Does the Almas/ Russian Bigfoot Exist? A study of Sequence >KJ155705.1

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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. In conclusion the DNA Sample was from the Domesticated Horse (*Equus caballus*).

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 a 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, Rhettman 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 56ºC 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 >KJ155705.1 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: A photo the American Sasquatch, which many believe is a cousin to the Russian Almas.
https://www.skepticblog.org/2014/06/01/the-profound-awfulness-of-discoverys-russian-yeti-the-killer-lives/

Methods

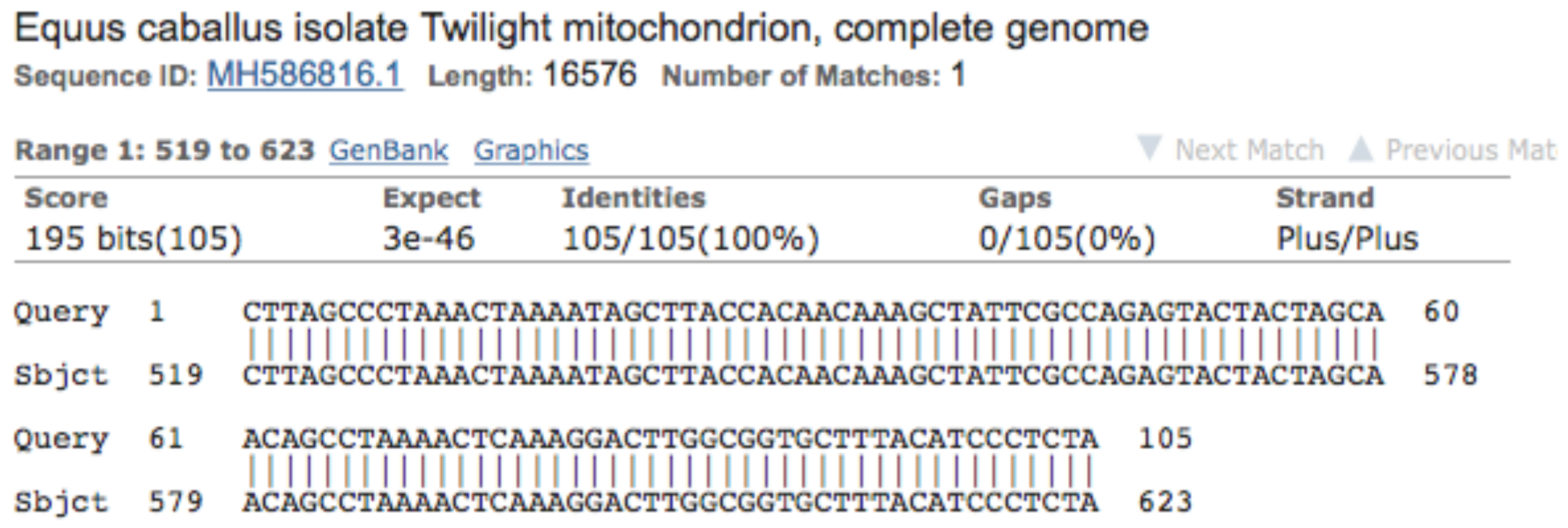
Websites that were used:

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.

```
>KJ155705.1 isolate 25041
CTTAGCCCTAAACTAAAATAGCTTACCACAACAAAG
CTATTCGCCAGAGTACTACTAGCAACAGCCTAAAAC
TCAAAGGACTTGGCGGTGCTTTACATCCCTCTA
```

Raw DNA Nucleotide Sequence

Results



Equus caballus isolate Twilight mitochondrion, complete genome
Sequence ID: MH586816.1 Length: 16576 Number of Matches: 1

Range 1: 519 to 623 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
195 bits(105)	3e-46	105/105(100%)	0/105(0%)	Plus/Plus

