GEPHE SUMMARY

Gephebase Gene
Period (per) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Period (per)^#gephebase-summary-title)

Entry Status
Published

GepheID
GP00002427

Main curator
Courtier

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
Pararge aegeria - different critical photoperiod for diapause induction

Trait State in Taxon B
Pararge aegeria - different critical photoperiod for diapause induction

Ancestral State
Unknown

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

Taxon A

Latin Name
Pieris napi (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Pieris napi^#gephebase-summary-title)

Common Name
-

Synonyms
Artogeia napi; Pieris napi (Linnaeus, 1758)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Pieridae; Pierinae; Pierini; Pieris

Parent
Pieris () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7115)

NCBI Taxonomy ID
78633 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 78633)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Pieris napi (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Pieris napi^#gephebase-summary-title)

Common Name
-

Synonyms
Artogeia napi; Pieris napi (Linnaeus, 1758)

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Endopterygota; Amphiesmenoptera; Lepidoptera; Glossata; Neolepidoptera; Heteroneura; Ditrysia; Obtectomera; Papilionoidea; Pieridae; Pierinae; Pierini; Pieris

Parent
Pieris () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7115)

NCBI Taxonomy ID
78633 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 78633)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
per

Synonyms
CG2647; Clk; clk-6; Dmel\CG2647; dmper; dper; dPER; EG:155E2.4; mel_per; Per; PER; Per-2

String
7227.FBpp0070455 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0070455)

Sequence Similarities
-

GO - Molecular Function
GO:0042802 : identical protein binding (https://www.ebi.ac.uk/QuickGO/term/GO:0042802)
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)
GO:0046982 : protein heterodimerization activity

UniProtKB Drosophila melanogaster
P07663 (http://www.uniprot.org/uniprot/P07663)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0046982)
GO:0008134 : transcription factor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0008134)
GO:0003714 : transcription corepressor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003714)
GO:0003712 : transcription coregulator activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003712)
GO:0000976 : transcription regulatory region sequence-specific DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0000976)
GO:0001222 : transcription corepressor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0001222)

GO - Biological Process

GO:0009416 : response to light stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009416)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
GO:0045892 : negative regulation of transcription, DNA-templated
(https://www.ebi.ac.uk/QuickGO/term/GO:0045892)
GO:0007616 : long-term memory (https://www.ebi.ac.uk/QuickGO/term/GO:0007616)
GO:0032922 : circadian regulation of gene expression
(https://www.ebi.ac.uk/QuickGO/term/GO:0032922)
GO:0007623 : circadian rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0007623)
GO:0042752 : regulation of circadian rhythm
(https://www.ebi.ac.uk/QuickGO/term/GO:0042752)
GO:0045187 : regulation of circadian sleep/wake cycle, sleep
(https://www.ebi.ac.uk/QuickGO/term/GO:0045187)
GO:0007619 : courtship behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007619)
GO:0045433 : male courtship behavior, veined wing generated song production
(https://www.ebi.ac.uk/QuickGO/term/GO:0045433)
GO:0045475 : locomotor rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0045475)
GO:0008340 : determination of adult lifespan
(https://www.ebi.ac.uk/QuickGO/term/GO:0008340)
GO:0009266 : response to temperature stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:0009266)
GO:0006979 : response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0006979)
GO:0001932 : regulation of protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0001932)
GO:0001306 : age-dependent response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0001306)
GO:0048148 : behavioral response to cocaine
(https://www.ebi.ac.uk/QuickGO/term/GO:0048148)
GO:0048512 : circadian behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0048512)
GO:0042745 : circadian sleep/wake cycle
(https://www.ebi.ac.uk/QuickGO/term/GO:0042745)
GO:0060086 : circadian temperature homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0060086)
GO:0007620 : copulation (https://www.ebi.ac.uk/QuickGO/term/GO:0007620)
GO:0008062 : eclosion rhythm (https://www.ebi.ac.uk/QuickGO/term/GO:0008062)
GO:0009649 : entrainment of circadian clock
(https://www.ebi.ac.uk/QuickGO/term/GO:0009649)
GO:0043153 : entrainment of circadian clock by photoperiod
(https://www.ebi.ac.uk/QuickGO/term/GO:0043153)
GO:0007617 : mating behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007617)
GO:2000678 : negative regulation of transcription regulatory region DNA binding
(https://www.ebi.ac.uk/QuickGO/term/GO:2000678)
GO:1904059 : regulation of locomotor rhythm
(https://www.ebi.ac.uk/QuickGO/term/GO:1904059)
GO:0007622 : rhythmic behavior (https://www.ebi.ac.uk/QuickGO/term/GO:0007622)

GO - Cellular Component

GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0044297 : cell body (https://www.ebi.ac.uk/QuickGO/term/GO:0044297)
GO:0048471 : perinuclear region of cytoplasm
(https://www.ebi.ac.uk/QuickGO/term/GO:0048471)

Presumptive Null

No (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^No^#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

Multiple amino acid differences. Presence of five fixed SNPs between the N and S populations (one intergenic, two intronic and two exonic nonsynonymous substitutions).

Experimental Evidence

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

Main Reference

A region of the sex chromosome associated with population differences in diapause induction contains highly divergent alleles at clock genes. (2021) (https://pubmed.ncbi.nlm.nih.gov/33340097)

Authors

Pruisscher P; Nylin S; Wheat CW; Gotthard K

Abstract

Developmental plasticity describes the capacity of individuals with the same genotype to induce permanent change in a phenotype depending on a specific external input. One well-studied example of adaptive developmental plasticity is the induction of facultative diapause in insects. Studies investigating the inheritance of diapause induction have suggested diverse genetic origins. However, only few studies have performed genome-wide scans to identify genes affecting the induction decision. Here we compare two populations of the butterfly Pieris napi that differ in the propensity to enter diapause, and despite showing a low genome-wide divergence, we identify a few genomic regions that show high divergence between populations. We then identified a single genomic region associated with diapause induction by genotyping diapausing and directly developing siblings from backcrosses of these populations. This region is located on the Z chromosome and contained three circadian clock genes, cycle, clock, and period. Additionally, period harbored the largest number of SNPs showing complete fixation between populations. We conclude that the heritable basis of between-population variation in the plasticity that determines diapause induction resides on the Z chromosome, with the period gene being the prime candidate for the genetic basis of adaptive plasticity.

Additional References

A region of the sex chromosome associated with population differences in diapause induction contains highly divergent alleles at clock genes. (2021) (https://pubmed.ncbi.nlm.nih.gov/33340097)

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

The main reference article is: Genetic variation underlying local adaptation of diapause induction along a cline in a butterfly Pruisscher, Nylin, Gotthard, et al https://onlinelibrary.wiley.com/doi/10.1111/mec.14829