

An Investigation of reported Sasquatch (*Homo sapiens cognatus*) sequence M16.

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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 M16 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 M16 appears to have more in common with a bonobo chimp than a human. More Research must be done before the existence of a Sasquatch can be documented.

Introduction

On February 13, 2013, Dr. Melba Ketcham of the Sasquatch genome project (sasquatchgenomeproject.org/) and DNA Diagnostics, Inc. published her 5 year study 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 "DeNovo: 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 a 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.

What Are We Going To Do Differently?

The purpose of this project is to determine if sequence M16 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*).

Figure 1: Sketch of what Sasquatch (*Homo sapiens cognatus*) is suppose to look like. (Source: <http://cryptidz.wikia.com/wiki/Sasquatch> <http://cryptidz.wikia.com/wiki/Sasquatch>).



Methods Used

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.

Raw Nucleotide Sequence for Sasquatch Supplemental M16

```
TTTTAAGTGAATAAACTTTAAACAA-
ATACCTCCCTCGTGGCAGCAGTCTACAGTGTGGCAGGAAATGT-
GATCACATCCATCTCTGGGCTTAAGTACCTGAGGTCAGACAGA-
CAAGCTGATGACCACCCTCCATAGCCGACCC-
CATTGTGTCGGCTGTATTATCCCAATGAGTTAAAGCAATCGGGT
ATGTTGTGGGGTTCACGGCTCCCTGGAAGTCTGAGGTT-
CTGT
```

Source: http://sasquatchgenomeproject.org/sasquatch_genome_project_003.htm

Results

Homo sapiens BAC clone CTB-132J19 from 7, complete sequence
Sequence ID: [AC005163.3](#) Length: 9161 Number of Matches: 2

Score	Expect	Identities	Gaps	Strand
228 bits(123)	6e-56	123/123(100%)	0/123(0%)	Plus/Minus

Range 1: 5067 to 5189 GenBank Graphics

Query 113 ACAAGCTGATGACACCCCTCCATAGCCGACCCCAATTTTCCCGCTGTATTATCCCAAT 172
Sbjct 5189 ACAAGCTGATGACACCCCTCCATAGCCGACCCCAATTTTCCCGCTGTATTATCCCAAT 5130

Query 173 GAGTTTAAAGCAATCGGGTATGTTGTGGGTCACGGCTCCCTGGAAGTCTGAGGTTTC 232
Sbjct 5129 GAGTTTAAAGCAATCGGGTATGTTGTGGGTCACGGCTCCCTGGAAGTCTGAGGTTTC 5070

Query 233 TGT 235
Sbjct 5069 TGT 5067

Figure 2: Result of BLASTN for sequence M16 . Top Hit (6e-15) is from a Human (*Homo sapiens*) BAC clone. BAC stands for bacterial artificial chromosome. BAC clones are used to sequence genomes. A short piece of the organism's DNA is amplified as an insert in BACs, and then sequenced. This result offers no clue as to function.

TPA_exp: Homo sapiens myosin heavy chain (MYH16) pseudogene, complete sequence
Sequence ID: [BK001410.1](#) Length: 83303 Number of Matches: 2

Score	Expect	Identities	Gaps	Strand
228 bits(123)	6e-56	123/123(100%)	0/123(0%)	Plus/Plus

Range 1: 36308 to 36430 GenBank Graphics

Query 113 ACAAGCTGATGACACCCCTCCATAGCCGACCCCAATTTTCCCGCTGTATTATCCCAAT 172
Sbjct 36308 ACAAGCTGATGACACCCCTCCATAGCCGACCCCAATTTTCCCGCTGTATTATCCCAAT 36367

Query 173 GAGTTTAAAGCAATCGGGTATGTTGTGGGTCACGGCTCCCTGGAAGTCTGAGGTTTC 232
Sbjct 36368 GAGTTTAAAGCAATCGGGTATGTTGTGGGTCACGGCTCCCTGGAAGTCTGAGGTTTC 36427

Query 233 TGT 235
Sbjct 36428 TGT 36430

Figure 3: Another Result of BLASTN for sequence M16 . Top Hit (6e-56) is also from a Human (*Homo sapiens*) This time it is a myosin heavy chain (MYH16) pseudogene. Pseudogenes are segments of DNA that have lost some functionality. (<https://en.wikipedia.org/wiki/Pseudogene>). Myosin proteins are related to muscle contraction (<https://en.wikipedia.org/wiki/Myosin>). This result offers clues to M16's function.

Results continued.

How does the Sequence compare to other Primates?

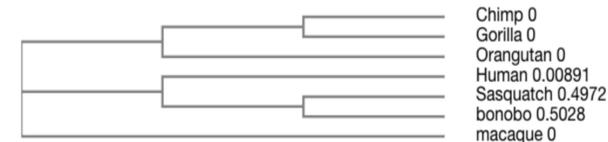


Figure 4: Phylogenetic tree from T-COFFEE of M16 or MYH16 DNA sequences from Primates taken from Uniprot.org. The Sasquatch sequenced is on the same branch as bonobo (Pan paniscus) and on a separate branch than humans. This means that Dr. Ketcham's theory may be wrong.

How does the Sequence compare to other North American Mammals found on Uniprot.org?

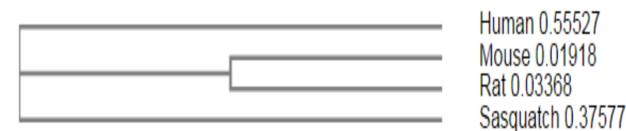


Figure 4: Phylogenetic tree from T-COFFEE of M16 or MYH16 DNA sequences from two Mammals found in North America taken from Uniprot.org. The Sasquatch sequence is on its own branch far from humans.



How does the Sequence compare to Domesticated Mammals found on Uniprot.org?

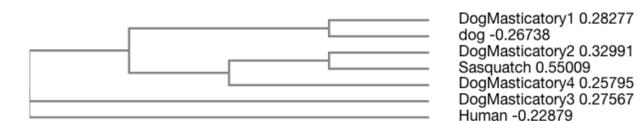


Figure 4: Phylogenetic tree from T-cofee of M16 or MYH16 DNA sequences from Sasquatch, humans, and dog. The Sasquatch sequence is on a branch with a fragment of a Dog masticatory (chewing) myosin protein sequence > Masticatory myosin heavy chain 16 (Fragment) OS=Canis lupus familiaris RKLAARLQEAEEETAEAAQARAASLEKNKQRLQAEVEDLTIDLEK DLTIDLEK (<http://www.uniprot.org/uniprot/Q6RY93.fasta>). The Human sequence is on its own branch.

Can you fit a nice dog photo here? Like your mouse to fill the white space.

How does the M16 Sequence compare to Human, Bonobo, and Dog Masticatory Protein?

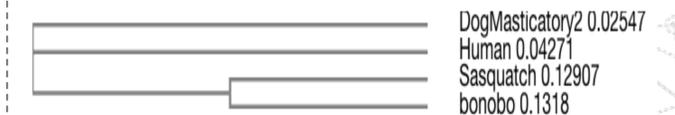


Figure 5: Phylogenetic tree from T-COFFEE of M16 or MYH16 for Human, bonobo, "Sasquatch", and Dog Masticatory Protein. Sasquatch is on the same branch as the bonobo.

masticatory myosin heavy chain, partial [Pan paniscus]
Sequence ID: [AAQ89688.1](#) Length: 29 Number of Matches: 1

Score	Expect	Method	Identities	Positives	Gaps
39.3 bits(90)	2e-06	Compositional matrix adjust.	16/17(94%)	16/17(94%)	0/17(0%)

Range 1: 13 to 29 GenPep Graphics

Query 10 AAPHFVRCIIPNEFKQS 26
Sbjct 13 TAPHFVRCIIPNEFKQS 29

Figure 6 : BLAST of Sasquatch Sequence M16 versus the genome of bonobo (Pan paniscus). E-value - 2e-06. Masticatory Myosin heavy chain Protein, partial.

Conclusion

The Top BLAST Hit for the Nucleotide sequence was a BAC clone. The first hit that offered a clue as to function was a M16, a myosin heavy chain. M16 from other primates were compared using a phylogenetic tree. It discovered that our sequence is closer related to a bonobo chimp (*Pan paniscus*) than to Sasquatch (*Homo sapiens cognatus*). How did Dr. Malba Ketcham and her team find something resembling Bonobo DNA in the forest of North America. Bonobos originate from Africa. Further research must be done before we can make any conclusions about "Sasquatch."

References

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

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