

GEPHE SUMMARY

<p>BMP6 (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=BMP6#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00000154</p> <p>Martin</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (https://www.gephebase.org/search-criteria?/and+Trait+Category=Morphology#gephebase-summary-title)</p> <p>Tooth number (https://www.gephebase.org/search-criteria?/and+Trait=Tooth+number#gephebase-summary-title)</p> <p>Gasterosteus aculeatus - marine; Rabbit Slough; Alaska (RABS)</p> <p>Gasterosteus aculeatus - benthic (Paxton Lake; Canada (PAXB))</p> <p>Taxon A</p> <p>Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=Intraspecific#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p>Gasterosteus aculeatus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Gasterosteus+aculeatus#gephebase-summary-title)</p> <p>Common Name</p> <p>three-spined stickleback</p> <p>Synonyms</p> <p>three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostei; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus</p> <p>Parent</p> <p>Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292)</p> <p>NCBI Taxonomy ID</p> <p>69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Gasterosteus aculeatus - marine; Rabbit Slough; Alaska (RABS)</p>	<p>Taxon B</p> <p>Latin Name</p> <p>Gasterosteus aculeatus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=Gasterosteus+aculeatus#gephebase-summary-title)</p> <p>Common Name</p> <p>three-spined stickleback</p> <p>Synonyms</p> <p>three-spined stickleback; three spined stickleback; Gasterosteus aculeatus Linnaeus, 1758</p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Actinopterygii; Actinopteri; Neopterygii; Teleostei; Osteoglossocephalai; Clupeocephala; Euteleostei; Neoteleostei; Eurypterygia; Ctenosquamata; Acanthomorpha; Euacanthomorpha; Perciformes; Cottioidei; Gasterosteales; Gasterosteidae; Gasterosteus</p> <p>Parent</p> <p>Gasterosteus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69292)</p> <p>NCBI Taxonomy ID</p> <p>69293 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=69293)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Gasterosteus aculeatus - benthic (Paxton Lake; Canada (PAXB))</p>
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GENOTYPIC CHANGE

<p>Bmp6</p> <p>Vgr1; D13Wsu115e; Bmp-6</p> <p>10090.ENSMUSP00000126999 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000126999)</p> <p>Sequence Similarities</p> <p>Belongs to the TGF-beta family.</p> <p>GO - Molecular Function</p> <p>GO:0046982 : protein heterodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046982)</p> <p>GO:0005125 : cytokine activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005125)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>P20722 (http://www.uniprot.org/uniprot/P20722)</p> <p>()</p> <p>UniProtKB Mus musculus</p> <p>GenebankID or UniProtKB</p>
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GO:0008083 : growth factor activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0008083>)
GO:0005160 : transforming growth factor beta receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005160>)
GO:0070700 : BMP receptor binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0070700>)

GO - Biological Process

GO:0006955 : immune response (<https://www.ebi.ac.uk/QuickGO/term/GO:0006955>)
GO:0045944 : positive regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045944>)
GO:0030154 : cell differentiation (<https://www.ebi.ac.uk/QuickGO/term/GO:0030154>)
GO:0000122 : negative regulation of transcription by RNA polymerase II
(<https://www.ebi.ac.uk/QuickGO/term/GO:0000122>)
GO:0030509 : BMP signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030509>)
GO:0048468 : cell development (<https://www.ebi.ac.uk/QuickGO/term/GO:0048468>)
GO:0010862 : positive regulation of pathway-restricted SMAD protein phosphorylation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010862>)
GO:0042981 : regulation of apoptotic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0042981>)
GO:0043408 : regulation of MAPK cascade
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043408>)
GO:0060395 : SMAD protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060395>)
GO:0051216 : cartilage development (<https://www.ebi.ac.uk/QuickGO/term/GO:0051216>)
GO:0001503 : ossification (<https://www.ebi.ac.uk/QuickGO/term/GO:0001503>)
GO:0001649 : osteoblast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001649>)
GO:0006879 : cellular iron ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006879>)
GO:0071773 : cellular response to BMP stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071773>)
GO:0031668 : cellular response to extracellular stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031668>)
GO:0071281 : cellular response to iron ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071281>)
GO:0071260 : cellular response to mechanical stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071260>)
GO:0001958 : endochondral ossification
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001958>)
GO:0001654 : eye development (<https://www.ebi.ac.uk/QuickGO/term/GO:0001654>)
GO:0006954 : inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0001822 : kidney development (<https://www.ebi.ac.uk/QuickGO/term/GO:0001822>)
GO:0030539 : male genitalia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030539>)
GO:0060586 : multicellular organismal iron ion homeostasis
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060586>)
GO:0032349 : positive regulation of aldosterone biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032349>)
GO:2000860 : positive regulation of aldosterone secretion
(<https://www.ebi.ac.uk/QuickGO/term/GO:2000860>)
GO:0030501 : positive regulation of bone mineralization
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030501>)
GO:0032332 : positive regulation of chondrocyte differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032332>)
GO:0045603 : positive regulation of endothelial cell differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045603>)
GO:0001938 : positive regulation of endothelial cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0001938>)
GO:0050679 : positive regulation of epithelial cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0050679>)
GO:0031666 : positive regulation of lipopolysaccharide-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031666>)
GO:0045666 : positive regulation of neuron differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045666>)
GO:0045669 : positive regulation of osteoblast differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045669>)
GO:0060391 : positive regulation of SMAD protein signal transduction
(<https://www.ebi.ac.uk/QuickGO/term/GO:0060391>)
GO:0014823 : response to activity (<https://www.ebi.ac.uk/QuickGO/term/GO:0014823>)
GO:0051384 : response to glucocorticoid
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051384>)
GO:0032026 : response to magnesium ion
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032026>)
GO:0032526 : response to retinoic acid
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032526>)
GO:0003323 : type B pancreatic cell development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0003323>)

