

Testing a Sasquatch's (*Homo sapiens cognatus*) gene AMEL_Y.

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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](http://www.ncbi.nlm.nih.gov/BLAST) to test the claims of this article. A supplemental sequence titled Amel_Y 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. (Add one or more sentences from your conclusion here).

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 "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.

The purpose of this project is to determine if sequence Amel_Y 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 may look like. (Source: incolors.club)

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.

Results

>Amel_Y, Exon 2, Sequence for 25-26
AGTAAAGATGAAATGTGCCGCTGTGAGCATGTGTGCATGCCAAGAG
GAGAAAGAAGCTGGATGGCTGGGATGACTGTAGCCTCTCCCATGA
CTTCACGGAGAGATAAAGTTGAGCAGGTGTCTGGGGAAAAAAAAT
TAAACTTCTGATACTAATAAGGAAGAGAGAGAAAAAGAC
TGAGCCATCACGGTCTTATTACAGACTTGAATCTCAGTGTCTGT
AAGCCAAGGAGGGTGACCAGATGAGACAAATGGCTTTTCTTTGGA
ATTACTGAGTAGTTAGAAGTTGACAAAACTGGATTTCTTCCAAG
GTGATGGGTCTGAGCTCAAGCCAGAATCCGCCTGTCTGTTTCATG
CAGCAGCAGGCACCTCGTGGCAGCAGTCTACAGTGTGTTGCACGG
AATGTGACACATCCATCTCTGGGCTTAAGTACCTGAGGTGACAG
AGGCCATTTGTCTGTGGGGTA

Figure 2: Raw Amino acid sequence for Amel_Y gene for "Sasquatch"

PREDICTED: Equus przewalskii mitogen-activated protein kinase kinase kinase 4 (MAP4K4), transmembrane protein
Sequence ID: XM_008532659.1 Length: 6517 Number of Matches: 1

Score	Expect	Identities	Gaps	Strand
112 bits(58)	1e-20	216/280(77%)	7/280(2%)	Plus/Plus
Query 22	GTGACATGTTGTCATCCAGAGAGAGAAAGAACTGGATGGGATGACTGTAGCCTCT	81		
Sbjct 5336	GTGACACGCTGTGTCATCCAGAGAGAGAAAGAACTGGATGGGATGACTGTAGCCTCT	5395		
Query 82	TCCCAATCCTTACAGAGAGAT-AAAATTGACAGTGTCTGGGAAAAAATAAAT	140		
Sbjct 5396	T-CCACGCTTTAGAGAGAGTAAAGTTGGCAGGTTTCTTGG-AAAAATACTAACT	5453		
Query 141	TCTGATACTAATAAGGAGAGAGAGAAAGAACTGACCCATCAGGCTCTT-CTAT-ACA	197		
Sbjct 5454	TCTGATCAGTGTGAAAAAATAAGGAGAGAGAAAGAACTGACCCATCAGGCTCTT-CTAT-ACA	5513		
Query 198	GACTGAAATCTCAGTGTCTTAAAGCAAGAGGGGAGAC-CAGATGAGCAAAAGGCTTTT	256		
Sbjct 5514	GACTGAAAGCTCAGTGTCTTAAAGCAAGAGGGGAGAC-CAGATGAGCAAAAGGCTTTT	5573		
Query 257	CTTTGGAATTAAGTGTGAACTTGAACCTGACAAAACCTGG	296		
Sbjct 5574	CATTTGGAATTAAGTGTGAACTTGAACCTGACAAAACCTGG	5613		

Figure 3: top BLASTN for Sequence Amel_Y which is a Przewalski's Horse (Equus przewalskii).



Figure 4. Photograph of a Przewalski's Horse, which is not a bipedal primate (Source: <http://www.horsetalk.co.nz/2016/03/09/przewalskis-horse-steppes-russia/>).

```
>SASQUTCH
KMKCAAVSMCACQEEKELDGWDDCSLSHDFTER.S.AGVVWGGKIKL
LILIRKREKRLSHHGLLIQT.ISVSVSQGG.PDETNGFLELLSS.NLTKT
GFPSKVMGLSSSNPPVLFMQQQAPRGSSSLQCLHGM.SHPSLGLSH
LRSDRPFVCGV
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Figure 5: Amino acid sequence of "Sasquatch" AMEL_Y (M4K4).

Sequence is a M4K4 gene conserved in Primates

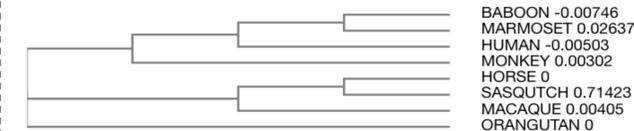


FIGURE 6. Phylogenetic tree made from T-Coffee aligning M4K4 gene for "SASQUTCH", horse, and Primates. Sasquatch sequence is on the same branch as horse M4K4 gene.



Figure 7 This is the ring tailed lemur which is the most closely related to sasquatch according to Figure 6.

<http://cincinnatizo.org/blog/animal/s/ring-tailed-lemur/>

Is AMEL-Y Sequence similar to Primates?

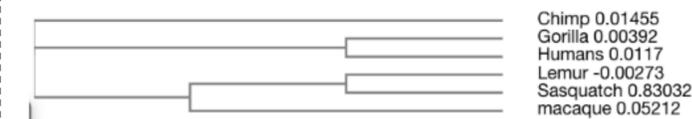


Figure 8: Phylogenetic Tree made from a T-Coffee alignment suspected Sasquatch with other Primates. "Sasquatch" Sequence in on the same branch as a lemur.
What happens if you add a Horse AMEL_Y Sequence to the alignment



Figure 9: Phylogenetic Tree made from a T-Coffee aligning suspected Sasquatch with other Primates with the horse AMEL_Y sequence added in. "Sasquatch" Sequence in on the same branch as horse again.

Could AMEL_Y have come from an indigenous North American mammal that is horse-like?

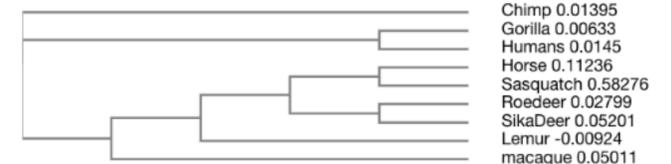


Figure 10: Phylogenetic Tree made from a T-Coffee aligning suspected Sasquatch sequence with other primates, the horse and deer for the AMEL_Y gene. White-tailed deer Was not available on uniprot.org. "Sasquatch" sequence Is still on the branch with horse.



Figure 11 As shown in figure 10 the sasquatch does not have the same DNA as Roedeer.

<http://www.coniferousorest.com/roe-deer.htm>

Conclusion

The first BLAST hit for the nucleotide sequence was a M4K4 gene in a horse. E-value 1e-20 and 112 bits. Dr. Ketcham labels this sequences as an AMEL_Y gene from a human. A Phylogenetic tree of AMEL_Y in Primates showed the sequence is closest to a lemur. A Horse was added to the previous phylogenetic tree and the Sasquatch sequence was on the same branch as the horse. Large North American animals like deer were added to the phylogenetic tree and AMEL_Y was still closest to the horse. The reported Sasquatch sequence is from a horse and not a primate. As a next step, The sequece could be comapred with other horse-like mammals. The M4K4 path could also be explored. The Sasquatch genome project has not gathered enough DNA evidence to show Sasquatch (*Homo sapeins cognatus*). More sequences will be needed in order to show that a large primate lives in the forests of North America.

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

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Subtitle for Academic Research Poster (48x36 inches)

Your names and the names of the people who contributed to this presentation



Introduction

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Methods

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MAURIS ORCI VARIUS ID DIAM

- Sed in risus nibh. In nisl quam, aliquet sed nibh sit amet, faucibus placerat dui.
- Fusce quis augue scelerisque, luctus rum sed, ut in pulvinar urna in eros posuere.

EUISMOD JUSTO VITAE PURUS

- Proin semper ipsum donec semper placerat.
- Finibus quam tempor, vitae consectetur.



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Data Analysis

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- B. Fusce quis augue scelerisque, luctus rum sed, ut dolor. pulvinar urna in eros posuere.
- C. in elementum orci dignissim. Proin semper ipsum finibus quam tempor, vitae consectetur.

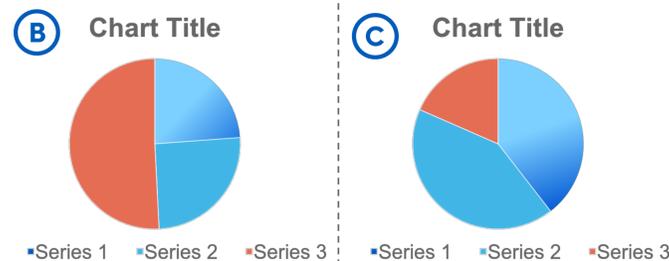
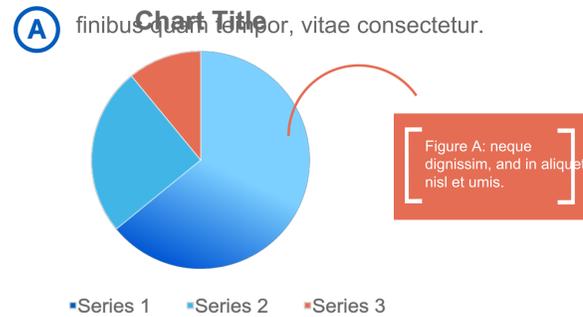
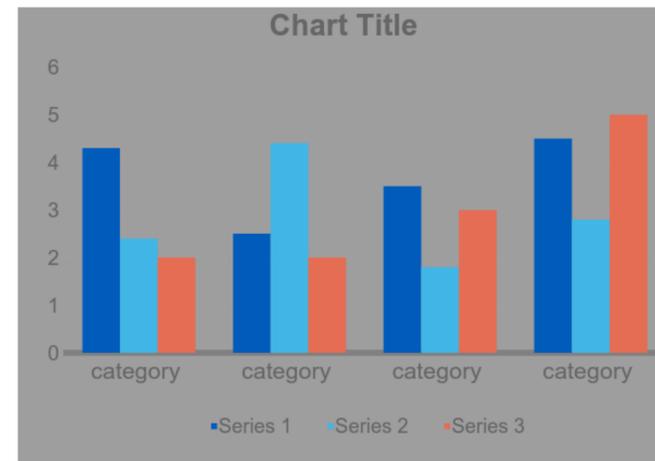


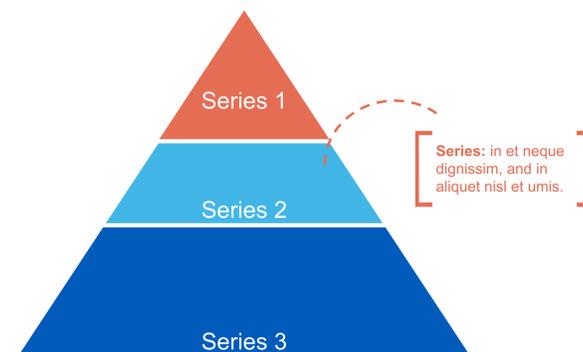
Chart Title			
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4.50	3.11	9.55	1.12
6.15	8.00	6.18	5.65
8.21	2.16	3.11*	7.17
3.00	9.70	10.50	4.45

*Unamcorper efficitur sed in nulla.



Results

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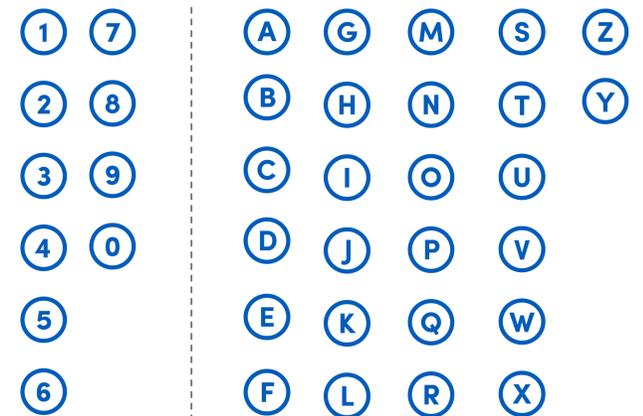
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Conclusion

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- Sed Risus Nibh:** CiIn nisl quam, aliquet sed nibh sit amet, faucibus placerat dui augue scelerisque.
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- Aenean Suscipit:** Proin semper Donec semper ipsum.
- Rutrum Gravida:** Ullamcorper efficitur sed in nulla.

Graphic Elements



References

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