

GEPHE SUMMARY

ATP4B (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ATP4B^#gephebase-summary-title)	Gephebase Gene	GP00001916	GepheID
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)	Trait Category		
Digestion (absence of stomach) (https://www.gephebase.org/search-criteria?/and+Trait=^Digestion+absence+of+stomach^#gephebase-summary-title)	Trait		
presence of stomach and gastric acid production	Trait State in Taxon A		
loss of stomach and no gastric acid production	Trait State in Taxon B		
	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		Taxon B
Scyliorhinus canicula (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Scyliorhinus+canicula^#gephebase-summary-title)	Latin Name	Callorhynchus milii (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Callorhynchus+milii^#gephebase-summary-title)	Latin Name
smaller spotted catshark	Common Name	elephant shark	Common Name
smaller spotted catshark; smaller spotted dogfish; spotted catshark; spotted dogfish; Scyliorhinus canicula (Linnaeus, 1758); Scyliorhinus caniculus	Synonyms	elephant shark; Australian ghost shark; elephant fish; ghost shark; makorepe; plownose chimaera; reperepe; Callorhynchus milii Bory de Saint-Vincent, 1823; Callorhynchus milii	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Chondrichthyes; Elasmobranchii; Selachii; Galeomorphii; Galeoidea; Carcharhiniformes; Scyliorhinidae; Scyliorhinus	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Chondrichthyes; Holocephali; Chimaeriformes; Callorhynchidae; Callorhynchus	Lineage
Scyliorhinus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7829)	Parent	Callorhynchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7866)	Parent
7830 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7830)	NCBI Taxonomy ID	7868 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7868)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	No	is Taxon B an Intraspecies?

GENOTYPIC CHANGE

ATP4B	Generic Gene Name	P51164 (http://www.uniprot.org/uniprot/P51164)	UniProtKB Homo sapiens
ATP6B	Synonyms	()	GenebankID or UniProtKB
9606.ENSPP00000334216 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000334216)	String		
Belongs to the X(+)/potassium ATPases subunit beta family.	Sequence Similarities		
GO:0001671 : ATPase activator activity (https://www.ebi.ac.uk/QuickGO/term/GO:0001671)	GO - Molecular Function		
GO:0008900 : potassium:proton exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008900)			
GO:0007155 : cell adhesion (https://www.ebi.ac.uk/QuickGO/term/GO:0007155)	GO - Biological Process		
GO:0034220 : ion transmembrane transport			

(<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](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](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](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](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; Gon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