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Essay

DOES MITOCHONDRIAL INTROGRESSION EXPLAIN THE SASQUATCH GENOME PROJECT DATA BETTER THAN A HUMAN HYBRID OF RECENT ORIGIN?

Kevin Leroy Harter

Harrisonburg, VA 22802

ABSTRACT. As Ketchum *et al*. (2013) sum up the findings of the Sasquatch Genome Project (SGP), "DNA analysis showed two distinctly different types of results; the mitochondrial DNA was unambiguously human, while the nuclear DNA was shown to harbor novel structure and sequence." This mito-nuclear discordance, they hypothesize, is the result of Late Pleistocene *Homo sapiens* interbreeding with an unknown species to give rise to a new hominin, the "human hybrid" known as Sasquatch. I discuss problems concerning hybridity and speciation to show that the simpler hypothesis of one unknown primate works better, the one Ketchum *et al*. call the "paternal lineage" of the human-hybrid Sasquatch. The SGP mtDNA data are best explained with concepts of population genetics, as the result of inter-specific asymmetric gene flow resulting in mitochondrial introgression—the replacement of mtDNA in one species with that of a related species. Rare hybridizing of Sapiens females and Sasquatch males could result, many generations later, in total replacement of the Sasquatch mitogenome. The SGP haplogroups are consistent with a known pattern of introgression from a locally established species (Sapiens) into an invading species on the frontier, beyond the normal range of conspecifics (Sasquatch). The direction of gene flow is against the direction of "invasion" and into the range of the colonizing species. Mitochondrial introgression is now recognized among fossil hominins: The Middle Pleistocene Neanderthal mitogenome was completely replaced with Sapiens mtDNA lineages, yet this did not signal the formation of a new species, hybrid or otherwise.

KEYWORDS: gene flow, hybridization, Neanderthals, population genetics, speciation

INTRODUCTION

The authors claim, concerning the findings of the Sasquatch Genome Project (SGP), "the data conclusively proves that the Sasquatch exist as an extant hominin and are a direct maternal descendent of modern humans," but they were not able to convince reviewers for an established scientific journal of this claim, and after several rejections, they chose to self-publish their article, "*Novel North American Hominins: Next Generation Sequencing of Three Whole Genomes and Associated Studies*," as Issue One of *DeNovo* (Ketchum *et al*. 2013). The project should have produced a breakthrough study. It brought to bear the latest in DNA sequencing and analytic technology on some 111 bio-samples supplied by dozens of experienced and knowledgeable field researchers and research groups. Yet the scientific world has not embraced the study's findings. Lead author, Melba S. Ketchum, Doctor of Veterinary Medicine, has decried the prejudices of the Academy and the biases of "mainstream science" against the study. Judging from the peer reviews and authors' responses posted on the SGP website (http://sasquatchgenome-project.org/), the

*correspondence to Kevin L. Harter, email: harterkevin@msn.com.

manuscript may have met with some incredulous reviewers, but that the study was denied a fair hearing seems doubtful. Of course, even a fair hearing does not necessarily arrive at the truth.

A newly discovered extant hominin! Is it possible to make a compelling argument for such an astonishing claim without even one partial type specimen to offer in evidence? Sasquatch Genome Project researchers made a serious and laborious effort to do so, relying on genomic data supposedly representing dozens of individuals (and supporting materials, including video of living specimens in the field) instead of a single Sasquatch cadaver. This approach to the scientific study of Sasquatch is consistent with the SGP assessment of its ontological status as "an indigenous, aboriginal people." So says the "Q & A" portion of the SGP website (part of the answer to "What is Sasquatch?") which also contends (in reply to "Is hunting Sasquatch legal?") "The Sasquatch are people, not animals. They are a hybrid human. Killing one is murder." The article by Ketchum, *et al*. (2013) asserts further that SGP data indicate they are "human hybrids originating from human females," and that these origins date to a surprisingly recent period in the Late Pleistocene. Although I do not agree that the Sasquatch is a human hybrid, and I do not concur that it is a descendant of *H. sapiens,* nor that it is of such recent origin, nevertheless, I do agree with the "no-kill" ethos of the SGP, and I do prefer to regard Sasquatches as people, though not as *a* people. Even so, lack of a type specimen is a basic problem hindering "mainstream" acceptance of the species and reception of the SGP study, as well as preventing a much more informed analysis of Sasquatch nuclear DNA.

