GEPHE SUMMARY

Gephebase Gene
srx-43 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^srx-43^#gephebase-summary-title)
Entry Status
Published

GepheID
GP00001319
Main curator
Courtier

PHENOTYPIC CHANGE

Trait Category
Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)
Trait
Pheromone response (ascaroside) (https://www.gephebase.org/search-criteria?/and+Trait=^Pheromone response (ascaroside)^#gephebase-summary-title)
Trait State in Taxon A
C. elegans
Trait State in Taxon B
C. elegans - strains MY14; MY16; JU1171; MY6; JU360; ED3021; MY2 - less sensitive
Ancestral State
Taxon A
Taxonomic Status
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

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

Taxon B

Latin Name
Caenorhabditis elegans
(https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Caenorhabditis elegans^#gephebase-summary-title)
Common Name
-
Synonyms
roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900
Rank
species
Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Nematoda; Chromadorea; Rhabditida; Rhabditina; Rhabditomorpha; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
Parent
Caenorhabditis () - (Rank: genus)
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237)
NCBI Taxonomy ID
6239
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239)
is Taxon B an Infraspecies?
Yes
Taxon B Description
C. elegans - strains MY14; MY16; JU1171; MY6; JU360; ED3021; MY2 - less sensitive

GENOTYPIC CHANGE

Generic Gene Name
srx-43
Synonyms
T10C6.3
String
6239.T10C6.3
(http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 6239.T10C6.3)
Sequence Similarities
Belongs to the G-protein coupled receptor 1 family.
GO - Molecular Function
GO:0016503 : pheromone receptor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0016503)
GO - Biological Process
GO:0035641 : locomotory exploration behavior
(https://www.ebi.ac.uk/QuickGO/term/GO:0035641)
GO:0019722 : calcium-mediated signaling

UniProtKB Caenorhabditis elegans
O45767 (http://www.uniprot.org/uniprot/O45767)
GenebankID or UniProtKB
NM_074621.2 (https://www.ncbi.nlm.nih.gov/nuccore/NM_074621.2)

(https://www.ebi.ac.uk/QuickGO/term/GO:0019722)
GO:0071444 : cellular response to pheromone
(https://www.ebi.ac.uk/QuickGO/term/GO:0071444)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0043204 : perikaryon (https://www.ebi.ac.uk/QuickGO/term/GO:0043204)
GO:0097730 : non-motile cilium (https://www.ebi.ac.uk/QuickGO/term/GO:0097730)

Presumptive Null

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

Molecular Type

Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title)

Aberration Type

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

Molecular Details of the Mutation

unknown

Experimental Evidence

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

Main Reference

Balancing selection shapes density-dependent foraging behaviour. (2016) (https://pubmed.ncbi.nlm.nih.gov/27799655)

Authors

Greene JS; Brown M; Dobosiewicz M; Ishida IG; Macosko EZ; Zhang X; Butcher RA; Cline DJ; McGrath PT; Bargmann CI

Abstract

The optimal foraging strategy in a given environment depends on the number of competing individuals and their behavioural strategies. Little is known about the genes and neural circuits that integrate social information into foraging decisions. Here we show that ascaroside pheromones, small glycolipids that signal population density, suppress exploratory foraging in Caenorhabditis elegans, and that heritable variation in this behaviour generates alternative foraging strategies. We find that natural C. elegans isolates differ in their sensitivity to the potent ascaroside icas#9 (IC-asc-C5). A quantitative trait locus (QTL) regulating icas#9 sensitivity includes srx-43, a G-protein-coupled icas#9 receptor that acts in the ASI class of sensory neurons to suppress exploration. Two ancient haplotypes associated with this QTL confer competitive growth advantages that depend on ascaroside secretion, its detection by srx-43 and the distribution of food. These results suggest that balancing selection at the srx-43 locus generates alternative density-dependent behaviours, fulfilling a prediction of foraging game theory.

Additional References

Regulatory changes in two chemoreceptor genes contribute to a Caenorhabditis elegans QTL for foraging behavior. (2016) (https://pubmed.ncbi.nlm.nih.gov/27893361)

RELATED GEPHE

Related Genes

1 (srx-44) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^6239^/and+Trait=Pheromone response/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE @Epistasis @BalancingSelection - The srx-43 gene is expressed at a level fivefold lower in strain MY14 than in strain N2. Both the ascaroside insensitity phenotype and the srx-43 haplotype are found in 7 strains with different geographical origins and genetic backgrounds. Phylogenetic analysis suggests a single mutational event. Data is consistent with balancing selection; with two co-existing haplotypes in C. elegans that are 30kb long; GxE effect (food distribution and addition of pheromones to the medium) ; GxG interaction with daf-22 mutation ; loss-of-function; not null ; The underlying QTL is actually multigenic and includes alternative alleles of a second chemoreceptor gene that modifies pheromone sensitivity: srx-44 . GxG interaction with srx-44.