GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001378

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Threespined stickleback fish ; marine habitat

Trait State in Taxon B

Threespined stickleback fish ; freshwater habitat

Ancestral State

Unknown

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

Threespined stickleback fish ; marine habitat

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

Threespined stickleback fish ; freshwater habitat

GENOTYPIC CHANGE

Generic Gene Name

MUC1

Synonyms

EMA; MCD; PEM; PUM; KL-6; MAM6; MCKD; PEMT; CD227; H23AG; MCKD1; MUC-1; ADMCKD; ADMCKD1; CA 15-3; MUC-1/X; MUC1/ZD; MUC-1/SEC

String

9606.ENSP00000357380 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000357380)

Sequence Similarities

-

GO - Molecular Function

GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000978)

UniProtKB Homo sapiens

P15941 (http://www.uniprot.org/uniprot/P15941)

GenebankID or UniProtKB

()

GO:0003712 : transcription coregulator activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0003712)
GO:0002039 : p53 binding (https://www.ebi.ac.uk/QuickGO/term/GO:0002039)

GO - Biological Process

GO:0010944 : negative regulation of transcription by competitive promoter binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0010944)
GO:0019221 : cytokine-mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0019221)
GO:0006977 : DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest (https://www.ebi.ac.uk/QuickGO/term/GO:0006977)
GO:0006978 : DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator (https://www.ebi.ac.uk/QuickGO/term/GO:0006978)
GO:0033629 : negative regulation of cell adhesion mediated by integrin
(https://www.ebi.ac.uk/QuickGO/term/GO:0033629)
GO:1902166 : negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator (https://www.ebi.ac.uk/QuickGO/term/GO:1902166)
GO:0016266 : O-glycan processing (https://www.ebi.ac.uk/QuickGO/term/GO:0016266)
GO:0090240 : positive regulation of histone H4 acetylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0090240)
GO:0036003 : positive regulation of transcription from RNA polymerase II promoter in response to stress (https://www.ebi.ac.uk/QuickGO/term/GO:0036003)
GO:0043618 : regulation of transcription from RNA polymerase II promoter in response to stress (https://www.ebi.ac.uk/QuickGO/term/GO:0043618)
GO:0002223 : stimulatory C-type lectin receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0002223)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0016324 : apical plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0016324)
GO:0070062 : extracellular exosome (https://www.ebi.ac.uk/QuickGO/term/GO:0070062)
GO:0005887 : integral component of plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0005887)
GO:0031982 : vesicle (https://www.ebi.ac.uk/QuickGO/term/GO:0031982)
GO:0005796 : Golgi lumen (https://www.ebi.ac.uk/QuickGO/term/GO:0005796)
GO:0005615 : extracellular space (https://www.ebi.ac.uk/QuickGO/term/GO:0005615)
GO:0000790 : nuclear chromatin (https://www.ebi.ac.uk/QuickGO/term/GO:0000790)

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

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

Main Reference

A genome-wide SNP genotyping array reveals patterns of global and repeated species-pair divergence in sticklebacks. (2012) (https://pubmed.ncbi.nlm.nih.gov/22197244)

Authors

Jones FC; Chan YF; Schmutz J; Grimwood J; Brady SD; Southwick AM; Absher DM; Myers RM; Reimchen TE; Deagle BE; Schluter D; Kingsley DM

Abstract

Genes underlying repeated adaptive evolution in natural populations are still largely unknown. Stickleback fish (Gasterosteus aculeatus) have undergone a recent dramatic evolutionary radiation, generating numerous examples of marine-freshwater species pairs and a small number of benthic-limnetic species pairs found within single lakes [1]. We have developed a new genome-wide SNP genotyping array to study patterns of genetic variation in sticklebacks over a wide geographic range, and to scan the genome for regions that contribute to repeated evolution of marine-freshwater or benthic-limnetic species pairs. Surveying 34 global populations with 1,159 informative markers revealed substantial genetic variation, with predominant patterns reflecting demographic history and geographic structure. After correcting for geographic structure and filtering for neutral markers, we detected large repeated shifts in allele frequency at some loci, identifying both known and novel loci likely contributing to marine-freshwater and benthic-limnetic divergence. Several novel loci fall close to genes implicated in epithelial barrier or immune functions, which have likely changed as sticklebacks adapt to contrasting environments. Specific alleles differentiating sympatric benthic-limnetic species pairs are shared in nearby solitary populations, suggesting an allopatric origin for adaptive variants and selection pressures unrelated to sympatry in the initial formation of these classic vertebrate species pairs.

Additional References

RELATED GEPHE

Related Genes

1 (Na/K ATPase) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^69293^/and+Trait=Salt tolerance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Candidate locus ; mapping is not precise enough