GEPHE SUMMARY

Gephebase Gene
ephrin-a4 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ephrin-a4^#gephebase-summary-title)

GepheID
GP00001420

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

Trait State in Taxon A
Labeotropheus fuelleborni with more xanthophore on caudal region of the flank

Trait State in Taxon B
Tropheops red cheek with less xanthophores on caudal region of the flank

Ancestral State
Unknown

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

Taxon A

Latin Name
Labeotropheus fuelleborni (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Labeotropheus fuelleborni^#gephebase-summary-title)

Common Name
blue mbuna

Synonyms
blue mbuna; Labeotropheus fuelleborni Ahl, 1926

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Cichlomorphae; Cichliformes; Cichlidae; African cichlids; Pseudocrenilabrinae; Haplochromini; Labeotropheus

Parent
Labeotropheus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 57306)

NCBI Taxonomy ID
57307 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 57307)

is Taxon A an Infraspecies?
No

Taxon B

Latin Name
Tropheops sp. 'red cheek' (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Tropheops sp. 'red cheek'^#gephebase-summary-title)

Common Name
-

Synonyms
Tropheops redcheek

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percomorphaceae; Ovalentaria; Cichlomorphae; Cichliformes; Cichlidae; African cichlids; Pseudocrenilabrinae; Haplochromini; Tropheops

Parent
Tropheops () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702376)

NCBI Taxonomy ID
702379 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 702379)

is Taxon B an Infraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
EFNA4

Synonyms
EFL4; EPLG4; LERK4

String
9606.ENSP00000414378 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000414378)

Sequence Similarities
Belongs to the ephrin family.

GO - Molecular Function
GO:0005005 : transmembrane-ephrin receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005005)
GO:0046875 : ephrin receptor binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046875)

GO - Biological Process

UniProtKB Homo sapiens
P52798 (http://www.uniprot.org/uniprot/P52798)

GenebankID or UniProtKB
()

GO:0007267 : cell-cell signaling (https://www.ebi.ac.uk/QuickGO/term/GO:0007267)
GO:0007411 : axon guidance (https://www.ebi.ac.uk/QuickGO/term/GO:0007411)
GO:0048013 : ephrin receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0048013)
GO:0030316 : osteoclast differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0030316)
GO:0046849 : bone remodeling (https://www.ebi.ac.uk/QuickGO/term/GO:0046849)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0031225 : anchored component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0031225)
GO:0031226 : intrinsic component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0031226)

Presumptive Null

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

Molecular Type

Unknown (https://www.gephebase.org/search-criteria?/and+Molecular Type=^Unknown^#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

Experimental Evidence

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

Main Reference

Genetic basis of continuous variation in the levels and modular inheritance of pigmentation in cichlid fishes. (2014) (https://pubmed.ncbi.nlm.nih.gov/25156298)

Authors

Albertson RC; Powder KE; Hu Y; Coyle KP; Roberts RB; Parsons KJ

Abstract

Variation in pigmentation type and levels is a hallmark of myriad evolutionary radiations, and biologists have long been fascinated by the factors that promote and maintain variation in coloration across populations. Here, we provide insights into the genetic basis of complex and continuous patterns of colour variation in cichlid fishes, which offer a vast diversity of pigmentation patterns that have evolved in response to both natural and sexual selection. Specifically, we crossed two divergent cichlid species to generate an F2 mapping population that exhibited extensive variation in pigmentation levels and patterns. Our experimental design is robust in that it combines traditional quantitative trait locus (QTL) analysis with population genomics, which has allowed us to move efficiently from QTL interval to candidate gene. In total, we detected 41 QTL and 13 epistatic interactions that underlie melanocyte- and xanthophore-based coloration across the fins and flanks of these fishes. We also identified 2 QTL and 1 interaction for variation in the magnitude of integration among these colour traits. This finding in particular is notable as there are marked differences both within and between species with respect to the complexity of pigmentation patterns. While certain individuals are characterized by more uniform 'integrated' colour patterns, others exhibit many more degrees of freedom with respect to the distribution of colour 'modules' across the fins and flank. Our data reveal, for the first time, a genetic basis for this difference. Finally, we implicate pax3a as a mediator of continuous variation in the levels of xanthophore-based colour along the cichlid flank.

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Additional References

RELATED GEPHE

Related Genes

4 (pax3a, pax3b, zeb1a, Pax7) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^57307^/and+Trait=Coloration/or+Taxon ID=^702379^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

SNP adjacent to ephrin-a4