

Sequence >KJ155698.1, from an Almas/Russian Bigfoot or a Bear?

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Abstract

In the July 2, 2014 issue of the *Journal of the The Proceedings of the Royal Society: Biological Science* Volume 281, Issue 2014.0161, Sykes, Mullis, Hagenmuller, Melton, and Sartori conducted a comprehensive genetic survey of individual and museum collected specimens to explore their identity. The purpose of this project was to verify the claims of this article regarding the Russian Bigfoot or Almas.. Sequences cited in the article are stored in GenBank and translated into six reading frames using <http://insilico.ehu.es/translate/>. Protein BLASTs were conducted of the results. Multiple sequence alignments and phylogenetic trees were constructed comparing the sequence to humans, other primates, and Russian mammals to determine the source of the sequence. Sequence >155698.1 appears to be from a brown bear (*Ursus arctos*).

Introduction

Regions of Northern Asia are famous for the legend of the Russian Bigfoot 'Almas' or Relic Neanderthal. If such a creature exists, there must be hair samples in the area that contain unique DNA sequences that would align with other known "higher" primates such as humans, chimpanzees, gorillas, and orangutans.

In the July 2, 2014 issue of the *Journal The Proceedings of the Royal Society: Biological Science* Volume 281, Bryan Sykes, Rhetman Mullis, Christophe Hagenmuller, Terry Melton, and Michel Sartori conducted a comprehensive genetic survey of field-collected and museum specimens to explore their identity. The resulting journal article was entitled "Genetics Analysis of Hair Samples attributed to Yeti, Bigfoot and Other Anomalous Primate". A total of 37 individual and museum collected hair samples were selected for genetic analysis based on their place of origin.

Samples were placed in proteinase K for 2 hours at 56°C before DNA extraction using phenol, chloroform, and isoamyl alcohol. Extracted DNA was amplified for the ribosomal mitochondrial DNA 12S fragment using Polymerase Chain The resulting DNA were compared to GenBank for species identification..

The purpose of this project is to determine if sequence >KJ155698.1 came from a scientifically unknown relic bipedal Hominidae (commonly called the Almas or Russian Bigfoot), or another known primate or another Russian mammal. Critical thinking skills and gene annotation skills were used to scientifically investigate a popular cryptid. The second purpose is to independently verify the work of Oxford's Dr. Bryan Sykes and the other scientists.



Figure 1: Russian Almas

Source:
https://www.google.com/search?q=almas&safe=active&rlz=1C1GCEA_enUS813US813&source=lnms&tbm=isch&sa=X&ved=0ahUKEwifjLnlulniAhVw1KkHVxfBe4Q_AUJDigB&biw=1366&bih=639&url=1#imgrc=C1EK9a9BnM

Methods

Websites that were used:

- 1) Proceedings of the Royal Society Biological Sciences <https://royalsocietypublishing.org/doi/10.1098/rspb.2014.0161#d661480e838s> reference Number 25027-25194 to obtain sequence identifiers for GenBank.
- 2) DNA to Protein translation <http://insilico.ehu.es/translate/> to obtain 6 possible reading frame translation for sequences.
- 3) BLAST <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- 4) GenBank: <https://www.ncbi.nlm.nih.gov/nucleotide/> to find test sequences, comparable primate sequences, and Himalayan mammal sequences.
- 5) T-COFFEE <http://www.ebi.ac.uk/Tools/msa/tcoffee/> to construct multiple sequence alignments and Phylogenetic Trees.

>KJ155698.1 Almas from Russia isolate 25027
CTTAGCCTTAAACATAAATAATTATTAAACAAAATTATTCCGCCAGA
GAACTACTAGCAACAGCTTAAACTCAAAGGACTTGGCGGTGCTT
TAAACCCCTA

Raw DNA Nucleotide Sequence

Results

Ursus arctos isolate Tver203 mitochondrion, partial genome
Sequence ID: KY419702.1 Length: 16555 Number of Matches: 1

Score	Expect	Identities	Gaps	Strand
188 bits (208)	2e-44	104/104(100%)	0/104(0%)	Plus/Plus

Query 1 CTTAGCCTTAAACATAAATAATTATTAAACAAAATTATTCCGCCAGA 60
Sbjct 519 CTTAGCCTTAAACATAAATAATTATTAAACAAAATTATTCCGCCAGA 578

Query 61 CAGCTTAAACTCAAAGGACTTGGCGGTGCTTAAACCCCTA 104
Sbjct 579 CAGCTTAAACTCAAAGGACTTGGCGGTGCTTAAACCCCTA 622

Figure 2. Blast results from raw nucleotide. Ursus arctos (Brown Bear). Score 188 bits. E-value 2e-44. 100 identity, 0 gaps.