The human-hybrid Sasquatch of Ketchum *et al*. (2013), which is a particularly confusing concept for the intended audience of scientific and academic specialists, is itself an attempt to resolve what might be called the central problem of Sasquatch genomics: Instead of one or more unique mitochondrial lineages, which could represent a distinctive Sasquatch mitogenome, why have the most promising research efforts so far turned up, at best, only mitochondrial DNAs which belong to haplogroups already identified with "humans" (Sapiens)? Ketchum *et al*. reason that the Sasquatch must be a "human hybrid," or maybe a hybrid species. Critics suggest, instead, that the study samples are merely human, and cynics claim all too readily that the fictive nature of the Sasquatch is hereby proven, again. But this problem has an alternate, possibly better solution.

With this essay I will explain how the SGP mitochondrial DNA (mtDNA) data may have been broadly mis-interpreted in a way which dramatically over-states the "human" component of the Sasquatch phylogeny—"human" in the restrictive sense, the sense used by Ketchum *et al*. (2013), in which it refers to Sapiens only. And I will suggest how these data might be re-interpreted as the result of mitochondrial introgression, which is the accumulating effect of mitochondrial gene flow such that, over the course of many generations, the mitogenome of one species is replaced, in whole or in part, with that of a related species which has been acquired through past interbreeding. This explanation is simpler and better in keeping with population genetics, and it better supports the objective reality of Sasquatch—not as a human hybrid, a hybrid species, or a human subspecies, but as an unrecognized extant hominin.

Since the (self-)publication of "*Novel North American Hominins*..." (Ketchum *et al*. 2013), the human-hybrid Sasquatch theory has been extensively debated in the social media universe and promoted in works of vanity-press pseudo-science, but scholarly attention has been mainly limited to a pair of articles (2016, 2016a) by Haskell V Hart, Ph.D., Chemistry. Recently, Dr. Hart has combined the points of his earlier work with an expanded treatment of the SGP analyses and results

in *The Sasquatch Genome Project: A Failed DNA Study* (2020, Kindle Direct Publishing). This book-length, detailed assessment is extremely helpful for anyone who wants to understand the methods of DNA analysis employed by the SGP, and exactly what went wrong or may have gone wrong with these molecular studies. I will refer to Hart (2016, 2020) extensively, especially in Section 1, for a well-informed, independent evaluation of the SGP study and its findings. My subsequent treatment, which builds on Hart's expert treatment of the molecular data, is focused primarily on issues of sociobiology and population genetics.

To fans of the human-hybrid young Sasquatch, I say: Take heart! The mitochondrial introgression hypothesis does not deny or disprove the existence of Sasquatch, nor does it deny the history of hybridizing which the SGP data indicate. Instead, it provides a more plausible explanation for the SGP data as evidence of an unrecognized hominin species—a conclusion to be celebrated, because it affords Sasquatch the dignity of independent taxonomic status and an older phylogeny which is not bounded by or derived from *H. sapiens*, as Ketchum *et al*. (2013) have claimed.

1. MITOCHONDRIAL MYSTERY OR MISTAKE?

Mitochondria are descended from bacteria, single-celled organisms with their own DNA but without nuclei (prokaryotes) which long ago took up symbiotic residence in the cytoplasm of nucleated cells (eukaryotes). Mitochondria reproduce asexually, independently of the rest of the cell, and they are transmitted to the next generation of the larger organism (their "host" species) without changes in the mtDNA, exclusively through the female line, as fully functional organelles in the cytoplasm of the egg. During the lifetime of the individual organism or specimen, its mitochondrial genome does not change, except perhaps for the occurrence of a new mutation, which is rare from the point of view of an individual. However, the mitogenome of a species does change, slowly and incrementally, with the accumulation of new mutations, and it is this process which produces a unique set of mitochondrial lineages for every eukaryotic species. But the mitogenome of a species can also change more substantially and less slowly, via hybridizing and "horizontal" gene flow across the usual boundary between species, through which it is possible to acquire new mitochondrial lineages from other forms in the same genus.

Mitochondrial DNA has been used for decades as the preferred molecular means for the systematic definition and identification of species, and determination of the mitochondrial genotype is standard practice as a first step for identification of an unknown bio-sample. If a sufficiently close match can be identified in a genomic database, it should enable the inference of species for the unknown sample, assuming that contamination, degradation, or other problems have not skewed the results. However, for any species which might have even a slight history of hybridizing or interbreeding (terms which will be used interchangeably here to refer to the reproduction of mating pairs consisting of two distinct species), the likelihood of mitochondrial introgression means that the mtDNA genotype may be misleading, even if it does match a known haplogroup of a recognized species (Liu and Wang *et al*. 2010).

