-title)		GP00001026	
	Entry Status	Martin	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	
Diapause (<a +diapause+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Diapause+"#gephebase-summary-title)			
	Trait State in Taxon A		
C. elegans - desert strain		Trait State in Taxon B	
C. elegans - N2			
	Ancestral State		
Data not curated		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)	
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
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
C. elegans - desert strain		C. elegans - N2	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Caenorhabditis elegans
scd-2		O76411 (http://www.uniprot.org/uniprot/O76411)	
	Synonyms		GenebankID or UniProtKB
T10H9.2		BX284605 (https://www.ncbi.nlm.nih.gov/nucleotide/BX284605)	
	String		
6239.T10H9.2 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=6239.T10H9.2)			
	Sequence Similarities		
Belongs to the protein kinase superfamily. Tyr protein kinase family. Insulin receptor subfamily.			
	GO - Molecular Function		
GO:0004888 : transmembrane signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004888)			
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: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>)

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~No^#gephebase-summary-title)	Presumptive Null
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding^#gephebase-summary-title)	Molecular Type
SNP (https://www.gephebase.org/search-criteria?/and+Aberration Type=~SNP^#gephebase-summary-title)	Aberration Type
Nonsynonymous	SNP Coding Change
Gly985Arg	Molecular Details of the Mutation
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title)	Experimental Evidence

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

C. elegans anaplastic lymphoma kinase ortholog SCD-2 controls dauer formation by modulating TGF-beta signaling. (2008) (https://pubmed.ncbi.nlm.nih.gov/18674914)	Main Reference
Reiner DJ; Ailion M; Thomas JH; Meyer BJ	Authors
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.	Abstract
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 Genes
No matches found.	Related Haplotypes

EXTERNAL LINKS

COMMENTS

