GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00001381

Main curator

Prigent

PHENOTYPIC CHANGE

Trait Category

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

Trait

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

Trait State in Taxon A

Threespined stickleback fish ; marine habitat of Pacific basin

Trait State in Taxon B

Threespined stickleback fish ; freshwater habitat of Pacific basin

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 of Pacific basin

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 of Pacific basin

GENOTYPIC CHANGE

Generic Gene Name

PRKCD

Synonyms

MAY1; PKCD; ALPS3; CVID9; nPKC-delta

String

9606.ENSP00000331602 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000331602)

Sequence Similarities

Belongs to the protein kinase superfamily. AGC Ser/Thr protein kinase family. PKC subfamily.

GO - Molecular Function

GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)

UniProtKB Homo sapiens

Q05655 (http://www.uniprot.org/uniprot/Q05655)

GenebankID or UniProtKB

()

GO:0019899 : enzyme binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019899)
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)
GO:0004674 : protein serine/threonine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004674)
GO:0004672 : protein kinase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0004672)
GO:0043560 : insulin receptor substrate binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0043560)
GO:0019900 : kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019900)
GO:0004699 : calcium-independent protein kinase C activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004699)
GO:0008047 : enzyme activator activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0008047)
GO:0004715 : non-membrane spanning protein tyrosine kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004715)
GO:0004697 : protein kinase C activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0004697)

GO - Biological Process

GO:0007165 : signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0007165)
GO:0050728 : negative regulation of inflammatory response
(https://www.ebi.ac.uk/QuickGO/term/GO:0050728)
GO:0043407 : negative regulation of MAP kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0043407)
GO:0006468 : protein phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0006468)
GO:0060326 : cell chemotaxis (https://www.ebi.ac.uk/QuickGO/term/GO:0060326)
GO:0042742 : defense response to bacterium
(https://www.ebi.ac.uk/QuickGO/term/GO:0042742)
GO:0090398 : cellular senescence (https://www.ebi.ac.uk/QuickGO/term/GO:0090398)
GO:0006915 : apoptotic process (https://www.ebi.ac.uk/QuickGO/term/GO:0006915)
GO:0018105 : peptidyl-serine phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0018105)
GO:0043312 : neutrophil degranulation
(https://www.ebi.ac.uk/QuickGO/term/GO:0043312)
GO:0070301 : cellular response to hydrogen peroxide
(https://www.ebi.ac.uk/QuickGO/term/GO:0070301)
GO:0060333 : interferon-gamma-mediated signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0060333)
GO:2001022 : positive regulation of response to DNA damage stimulus
(https://www.ebi.ac.uk/QuickGO/term/GO:2001022)
GO:0035556 : intracellular signal transduction
(https://www.ebi.ac.uk/QuickGO/term/GO:0035556)
GO:0050732 : negative regulation of peptidyl-tyrosine phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0050732)
GO:0050821 : protein stabilization (https://www.ebi.ac.uk/QuickGO/term/GO:0050821)
GO:0016064 : immunoglobulin mediated immune response
(https://www.ebi.ac.uk/QuickGO/term/GO:0016064)
GO:0046627 : negative regulation of insulin receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0046627)
GO:0032091 : negative regulation of protein binding
(https://www.ebi.ac.uk/QuickGO/term/GO:0032091)
GO:0007049 : cell cycle (https://www.ebi.ac.uk/QuickGO/term/GO:0007049)
GO:0032956 : regulation of actin cytoskeleton organization
(https://www.ebi.ac.uk/QuickGO/term/GO:0032956)
GO:0002223 : stimulatory C-type lectin receptor signaling pathway
(https://www.ebi.ac.uk/QuickGO/term/GO:0002223)
GO:0032147 : activation of protein kinase activity
(https://www.ebi.ac.uk/QuickGO/term/GO:0032147)
GO:0042100 : B cell proliferation (https://www.ebi.ac.uk/QuickGO/term/GO:0042100)
GO:1904385 : cellular response to angiotensin
(https://www.ebi.ac.uk/QuickGO/term/GO:1904385)
GO:0071447 : cellular response to hydroperoxide
(https://www.ebi.ac.uk/QuickGO/term/GO:0071447)
GO:0038096 : Fc-gamma receptor signaling pathway involved in phagocytosis
(https://www.ebi.ac.uk/QuickGO/term/GO:0038096)
GO:0016572 : histone phosphorylation
(https://www.ebi.ac.uk/QuickGO/term/GO:0016572)
GO:0032613 : interleukin-10 production
(https://www.ebi.ac.uk/QuickGO/term/GO:0032613)
GO:0032615 : interleukin-12 production
(https://www.ebi.ac.uk/QuickGO/term/GO:0032615)
GO:0008631 : intrinsic apoptotic signaling pathway in response to oxidative stress
(https://www.ebi.ac.uk/QuickGO/term/GO:0008631)
GO:0030837 : negative regulation of actin filament polymerization
(https://www.ebi.ac.uk/QuickGO/term/GO:0030837)
GO:0051490 : negative regulation of filopodium assembly
(https://www.ebi.ac.uk/QuickGO/term/GO:0051490)
GO:0034351 : negative regulation of glial cell apoptotic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0034351)

