

GEPHE SUMMARY

ALX1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~ALX1~#gephebase-summary-title)	Gephebase Gene	GP00000081	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Morphology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~#gephebase-summary-title)	Trait Category		
Beak size (https://www.gephebase.org/search-criteria?/and+Trait=~Beak size~#gephebase-summary-title)	Trait		
Geospiza magnirostris ; Geospiza spp. (blunt beaks) ; Darwin finches	Trait State in Taxon A		
Geospiza conirostris ; other Geospiza spp. (pointed beaks) ; Darwin finches	Trait State in Taxon B		
	Ancestral State		
Taxon A		Taxon B	
Interspecific (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Interspecific~#gephebase-summary-title)	Taxonomic Status		
Geospiza	Latin Name	Geospiza	Latin Name
(https://www.gephebase.org/search-criteria?/and+Taxon andSynonyms=~Geospiza~#gephebase-summary-title)		(https://www.gephebase.org/search-criteria?/and+Taxon andSynonyms=~Geospiza~#gephebase-summary-title)	
-	Common Name	-	Common Name
-	Synonyms	-	Synonyms
genus	Rank	genus	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; Thraupidae	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; Thraupidae	Lineage
Thraupidae (tanagers) - (Rank: family)	Parent	Thraupidae (tanagers) - (Rank: family)	Parent
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 400783)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 400783)	
48881	NCBI Taxonomy ID	48881	NCBI Taxonomy ID
(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 48881)		(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 48881)	
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

Alx1	Generic Gene Name	Q8C8B0 (http://www.uniprot.org/uniprot/Q8C8B0)	UniProtKB Mus musculus
Cart1; A1314867; C130005102	Synonyms	XP_005421635 (https://www.ncbi.nlm.nih.gov/nuccore/XP_005421635)	GenebankID or UniProtKB
10090.ENSMUSP00000042512	String		
(http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000042512)			
Belongs to the paired homeobox family.	Sequence Similarities		
GO:0042803 : protein homodimerization activity	GO - Molecular Function		
(https://www.ebi.ac.uk/QuickGO/term/GO:0042803)			
GO:0001228 : DNA-binding transcription activator activity, RNA polymerase II-specific			
(https://www.ebi.ac.uk/QuickGO/term/GO:0001228)			
GO:0003700 : DNA-binding transcription factor activity			
(https://www.ebi.ac.uk/QuickGO/term/GO:0003700)			

GO:0046982 : protein heterodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046982>)
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000977>)
GO:0043565 : sequence-specific DNA binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043565>)

GO - Biological Process

GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0009952 : anterior/posterior pattern specification
(<https://www.ebi.ac.uk/QuickGO/term/GO:0009952>)
GO:0030326 : embryonic limb morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030326>)
GO:0048704 : embryonic skeletal system morphogenesis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048704>)
GO:0014031 : mesenchymal cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0014031>)
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:0001755 : neural crest cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001755>)
GO:0001843 : neural tube closure (<https://www.ebi.ac.uk/QuickGO/term/GO:0001843>)
GO:0010718 : positive regulation of epithelial to mesenchymal transition
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010718>)
GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0060021 : roof of mouth development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060021>)

GO - Cellular Component

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:0005794 : Golgi apparatus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005794>)
GO:0005667 : transcription factor complex
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005667>)
GO:0016604 : nuclear body (<https://www.ebi.ac.uk/QuickGO/term/GO:0016604>)

	Presumptive Null
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Presumptive Null=">https://www.gephebase.org/search-criteria?/and+Presumptive Null="+Unknown`#gephebase-summary-title)	
	Molecular Type
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Molecular Type=">https://www.gephebase.org/search-criteria?/and+Molecular Type="+Unknown`#gephebase-summary-title)	
	Aberration Type
Unknown (<a +unknown`#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Aberration Type=">https://www.gephebase.org/search-criteria?/and+Aberration Type="+Unknown`#gephebase-summary-title)	
240kb haplotype with complex variation	Molecular Details of the Mutation
	Experimental Evidence
Association Mapping (<a +association="" href="https://www.gephebase.org/search-criteria?/and+Experimental Evidence=" mapping`#gephebase-summary-title"="">https://www.gephebase.org/search-criteria?/and+Experimental Evidence="+Association Mapping`#gephebase-summary-title)	
	Main Reference
Evolution of Darwin’s finches and their beaks revealed by genome sequencing. (2015) (https://pubmed.ncbi.nlm.nih.gov/25686609)	
	Authors
Lamichhaney S; Berglund J; AlmÃn MS; Maqbool K; Grabherr M; Martinez-Barrio A; PromerovÃi M; Rubin CJ; Wang C; Zamani N; Grant BR; Grant PR; Webster MT; Andersson L	
	Abstract
Darwin’s finches, inhabiting the GalÃpagos archipelago and Cocos Island, constitute an iconic model for studies of speciation and adaptive evolution. Here we report the results of whole-genome re-sequencing of 120 individuals representing all of the Darwin’s finch species and two close relatives. Phylogenetic analysis reveals important discrepancies with the phenotype-based taxonomy. We find extensive evidence for interspecific gene flow throughout the radiation. Hybridization has given rise to species of mixed ancestry. A 240Ãkilobase haplotype encompassing the ALX1 gene that encodes a transcription factor affecting craniofacial development is strongly associated with beak shape diversity across Darwin’s finch species as well as within the medium ground finch (<i>Geospiza fortis</i>), a species that has undergone rapid evolution of beak shape in response to environmental changes. The ALX1 haplotype has contributed to diversification of beak shapes among the Darwin’s finches and, thereby, to an expanded utilization of food resources.	
	Additional References
Adaptive radiation of Darwin’s finches revisited using whole genome sequencing. (2016) (https://pubmed.ncbi.nlm.nih.gov/26606649)	

RELATED GEPHE

	Related Genes
No matches found.	
	Related Haplotypes
No matches found.	

EXTERNAL LINKS

COMMENTS

Adaptive Introgression in the genus - underlying both intraspecific and interspecific variation