

Gephebase Gene		GepheID
exp-1 (https://www.gephebase.org/search-criteria?and+Gene+Gephebase=^exp-1^#gephebase-summary-title)	GP00000300	Main curator
Published	Entry Status: Martin	

Behavior (#gephebase-summary-title)		Trait Category	
Aggregation behavior (#gephebase-summary-title)		Trait	
C. elegans - CB4856 (wild isolate)		Trait State in Taxon A	
C. elegans - N2		Trait State in Taxon B	
Data not curated		Ancestral State	
Intraspecific (#gephebase-summary-title)		Taxonomic Status	
Taxon A		Taxon B	
Caenorhabditis elegans (#gephebase-summary-title)		Caenorhabditis elegans (#gephebase-summary-title)	
-		-	
roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900		roundworm; Rhabditis elegans; Caenorhabditis elegans (Maupas, 1900); Rhabditis elegans Maupas, 1900	
species		species	
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	
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)		6239 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=6239)	
is Taxon A an Intraspecies?		is Taxon B an Intraspecies?	
Yes		Yes	
C. elegans - CB4856 (wild isolate)		C. elegans - N2	

exp-1	Generic Gene Name	G5ECJ0 (http://www.uniprot.org/uniprot/G5ECJ0)	UniProtKB <i>Caenorhabditis elegans</i>
H35N03.1	Synonyms	AY383563 (https://www.ncbi.nlm.nih.gov/nucore/AY383563)	GenebankID or UniProtKB
6239.H35N03.1 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=6239.H35N03.1)	String		
	Sequence Similarities		
Belongs to the ligand-gated ion channel (TC 1.A.9) family. Gamma-aminobutyric acid receptor (TC 1.A.9.5) subfamily.			
	GO - Molecular Function		
GO:0005231 : excitatory extracellular ligand-gated ion channel activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005231)			
GO:0016917 : GABA receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0016917)			
	GO - Biological Process		

GO:0007165 : signal transduction (<https://www.ebi.ac.uk/QuickGO/term/GO:0007165>)
GO:0007268 : chemical synaptic transmission
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007268>)
GO:0010877 : lipid transport involved in lipid storage
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010877>)
GO:0006813 : potassium ion transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)
GO:0006814 : sodium ion transport (<https://www.ebi.ac.uk/QuickGO/term/GO:0006814>)
GO:0034220 : ion transmembrane transport
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034220>)
GO:0050877 : nervous system process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050877>)
GO:0042391 : regulation of membrane potential
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042391>)
GO:0030421 : defecation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030421>)
GO:1904731 : positive regulation of intestinal lipid absorption
(<https://www.ebi.ac.uk/QuickGO/term/GO:1904731>)
GO:0045933 : positive regulation of muscle contraction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045933>)

GO - Cellular Component

GO:0005887 : integral component of plasma membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
GO:0030054 : cell junction (<https://www.ebi.ac.uk/QuickGO/term/GO:0030054>)
GO:0043005 : neuron projection (<https://www.ebi.ac.uk/QuickGO/term/GO:0043005>)
GO:0045202 : synapse (<https://www.ebi.ac.uk/QuickGO/term/GO:0045202>)
GO:0031594 : neuromuscular junction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031594>)
GO:0098794 : postsynapse (<https://www.ebi.ac.uk/QuickGO/term/GO:0098794>)

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

unidentified; 6.2kb wide genetic interval 3' of the exp-1 gene

Experimental Evidence

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

Main Reference

Long-range regulatory polymorphisms affecting a GABA receptor constitute a quantitative trait locus (QTL) for social behavior in *Caenorhabditis elegans*. (2012)
(<https://pubmed.ncbi.nlm.nih.gov/23284308>)

Authors

Bendesky A; Pitts J; Rockman MV; Chen WC; Tan MW; Kruglyak L; Bargmann CI

Abstract

Aggregation is a social behavior that varies between and within species, providing a model to study the genetic basis of behavioral diversity. In the nematode *Caenorhabditis elegans*, aggregation is regulated by environmental context and by two neuromodulatory pathways, one dependent on the neuropeptide receptor NPR-1 and one dependent on the TGF- β family protein DAF-7. To gain further insight into the genetic regulation of aggregation, we characterize natural variation underlying behavioral differences between two wild-type *C. elegans* strains, N2 and CB4856. Using quantitative genetic techniques, including a survey of chromosome substitution strains and QTL analysis of recombinant inbred lines, we identify three new QTLs affecting aggregation in addition to the two known N2 mutations in *npr-1* and *glb-5*. Fine-mapping with near-isogenic lines localized one QTL, accounting for 5%-8% of the behavioral variance between N2 and CB4856, 3' to the transcript of the GABA neurotransmitter receptor gene *exp-1*. Quantitative complementation tests demonstrated that this QTL affects *exp-1*, identifying *exp-1* and GABA signaling as new regulators of aggregation. *exp-1* interacts genetically with the *daf-7* TGF- β pathway, which integrates food availability and population density, and *exp-1* mutations affect the level of *daf-7* expression. Our results add to growing evidence that genetic variation affecting neurotransmitter receptor genes is a source of natural behavioral variation.

Additional References

RELATED GEPHE

Related Genes

3 (*arcp-1*, *glb-5*, *npr-1*) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=^6239^/and+Trait=Aggregation behavior/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE

