

GEPHE SUMMARY

ATP4A (https://www.gephebase.org/search-criteria?/and+Gene Gephebase=%ATP4A%#gephebase-summary-title)	Gephebase Gene	GP00001908	GephelD
Published	Entry Status	Courtier	Main curator

PHENOTYPIC CHANGE

Trait Category		Trait	
Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=%Physiology%#gephebase-summary-title)			
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	
Monodelphis domestica (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Monodelphis+domestica%#gephebase-summary-title)	Latin Name	Ornithorhynchus anatinus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=%Ornithorhynchus+anatinus%#gephebase-summary-title)	Latin Name
gray short-tailed opossum	Common Name	platypus	Common Name
gray short-tailed opossum; Monodelphis domesticus	Synonyms	platypus; duck-billed platypus; duckbill platypus; Ornithorhynchus anatinus	Synonyms
species	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Metatheria; Didelphimorpha; Didelphidae; Didelphinae; Monodelphis	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Prototheria; Monotremata; Ornithorhynchidae; Ornithorhynchus	Lineage
Monodelphis (short-tailed opossums) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 13615)	Parent	Ornithorhynchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9257)	Parent
13616 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 13616)	NCBI Taxonomy ID	9258 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9258)	NCBI Taxonomy ID
No	is Taxon A an Infraspecies?	No	is Taxon B an Infraspecies?

GENOTYPIC CHANGE

ATP4A	Generic Gene Name	P20648 (http://www.uniprot.org/uniprot/P20648)	UniProtKB Homo sapiens
ATP6A	Synonyms	0	GenebankID or UniProtKB
9606.ENSP00000262623 (http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9606.ENSP00000262623)	String		
Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIC subfamily. GO - Molecular Function	Sequence Similarities		
GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524) GO:0000287 : magnesium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000287) GO:0005391 : sodium:potassium-exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005391) GO:0008900 : potassium:proton exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008900)			

GO - Biological Process

GO:0034220 : ion transmembrane transport
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0034220>)
 GO:0015991 : ATP hydrolysis coupled proton transport
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0015991>)
 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 - Cellular Component

GO:0005886 : plasma membrane (<https://www.ebi.ac.uk/QuickGO/term/GO:0005886>)
 GO:0005887 : integral component of plasma membrane
 (<https://www.ebi.ac.uk/QuickGO/term/GO:0005887>)
 GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

Presumptive Null

Yes ([https://www.gephebase.org/search-criteria/?and+Presumptive Null=%27Yes%27#gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Presumptive%20Null=%27Yes%27#gephebase-summary-title))

Molecular Type

Gene Loss ([https://www.gephebase.org/search-criteria/?and+Molecular Type=%27Gene Loss%27#gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Molecular%20Type=%27Gene%20Loss%27#gephebase-summary-title))

Aberration Type

Deletion ([https://www.gephebase.org/search-criteria/?and+Aberration Type=%27Deletion%27#gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Aberration%20Type=%27Deletion%27#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=%27Candidate Gene%27#gephebase-summary-title](https://www.gephebase.org/search-criteria/?and+Experimental%20Evidence=%27Candidate%20Gene%27#gephebase-summary-title))

Main Reference

Loss of genes implicated in gastric function during platypus evolution. (2008) (<https://pubmed.ncbi.nlm.nih.gov/18482448>)

Authors

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Abstract

The duck-billed platypus (*Ornithorhynchus anatinus*) belongs to the mammalian subclass *Prototheria*, which diverged from the *Theria* line early in mammalian evolution. The platypus genome sequence provides a unique opportunity to illuminate some aspects of the biology and evolution of these animals.

We show that several genes implicated in food digestion in the stomach have been deleted or inactivated in platypus. Comparison with other vertebrate genomes revealed that the main genes implicated in the formation and activity of gastric juice have been lost in platypus. These include the aspartyl proteases pepsinogen A and pepsinogens B/C, the hydrochloric acid secretion stimulatory hormone gastrin, and the alpha subunit of the gastric H+/K+-ATPase. Other genes implicated in gastric functions, such as the beta subunit of the H+/K+-ATPase and the aspartyl protease cathepsin E, have been inactivated because of the acquisition of loss-of-function mutations. All of these genes are highly conserved in vertebrates, reflecting a unique pattern of evolution in the platypus genome not previously seen in other mammalian genomes.

The observed loss of genes involved in gastric functions might be responsible for the anatomical and physiological differences in gastrointestinal tract between monotremes and other vertebrates, including small size, lack of glands, and high pH of the monotreme stomach. This study contributes to a better understanding of the mechanisms that underlie the evolution of the platypus genome, might extend the less-is-more evolutionary model to monotremes, and provides novel insights into the importance of gene loss events during mammalian evolution.

Additional References

RELATED GEPHE

Related Genes

7 (gastrin, neurogenin 3, pepsinogen A, pepsinogen B, pepsinogen C, ATP4B, cathepsin E) ([https://www.gephebase.org/search-criteria/?or+Taxon ID=%2713616%27/and+Trait=Digestion/or+Taxon ID=%279258%27/and+Trait=Digestion/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria/?or+TaxonID=%2713616%27/and+Trait=Digestion/or+TaxonID=%279258%27/and+Trait=Digestion/and+groupHaplotypes=true#gephebase-summary-title))

Related Haplotypes

No matches found.

EXTERNAL LINKS

COMMENTS

lack of acid secretion in the platypus stomach - this is a characteristic feature of monotremes whose gastric juice is above pH 6