Source:

https://www.google.com/search?q=brown+be ar&safe=active&rlz=1C1GCEA_enUS813US813&source=lnms&tbm=isch&sa=X&ved=0ahUKEwifjLnlulniAhVw1KkHVxfBe4Q_AUJDigB&biw=1366&bih=639&url=1#imgrc=JhwWuG_BSvkUnM



The Brown Bear. (*Ursus arctos*)

Does the sequence come from a Primate?

Macaca mulatta putative NUMT 12S rRNA gene, clone 28
Sequence ID: AJ842856.1 Length: 385 Number of Matches: 1

Score	Expect	Identities	Gaps	Strand
119 bits (131)	1e-25	89/104(86%)	3/104(2%)	Plus/Plus

Query 1 CTTAGCCTTAAACATAAATAATTATTAAACAAAATTATTCCGCCAGA 60
Sbjct 2 CTTAGCCTTAAACCTCAAGTAAATAAACAAAATTATTCCGCCAGA 58

Query 61 CAGCTTAAACTCAAAGGACTTGGCGGTGCTTAAACCCCTA 104
Sbjct 59 CAGCTTAAACTCAAAGGACTTGGCGGTGCTTAAACCCCTA 102

Figure 3. Blast results from raw nucleotide. Macaca mulatta (Rhesus macaque). Score 119 bits. E-value 1e-25. 3 gaps. 89/104 base pairs. Identity 86%. The Brown Bear is a better match.

Source:

https://www.google.com/search?q=rhesus+macaque&safe=active&rlz=1C1GCEA_enUS813US813&source=lnms&tbm=isch&sa=X&ved=0ahUKEwifjLnlulniAhVw1KkHVxfBe4Q_AUJDigB&biw=1366&bih=639&url=1#imgrc=JhwWuG_BSvkUnM



Does the sequence come from a primate?

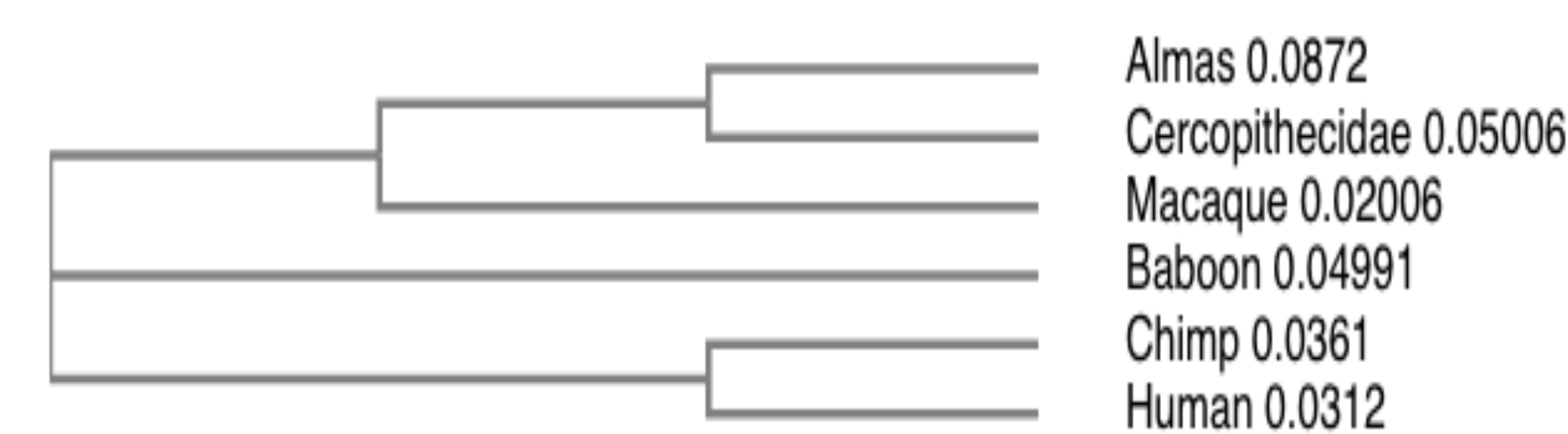


Figure 4. Shows the phylogenetic tree results. The Almas sequence is on the same branch as Cercopithecidae, a lower primate. If the Almas existed, it would be on the same branch as higher primates like the human and chimpanzee.



Figure 5. Bryan Clifford Sykes a Emeritus Professor of Human Genetics at the University of Oxford.