The Sasquatch Genome Project mtDNA data contained surprising results. As Ketchum *et al*. (2013) explain in the abstract:

"The mtDNA whole genome haplotypes obtained were uniformly consistent with modern humans. Of the 20 whole and 10 partial mitochondrial genomes sequenced, 16 diverse haplotypes were found suggesting that these hominins did not originate in a single geographic location."

Under most other circumstances, mtDNA which is so consistent with anatomically modern humans would be taken as an answer to the question of species identity, an answer rendering further investigation un-necessary. But Ketchum *et al.* maintain that Sasquatch DNA consists of a discordant alliance (mito-nuclear discordance) of "human" mtDNA and the nuclear genome of an unknown primate species. Also surprising, and puzzling: The geographic regions associated with 12 of the 16 human mtDNA haplogroups identified by Ketchum *et al.* are incongruous with the distribution of the sample collection sites, all of which are in North America, whereas only four samples match American haplogroups, one each for A and C, and two more for D. A contrasting example, the Caucasian European haplogroup, H, including 7 of its sub-groups, is represented by a total of 12 samples. To complicate matters further, Hart (2016, 2020) has demonstrated, citing additional independent DNA analyses and extensive comparative search (BLAST) results, that the sequencing and identifications of the 3 nuclear genomes (Samples 26, 31, and 140) referenced in the title of Ketchum *et al*. ("…*Next Generation Sequencing of Three Whole Genomes…*") are in fact erroneous. Specifically, those nuclear sequences match better overall with the American black bear (26), an un-mixed Sapiens (31), and a dog of some sort (140), as Hart explains in detail and at length.

To get to the mtDNA results summarized above, SGP researchers began with a much larger number of samples, most of which consisted of one or two strands of hair. A few samples of other kinds (blood, saliva/mucous, skin tissue, trace remains and a toenail) were also included for DNA testing, The hair samples were examined by a forensic fiber and hair expert, who removed any which could be positively identified through comparison with reference samples representing most North American mammal species, domestic and wild. The hair samples retained for testing could not be positively identified, but researchers proceeded with high confidence that they were not of Sapiens origin. Although the best of these samples were reserved for nuclear DNA analysis, SGP researchers had great difficulty recovering nuclear sequences of sufficient size from any of the hair samples. The three whole genome nuclear sequences referenced in the title of the paper by Ketchum *et al.* (2013) were recovered from other sample types (blood, mucous, skin tissue) which did not allow for the same phenotypic analysis which was used to evaluate the hair samples, nor could they be treated with the same decontamination procedure applied to the hair samples.

For the first stage of molecular analysis, the SGP researchers made use of two methods of mtDNA sequencing, each of which focuses on a different segment of the mtDNA molecule. As Ketchum *et al*. (2013) explain:

"Universal mitochondrial DNA cytochrome b primers for species determination as well as universal mammalian primers designed for species identification in the hypervariable region 1 were utilized. All 111 screened samples revealed 100% human cytochrome b and hypervariable region 1 sequences with no heteroplasmic bases that would indicate contamination or a mixture. These samples were then sent out to another laboratory for mitochondrial whole genome sequencing."

In the extractions of the samples being tested, universal primers should amplify the DNA of almost any animal species which is present, and universal mammalian primers should amplify that of any mammal species which is present. Notwithstanding the use of these primers, which is in keeping with the later recommendations of Hart (2016, 2020), the authors claim that the mtDNA analysis indicated "100% human" matches for 111 samples.

If Ketchum *et al*. (2013) are correct in their

attribution of these samples to something which is not *H. sapiens*, an unknown primate species, then these molecular analyses could be consistent with a history of mitochondrial introgression from Sapiens into that species. But before developing this scenario further, we should consider a caveat from Hart (2020) who notes that the laboratory work for such sequencing could cost several hundred thousand dollars, and yet these data have not been published:

"There is no proof anywhere of the veracity of the above statement. It is very unlikely to be true. With universal and mammalian primers employed, [53] surely some of these samples would turn out to be animals unless they were so severely contaminated by human handling that there was more human DNA extracted than animal DNA."

The lack of published data does seem strange. That information would presumably include data generated before Dr. Ketchum's conversion from unbelieving skeptic to "knowing" advocate for the human-hybrid Sasquatch.