GO:0005737 : cytoplasm (<https://www.ebi.ac.uk/QuickGO/term/GO:0005737>)

GO:0031982 : vesicle (<https://www.ebi.ac.uk/QuickGO/term/GO:0031982>)

GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

No ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Presumptive+Null+No))

Presumptive Null

Cis-regulatory ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Molecular+Type+Cis-regulatory))

Molecular Type

Unknown ([#gpepbase-summary-title](https://www.gephebase.org/search-criteria?/and+Aberration+Type+Unknown))

Aberration Type

Molecular Details of the Mutation

Candidate enhancer of 190bp recapitulating tooth and fin expression of Bmp6

Experimental Evidence

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

Main Reference

Evolved tooth gain in sticklebacks is associated with a cis-regulatory allele of Bmp6. (2014) (<https://pubmed.ncbi.nlm.nih.gov/25205810>)

Authors

Cleves PA; Ellis NA; Jimenez MT; Nunez SM; Schluter D; Kingsley DM; Miller CT

Abstract

Developmental genetic studies of evolved differences in morphology have led to the hypothesis that cis-regulatory changes often underlie morphological evolution. However, because most of these studies focus on evolved loss of traits, the genetic architecture and possible association with cis-regulatory changes of gain traits are less understood. Here we show that a derived benthic freshwater stickleback population has evolved an approximate twofold gain in ventral pharyngeal tooth number compared with their ancestral marine counterparts. Comparing laboratory-reared developmental time courses of a low-toothed marine population and this high-toothed benthic population reveals that increases in tooth number and tooth plate area and decreases in tooth spacing arise at late juvenile stages. Genome-wide linkage mapping identifies largely separate sets of quantitative trait loci affecting different aspects of dental patterning. One large-effect quantitative trait locus controlling tooth number fine-maps to a genomic region containing an excellent candidate gene, Bone morphogenetic protein 6 (Bmp6). Stickleback Bmp6 is expressed in developing teeth, and no coding changes are found between the high- and low-toothed populations. However, quantitative allele-specific expression assays of Bmp6 in developing teeth in F1 hybrids show that cis-regulatory changes have elevated the relative expression level of the freshwater benthic Bmp6 allele at late, but not early, stages of stickleback development. Collectively, our data support a model where a late-acting cis-regulatory up-regulation of Bmp6 expression underlies a significant increase in tooth number in derived benthic sticklebacks.

Additional References

Distinct developmental genetic mechanisms underlie convergently evolved tooth gain in sticklebacks. (2015) (<https://pubmed.ncbi.nlm.nih.gov/26062935>)

A 190 base pair, TGF- β 2 responsive tooth and fin enhancer is required for stickleback Bmp6 expression. (2015) (<https://pubmed.ncbi.nlm.nih.gov/25732776>)

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Trait Gain ; Functional Characterization in Additional References; Cleves et al. correction about Bmp6 expression : the benthic allele is downregulated compared to the marine allele; <http://www.pnas.org/content/111/50/18090.2.full>