Source:

https://www.google.com/search?q=bryan+sykes&safe=active&rlz=1C1GCEA_enUS813US813&source=lnms&tbm=isch&sa=X&ved=0ahUKEwifjLnlulniAhVw1KkHVxfBe4Q_AUJDigB&biw=1366&bih=639&url=1#imgrc=5_rpo49nfcqM

Does the sequence come from a Primate or a Bear?

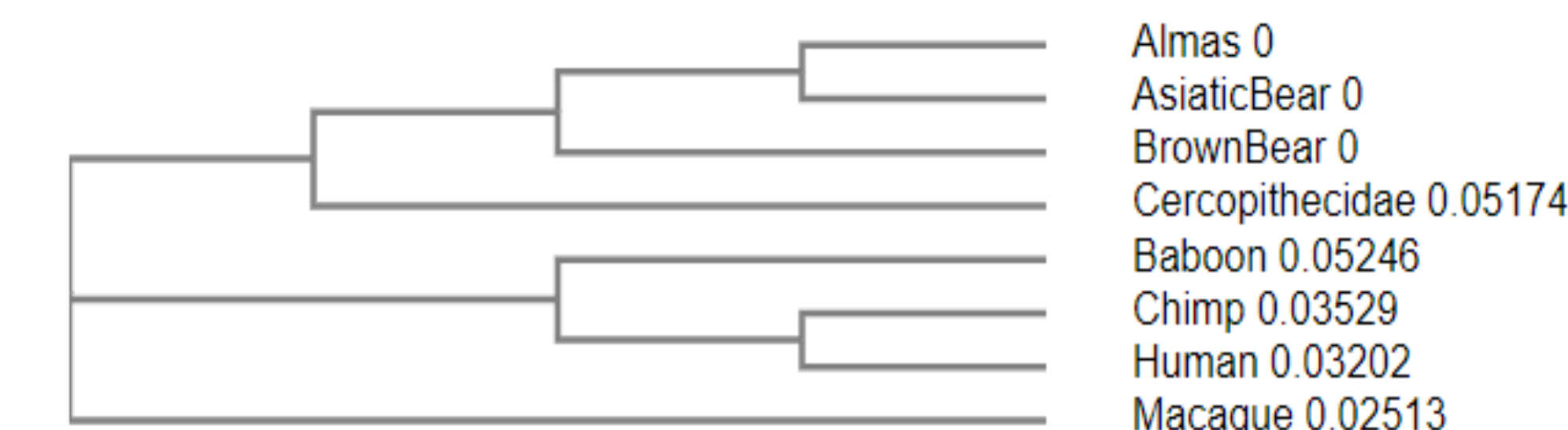


Figure 6. Shows the phylogenetic tree results. The blast best matches the Brown Bear (*Ursus arctos*) and the Asiatic Bear (*Ursus thibetanus*). Humans and Chimpanzees are on an entirely different branch. The macaque (*Macaca* sp.) is even farther away.

Does the sequence come from a Domesticated Mammal?

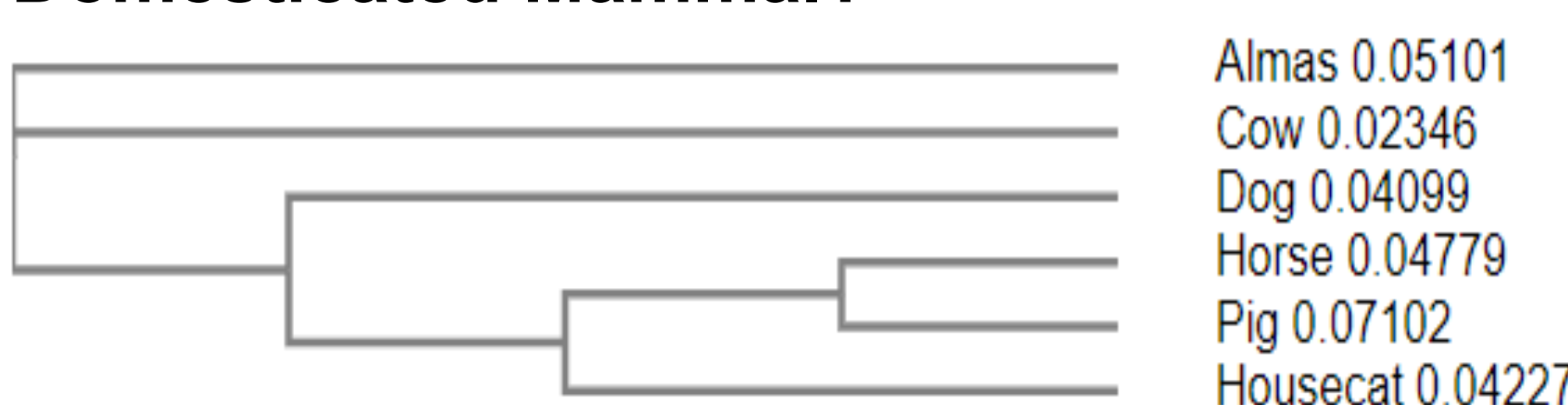


Figure 8. Shows the phylogenetic tree results. The phylogenetic tree shows that the "Almas" DNA sequence isn't even on the same branch as any of the domesticated mammals.

