

## GEPHE SUMMARY

	Gephebase Gene		GepheID
Mucin gene family ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a> Gephebase="Mucin gene family"#gephebase-summary-title)		GP00001378	Main curator
Published	Entry Status	Prigent	

## PHENOTYPIC CHANGE

	Trait Category		
Physiology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> Category="Physiology"#gephebase-summary-title)			
	Trait		
Salt tolerance ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a> ="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 ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a> Status="Intraspecific"#gephebase-summary-title)			
Taxon A		Taxon B	
	Latin Name		Latin Name
Gasterosteus aculeatus ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon">https://www.gephebase.org/search-criteria?/and+Taxon</a> and Synonyms="Gasterosteus aculeatus"#gephebase-summary-title)		Gasterosteus aculeatus ( <a href="https://www.gephebase.org/search-criteria?/and+Taxon">https://www.gephebase.org/search-criteria?/and+Taxon</a> and Synonyms="Gasterosteus aculeatus"#gephebase-summary-title)	
	Common Name		Common Name
three-spined stickleback		three-spined stickleback	
	Synonyms		Synonyms
three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758		three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758	
	Rank		Rank
species		species	
	Lineage		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; Perciformes; Cottiidae; Gasterosteales; Gasterosteidae; Gasterosteus		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; Perciformes; Cottiidae; Gasterosteales; Gasterosteidae; Gasterosteus	
	Parent		Parent
Gasterosteus () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292</a> )		Gasterosteus () - (Rank: genus) ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292</a> )	
	NCBI Taxonomy ID		NCBI Taxonomy ID
69293 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293</a> )		69293 ( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293</a> )	
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
Yes		Yes	
	Taxon A Description		Taxon B Description
Threespined stickleback fish ; marine habitat		Threespined stickleback fish ; freshwater habitat	

## GENOTYPIC CHANGE

	Generic Gene Name		UniProtKB Homo sapiens
MUC1		P15941 ( <a href="http://www.uniprot.org/uniprot/P15941">http://www.uniprot.org/uniprot/P15941</a> )	GenebankID or UniProtKB
	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 ( <a href="http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000357380">http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSP00000357380</a> )			
	Sequence Similarities		
-			
	GO - Molecular Function		
GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding ( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0000978">https://www.ebi.ac.uk/QuickGO/term/GO:0000978</a> )			

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.

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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