

## GEPHE SUMMARY

**Gephebase Gene**  
KCNH4 - uncertain

**Entry Status**  
Published

**GepheID**  
GP00000510

**Main curator**  
Martin

## PHENOTYPIC CHANGE

**Trait Category**  
Physiology

**Trait**  
Freshwater adaptation

**Trait State in Taxon A**  
Gasterosteus aculeatus - marine

**Trait State in Taxon B**  
Gasterosteus aculeatus - freshwater

**Ancestral State**  
Taxon A

**Taxonomic Status**  
Intraspecific

### Taxon A

**Latin Name**

*Gasterosteus aculeatus*

**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; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Eupercaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus

**Parent**

Gasterosteus () - (Rank: genus)

**NCBI Taxonomy ID**

69293

**is Taxon A an Intraspecies?**

Yes

**Taxon A Description**

Gasterosteus aculeatus - marine

### Taxon B

**Latin Name**

*Gasterosteus aculeatus*

**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; Euteleostomorpha; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Percormorphaceae; Eupercaria; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus

**Parent**

Gasterosteus () - (Rank: genus)

**NCBI Taxonomy ID**

69293

**is Taxon B an Intraspecies?**

Yes

**Taxon B Description**

Gasterosteus aculeatus - freshwater

## GENOTYPIC CHANGE

**Generic Gene Name**  
KCNH4

**Synonyms**

BEC2; ELK1; Kv12.3

**String**

9606.ENSP00000264661

**Sequence Similarities**

Belongs to the potassium channel family. H (Eag) (TC 1.A.1.20) subfamily. Kv12.3/KCNH4 sub-subfamily.

**GO - Molecular Function**

GO:0000155 : phosphorelay sensor kinase activity

GO:0005249 : voltage-gated potassium channel activity

**GO - Biological Process**

GO:0006813 : potassium ion transport

GO:0042391 : regulation of membrane potential

**UniProtKB** Homo sapiens

Q9UQ05

**GenebankID or UniProtKB**

GO:0071805 : potassium ion transmembrane transport  
GO:0034765 : regulation of ion transmembrane transport

**GO - Cellular Component**

GO:0005886 : plasma membrane  
GO:0005887 : integral component of plasma membrane  
GO:0008076 : voltage-gated potassium channel complex

**Presumptive Null**

Unknown

**Molecular Type**

Unknown

**Aberration Type**

Unknown

**Molecular Details of the Mutation**

Large Inversion resulting in alternative transcripts

**Experimental Evidence**

Association Mapping

**Main Reference**

The genomic basis of adaptive evolution in threespine sticklebacks. (2012)

**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**