Does the sequence come from a Domesticated Mammal or a Bear?

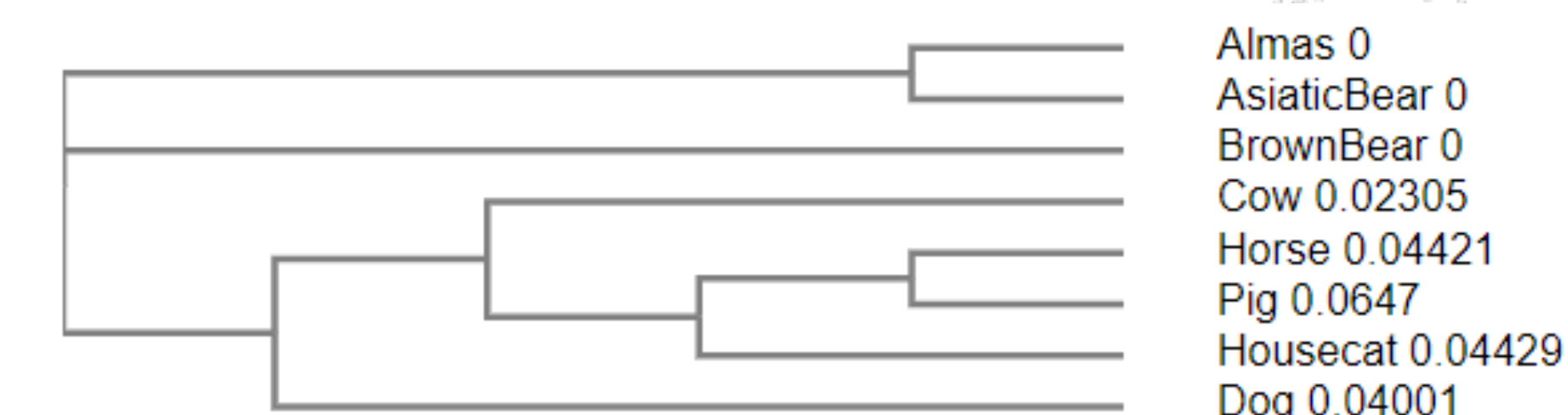


Figure 8. Shows the phylogenetic tree results. The blast best matches the Asiatic Bear and the brown bear (*Ursus arctos*). The comparison to domesticated mammals shows no close match.



Figure 9. shows a Asiatic Black Bear which is our second best match.

https://www.google.com/search?safe=active&rlz=1C1GCEA_enUS813US813&biw=1366&bih=639&tbm=isch&sa=X&ved=0ahUKEwifjLnlulniAhVw1KkHVxfBe4Q_AUJDigB&biw=1366&bih=639&url=1#imgrc=5_rpo49nfcqM

Conclusion

At the start of the experiment, the raw nucleotide sequence was BLASTed to determine whether it was from an "Almas", or some other mammal. The raw nucleotide sequence from the "Almas" was compared to thousands of other sequences. Our results showed that the closest match to the DNA sequence was a Brown Bear (*Ursus arctos*). After matching it to a Brown Bear, we blasted our sequence against humans, primates and gorillas. The best result we got was a *Macaca mulatta* (Rhesus macaque). The blast against the Brown Bear had an identity of 100% with 0 gaps while the *Macaca mulatta* had an identity of 86% with 3 gaps. Phylogenetic trees were then to show that the DNA sequence was not the "Almas" but from a bear. Our results came up as not being on the same branch as any of the Domesticated Mammals and not close to being on the same branch as the Primates, but it was on the same branch as the Asiatic Bear and the Brown Bear. It was concluded that the sequence came from an Asian bear and not from a large bipedal primate.

References

- 1 Sykes, B.C., Mullis R. A, Hagenmuller, C., Melton, T. W., Sartori, M. July 2014 Genetic analysis of hair samples attributed to yeti, bigfoot and other anomalous primates. Proc. R. Soc. B 281:2014.0161. <https://royalsocietypublishing.org/doi/10.1098/rspb.2014.0161#d661480e838s>

Acknowledgments

Supported by an NIH Science Education Partnership Award R25OD010536.

Thank you to Dr. Stephen Koury and Dr. Rama Dey-Rao. University at Buffalo.

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