Nevertheless, to return to my claim, mitochondrial introgression could provide a reasonable, not unlikely explanation for the "human" mtDNA identifications, however many of them are truly valid. The SGP mtDNA data could be exactly what Ketchum *et al*. (2013) claim them to be, a collection of "human" (Sapiens) mitochondrial lineages which have been recovered from purported Sasquatch biosamples, rather than contamination from human handlers, because this is precisely the effect of mitochondrial introgression, replacement of the older mtDNA lineages in one species with those of a closely related species, which have been acquired through hybridizing. The SGP mtDNA results could be consistent, as summarized, with a history of mitochondrial introgression which is recent and "complete" (Stoeckle and Thaler 2018), meaning the older mtDNA lines have been completely replaced with mtDNA derived from Sapiens, leaving no mtDNA which could represent the Sasquatch mitogenome prior to introgression (Irwin and Rubtsov *et al*. 2009). This scenario is sometimes called "mitochondrial capture" (Cortez-Ortiz and Roos *et al*. 2019), and it constitutes a more likely explanation for the SGP mtDNA data than either the appearance of a hybrid species in the Late Pleistocene, or ongoing hybridizing between Sapiens and an unknown primate species in present-day North America.

Many of the SGP samples were consumed entirely with the first phase of mtDNA analysis, especially those consisting of single hairs, and of the 111 samples identified as containing Sapiens mtDNA, only 30 samples (or 29, as corrected below) yielded enough mtDNA for "whole mitochondrial genome sequencing." As Ketchum *et al*. (2013) summarize these results, "All 16 haplotypes from 20 completed whole mitochondrial sequences and 10 partial mitochondrial genomes have indicated 100% homology with human mitochondrial sequences without any significant deviation." If we refer to the chart which contains these data, "Supplementary Data 2 mito mutation chart complete final," posted with the article on the SGP website, we see that it includes, for each sample, the nearest human haplogroup and a name indicating a reference sequence, followed by a list of "extra" mutations, each of which marks a departure from the reference sequence at a precise location on the mtDNA molecule.

The SGP mitochondrial DNA mutation chart itself is somewhat confusing. The last entry in the list of 30 samples is identified as a "human" control sample, and of the remaining 29 field samples, those corresponding to the whole mtDNA sequences are mixed with those samples corresponding to the partial sequences, without labels to distinguish them. Hart (2016, 2020) has reorganized these data and has deduced, based on the mutations listed for each sample, that only 18 samples yielded

whole mtDNA sequences, and 11 others yielded partial sequences. His statistical analysis of these mutations conflicts with the authors' claim, quoted above, of 100% homology with human sequences "without any significant deviation." For the 18 samples yielding whole mtDNA sequences, Hart argues that eight of them "…have '*significant deviation*' from human, i.e., less than 1% probability of occurrence based on extra mutations." Of the samples yielding partial mtDNA sequences, Hart explains:

"…only three of the 11 samples (33, 95, and 168) show a normal pattern of mutations although for the others one extra or one missing mutation does not necessarily mean a *significant deviation*, since a complete sequence was not obtained. However, the frequency of extra mutations (4/11) and ambiguous haplogroups (4/11) in these samples raises suspicions of multiple human contaminations or that the 'human female' hypothesis is flawed."

So, by Hart's reckoning, 13 of the 29 mtDNA genotypes (10 whole and 3 partial sequences) are consistent with regular human haplogroups. Eight more contain enough extra mutations to have less than one percent chance of occurring among Sapiens. And eight others are ambiguously human: closer to Sapiens than anything else—not necessarily wrong, but an inexact match using an incomplete sequence. For these last two groups, the variance from normal Sapiens mtDNA could be attributable to a period of thousands of years during which these mtDNAs replicated themselves in a new context as part of a different hominin species. Some mutations or changes in the mtDNA molecule are more likely to occur than others, depending (in part) on exactly which species the mitochondria inhabit. In this connection, Hart (2020) provides interesting analysis of some of the unusual mutations contained within the SGP mitochondrial data. He explains, in summary:

"The mtDNA sequences of five samples (24, 26, 28, 29, and 138) which have in common the same rare human mutations common in other primates may actually be from Sasquatch (Chapter 16). Additional sample collection in these areas of CA, NM, and BC may be fruitful. If new mtDNA sequences show the same mutations, a case could be made that it is an unknown, but very human-like primate."

These five mtDNA sequences might be regarded as the most likely of the SGP data to represent authentic Sasquatch specimens. The other mtDNA samples could be authentic also, but the rare mutations in this group of five provide some additional evidence of a changed context for those Sapiens mitochondrial lineages. We will consider Dr. Hart's revisions to the list of SGP haplogroups in Section 8.