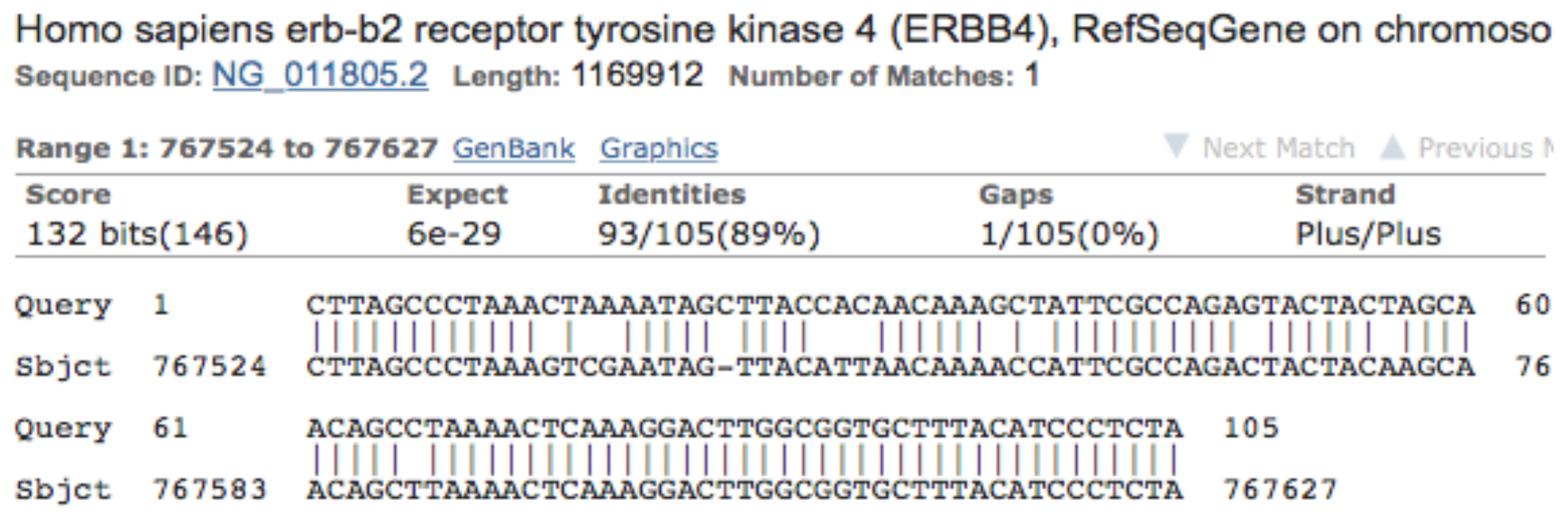
```
Query  1    CTTAGCCCTAAACTAAAATAGCTTACCACAACAAAGCTATTCGCCAGAGTACTACTAGCA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  519  CTTAGCCCTAAACTAAAATAGCTTACCACAACAAAGCTATTCGCCAGAGTACTACTAGCA  578

Query  61   ACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTTACATCCCTCTA  105
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  579  ACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTTACATCCCTCTA  623
```

Figure 2. BLAST results of Raw Nucleotide sequence. It is Equus caballus (Domesticated Horse). Score 195 bits. E-value 3e-46. 0 gaps.

https://equineguelph.ca/learn_objects/evolutiontimeline/equus.html

Does the Sequence come from a Primate?



Homo sapiens erb-b2 receptor tyrosine kinase 4 (ERBB4), RefSeqGene on chromoso
Sequence ID: NG_011805.2 Length: 1169912 Number of Matches: 1

Range 1: 767524 to 767627 GenBank Graphics

Score	Expect	Identities	Gaps	Strand
132 bits(146)	6e-29	93/105(89%)	1/105(0%)	Plus/Plus

```
Query  1       CTTAGCCCTAAACTAAAATAGCTTACCACAACAAAGCTATTCGCCAGAGTACTACTAGCA  60
               ||||||||||||  |    |||||  ||||      ||||||  |  ||||||||||  ||||||  ||||
Sbjct  767524  CTTAGCCCTAAAGTCGAATAG-TTACATTAACAAAACCATTCGCCAGACTACTACAAGCA  76

Query  61      ACAGCCTAAAACTCAAAGGACTTGGCGGTGCTTTACATCCCTCTA  105
               |||||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  767583  ACAGCTTAAAACTCAAAGGACTTGGCGGTGCTTTACATCCCTCTA  767627
```

Figure 3: Nucleotide BLAST of sequence against Homo/Pan/Gorilla. Results are for a Human kinase. Score 132 bits. e-value 6e-29. Just 89% identity with 1 Gap. The Horse is a better match.

