

GEPHE SUMMARY

<p>ATP4A (https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=^ATP4A^#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>Entry Status</p>	<p>GP00001908</p> <p>Courtier</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Physiology (https://www.gephebase.org/search-criteria?/and+Trait+Category=^Physiology^#gephebase-summary-title)</p> <p>Digestion (absence of stomach) (https://www.gephebase.org/search-criteria?/and+Trait=^Digestion (absence of stomach)^#gephebase-summary-title)</p> <p>presence of stomach and gastric acid production</p> <p>loss of stomach and no gastric acid production</p> <p>Taxon A</p> <p>Intergeneric or Higher (https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=^Intergeneric or Higher^#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>Ornithorhynchus anatinus (https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Ornithorhynchus anatinus^#gephebase-summary-title)</p> <p>platypus</p> <p>platypus; duck-billed platypus; duckbill platypus; Ornithorhynchus anatinus</p> <p>species</p> <p>cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Metatheria; Didelphimorphia; Didelphidae; Didelphinae; Monodelphis</p> <p>Ornithorhynchus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9257)</p> <p>9258 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9258)</p> <p>No is Taxon B an Intraspecies?</p>	<p>Latin Name</p> <p>Common Name</p> <p>Synonyms</p> <p>Rank</p> <p>Lineage</p> <p>Parent</p> <p>NCBI Taxonomy ID</p> <p>is Taxon B an Intraspecies?</p>
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GENOTYPIC CHANGE

<p>ATP4A</p> <p>ATP6A</p> <p>9606.ENSPP00000262623 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000262623)</p> <p>Belongs to the cation transport ATPase (P-type) (TC 3.A.3) family. Type IIC subfamily.</p> <p>GO:0005524 : ATP binding (https://www.ebi.ac.uk/QuickGO/term/GO:0005524)</p> <p>GO:0000287 : magnesium ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000287)</p> <p>GO:0005391 : sodium:potassium-exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005391)</p> <p>GO:0008900 : potassium:proton exchanging ATPase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008900)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>P20648 (http://www.uniprot.org/uniprot/P20648)</p> <p>()</p> <p>UniProtKB Homo sapiens</p> <p>GenebankID or UniProtKB</p>
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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>)

Yes (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Yes^#gephebase-summary-title)	Presumptive Null
Gene Loss (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Gene Loss^#gephebase-summary-title)	Molecular Type
Deletion (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Deletion^#gephebase-summary-title)	Aberration Type
-	Deletion Size
Absence of the gene in the genome sequence	Molecular Details of the Mutation
Candidate Gene (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Candidate Gene^#gephebase-summary-title)	Experimental Evidence
Loss of genes implicated in gastric function during platypus evolution. (2008) (https://pubmed.ncbi.nlm.nih.gov/18482448)	Main Reference
Ordoñez GR; Hillier LW; Warren WC; Grützner F; López-Otin C; Puente XS	Authors
The duck-billed platypus (<i>Ornithorhynchus anatinus</i>) 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.	Abstract
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

7 (gastrin, neurogenin 3, pepsinogen A, pepsinogen B, pepsinogen C, ATP4B, cathepsin E) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~13616^/and+Trait=Digestion/or+Taxon ID=~9258^/and+Trait=Digestion/and+groupHaplotypes=true#gephebase-summary-title>)

Related Genes

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

