Research on a Reported Sasquatch (Homo sapien cognatus) gene HAR1

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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 titled HAR1 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. Ant many tests, the sequence is more like a carnivire, such as a mink (Neovison) than a primate.....

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 HiSeg 2000 "next generation sequencer." Dr.

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 cagnatus* ("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 HAR 1 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 in 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).

Methods

Websites that were used:

- Sasquatch genome Project-Supplmental raw data http://sasquatch.genomeproject.org/sasquatch.genomepr
- 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
- 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 HAR1

ATCTGAAATGTGAGACCCAGGGAAAGAGAATGATATTCTACCAAATAACAGGTCTGTAATCT

TTAAAAACTGGTCGTAAAGGTCAGGGAAAGGCGGTGGAACGGTTT CAGATCACGGAGACTAACGAGGCTTGAGTGGTTGAACCGGACCCT CTCCGTGGGGAGGACG

GGCCGCTCCCGAGTGGGTGTGAGGACTGGCCCGCCGCACAGTAA
CA AGCTACCTGCCCGCTCCTGGTGGCCGCTTAGGTGGCATA

Results

Homo sapiens 3 BAC RP11-788A4 (Roswell Park Cancer Institute Human BAC Library) complete sequence

Score		Expect	Identities	Gaps	Strand
57.2	bits(62)	9e-06	70/93(75%)	2/93(2%)	Plus/Minus
Query	32	GATATTCTACCAAATAA	CAGGECTUTAATCTTTA	AAAAC-TGGTCGTAAAGGT	DAGOGAA 90
Sbjet	94306	GACATTCTACAMATAA	CTGGCCTRTAATCTTAA	AGAMTRYCOTCATGAAACTY	34000AA 94247
Query	91	AGCCCCTGGAACGCTTT	CAGATCACOGAGACTA	123	
Dites	94246	A-GAGTINGAAACTETT	COGATCABABAGECTA	94215	

Figure 1: Top BLASTn Result for HAR1. BLASTN produced no significant results. This result is a Human (Homo sapiens) BAC. Score 57.2. e-value =9e-06. BAC stands for bacterial artificial chromosome. No function was given.

Homo sapiens ubiquitin specific peptidase 9, X-linked (USP9X), RefSeqGene on chromosome X Sequence ID: NG_012547.1 Length: 157945 Number of Matches: 1

Score 48.2 bits(52)		Expect	Identities	Gaps	Strand Plus/Minus			
		0.005	74/103(72%)	6/103(5%)				
Query	28	GARTGATATTCTACCAAATAACAGGTCTGTAATCTTTAAAAACTGGTCGTAAAGGTCA 85						
Sbjot	93870	GAAGGACATTCTAT-AATTAACTGGCCTGTAATCTTTAAGAGTCAAGGTCATGAAGGTCA 93812						
	86	COCANAGGCGGTGGAA	COCTTTCAGATCACGGAGAC	TAACGAG 128				
Query								

Figure 2: Another BLASTn Result for HAR1. This results i s ubiquitin specific peptidase. Score 46.2. e-value 0.005, which is not significant, but gives a place to start. HAR1 stands for Human accelerated regions. It is found on chromosome 20 and is found between 2 non-coding RNA regions (en.m.wikipedia.org). Ubiquitin is a small protein that performs many functions.



Figure 3: Picture of Ubiquitin. (Source: en.m.wikipedia.org/wiki/Ubiquit

HAR1 Sequence compared to USP9X in other primates



Figure 4: Phylogenetic tree from T-COFFEE of HAR_1 from primates. The sasquatch is on the same branch as the macaque, which means Dr.Ketcham may be wrong. Sasqutch should be on the branch with Chimps and Humans.

HAR1 Sequence compared to USP9X in Domesticated animals and 4 other primates

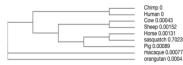


Figure 4: Phylogenetic tree from T-COFFEE of sequence HAR_1 for a human, chimpanzee, orangutan, macaque and four farm animals.. The sasquatch is on the same branch as the horse and pig.

Sequence compared to USP9X in Mammals found in the USA

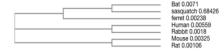


Figure 5: Phylogenic tree from T-COFFEE of USP9X DNA sequences for a few animals found in North America. Sasquatch is found on a branch with bats distant from humans. The human sequence is on the same branch as a rabbit.

What other animals are like a bat?

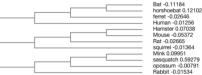


Figure 6: Phylogenetic tree from T-COFFEE of USP9X DNA sequences for two bats, four rodents, two carnivores, human, a lagomorph, and a marsupial. Sasquatch is next to a mink. Sasquatch is no longer on the same branch as a bat.

What if you add in another carnivore like a cat?

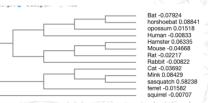


Figure 7: Phylogenetic tree from T-COFFEE of USP9X DNA sequences for Figure 6 plus a cat (felis domesticus). The sasquatch sequence is still next to the mink, but on the same branch as the cat.



Figure 8 : The American mink (Neovison vison). Source: pixgood.com.

Conclusion

According to the phylogenetic trees, there no direct correlations from sasquatch to any of the other tested organisms. The sample that was tested, was more closely correlated to the hair of a carnivore like a mink than any primate.

Dr. Melba Ketchum



http://midnightinthedesert.com/melba-ketchum/

References

http://satquatchgenomeproject.org/ http://sasquatchgenomeproject.org/linked/novel-north-americanhominins-final-pdf-download.pdf

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