GEPHE SUMMARY

Gephebase Gene

G protein-coupled receptor rhodopsin (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^G protein-coupled receptor rhodopsin^#gephebase-summary-title)

Entry Status

Published

GepheID

GP00001539

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category=^Physiology^#gephebase-summary-title)

Trait

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

Trait State in Taxon A

Daphnia magna from Germany

Trait State in Taxon B

Daphnia magna from Finland

Ancestral State

Unknown

Taxonomic Status

Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intraspecific^#gephebase-summary-title)

Taxon A

Latin Name

Daphnia magna (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Daphnia magna^#gephebase-summary-title)

Common Name

-

Synonyms

Daphnia magna Straus, 1820

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Branchiopoda; Phyllopoda; Diplostraca; Cladocera; Anomopoda; Daphniidae; Daphnia

Parent

Daphnia (common water fleas) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6668)

NCBI Taxonomy ID

35525 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35525)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Daphnia magna from Germany

Taxon B

Latin Name

Daphnia magna (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Daphnia magna^#gephebase-summary-title)

Common Name

-

Synonyms

Daphnia magna Straus, 1820

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Crustacea; Branchiopoda; Phyllopoda; Diplostraca; Cladocera; Anomopoda; Daphniidae; Daphnia

Parent

Daphnia (common water fleas) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 6668)

NCBI Taxonomy ID

35525 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 35525)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Daphnia magna from Finland

GENOTYPIC CHANGE

Generic Gene Name

RHO

Synonyms

RP4; OPN2; CSNBAD1

String

9606.ENSP00000296271 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000296271)

Sequence Similarities

Belongs to the G-protein coupled receptor 1 family. Opsin subfamily.

GO - Molecular Function

GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0004930 : G protein-coupled receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004930)
GO:0008020 : G protein-coupled photoreceptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008020)

UniProtKB Homo sapiens

P08100 (http://www.uniprot.org/uniprot/P08100)

GenebankID or UniProtKB

()

GO:0005502 : 11-cis retinal binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005502)

GO - Biological Process

GO:0007186 : G protein-coupled receptor signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0007186)
GO:0001523 : retinoid metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0001523)
GO:0006468 : protein phosphorylation (https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:0018298 : protein-chromophore linkage (https://www.ebi.ac.uk/QuickGO/term/GO:0018298)
GO:0007601 : visual perception (https://www.ebi.ac.uk/QuickGO/term/GO:0007601)
GO:0071482 : cellular response to light stimulus (https://www.ebi.ac.uk/QuickGO/term/GO:0071482)
GO:0007602 : phototransduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007602)
GO:0016038 : absorption of visible light (https://www.ebi.ac.uk/QuickGO/term/GO:0016038)
GO:0045494 : photoreceptor cell maintenance (https://www.ebi.ac.uk/QuickGO/term/GO:0045494)
GO:0007603 : phototransduction, visible light (https://www.ebi.ac.uk/QuickGO/term/GO:0007603)
GO:0022400 : regulation of rhodopsin mediated signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0022400)
GO:0060041 : retina development in camera-type eye (https://www.ebi.ac.uk/QuickGO/term/GO:0060041)
GO:0016056 : rhodopsin mediated signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:0016056)

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:0000139 : Golgi membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0000139)
GO:0005887 : integral component of plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0005794 : Golgi apparatus (https://www.ebi.ac.uk/QuickGO/term/GO:0005794)
GO:0005911 : cell-cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0005911)
GO:0001750 : photoreceptor outer segment (https://www.ebi.ac.uk/QuickGO/term/GO:0001750)
GO:0097381 : photoreceptor disc membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0097381)
GO:0060170 : ciliary membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0060170)
GO:0030660 : Golgi-associated vesicle membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0030660)
GO:0001917 : photoreceptor inner segment (https://www.ebi.ac.uk/QuickGO/term/GO:0001917)
GO:0060342 : photoreceptor inner segment membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0060342)
GO:0042622 : photoreceptor outer segment membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0042622)

Presumptive Null

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

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#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

A Photoreceptor Contributes to the Natural Variation of Diapause Induction in Daphnia magna. (2016) (https://pubmed.ncbi.nlm.nih.gov/27660296)

Authors

Roulin AC; Bourgeois Y; Stiefel U; Walser JC; Ebert D

Abstract

Diapause is an adaptation that allows organisms to survive harsh environmental conditions. In species occurring over broad habitat ranges, both the timing and the intensity of diapause induction can vary across populations, revealing patterns of local adaptation. Understanding the genetic architecture of this fitness-related trait would help clarify how populations adapt to their local environments. In the cyclical parthenogenetic crustacean Daphnia magna, diapause induction is a phenotypic plastic life history trait linked to sexual reproduction, as asexual females have the ability to switch to sexual reproduction and produce resting stages, their sole strategy for surviving habitat deterioration. We have previously shown that the induction of resting stage production correlates with changes in photoperiod that indicate the imminence of habitat deterioration and have identified a Quantitative Trait Locus (QTL) responsible for some of the variation in the induction of resting stages. Here, new data allows us to anchor the QTL to a large scaffold and then, using a combination of a new mapping panel, targeted association mapping and selection analysis in natural populations, to identify candidate genes within the QTL. Our results show that variation in a rhodopsin photoreceptor gene plays a significant role in the variation observed in resting stage induction. This finding provides a mechanistic explanation for the link between diapause and day-length perception that has been suggested in diverse arthropod taxa.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@GxE @SexualTrait - 1 SNP located in the middle of the intron explained 11% of the variance in resting stage production