Phylogenetic trees for Sequence and Domesticated Animals

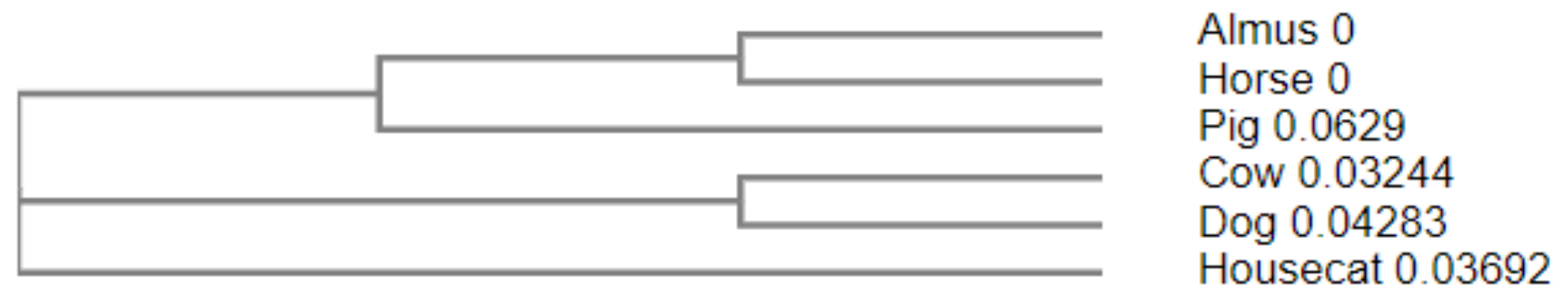


Figure 4. The Almas sequence is on the same branch as the Horse This is further evidence that the sequence isn't from a Russian Bigfoot, but from a horse.

Phylogenetic trees for Sequence and Primates.

Figure 5. The Almas sequence is on its own branch, but near chimpanzees and humans. This is what you would expect if the Almas was a large primate.

Phylogenetic trees for Sequence and Wild Mammals of Russia.

Figure 6. The Almas is on its own branch of the phylogenetic tree and not closely related to the four mammals of Russia.

Phylogenetic trees for Almas sequence Wild Mammals of Russia and Horse.

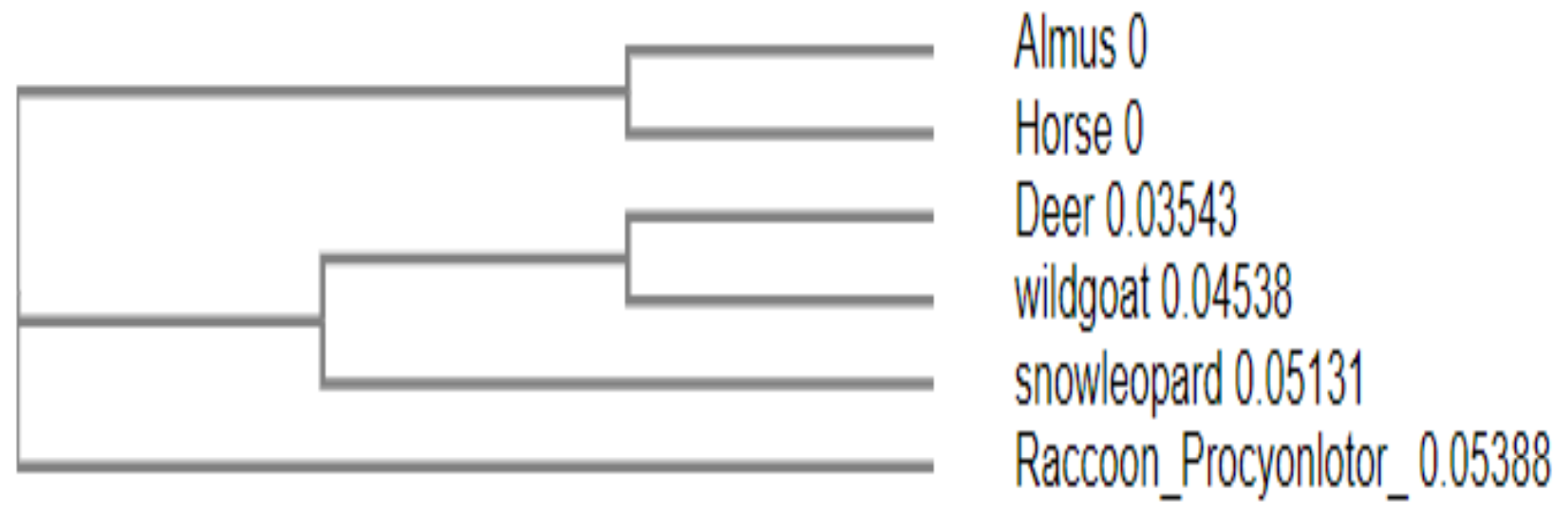


Figure 7. The Almas and the Horse are on the same branch after adding the Horse sequence with Wild Mammals of Russia. This is further evidence that the sequence is from a horse.

Phylogenetic trees for >KJ155705.1 Sequence and Russian Bears

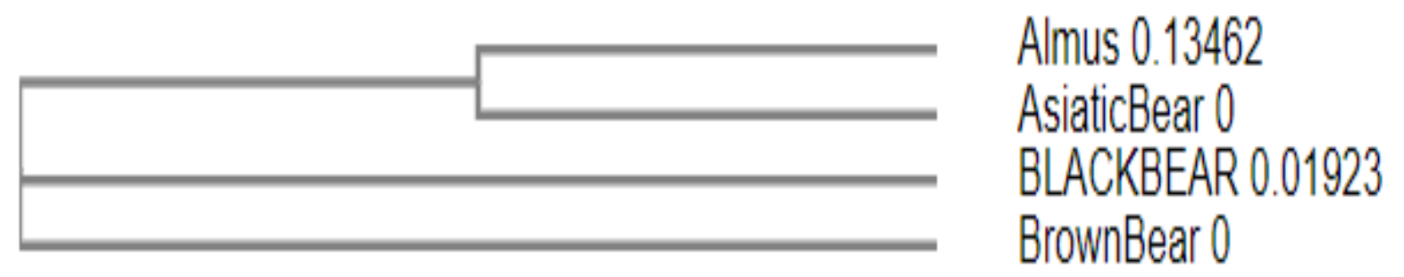


Figure 8. The Almas sequence is on the same branch as the Asiatic Bear.

Phylogenetic trees for Sequence and Primates Plus Horse

Figure 9. The Almas sequence is on the same branch as a horse sequence and near the chimpanzee and human sequences. This helps with the understanding of Figure 5.

Conclusion

The first BLAST was 100% Identity and extremely significant (3e-46) and was a good match for a horse (0 gaps) It does not appear to be from a Russian Bigfoot. The human BLAST values showed that the horse hit was better. This is even more evidence that the sequence is not from a primate. The chimp is on a different branch on the phylogenetic tree. If the Russian Almas was a bipedal primate, then the chimp or human would be on the same branch. Horses are distantly related to primates. The hair probably came from a horse. Figure 7 BLAST results were tested with Phylogenetic trees for Wild Mammals of Russia Plus Horse. The Almas and the Horse were on the same branch. Figure 9. The Almas sequence is on the same branch as the Horse. Phylogenetic trees for Sequence and Primates Plus Horse. These pieces of evidence is is further evidence that the sequence is not from a Russian Bigfoot, but from a horse (*Equus caballus*).

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

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