Regarding the SGP molecular findings in Ketchum *et al*. (2013), the *Nature* referees, writing in 2012, without access to the sequencing data (which was omitted from the original submission) were inclined to interpret the human mtDNA as evidence of ordinary, contemporary *H. sapiens*, and they blamed degraded or contaminated nuclear DNA for those results which appear to be non-human. As point 2 of the first-round peer review from *Nature* Referee 3 explains:

"The nuDNA, however, is too poor quality for amplifying the attempted sequence length and creating PCR artifacts. It makes good sense even for the hair sharft samples that by nature has degraded DNA (even when taken "fresh"). I am sorry but this appears to be a much more straightforward scenario than having a previously undetected (by science) hominin subspecies running around in the forest mating with Caucasian woman. [*sic*]"

The mention of Caucasian women refers to the numerous samples representing the H family

of human haplogroups among the SGP mtDNA identifications (12 of the 29 samples, representing 7 of the 16 total haplogroups), and which seem to conflict most profoundly with the geographic distribution of sample collection sites. For *Nature* Referee 3, degraded nuclear DNA of ordinary Sapiens, mistakenly interpreted as mito-nuclear discordance, would be easier to accept as explanation of the SGP data than widespread, ongoing interbreeding of Sapiens and an unrecognized primate. *Nature* Referees 2 and 4 express broadly similar concerns, but also suggest a possible role for contamination, including "background contamination" from "previous primate sequencing projects."

Ketchum *et al*. (2013) refute the suggestion of primate contamination with the assertion that the next-generation sequencing was done at laboratories that do not work with non-human primates. The authors also remind the reviewers who refer to problems arising from ancient DNA that the SGP has been working exclusively with "fresh" DNA (which may be degraded, nonetheless) and without the use of any special techniques for the recovery of ancient DNA. Ketchum *et al*. address the issues of contamination and degradation at length in their article, and in the detailed Materials and Methods supplement ("Supplementary Materials and Methods S1," available for download with the article on the SGP website), and in the authors' responses to peer reviews. The authors express great confidence in the quality and purity of their DNA extractions, citing their adherence to forensic methods, their use of universal primers, the sharp separation of components in chromatographic yield gels, and "Q30 scores" indicating single-source amplifications, a new proprietary technique which particularly impressed Referee B. As summarized in the Discussion section of "*Novel North American Hominins…*":

"In all cases, as demonstrated by clean sequences without false heteroplasmic bases denoting mixture or contamination and single source profiles with the PowerPlex® 16 amplification kit, no evidence was obtained that the DNA extracted from collectors or scientists or any other secondary source was present as a contaminant in any of the samples."

Ketchum *et al*. (2013) had no indications that a "secondary source" of DNA was present in their sample extractions; however, such assurances of purity can do nothing to correct mistakes in the assembly of sequencing data, nor can they correct errors in matching the assembled sequences with known species in genomic databases. And as Hart (2020) explains, errors in assembly and identification are the main problems behind the faulty results of the SGP nuclear DNA analyses: the use of a human reference sequence in the assembly of "Sasquatch" nuclear DNA, which biased the results toward hominin sequences; over-reliance on highly conserved nuclear sequences, which do not vary enough between species for exclusive identifications; and over-reliance on the NCBI [National Center for Biotechnology Information, part of the National Institutes of Health] nucleotide database, which, at the time, did not adequately represent likely species such as the black bear, but which over-represented certain rare species like the giant panda.

Sasquatch Genome Project researchers were aware of several earlier efforts to identify Sasquatch DNA, including the identifications of exclusively human haplogroups in the mtDNA results of these other studies:

"It should be emphasized that there have been attempts by other groups around the world to obtain mitochondrial DNA sequence from Sasquatch (aka Yeti, Bigfoot) with remarkably consistent outcomes. Hence, the mitochondrial DNA findings have been unvarying between samples in this study and between seven different laboratories, four of which were independent of this project and predated it."

(Ketchum *et al*. 2013.)

The earlier efforts had been stymied by the "human" mtDNA results, which suggested contamination and error, and failed to provide what everyone would have recognized as success: mtDNA sequences which did not match any known sources, and which could be identified as something new and distinct. And it appears that Ketchum *et al*. have added to the body of ambiguous evidence which suggests that bio-samples which are attributed to Sasquatch nevertheless often (always?) contain mtDNA which matches closely with historical patterns of Sapiens mtDNA. Peer reviews dismissed the SGP mtDNA data as merely human, but Ketchum *et al*. (2013), knowing of the mtDNA results of earlier studies, have maintained that their mtDNA data accurately represent a non-human primate. However, in the steadfast defense of their findings against the dismissive judgments of "mainstream" science, Ketchum *et al*. have never presented the SGP data in a neutral way, but have always advanced a problematic interpretation of their own, the human-hybrid young Sasquatch.

