

GEPHE SUMMARY

	Gephebase Gene	GephelD
Agouti (ASIP) (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^Agouti (ASIP)^#gephebase-summary-title)	GP00001331	
	Entry Status	Main curator
Published	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		Taxon B	
	Latin Name		Latin Name
Vermivora chrysoptera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Vermivora chrysoptera^#gephebase-summary-title)		Vermivora cyanoptera (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Vermivora cyanoptera^#gephebase-summary-title)	
Golden-winged warbler	Common Name		Common Name
Motacilla chrysoptera; Golden-winged warbler; Motacilla chrysoptera Linnaeus 1766; Vermivora chrysoptera (Linnaeus, 1766)	Synonyms	blue-winged warbler	Synonyms
species	Rank	species	Rank
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	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	Lineage
Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62258)	Parent	Vermivora () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 62258)	Parent
231561 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 231561)	NCBI Taxonomy ID	1871067 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 1871067)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Mus musculus
Asip	Q03288 (http://www.uniprot.org/uniprot/Q03288)	
As; ASP; A<y>; ASIP; a	String	GenebankID or UniProtKB
10090.ENSMUSP00000029123 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=10090.ENSMUSP00000029123)	0	
	Sequence Similarities	
	GO - Molecular Function	
GO:0031779 : melanocortin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031779)		
GO:0031781 : type 3 melanocortin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0031781)		
GO:0031782 : type 4 melanocortin receptor binding		

GO:0008343 : adult feeding behavior

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008343>)

GO:0006091 : generation of precursor metabolites and energy

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006091>)

GO:0071514 : genetic imprinting (<https://www.ebi.ac.uk/QuickGO/term/GO:0071514>)

GO:0009755 : hormone-mediated signaling pathway

(<https://www.ebi.ac.uk/QuickGO/term/GO:0009755>)

GO:0042438 : melanin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042438>)

GO:0032438 : melanosome organization

(<https://www.ebi.ac.uk/QuickGO/term/GO:0032438>)

GO:0032402 : melanosome transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0032402>)

GO:0043473 : pigmentation (<https://www.ebi.ac.uk/QuickGO/term/GO:0043473>)

GO:0048023 : positive regulation of melanin biosynthetic process

(<https://www.ebi.ac.uk/QuickGO/term/GO:0048023>)

GO:0040030 : regulation of molecular function, epigenetic

(<https://www.ebi.ac.uk/QuickGO/term/GO:0040030>)

GO - Cellular Component

GO:0005576 : extracellular region (<https://www.ebi.ac.uk/QuickGO/term/GO:0005576>)

GO:0005623 : cell (<https://www.ebi.ac.uk/QuickGO/term/GO:0005623>)

Presumptive Null

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

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Additional References

RELATED GEPHE

Related Genes

1 (BCO2 = beta-carotene oxygenase 2) (<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 ASIP is a candidate gene supposed to be involved in the throat color (black or yellow-white)

