## GEPHE SUMMARY

Gephebase Gene
ATP4B (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=^ATP4B^#gephebase-summary-title)

GepheID
GP00001916

Entry Status
Published

Main curator
Courtier

## PHENOTYPIC CHANGE

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

Trait
Digestion (absence of stomach) (https://www.gephebase.org/search-criteria?/and+Trait=^Digestion (absence of stomach)^#gephebase-summary-title)

Trait State in Taxon A
presence of stomach and gastric acid production

Trait State in Taxon B
loss of stomach and no gastric acid production

Ancestral State
Taxon A

Taxonomic Status
Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic Status=^Intergeneric or Higher^#gephebase-summary-title)

### Taxon A

Latin Name
Scyliorhinus canicula (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Scyliorhinus canicula^#gephebase-summary-title)

Common Name
smaller spotted catshark

Synonyms
smaller spotted catshark; smaller spotted dogfish; spotted catshark; spotted dogfish; Scyliorhinus canicula (Linnaeus, 1758); Scyliorhinus caniculus

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Chondrichthyes; Elasmobranchii; Selachii; Galeomorphii; Galeoidea; Carcharhiniformes; Scyliorhinidae; Scyliorhinus

Parent
Scyliorhinus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7829 )

NCBI Taxonomy ID
7830 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7830 )

is Taxon A an Infraspecies?
No

### Taxon B

Latin Name
Callorhinchus milii (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Callorhinchus milii^#gephebase-summary-title)

Common Name
elephant shark

Synonyms
elephant shark; Australian ghost shark; elephant fish; ghost shark; makorepe; plownose chimaera; reperepe; Callorhinchus milii Bory de Saint-Vincent, 1823; Callorhynchus milii

Rank
species

Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Chondrichthyes; Holocephali; Chimaeriformes; Callorhinchidae; Callorhinchus

Parent
Callorhinchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7866 )

NCBI Taxonomy ID
7868 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 7868 )

is Taxon B an Infraspecies?
No

## GENOTYPIC CHANGE

Generic Gene Name
ATP4B

Synonyms
ATP6B

String
9606.ENSP00000334216 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier= 9606.ENSP00000334216 )

Sequence Similarities
Belongs to the X(+)/potassium ATPases subunit beta family.

GO - Molecular Function
GO:0001671 : ATPase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0001671)
GO:0008900 : potassium:proton exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008900)

GO - Biological Process
GO:0007155 : cell adhesion (https://www.ebi.ac.uk/QuickGO/term/GO:0007155)
GO:0034220 : ion transmembrane transport

UniProtKB Homo sapiens
P51164 (http://www.uniprot.org/uniprot/P51164)

GenebankID or UniProtKB
()

(https://www.ebi.ac.uk/QuickGO/term/GO:0034220)
GO:0032496 : response to lipopolysaccharide
(https://www.ebi.ac.uk/QuickGO/term/GO:0032496)
GO:0030007 : cellular potassium ion homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0030007)
GO:0006883 : cellular sodium ion homeostasis
(https://www.ebi.ac.uk/QuickGO/term/GO:0006883)
GO:1990573 : potassium ion import across plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:1990573)
GO:0036376 : sodium ion export across plasma membrane
(https://www.ebi.ac.uk/QuickGO/term/GO:0036376)
GO:0010243 : response to organonitrogen compound
(https://www.ebi.ac.uk/QuickGO/term/GO:0010243)
GO:0010248 : establishment or maintenance of transmembrane electrochemical gradient
(https://www.ebi.ac.uk/QuickGO/term/GO:0010248)

GO - Cellular Component

GO:0005886 : plasma membrane (https://www.ebi.ac.uk/QuickGO/term/GO:0005886)
GO:0005890 : sodium:potassium-exchanging ATPase complex
(https://www.ebi.ac.uk/QuickGO/term/GO:0005890)

Presumptive Null

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=^Yes^#gephebase-summary-title)

Molecular Type

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

Aberration Type

Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=^Deletion^#gephebase-summary-title)

Deletion Size

-

Molecular Details of the Mutation

Absence of the gene in the genome sequence

Experimental Evidence

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

Main Reference

Recurrent gene loss correlates with the evolution of stomach phenotypes in gnathostome history. (2014) (https://pubmed.ncbi.nlm.nih.gov/24307675)

Authors

Castro LF; GonÃ§alves O; Mazan S; Tay BH; Venkatesh B; Wilson JM

Abstract

The stomach, a hallmark of gnathostome evolution, represents a unique anatomical innovation characterized by the presence of acid- and pepsin-secreting glands. However, the occurrence of these glands in gnathostome species is not universal; in the nineteenth century the French zoologist Cuvier first noted that some teleosts lacked a stomach. Strikingly, Holocephali (chimaeras), dipnoids (lungfish) and monotremes (egg-laying mammals) also lack acid secretion and a gastric cellular phenotype. Here, we test the hypothesis that loss of the gastric phenotype is correlated with the loss of key gastric genes. We investigated species from all the main gnathostome lineages and show the specific contribution of gene loss to the widespread distribution of the agastric condition. We establish that the stomach loss correlates with the persistent and complete absence of the gastric function gene kit--H(+)/K(+)-ATPase (Atp4A and Atp4B) and pepsinogens (Pga, Pgc, Cym)--in the analysed species. We also find that in gastric species the pepsinogen gene complement varies significantly (e.g. two to four in teleosts and tens in some mammals) with multiple events of pseudogenization identified in various lineages. We propose that relaxation of purifying selection in pepsinogen genes and possibly proton pump genes in response to dietary changes led to the numerous independent events of stomach loss in gnathostome history. Significantly, the absence of the gastric genes predicts that reinvention of the stomach in agastric lineages would be highly improbable, in line with Dollo's principle.

Additional References

## RELATED GEPHE

Related Genes

No matches found.

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS