

# GEPHE SUMMARY

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

## PHENOTYPIC CHANGE

	Trait Category
Behavior ( <a href="https://www.gephebase.org/search-criteria/?and+Trait Category=^Behavior^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait Category=^Behavior^#gephebase-summary-title</a> )	Trait
Aggregation behavior ( <a href="https://www.gephebase.org/search-criteria/?and+Trait=^Aggregation behavior^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Trait=^Aggregation behavior^#gephebase-summary-title</a> )	Trait State in Taxon A
C. elegans - CB4856 (wild isolate)	Trait State in Taxon B
C. elegans - N2	Ancestral State
Data not curated	Taxonomic Status
Intraspecific ( <a href="https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Intraspecific^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxonomic Status=^Intraspecific^#gephebase-summary-title</a> )	

Taxon A		Taxon B	
	Latin Name		Latin Name
Caenorhabditis elegans ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Caenorhabditis elegans^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Caenorhabditis elegans^#gephebase-summary-title</a> )	Common Name	Caenorhabditis elegans ( <a href="https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Caenorhabditis elegans^#gephebase-summary-title">https://www.gephebase.org/search-criteria/?and+Taxon and Synonyms=^Caenorhabditis elegans^#gephebase-summary-title</a> )	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	
species	Rank	species	Rank
	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) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237</a> )	NCBI Taxonomy ID	Caenorhabditis () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6237</a> )	NCBI Taxonomy ID
6239 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239</a> )		6239 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6239</a> )	
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
C. elegans - CB4856 (wild isolate)	Taxon A Description	C. elegans - N2	Taxon B Description

## GENOTYPIC CHANGE

exp-1	Generic Gene Name	UniProtKB Caenorhabditis elegans
H35N03.1	Synonyms	GenebankID or UniProtKB
6239.H35N03.1 ( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 6239.H35N03.1">http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 6239.H35N03.1</a> )	String	AY383563 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/AY383563">https://www.ncbi.nlm.nih.gov/nuccore/AY383563</a> )
Belongs to the ligand-gated ion channel (TC 1.A.9) family. Gamma-aminobutyric acid receptor (TC 1.A.9.5) subfamily.	Sequence Similarities	
GO:0005231 : excitatory extracellular ligand-gated ion channel activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0005231">https://www.ebi.ac.uk/QuickGO/term/GO:0005231</a> )	GO - Molecular Function	
GO:0016917 : GABA receptor activity ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016917">https://www.ebi.ac.uk/QuickGO/term/GO:0016917</a> )		
	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.gephbase.org/search-criteria?/and+Presumptive Null=%27Unknown%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Presumptive%20Null=%27Unknown%27#gephbase-summary-title))

Molecular Type

Cis-regulatory ([https://www.gephbase.org/search-criteria?/and+Molecular Type=%27Cis-regulatory%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Molecular%20Type=%27Cis-regulatory%27#gephbase-summary-title))

Aberration Type

Unknown ([https://www.gephbase.org/search-criteria?/and+Aberration Type=%27Unknown%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Aberration%20Type=%27Unknown%27#gephbase-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.gephbase.org/search-criteria?/and+Experimental Evidence=%27Linkage Mapping%27#gephbase-summary-title](https://www.gephbase.org/search-criteria?/and+Experimental%20Evidence=%27Linkage%20Mapping%27#gephbase-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- $\beta$  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- $\beta$  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 (arc-1, glb-5, npr-1) ([https://www.gephbase.org/search-criteria?/or+Taxon ID=%276239%27/and+Trait=Aggregation behavior/and+groupHaplotypes=true#gephbase-summary-title](https://www.gephbase.org/search-criteria?/or+Taxon%20ID=%276239%27/and+Trait=Aggregation%20behavior/and+groupHaplotypes=true#gephbase-summary-title))

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS

@GxE

