GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00000523

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Gasterosteus aculeatus - Japanese marine

Trait State in Taxon B

Gasterosteus aculeatus - Paxton benthic

Ancestral State

Data not curated

Taxonomic Status

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

Taxon A

Latin Name

Gasterosteus aculeatus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Gasterosteus aculeatus^#gephebase-summary-title)

Common Name

three-spined stickleback

Synonyms

three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758

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; Eupercaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus

Parent

Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69292)

NCBI Taxonomy ID

69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69293)

is Taxon A an Infraspecies?

Yes

Taxon A Description

Gasterosteus aculeatus - Japanese marine

Taxon B

Latin Name

Gasterosteus aculeatus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Gasterosteus aculeatus^#gephebase-summary-title)

Common Name

three-spined stickleback

Synonyms

three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758

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; Eupercaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus

Parent

Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69292)

NCBI Taxonomy ID

69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 69293)

is Taxon B an Infraspecies?

Yes

Taxon B Description

Gasterosteus aculeatus - Paxton benthic

GENOTYPIC CHANGE

Generic Gene Name

KITLG

Synonyms

SF; MGF; SCF; SLF; DCUA; FPH2; FPHH; KL-1; Kitl; SHEP7; DFNA69

String

9606.ENSP00000228280 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000228280)

Sequence Similarities

Belongs to the SCF family.

GO - Molecular Function

GO:0005125 : cytokine activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005125)
GO:0008083 : growth factor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008083)
GO:0046934 : phosphatidylinositol-4,5-bisphosphate 3-kinase activity

UniProtKB Homo sapiens

P21583 (http://www.uniprot.org/uniprot/P21583)

GenebankID or UniProtKB

AAC04337 (https://www.ncbi.nlm.nih.gov/nuccore/AAC04337)

(https://www.ebi.ac.uk/QuickGO/term/GO:0046934)
GO:0005088 : Ras guanyl-nucleotide exchange factor activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0005088)
GO:0005173 : stem cell factor receptor binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0005173)

GO - Biological Process

GO:0007155 : cell adhesion (https://www.ebi.ac.uk/QuickGO/term/GO:0007155)
GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0001755 : neural crest cell migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0001755)
GO:0008283 : cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0008283)
GO:0035234 : ectopic germ cell programmed cell death
(https://www.ebi.ac.uk/QuickGO/term/GO:0035234)
GO:0035162 : embryonic hemopoiesis
(https://www.ebi.ac.uk/QuickGO/term/GO:0035162)
GO:0097192 : extrinsic apoptotic signaling pathway in absence of ligand
(https://www.ebi.ac.uk/QuickGO/term/GO:0097192)
GO:0008584 : male gonad development
(https://www.ebi.ac.uk/QuickGO/term/GO:0008584)
GO:0000165 : MAPK cascade (https://www.ebi.ac.uk/QuickGO/term/GO:0000165)
GO:0033026 : negative regulation of mast cell apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0033026)
GO:0001541 : ovarian follicle development
(https://www.ebi.ac.uk/QuickGO/term/GO:0001541)
GO:0008284 : positive regulation of cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0008284)
GO:1902035 : positive regulation of hematopoietic stem cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:1902035)
GO:0002687 : positive regulation of leukocyte migration
(https://www.ebi.ac.uk/QuickGO/term/GO:0002687)
GO:0043406 : positive regulation of MAP kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043406)
GO:0070668 : positive regulation of mast cell proliferation
(https://www.ebi.ac.uk/QuickGO/term/GO:0070668)
GO:0045636 : positive regulation of melanocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0045636)
GO:0002763 : positive regulation of myeloid leukocyte differentiation
(https://www.ebi.ac.uk/QuickGO/term/GO:0002763)
GO:0050731 : positive regulation of peptidyl-tyrosine phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0050731)
GO:0051897 : positive regulation of protein kinase B signaling
(https://www.ebi.ac.uk/QuickGO/term/GO:0051897)
GO:0046579 : positive regulation of Ras protein signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0046579)

GO - Cellular Component

GO:0016021 : integral component of membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016021)
GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005737 : cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005737)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0005856 : cytoskeleton (https://www.ebi.ac.uk/QuickGO/term/GO:0005856)
GO:0030175 : filopodium (https://www.ebi.ac.uk/QuickGO/term/GO:0030175)
GO:0030027 : lamellipodium (https://www.ebi.ac.uk/QuickGO/term/GO:0030027)

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

Not identified

Experimental Evidence

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

Main Reference

cis-Regulatory changes in Kit ligand expression and parallel evolution of pigmentation in sticklebacks and humans. (2007) (https://pubmed.ncbi.nlm.nih.gov/18083106)

Authors

Miller CT; Beleza S; Pollen AA; Schluter D; Kittles RA; Shriver MD; Kingsley DM

Abstract

Dramatic pigmentation changes have evolved within most vertebrate groups, including fish and humans. Here we use genetic crosses in sticklebacks to investigate the parallel origin of pigmentation changes in natural populations. High-resolution mapping and expression experiments show that light gills and light ventrums map to a divergent regulatory allele of the Kit ligand (Kitlg) gene. The divergent allele reduces expression in gill and skin tissue and is shared by multiple derived freshwater populations with reduced pigmentation. In humans, Europeans and East Asians also share derived alleles at the KITLG locus. Strong signatures of selection map to regulatory regions surrounding the gene, and admixture mapping shows that the KITLG genomic region has a significant effect on human skin color. These experiments suggest that regulatory changes in Kitlg contribute to natural variation in vertebrate pigmentation, and that similar genetic mechanisms may underlie rapid evolutionary change in fish and humans.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS