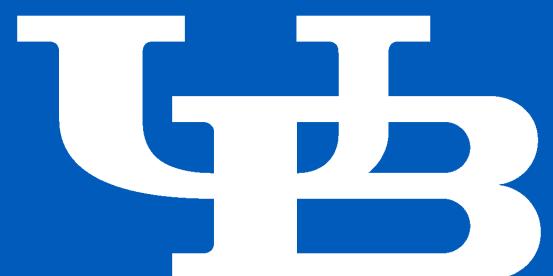


Has Sasquatch (*Homo sapiens cognatus*) DNA been sequenced?

Julio Lebron-Torres, Tyler Miles, Lon Knappenberger

Westfield Academy and Central School, 203 East Main Street, Westfield, New York, 14787 and The Western
New York Genetics in Research Partnership



University
at Buffalo

Abstract

In 2013, The Sasquatch Genome project, which includes Dr. Melba Ketcham and her colleagues, published a paper in the Journal DeNova: Accelerating Science in which they claimed they had sequenced genes from a creature unknown to science, which they named *Homo sapiens cognatus*. The purpose of this project was to use the newly acquired skills of [gene-act.org](#) to test the claims of this article. A supplemental sequence titled Amel_X from [www.sasquatchgenomeproject.org](#) was aligned using BLAST and the multiple sequence alignments and phylogenetic trees were constructed comparing the sequence to other primates, domesticated mammals and North American mammals to determine the source of the sequence. The sequence appears to be from a rodent and not from a primate. The possibility that the sequence is an olfactory receptor must also be explored.

Introduction

On February 13, 2013, Dr. Melba Ketcham of the Sasquatch genome project ([sasquatchgenomeproject.org](#)) and DNA Diagnostics, Inc. published her 5 year study on the DNA from a bipedal primate called Sasquatch or "Big Foot." The article titled "Novel North American Hominins, Next Generation Sequencing of Three Whole Genomes and Associated Studies" was published in a new "peer-reviewed" journal called "DeNova: Accelerating Science" ([www.denovojournal.com](#)). According to the forty-one page document:

"One hundred-eleven samples of blood, tissue, hair, and other types of specimens were studied, characterized and hypothesized to be obtained from elusive hominins in North America commonly referred to as Sasquatch. DNA was extracted from the samples and Sanger sequenced by an Illumina HiSeq 2000 "next generation sequencer." Dr. Ketcham and her team concluded that the sequences were from a bipedal primate unknown to science. The scientific name *Homo sapiens cognatus* ("Blood relative of the wise people") was submitted to ZooBank, the International Commission on Zoological Nomenclature and the application was accepted.

The purpose of this project is to determine if sequence Amel_X came from an unknown hominin, *Homo sapiens cognatus*, modern human *Homo sapiens sapiens* or entire different organism. Due to the fact that genes are highly conserved and that Dr. Ketcham argues that Sasquatch is a member of our genus and species, it will be almost impossible to determine if highly significant sequences came from our subspecies (*sapiens*) or the proposed Sasquatch subspecies (*cognatus*).



"Sasquatch" from the famous 1967 Patterson-Gimlin film.
Source: <https://aeon.co/ideas/why-sasquatch-and-other-crypto-beasts-haunt-our-imaginationsc>

Methods

Websites that were used:

- 1) Sasquatch genome Project-Supplemental raw data http://sasquatchgenomeproject.org/sasquatch_genome_project_003.htm to obtain sequences for testing.
- 2) EXPASY <http://web.expasy.org/translate/> to obtain 6 possible reading frame translation for sequences.
- 3) BLAST <https://blast.ncbi.nlm.nih.gov/Blast.cgi>
- 4) UNIPROT: <http://www.uniprot.org/> to find comparable primate, domesticated and North American mammals sequences.
- 5) T-COFFEE <http://www.ebi.ac.uk/Tools/msa/tcoffee/> to construct multiple sequence alignments and Phylogenetic Trees.

Figure 1: Raw Nucleotide Sequence of Reported Sasquatch DNA titled AMEL_X

```
GCAGGGGGCCGATGTGAGACTCGATCCTGGGACTCCAGGATC  
ACACTCTGGATCAAAGGCAGGTGCTAACTGTATGAACCACCCAG  
GGATCCCTAGAGAGCACTTCTGAATTGAAAGGATTATTTGTT  
TATTCCTATCCCCCTCTTCACCCAGAAAAGGATTATAGCAGTC  
TTGGACAGC
```

http://sasquatchgenomeproject.org/sasquatch_genome_project_003.htm

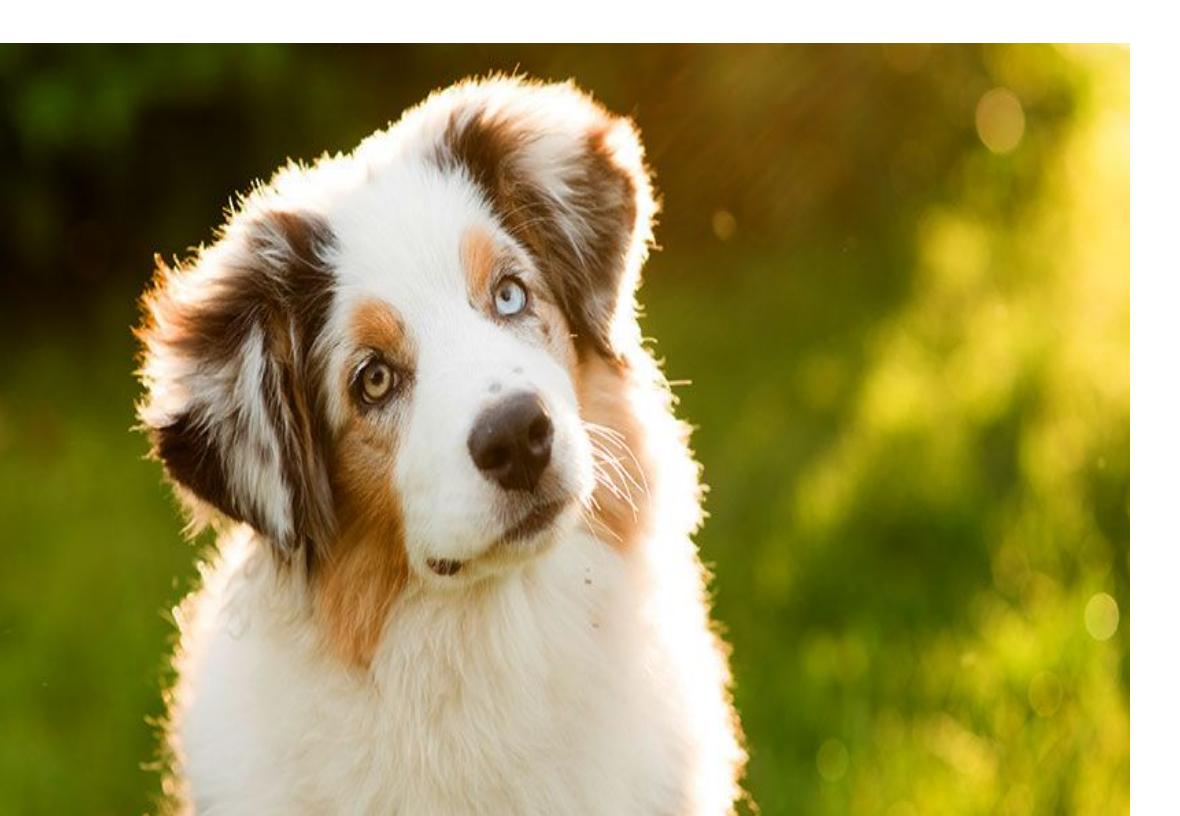
Results

The fifth reading frame of the Amel_X sequence is shown below.

```
>Sasquatch AMEL_X Reading Frame 5  
AVQRLL*SFSG*REGINKQI*SLQFRKCSLGIPGWFLSPLA  
FDPECDPGVPGSSLTSG PLX
```

olfactory receptor OR4137 [Canis lupus familiaris]
Sequence ID: [AEN80227_1](https://www.ncbi.nlm.nih.gov/blast/blast.cgi?text=AEN80227_1) Length: 358 Number of Matches: 1
Range 1: 301 to 334 GenPept Graphics
Score Expect Method Identities Positives Gaps
47.0 bits(110) 2e-04 Compositional matrix adjust. 24/34(71%) 24/34(70%) 0/34(0%)
Query 27 RKCSLGIPWFLSPLA FDPEDPGVPGSSLTSG 60
Subj 301 RKCSLGIPWFLSPLA FDPEDPGVPGSSLTSG 334

Figure 2: As shown in the first BLAST hit, there are many gaps in the alignment, which starts at position 27 of a *Canis lupus familiaris* olfactory receptor. The result is significant at 2e-04. The isn't very conclusive evidence, that Sasquatch is a primate.



Source: www.cesarsway.com/dog-behavior

Figure 3: *Canis lupus familiaris* is the scientific name of the domesticated dog, which does not resemble eye-witness accounts of Sasquatch, see left.

Comparison of AMEL_X gene in "Sasquatch" to AMEL_X gene in other primates using Uniprot.org.

Baboon 0.00462
Macaque 0.0005
Sasquatch 0.71582
Gorilla 0.00022
Chimp 0
Human 0

Figure 4: Phylogenetic Tree of a T-Coffee comparing Sasquatch gene with AMEL-X gene from other primates.. Sasquatch is on the same branch with macaques and baboons. Dr. Ketcham argues that Sasquatch is in the genus *Homo*.

Comparison of AMEL_X gene in "Sasquatch" to AMEL_X gene in human and domesticated farm animals using Uniprot.org.

Cat 0.01166
Dog -0.00205
Horse 0.0403
Sasquatch 0.71408
Human 0.05126
Cow -0.01137
sheep 0.03436
Pig 0.06081

Figure 5: Phylogenetic Tree of a T-Coffee comparing Sasquatch gene with AMEL-X gene from farm animals that may be found in North America. Sasquatch is on the same branch with humans and horses.

Comparison of AMEL_X gene in "Sasquatch" to AMEL_X gene in human and woodland animals using Uniprot.org.

Bear 0.03737
Wolf 0.01818
bat 0.02435
Horse 0.04765
Mouse 0
Rat 0
Sasquatch 0.63034
Human 0.03765
opossum 0.17524

Figure 6: Phylogenetic Tree of a T-Coffee comparing Sasquatch gene with AMEL-X gene from woodland that may be found in North America. Sasquatch is on the same branch with rats and mice.



The AMEL_X gene found in "Sasquatch" is most like the AMEL_X gene found in rodents, such as the house mouse (*Mus musculus*) and rat (*Rattus rattus*), than a human or a primate, so this sequence does not seem to be any type of sasquatch hair.

Photo souce:
www.orkin.com/rodents/deer-mice/what-do-deer-mice-look-like/
www.rentokil.com/rodents/rat-vs-mouse/

Baboon 0.00462
Horse 0.07677
Mouse 0
Rat 0
Sasquatch 0.69169
Human 0.00485
Macaque 0.00029

Figure 7: The results of the phylogenetic tree shown above shows that the sasquatch Amel_X sequence is more closely associated with rodents then human DNA.

Multiple Sequence Alignment for AMEL_X for Mouse, Rat and "Sasquatch". There are many gaps.

Figure 8: Multiple Sequence Alignment for AMEL_X for Mouse, Rat and "Sasquatch". There are many gaps.

Conclusion

As the results show this is not sasquatch DNA. This is more a rodent Amel_X sequence then a sasquatch's sequence. This sequence may not even be a Amel_X sequence as shown in the blast results for the reading frame, it may be a olfactory receptor gene. Our next step would be to see if the Amel_X sequence is even an Amel_X sequence through an investigation. This is most likely a an olfactory receptor OR4137, but UNIPROT only has one OR4137, so there is no way to compare.

The next thing we can do is compare the Amel_X sequence with other rodents like beavers, porcupine, nutria, muskrat, etc. With these results also it is hard to say that a Sasquatch can be called a *Homo sapiens* because it is too hard to differentiate a *Homo sapiens sapiens* to a *Homo sapiens congnatus*. This is why there is a problem when comparing humans to Sasquatches.

References

- 1.<http://sasquatchgenomeproject.org/>
- 2.<http://sasquatchgenomeproject.org/linked/novel-north-american-hominins-final-pdf-download.pdf>

Acknowledgments

Supported by an NSF Innovative Technology Experiences for Students and Teachers (ITEST) Award - 1311902

www.buffalo.edu