GEPHE SUMMARY

Gephebase Gene

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

GepheID

GP00002422

Entry Status

Published

Main curator

Courtier

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Plastic line - the dark red wing phenotype is induced by environmental cues

Trait State in Taxon B

Red line - the dark red wing phenotype is formed irrespective of the external conditions

Ancestral State

Taxon A

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

buckeye

Synonyms

Precis coenia; buckeye; peacock butterfly; Junonia coenia Hubner, 1822

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; Nymphalidae; Nymphalinae; Junoniini; Junonia

Parent

Junonia (buckeyes) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 39707)

NCBI Taxonomy ID

39708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 39708)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

buckeye

Synonyms

Precis coenia; buckeye; peacock butterfly; Junonia coenia Hubner, 1822

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; Nymphalidae; Nymphalinae; Junoniini; Junonia

Parent

Junonia (buckeyes) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 39707)

NCBI Taxonomy ID

39708 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 39708)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

rk

Synonyms

BG:DS00180.13; CG8930; CT25644; DLGR-2; dlgr2; DLgr2; DLGR2; dlgr2/rk; Dmel\CG8930; lgr2; Lgr2; LGR2; Rk; rk/CG8930; Dmel_CG8930

String

7227.FBpp0080183 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 7227.FBpp0080183)

Sequence Similarities

Belongs to the G-protein coupled receptor 1 family.

GO - Molecular Function

GO:0008528 : G protein-coupled peptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008528)
GO:0008188 : neuropeptide receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008188)
GO:0016500 : protein-hormone receptor activity

UniProtKB Drosophila melanogaster

Q7KTA0 (http://www.uniprot.org/uniprot/Q7KTA0)

GenebankID or UniProtKB

()

(https://www.ebi.ac.uk/QuickGO/term/GO:0016500)

GO - Biological Process

GO:0009755 : hormone-mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0009755)
GO:0007186 : G protein-coupled receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007186)
GO:0007298 : border follicle cell migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0007298)
GO:0001837 : epithelial to mesenchymal transition
(https://www.ebi.ac.uk/QuickGO/term/GO:0001837)
GO:0007189 : adenylate cyclase-activating G protein-coupled receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007189)
GO:0036335 : intestinal stem cell homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0036335)
GO:0007218 : neuropeptide signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0007218)
GO:0007190 : activation of adenylate cyclase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0007190)
GO:0030709 : border follicle cell delamination
(https://www.ebi.ac.uk/QuickGO/term/GO:0030709)
GO:0007564 : regulation of chitin-based cuticle tanning
(https://www.ebi.ac.uk/QuickGO/term/GO:0007564)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)

Presumptive Null

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

No variation in coding region. Strong association with cis-regulatory SNP. CRISPR mutant clones for the herfst gene display light tan scales.

Experimental Evidence

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

Main Reference

Genomic architecture of a genetically assimilated seasonal color pattern. (2020) (https://pubmed.ncbi.nlm.nih.gov/33154142)

Authors

van der Burg KRL; Lewis JJ; Brack BJ; Fandino RA; Mazo-Vargas A; Reed RD

Abstract

Developmental plasticity allows genomes to encode multiple distinct phenotypes that can be differentially manifested in response to environmental cues. Alternative plastic phenotypes can be selected through a process called genetic assimilation, although the mechanisms are still poorly understood. We assimilated a seasonal wing color phenotype in a naturally plastic population of butterflies (Junonia coenia) and characterized three responsible genes. Endocrine assays and chromatin accessibility and conformation analyses showed that the transition of wing coloration from an environmentally determined trait to a predominantly genetic trait occurred through selection for regulatory alleles of downstream wing-patterning genes. This mode of genetic evolution is likely favored by selection because it allows tissue- and trait-specific tuning of reaction norms without affecting core cue detection or transduction mechanisms.

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Additional References

RELATED GEPHE

Related Genes

2 (cortex, trehalase) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^39708^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

@Parallelism @GxE The two color morphs of Junonia coenia, light tan and dark red, depend on day length and temperature.