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December 19, 2012

NPG Executive Board
Nature
London, England

Re: Novel North American Hominins, Next Generation Sequencing of Three Whole Genomes and Associated Studies

Dear Executive Board,

I am the corresponding author for the above mentioned manuscript. We (the authors of this manuscript) are extremely unhappy with the ethics of the reviewers chosen by *Nature*. Please consider this letter as a formal appeal of your process on the previous manuscript, 2011-09-11671 and 2011-09-11671A-Z. We are resubmitting a revised manuscript in an effort to vindicate our reputations and also to give *Nature* a chance to rectify the scientific bias and the unethical behavior exhibited by the previous reviewers by giving our manuscript a fair chance at publication. Our manuscript and our reputations were tarnished by the reviewers as follows:

1. Release to the public of the first peer review as well as the fact that our manuscript was at *Nature*. One of the reviewers leaked the original peer review to a "celebrity" that is involved with our subject and it was put on the internet. Since it has not been published in *Nature*, this "celebrity" is now calling our study a "fake" on Twitter and elsewhere. This is highly damaging to our careers and never should have happened. The link states the source of the information as being one of the reviewers. (http://www.cryptomundo.com/bigfoot-report/mm-sasquatch-dna-project/)
2. Reviewers accused our genomes of having contamination even though we went to great lengths to explain how the samples were extracted and screened to rule out contamination. To tell us, as scientists, especially those of us that are forensic scientists, that our samples are contaminated can be likened to accusing us of hoaxing a scientific study or perjuring ourselves in court. As forensic scientists that testify in court, this can be highly damaging and has caused all of the authors tremendous worry and concern. Since we were not given a chance to defend ourselves on the second peer review and our manuscript refused because of these accusations (since all other revisions were verbiage and extremely minor), we contacted Illumina (manufacturers of the HiSeq 2000 next generation sequencing platform that we used to sequence the genomes) in an effort to prove, once and for all, that the three genomes were single source and not contaminated. We spoke with two supervisors specializing in technical support for next generation

sequencing. We asked them if it was possible to prove if there was contamination in a genome or not. They immediately answered "yes"! They told us that the average Q30 score for a genome was 85, but if there was contamination, which would cause the divergent sequences to compete against one another, that a contaminated sample would have a Q30 score of only 40 to 50. A pure, single source sample would have a Q30 score of about 85. When we checked our Q30 scores for the first read, our three genomes had Q30 scores of 92, 88 and 89 respectively. The second read was a little lower 88, 84.25 and 83.66 but still very close to the average of 85. The Q30 is the percent of the reads that have the statistical probability greater than 1:1000 of being correctly sequenced. Therefore, with the help of the scientists at Illumina, it was determined that not only were the sequences from a single source, but the quality of the sequences were far above the average genome sequenced using their platform. I can furnish contact information if you desire it. We attribute the high quality of the genomes to the stringent extraction procedures utilized whereby the DNA was repeatedly purified. This gave us greater than 30X coverage of the three genomes. Furthermore, it supported our original findings of human mitochondrial DNA since the whole genomes yielded human mitochondrial DNA consistent with the original individual mtDNA genome sequencing. The nuDNA findings were also supported in that there was novel primate sequence in the nuDNA. So, the original submission was indeed supported by the next generation sequencing that we included in the revised submission. The three genomes aligned with one another also supporting that all three genomes came from the same species and they were NOT contaminated. Most importantly, the Q30 scores absolutely disproved the reviewers' assumption that the whole genomes were a mixture of human with animal DNA contaminants. The summary of the next generation sequencing generated by the Illumina HiSeq 2000 sequencer is now furnished as Supplementary Data 7 to support this discussion that is now included in our manuscript, Lines 544-558.

3. The peer reviewers failed to even read the manuscript because we were asked for data or criticized for not having data that was already in the manuscript or supplementary information.

Because of the ethical problems listed above, our group is therefore re-submitting this revised manuscript having addressed all of the concerns raised by the reviewers. We are supplying the authors' response to each concern the reviewers had as proof of the bias and in defense of the manuscript. We have corrected all of the verbiage concerns and added the definitive proof that the genomes are not contaminated. We are also available for questions and any further requested revision. We also added a conclusion concerning human hybridization likened to Neanderthal and Denisovan hybridization to satisfy Reviewer 3. If it is preferred that the data speak for itself without theory, we will gladly remove the added conclusion.

