

GEPHE SUMMARY

	Gephebase Gene	GephelD
KCNH4 - uncertain (https://www.gephebase.org/search-criteria/?and+Gene)	GP00000510	Main curator
Gephebase=^KCNH4 - uncertain #gephebase-summary-title)		
Entry Status	Martin	
Published		

PHENOTYPIC CHANGE

	Trait Category		
Physiology (https://www.gephebase.org/search-criteria/?and+Trait)			
Category=^Physiology #gephebase-summary-title)			
Freshwater adaptation (https://www.gephebase.org/search-criteria/?and+Trait=^Freshwater+adaptation#gephebase-summary-title)	Trait		
Gasterosteus aculeatus - marine	Trait State in Taxon A		
Gasterosteus aculeatus - freshwater	Trait State in Taxon B		
Taxon A	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria/?and+Taxonomic+Status=^Intraspecific#gephebase-summary-title)	Taxonomic Status		
Taxon A	Latin Name	Taxon B	Latin Name
Gasterosteus aculeatus (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Gasterosteus+aculeatus#gephebase-summary-title)		Gasterosteus aculeatus (https://www.gephebase.org/search-criteria/?and+Taxon+and+Synonyms=^Gasterosteus+aculeatus#gephebase-summary-title)	
three-spined stickleback	Common Name	three-spined stickleback	Common Name
three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758	Synonyms	three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleoste; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percormorphaceae; Euperaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleosteomorpha; Neoteleoste; Eurypterygia; Ctenosquamata; Acanthomorphata; Euacanthomorphacea; Percormorphaceae; Euperaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus	Lineage
Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69292)	Parent	Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69292)	Parent
69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69293)	NCBI Taxonomy ID	69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69293)	NCBI Taxonomy ID
Yes	is Taxon A an Infraspecies?	Yes	is Taxon B an Infraspecies?
Taxon A Description		Taxon B Description	
Gasterosteus aculeatus - marine		Gasterosteus aculeatus - freshwater	

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Homo sapiens
KCNH4		
BEC2; ELK1; Kv12.3	Synonyms	GenebankID or UniProtKB
9606.ENSP0000264661 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP0000264661)	String	
Belongs to the potassium channel family. H (Eag) (TC 1.A.1.20) subfamily. Kv12.3/KCNH4 sub-subfamily.	Sequence Similarities	
GO:0000155 : phosphorelay sensor kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0000155)	GO - Molecular Function	

GO:0005249 : voltage-gated potassium channel activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005249>)

GO - Biological Process

GO:0006813 : potassium ion transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0006813>)

GO:0042391 : regulation of membrane potential

(<https://www.ebi.ac.uk/QuickGO/term/GO:0042391>)

GO:0071805 : potassium ion transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0071805>)

GO:0034765 : regulation of ion transmembrane transport

(<https://www.ebi.ac.uk/QuickGO/term/GO:0034765>)

GO - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)

GO:0005887 : integral component of plasma membrane

(<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)

GO:0008076 : voltage-gated potassium channel complex

(<https://www.ebi.ac.uk/QuickGO/term/GO:0008076>)

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

Large Inversion resulting in alternative transcripts

Experimental Evidence

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

Main Reference

The genomic basis of adaptive evolution in threespine sticklebacks. (2012) (<https://pubmed.ncbi.nlm.nih.gov/22481358>)

Authors

Jones FC; Grabherr MG; Chan YF; Russell P; Mauceli E; Johnson J; Swofford R; Pirun M; Zody MC; White S; Birney E; Searle S; Schmutz J; Grimwood J; Dickson MC; Myers RM; Miller CT; Summers BR; Knecht AK; Brady SD; Zhang H; Pollen AA; Howes T; Amemiya C; Baldwin J; Bloom T; Jaffe DB; Nicol R; Wilkinson J; Lander ES; Di Palma F; Lindblad-Toh K; Kingsley DM

Abstract

Marine stickleback fish have colonized and adapted to thousands of streams and lakes formed since the last ice age, providing an exceptional opportunity to characterize genomic mechanisms underlying repeated ecological adaptation in nature. Here we develop a high-quality reference genome assembly for threespine sticklebacks. By sequencing the genomes of twenty additional individuals from a global set of marine and freshwater populations, we identify a genome-wide set of loci that are consistently associated with marine-freshwater divergence. Our results indicate that reuse of globally shared standing genetic variation, including chromosomal inversions, has an important role in repeated evolution of distinct marine and freshwater sticklebacks, and in the maintenance of divergent ecotypes during early stages of reproductive isolation. Both coding and regulatory changes occur in the set of loci underlying marine-freshwater evolution, but regulatory changes appear to predominate in this well known example of repeated adaptive evolution in nature.

Additional References

RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS