GEPHE SUMMARY

Gephebase Gene

BCO2 = beta-carotene oxygenase 2 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^BCO2 = beta-carotene oxygenase 2^#gephebase-summary-title)

GepheID

GP00001332

Entry Status

Published

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Golden-winged warbler

Trait State in Taxon B

Blue-winged warbler

Ancestral State

Unknown

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

Golden-winged warbler

Synonyms

Motacilla chrysoptera; Golden-winged warbler; Motacilla chrysoptera Linnaeus 1766; Vermivora chrysoptera (Linnaeus, 1766)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea; Parulidae; Vermivora

Parent

Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62258)

NCBI Taxonomy ID

231561 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 231561)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

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

Common Name

blue-winged warbler

Synonyms

Vermivora pinus; blue-winged warbler; Vermivora cyanoptera (Olson & Reveal, 2009)

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea; Parulidae; Vermivora

Parent

Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62258)

NCBI Taxonomy ID

1871067 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1871067)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

BCO2

Synonyms

BCDO2; B-DIOX-II

String

9606.ENSP00000350314 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000350314)

Sequence Similarities

Belongs to the carotenoid oxygenase family.

GO - Molecular Function

GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)
GO:0003834 : beta-carotene 15,15'-monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003834)
GO:0010436 : carotenoid dioxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0010436)

UniProtKB Homo sapiens

Q9BYV7 (http://www.uniprot.org/uniprot/Q9BYV7)

GenebankID or UniProtKB

()

GO:0004744 : retinal isomerase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004744)
GO:0102076 : beta,beta-carotene-9′,10′-cleaving oxygenase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0102076)
GO:0016702 : oxidoreductase activity, acting on single donors with incorporation of
molecular oxygen, incorporation of two atoms of oxygen
(https://www.ebi.ac.uk/QuickGO/term/GO:0016702)

GO - Biological Process

GO:0055114 : oxidation-reduction process
(https://www.ebi.ac.uk/QuickGO/term/GO:0055114)
GO:0001523 : retinoid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001523)
GO:0016121 : carotene catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016121)
GO:0042574 : retinal metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042574)
GO:0016119 : carotene metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016119)
GO:0016116 : carotenoid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016116)
GO:0051881 : regulation of mitochondrial membrane potential
(https://www.ebi.ac.uk/QuickGO/term/GO:0051881)
GO:2000377 : regulation of reactive oxygen species metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:2000377)
GO:0042573 : retinoic acid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042573)
GO:0016122 : xanthophyll metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016122)

GO - Cellular Component

GO:0005739 : mitochondrion (https://www.ebi.ac.uk/QuickGO/term/GO:0005739)
GO:0005622 : intracellular (https://www.ebi.ac.uk/QuickGO/term/GO:0005622)
GO:0005759 : mitochondrial matrix (https://www.ebi.ac.uk/QuickGO/term/GO:0005759)

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

unknown - the divergent region falls in the 5prime region that is directly upstream of the associated coding region

Experimental Evidence

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

Main Reference

Plumage Genes and Little Else Distinguish the Genomes of Hybridizing Warblers. (2016) (https://pubmed.ncbi.nlm.nih.gov/27546575)

Authors

Toews DP; Taylor SA; Vallender R; Brelsford A; Butcher BG; Messer PW; Lovette IJ

Abstract

When related taxa hybridize extensively, their genomes may become increasingly homogenized over time. This mixing via hybridization creates conservation challenges when it reduces genetic or phenotypic diversity and when it endangers previously distinct species via genetic swamping [1]. However, hybridization also facilitates admixture mapping of traits that distinguish each species and the associated genes that maintain distinctiveness despite ongoing gene flow [2]. We address these dual aspects of hybridization in the golden-winged/blue-winged warbler complex, two phenotypically divergent warblers that are indistinguishable using traditional molecular markers and that draw substantial conservation attention [3-5]. Whole-genome comparisons show that differentiation is extremely low: only six small genomic regions exhibit strong differences. Four of these divergence peaks occur in proximity to genes known to be involved in feather development or pigmentation: agouti signaling protein (ASIP), follistatin (FST), ecodysplasin (EDA), wingless-related integration site (Wnt), and beta-carotene oxygenase 2 (BCO2). Throat coloration-the most striking plumage difference between these warblers-is perfectly associated with the promoter region of agouti, and genotypes at this locus obey simple Mendelian recessive inheritance of the black-throated phenotype characteristic of golden-winged warblers. The more general pattern of genomic similarity between these warblers likely results from a protracted period of hybridization, contradicting the broadly accepted hypothesis that admixture results from solely anthropogenic habitat change in the past two centuries [4]. Considered in concert, these results are relevant to both the genetic architecture of avian feather pigmentation and the evolutionary history and conservation challenges associated with these declining songbirds.

Copyright Â© 2016 Elsevier Ltd. All rights reserved.

Additional References

RELATED GEPHE

Related Genes

1 (Agouti (ASIP)) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^231561^/and+Trait=Coloration/or+Taxon ID=^1871067^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

the two taxa are possibly the same species (subspecies or races). Among six divergent genomic regions identified by SNP BCO2 is a candidate gene supposed to be involved in the range of yellow feathers (yellow against white)