GO:0090331 : negative regulation of platelet aggregation (https://www.ebi.ac.uk/QuickGO/term/GO:0090331)
GO:0042119 : neutrophil activation (https://www.ebi.ac.uk/QuickGO/term/GO:0042119)
GO:0018107 : peptidyl-threonine phosphorylation (https://www.ebi.ac.uk/QuickGO/term/GO:0018107)
GO:0030168 : platelet activation (https://www.ebi.ac.uk/QuickGO/term/GO:0030168)
GO:2001235 : positive regulation of apoptotic signaling pathway (https://www.ebi.ac.uk/QuickGO/term/GO:2001235)
GO:2000304 : positive regulation of ceramide biosynthetic process (https://www.ebi.ac.uk/QuickGO/term/GO:2000304)
GO:0032079 : positive regulation of endodeoxyribonuclease activity (https://www.ebi.ac.uk/QuickGO/term/GO:0032079)
GO:2000753 : positive regulation of glucosylceramide catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:2000753)
GO:1900163 : positive regulation of phospholipid scramblase activity (https://www.ebi.ac.uk/QuickGO/term/GO:1900163)
GO:0035307 : positive regulation of protein dephosphorylation (https://www.ebi.ac.uk/QuickGO/term/GO:0035307)
GO:0042307 : positive regulation of protein import into nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0042307)
GO:2000755 : positive regulation of sphingomyelin catabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:2000755)
GO:0032930 : positive regulation of superoxide anion generation (https://www.ebi.ac.uk/QuickGO/term/GO:0032930)
GO:0043488 : regulation of mRNA stability (https://www.ebi.ac.uk/QuickGO/term/GO:0043488)
GO:0010469 : regulation of signaling receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0010469)
GO:0023021 : termination of signal transduction (https://www.ebi.ac.uk/QuickGO/term/GO:0023021)

GO - Cellular Component

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:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)
GO:0005654 : nucleoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0005654)
GO:0070062 : extracellular exosome (https://www.ebi.ac.uk/QuickGO/term/GO:0070062)
GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
GO:0005576 : extracellular region (https://www.ebi.ac.uk/QuickGO/term/GO:0005576)
GO:0005783 : endoplasmic reticulum (https://www.ebi.ac.uk/QuickGO/term/GO:0005783)
GO:0048471 : perinuclear region of cytoplasm (https://www.ebi.ac.uk/QuickGO/term/GO:0048471)
GO:0035578 : azurophil granule lumen (https://www.ebi.ac.uk/QuickGO/term/GO:0035578)
GO:0005911 : cell-cell junction (https://www.ebi.ac.uk/QuickGO/term/GO:0005911)
GO:0016363 : nuclear matrix (https://www.ebi.ac.uk/QuickGO/term/GO:0016363)

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.

Copyright Â© 2012 Elsevier Ltd. All rights reserved.

Additional References

Related Genes

1 (IGK) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^69293^/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

Candidate locus ; mapping is not precise enough