GEPHE SUMMARY

Gephebase Gene

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

Entry Status

Published

GepheID

GP00000557

Main curator

Martin

PHENOTYPIC CHANGE

Trait Category

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

Trait

Digestion (anaerobic enzymatic activity) (https://www.gephebase.org/search-criteria?/and+Trait=^Digestion (anaerobic enzymatic activity)^#gephebase-summary-title)

Trait State in Taxon A

Other mammals

Trait State in Taxon B

Bos bovis

Ancestral State

Data not curated

Taxonomic Status

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

Taxon A

Latin Name

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

Common Name

mammals

Synonyms

mammals

Rank

class

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota

Parent

Amniota (amniotes) - (Rank: no rank) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 32524)

NCBI Taxonomy ID

40674 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 40674)

is Taxon A an Infraspecies?

No

Taxon B

Latin Name

Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)

Common Name

cattle

Synonyms

Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Tauurus

Rank

species

Lineage

cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos

Parent

Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)

NCBI Taxonomy ID

9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)

is Taxon B an Infraspecies?

No

GENOTYPIC CHANGE

Generic Gene Name

LYZ1

Synonyms

-

String

-

Sequence Similarities

Belongs to the glycosyl hydrolase 22 family.

GO - Molecular Function

GO:0003796 : lysozyme activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003796)

GO - Biological Process

GO:0050829 : defense response to Gram-negative bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0050829)
GO:0050830 : defense response to Gram-positive bacterium (https://www.ebi.ac.uk/QuickGO/term/GO:0050830)
GO:0019835 : cytolysis (https://www.ebi.ac.uk/QuickGO/term/GO:0019835)
GO:0007586 : digestion (https://www.ebi.ac.uk/QuickGO/term/GO:0007586)

UniProtKB Bos taurus

P04421 (http://www.uniprot.org/uniprot/P04421)

GenebankID or UniProtKB

M95099 (https://www.ncbi.nlm.nih.gov/nuccore/M95099)

GO:0008152 : metabolic process (https://www.ebi.ac.uk/QuickGO/term/GO:0008152)

GO - Cellular Component

-

Mutation #1

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

R14K

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Arg	Lys	14

Main Reference

Adaptive evolution in the stomach lysozymes of foregut fermenters. (1987 Nov 26-Dec 2) (https://pubmed.ncbi.nlm.nih.gov/3120013)

Authors

Stewart CB; Schilling JW; Wilson AC

Abstract

The convergent evolution of a fermentative foregut in two groups of mammals offers an opportunity to study adaptive evolution at the protein level. The appearance of this mode of digestion has been accompanied by the recruitment of lysozyme as a bacteriolytic enzyme in the stomach both in the ruminants (for example the cow) and later in the colobine monkeys (for example the langur). The stomach lysozymes of these two groups share some physicochemical and catalytic properties that appear to adapt them for functioning in the stomach fluid. To examine the basis for these shared properties, we sequenced langur stomach lysozyme and compared it to other lysozymes of known sequence. Tree analysis suggest that, after foregut fermentation arose in monkeys, the langur lysozyme gained sequence similarity to cow stomach lysozyme and evolved two times faster than the other primate lysozymes. This rapid evolution, coupled with functional and sequence convergence upon cow stomach lysozyme, could imply that positive darwinian selection has driven about 50% of the evolution of langur stomach lysozyme.

Additional References

Molecular adaptation of a leaf-eating bird: stomach lysozyme of the hoatzin. (1994) (https://pubmed.ncbi.nlm.nih.gov/7815930)

Mutation #2

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

X21K (sequence in the closest ancestor with ancestral trait unknown)

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	Lys	21

Main Reference

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Authors

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The convergent evolution of a fermentative foregut in two groups of mammals offers an opportunity to study adaptive evolution at the protein level. The appearance of this mode of digestion has been accompanied by the recruitment of lysozyme as a bacteriolytic enzyme in the stomach both in the ruminants (for example the cow) and later in the colobine monkeys (for example the langur). The stomach lysozymes of these two groups share some physicochemical and catalytic properties that appear to adapt them for functioning in the stomach fluid. To examine the basis for these shared properties, we sequenced langur stomach lysozyme and compared it to other lysozymes of known sequence. Tree analysis suggest that, after foregut fermentation arose in monkeys, the langur lysozyme gained sequence similarity to cow stomach lysozyme and evolved two times faster than the other primate lysozymes. This rapid evolution, coupled with functional and sequence convergence upon cow stomach lysozyme, could imply that positive darwinian selection has driven about 50% of the evolution of langur stomach lysozyme.

Additional References

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Mutation #3

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

N75D

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Asn	Asp	75

Main Reference

Adaptive evolution in the stomach lysozymes of foregut fermenters. (1987 Nov 26-Dec 2) (https://pubmed.ncbi.nlm.nih.gov/3120013)

Authors

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Additional References

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Mutation #4

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

E87N

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	Glu	Asn	87

Main Reference

Adaptive evolution in the stomach lysozymes of foregut fermenters. (1987 Nov 26-Dec 2) (https://pubmed.ncbi.nlm.nih.gov/3120013)

Authors

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Additional References

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Mutation #5

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

X126E (sequence in the closest ancestor with ancestral trait unknown)

Experimental Evidence

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

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	Glu	126

Main Reference

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Authors

Stewart CB; Schilling JW; Wilson AC

Abstract

The convergent evolution of a fermentative foregut in two groups of mammals offers an opportunity to study adaptive evolution at the protein level. The appearance of this mode of digestion has been accompanied by the recruitment of lysozyme as a bacteriolytic enzyme in the stomach both in the ruminants (for example the cow) and later in the colobine monkeys (for example the langur). The stomach lysozymes of these two groups share some physicochemical and catalytic properties that appear to adapt them for functioning in the stomach fluid. To examine the basis for these shared properties, we sequenced langur stomach lysozyme and compared it to other lysozymes of known sequence. Tree analysis suggest that, after foregut fermentation arose in monkeys, the langur lysozyme gained sequence similarity to cow stomach lysozyme and evolved two times faster than the other primate lysozymes. This rapid evolution, coupled with functional and sequence convergence upon cow stomach lysozyme, could imply that positive darwinian selection has driven about 50% of the evolution of langur stomach lysozyme.

Additional References

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RELATED GEPHE

Related Genes

9 (ATP4A, gastrin, neurogenin 3, pepsinogen A, pepsinogen B, pepsinogen C, ATP4B, cathepsin E, RNASE1B) (https://www.gephebase.org/search-criteria?/or+Taxon ID=^40674^/and+Trait=Digestion/or+Taxon ID=^9913^/and+Trait=Digestion/and+groupHaplotypes=true#gephebase-summary-title)

Related Haplotypes

1 (https://www.gephebase.org/search-criteria?/or+Gene Gephebase=^lysozyme^/and+Taxon ID=^40674^/or+Gene Gephebase=^lysozyme^/and+Taxon ID=^9913^#gephebase-summary-title)

EXTERNAL LINKS

COMMENTS

@SeveralMutationsWithEffect