We want our findings published in *Nature* since it is perhaps the best journal published and our manuscript is being called the largest scientific find in the last 100 years. If it was not a *Nature* worthy manuscript, it would not have been given a second chance with revision, revision that we completed beyond what was asked of us. Besides fair review, we are asking for expedient treatment of our groundbreaking discovery since we have provided more proof of existence of these hominins than any manuscripts describing other novel species to date. We also have other scientific groups that are headed by "famous" scientists still trying to beat us to publication even though we have by far the most data. We know our manuscript is worthy of publication because we have had

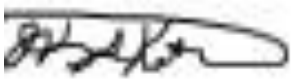
private peer review that was positive as well as your Reviewer #1. We just hope *Nature* is brave enough to do what we all know is right and that is publishing this manuscript. We would also note that a new monkey was found in Africa and published recently (PLOS One: Lesula paper) with only 6.8Kb of sequence. We have 20 samples with 16.5 Kb of mtDNA and 10 more with partial sequence but enough to obtain haplotypes with most of them coming from non-human hair yielding human sequence. This includes hair from 26, the first whole genome sample. We have three whole genomes comprising millions of reads and greater than 30X coverage. We have 2.7 million bases aligned to human chromosome 11 that are novel primate which is no small feat considering the sequence is novel and therefore difficult to align. That is not counting all of the other disciplines involved in our manuscript including forensic hair analysis, histopathology, forensics and electron microscopy. It has been stated that extraordinary claims require extraordinary proof. We have provided more than enough extraordinary proof. We even have high definition video of the donor of sample 37 sleeping in the forest and breathing at 6 breaths per minute (Supplementary Video 1). This sample was part of a field research study overseen by a PhD in wildlife biology so we are certain of the source of this sample and the video attached to it. We have a full facial video of her also that will be released after the paper publishes. I could arrange for the Editorial board to view it if they so desire and perhaps a copyright arrangement could be reached so that one frame could be used for the cover of the journal. The face is stunning.

We understand our subject is controversial; however solid scientific methods were used in this study. We are also attaching to this letter an overview of the laboratories utilized in the study to show how the data was produced using blind studies and reproduced and verified by other laboratories (see below).

If there is still any doubt concerning the existence of these hominins, we are also willing to allow a representative from *Nature* to travel here and see these individuals personally, preferably during a full moon to increase lighting since they are primarily nocturnal. Though there is never 100% guarantee that a sighting will occur, if a few (about 3) days are allowed, we predict that the chances of seeing one of these hominins approach 99%. So far, everyone that we have invited has had an experience, including myself and some of the co-authors. Seeing is believing and that is why we offer this opportunity. We will do whatever is necessary to support our manuscript.

Thank you in advance for fair unbiased treatment of our manuscript and for accepting it in its revised format.

Kind regards,



Dr. Melba S. Ketchum
Corresponding author

Table of Laboratories Participating in Study

#	Laboratory	Type of Testing	Paid	Authorship	Blind Study
1	North Lousiana Criminalistics Laboratory,	Forensic DNA Extraction and DNA	No	Yes	No

	Shreveport LA	quantification			
2	DNA Diagnostics, Nacogdoches, Texas	Forensic Extraction, Species Screening, Preliminary Species Sequencing and STR PP16 genotyping, mtDNA and nuDNA, testing known submitter (human) samples.	No	Yes	No
3	Southwestern Institute of Forensic Sciences, Dallas, TX	Hair analysis	No	Yes	No
4	Family Tree DNA, Houston, TX	mtDNA confirmation and mtDNA whole genome sequencing and haplotype assignment, PP16 STR confirmation testing and YSTR testing. Single locus Amelogenin testing	Yes	No	Yes
5	SeqWright, Houston, TX	mtDNA screening confirmation, sequenced various selected nuDNA loci and confirmation of mtDNA species sequencing, sequencing of various amelogenin exons	Yes	No	Yes
6	Helix Biological Laboratory, Department of Biological Sciences, Wayne State University, Detroit, Michigan	Blind parallel mtDNA testing of certain submitted samples. This work was done previous to our project and only became aware of this testing after we had confirmed mtDNA species ID on the same samples.	No	Yes	No
7	USC, Los Angeles, CA	Whole genome Bead Array SNP analysis	Yes	No	Yes
8	University of Texas at Arlington, Wakeland Laboratory	Next Generation whole genome sequencing and bioinformatics	Yes	No	Yes
9	UNT Center for Human Identification, University of North Texas Health Science Center, Fort Worth, TX	Confirmation of bioinformatics	Yes	Yes	No
10	Texas A&M University, College Station, TX	Electron Microscopy confirmation	Yes	Yes	Yes

11	University of North Carolina, Chapel Hill, North Carolina	Electron Microscopy. The director was unhappy about the blind study and refused recognition in the ms. He did give us the data to use.	No	No	Yes
12	Texas Veterinary Medical Diagnostic Laboratory, Texas A&M University, College Station, TX	Histopathology	Yes	No	No
13	Huguley Pathology Consultants, Ft. Worth, TX	Histopathology confirmation	No	Yes	No