

GEPHE SUMMARY

	Gephebase Gene		GepheID
BCO2 = beta-carotene oxygenase 2 (#Gephebase-summary-title)		GP00001332	
	Entry Status	Prigent	Main curator
Published			

PHENOTYPIC CHANGE

	Trait Category		
Morphology (#Gephebase-summary-title)			
	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 (#Gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Vermivora chrysoptera (#Gephebase-summary-title)		Vermivora cyanoptera (#Gephebase-summary-title)	
	Common Name		Common Name
Golden-winged warbler		blue-winged warbler	
	Synonyms		Synonyms
Motacilla chrysoptera; Golden-winged warbler; Motacilla chrysoptera Linnaeus 1766; Vermivora chrysoptera (Linnaeus, 1766)		Vermivora pinus; blue-winged warbler; Vermivora cyanoptera (Olson & Reveal, 2009)	
	Rank		Rank
species		species	
	Lineage		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		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		Parent
Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=62258)		Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=62258)	
	NCBI Taxonomy ID		NCBI Taxonomy ID
231561 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=231561)		1871067 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1871067)	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No		No	

GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
BCO2		Q9BYV7 (http://www.uniprot.org/uniprot/Q9BYV7)	
	Synonyms		GenebankID or UniProtKB
BCDO2; B-DIOX-II		0	
	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)			

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>)

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

Presumptive Null

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular Type=^Cis-regulatory^#gephebase-summary-title>)

Molecular Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration Type=^Unknown^#gephebase-summary-title>)

Aberration Type

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

Molecular Details of the Mutation

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

Experimental Evidence

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

Main Reference

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

Authors

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.

Abstract

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Additional References

RELATED GEPHE

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 Genes

No matches found.

Related Haplotypes

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)