2. HYBRIDITY AND SPECIES

The remarks of *Nature* Referee 3 (quoted above, page 82) highlight the ambiguity and confusion surrounding the human-hybrid Sasquatch concept: Does it refer to interbreeding in the distant past, or interbreeding in the present? Or both? "Hybrid," when used as a noun, as in "human hybrid," usually signifies a hybrid specimen, the offspring of parents of different species, always a product of contemporary inter-specific reproduction. "Hybrid species," in which "hybrid" is used as an adjective, signifies a species of hybrid origins—not unheard of in plants, but a rare occurrence in the Animal Kingdom, more so among vertebrates and mammals, and not easily defined. If it adheres to the meaning of "species" as a biological concept, a hybrid species should be inter-generationally stable in form without ongoing interbreeding. It may be of hybrid origins, but a hybrid species is not a hybrid any longer, and for this reason zoologists often regard "hybrid species" as a contradiction in terms (Khidas 2014).

Although they are common in nature, hybrids (hybrid specimens) are not afforded independent taxonomic status because they cannot produce offspring like themselves, if they can reproduce at all. The conditions which create the special properties of first generation (F1) hybrids—un-mixed parents each representing a different species—cannot be duplicated in later generations. "Hybrid vigor," or heterosis, often gives F1 hybrids, of both plant and animal species, increased fertility, size, and resilience, exceeding that of either parent species. But a mix of genetic influences in each of the parents does not produce the same heterotic effects which are possible in F1 specimens. As *Nature* Referee 1 observes, "It is stated throughout the ms that the animal is of hybrid origin. If this is so, it is highly debatable as to whether or not taxonomic novelty is warranted." The non-hybrid, non-human, progenitor species *would* warrant taxonomic novelty, however, and it would make more sense to focus on the identity of this parent species, which must currently exist in significant numbers if its hybrid offspring are as plentiful as the authors claim.

As Ketchum *et al*. (2013) put it in the Conclusions of their article, "DNA analysis showed two distinctly different types of results; the mitochondrial DNA was unambiguously human, while the nuclear DNA was shown to harbor novel structure and sequence." But this assessment of the mtDNA as "unambiguously human" discounts the glaringly ambiguous context. The authors further describe the nuclear DNA as a mosaic containing sequences homologous to humans and other sequences which are suggestive of other primate groups, and then go on to say, "These data clearly support that these hominins exist

as a novel species of primate. The data further suggests that they are human hybrids originating from human females." This last sentence is the mistaken inference seemingly justified by the presence of samples representing 16 human haplogroups within the purported Sasquatch mtDNA. If it is correct to describe the Sasquatch as "human hybrids originating from human females," this would literally mean that all Sasquatches are first generation (F1) hybrid specimens which have been born to Sapiens mothers, and that interbreeding has been recently ongoing near all of the sample collection sites. And this scenario does not seem plausible, especially because we do not have credible stories of any of the hundreds or thousands of Sapiens women who must have been recently involved. Nor is this "human hybrid" claim consistent with the previous sentence, which refers to the Sasquatch as a species of hominin. In fact, Ketchum *et al*. go on to propose formal recognition of the Sasquatch as a subspecies of Sapiens, for which they suggest the name *Homo sapiens cognatus*, the third term meaning "blood relative," in recognition of the kinship between Sapiens and Sasquatch which has been indicated in the mtDNA data.

Thus, Ketchum *et al.* (2013) confer upon the Sasquatch three conflicting levels of taxonomic status: a new hominin species, a subspecies of *H. sapiens*, and a "human hybrid"—not a species or subspecies, but an anomalous specimen. Clearly, the reviewers understand "human hybrid" in the sense of ongoing interbreeding in the present era, but they do not seem to consider this a realistic scenario. And, although Ketchum *et al*. use "hybrid" as a noun in their article but do not use the term "hybrid species," other statements, in the responses to peer reviews and in the "Q & A" section of the SGP website, suggest that "hybrid species" is the intended meaning. For example:

[Part C] "2. How do you know the samples came from Sasquatch and not some other species?

The DNA information provided by the genome clearly indicate a hybrid species of human and unknown hominin. Sasquatch is the only candidate. If it was not Sasquatch, then there is another hairy, hybrid human species living in the wild."

Astonishingly, this answer claims that the human-hybrid Sasquatch is the only possibility for identification of the SGP samples, but it also asserts the necessary existence of an additional unknown hominin parent species. The unjustified implication is that the unknown progenitor species has become extinct, and this I believe to be a mistaken view.

With one of the parent forms unknown, to designate the Sasquatch as a hybrid—whether hybrid specimen or hybrid species—does not seem warranted, nor does the suggestion that it came into being so recently, in the Late Pleistocene, which would make *H. sapiens* 15 to 20 times older, and most other hominin species older still. It is difficult to accept an evolutionary history so different from those of other species which are thought to be close relatives. Why should the Sasquatch be understood as a new species or subspecies rather than the continuation of the unknown, hominin or hominin-like species which existed before it, and which is said to have sired it? Nothing in the SGP data enables an understanding of the differences, or continuities, between the unknown primate parent form and its hybrid offspring or hybridized descendants, and without any such information, the human-hybrid or hybrid species claim is unverifiable and misleading.

As Chapman and Burke explain in their 2007 article, "*Genetic Divergence and Hybrid Speciation*," hybridizing is relatively common in nature, but the appearance of new hybrid animal species is most unusual, in part because it requires the hybrid offspring to reject the society of both parent types and to com-

pete with them:

"Although there are a great number of cases in which two species have come together to form a small number of hybrids, or even a hybrid zone consisting of thousands of hybrid individuals, the number of well-documented cases of hybrid speciation is much smaller, especially for animals (Coyne and Orr 2004). Perhaps the biggest reason for the paucity of hybrid species is the difficulty associated with producing a reproductively isolated hybrid lineage that can escape close competition with its parental taxa."

So, it seems likely that, if the pre-existing unknown primate species had persisted alongside the hybrid individuals, as I believe it did, the hybrids would have been absorbed into that breeding population, and, had they been able to reproduce, their descendants would have returned to the parent form within a few generations. Although present-day matrilineal descendants of those hybrids would possess mtDNA which is consistent with modern *H. sapiens*, this mitochondrial heritage alone would not qualify them as half human—as "human hybrid" implies—or human enough (if human means *H. sapiens*) even to be worth mentioning in the sense of genealogical ancestry. First generation (F1) hybrids would have been, genetically, half *H. sapiens*, but that would have changed quickly in subsequent generations without some superintendent agency to create additional hybrid specimens, bring them together, and enforce reproductive isolation from their parent species.

The pre-existing unknown hominin-like species is a necessary part of any viable hypothesis to explain the SGP mtDNA data, but the additional human-hybrid (or hybrid species, or human subspecies) is superfluous and problematic. The human-hybrid Sasquatch runs afoul of scientific parsimony, which is better served by a simpler hypothesis featuring only one unknown primate, the one that Ketchum *et al*. refer to as the "paternal" source of the human-hybrid Sasquatch. The general picture of the SGP mitochondrial data is perfectly consistent with this simpler hypothesis, in which the pre-existing species that hybridized with ancient Sapiens females was, at that time, prior to any interbreeding, more-or-less what Sasquatch is today.

Some of the peer reviews attempt to unpack the needless complexity of the human-hybrid Sasquatch hypothesis. The first-round review from *Nature* Referee 1 expresses concern about the additional mystery species:

[Referee 1] "I would like to know exactly what is meant by those statements noting that the 'paternal lineage [is] completely unknown', as the authors seems to be introducing a new layer of mystery to their conclusions. It seems radical enough that they are positing a hybrid origin for this putative animal, but are they also invoking the existence of an additional animal that was involved in the proposed hybridization event? This all seems very peculiar and I am not convinced that the evidence presented in this manuscript explains it adequately."

In reply, Ketchum *et al*. re-state the general summary of sequencing results and their flawed reasoning about them which leads to the same conclusion. The "3 whole genomes" mentioned below are the three nuclear whole genome sequences which are referenced in the title of Ketchum *et al*. (2013), Samples 26, 31, and 140:

[Authors' response] **"**By sequencing 3 whole genomes that failed to align with any animal or hominin found in NCBI there is no other conclusion other than that the paternal nuclear DNA origins are unknown… The nuDNA and mtDNA origins of the Sasquatch are discordant, with mtDNA indicating human maternal lineage."

Hart (2016, 2020) disputes the first assertion above, arguing instead that three known and uncontroversial species (bear, Sapiens, and dog) do align with the three SGP nuclear whole genomes. As we will see in later sections, the "discordant" relationship of the nuDNA and mtDNA which is mentioned here, mito-nuclear discordance, is most often attributable to mitochondrial introgression.

Referee A for the *Journal of Advanced Multidisciplinary Exploration in Zoology* (*JAMEZ*) also suggests that the second uncharacterized hominin species increases the difficulty of a challenging thesis:

[Referee A] "1. A difficult two-part thesis is posed that is inadequately substantiated by the analysis presented in the manuscript. Both parts (i.e. Part 1 - previously uncharacterized hominins exist in North America; Part 2 said hominins are the descendants of a putative hybridization event involving an ancient uncharacterized hominin and a modern human). A thesis this complex and counterintuitive requires significantly more in-depth analysis and consideration and should be developed through a series of peer-reviewed publications. Add in the idea that more than one species of hominin may be present in North America and the effort to make a convincing case is multiplied."

In reply, the authors explain that they have removed discussion of regional Sasquatch variants, and have included an alternate hypothesis which does not make use of hybridity. But the authors do not develop this alternative; instead, they retain the original thesis, including the untenable human-hybrid/hybrid species component.

Point 2 of the peer review from *JAMEZ* Referee B (not quoted here) poses concerns similar to those of Referee 1 and Referee A as quoted above, and, in reply, Ketchum *et al*. (2013) dogmatically insist again that the mtDNA data justify the identification as "human," yet the existence and identity of a second unknown primate species is also at issue:

[Authors' response to Referee B, point 2:] "Mitochondrial DNA has been universally utilized to determine species by the scientific community. Since the mtDNA in Sasquatch is not only unequivocally modern human in 100% of the samples included in this study, that places the Sasquatch as human. However, since the nuDNA is novel to a large extent, the speciation of a potential progenitor is what is in question, especially since there are gene sequences that align 100% with human interspersed in the nuclear genome."

The first sentence of this response may explain part of the confusion behind the superfluous secondary unknown primate. Mitochondrial DNA works as a means of species identification because, in theory, all eukaryotic species develop patterns of mutations in their mtDNA which are uniquely characteristic of that single species, and in such a context these distinctive mtDNA sequences define what are called haplogroups. But zero such haplogroups have been identified for Sasquatch; instead, all mtDNA attributed to Sasquatch has so far yielded only sequences belonging to "human" (Sapiens) haplogroups, and therefore it is not possible in this case to infer the identity of species from the mtDNA data.

Exactly this issue is raised in the first-round peer review from Referee 2, as conclusion to point 1:

"Moreover, the fragmentary mtDNA data does not support any unknown hominin lineage, because the haplotype/haplogroup attribution fits well in what is already known of the modern human mtDNA phylogeny."

Nature Referee 3 also makes the same point in the second-round remarks:

"The authors still lack explaining in any convincing way how this 'new species' carries mtDNA genomes identical to those of modern humans only."

However, the possibility of mitochondrial introgression from Sapiens to Sasquatch should satisfy these concerns about how exclusively "human" (Sapiens) mtDNA haplogroups could occur in a non-human primate species.

The assertion of "human" identity for the novel species is one of the main problems identified in the peer review from *JAMEZ* Referee B, as expressed in point 3:

[Referee B] "3…it is certainly premature and the evidence is not conclusive enough to make such close connections between this unknown species and *Homo sapiens*…Making such claims is far too premature for a manuscript like this. The manuscript demonstrates a universal bias toward a hominini hypothesis."

The mitochondrial introgression hypothesis should also satisfy this referee's concern, because it eliminates the need to identify the sample sources as "human" (Sapiens) or as hybrids. The mtDNA has been acquired from *H. sapiens* through hybridizing, but the later carriers of it are not thereby humans or hybrids themselves. Referee B's comments drew another defensively doctrinaire response from the authors, reflecting undue confidence in the reliability of mitochondrial DNA for distinguishing between closely related species:

[Authors' response] "Since the mitochondrial DNA places them as human, in both the original sequencing of the mitochondrial whole genomes as well as the Next Generation Sequencing, it is not premature to align them with Homo. We did add another hypothesis in addition to the hybridization theory on lines 692-696. In consideration of the mitochondrial whole genomes, these are the only two viable hypotheses available."

In general, the authors use "human" synonymously with *Homo sapiens*, except in the first sentence of the above response, which mentions the genus only. Yet, the additional, non-hybrid hypothesis (quoted in Section 7, page 99) absurdly suggests that the Sasquatch could be descended entirely from *Homo sapiens* in the time since the Late Pleistocene appearance of haplogroup H, which Ketchum *et al*. estimate to be about 15,000 years ago. So, as the authors see it, the Sasquatch is either a human-hybrid species or a non-hybrid human sub-species, which begs the question: Why can't the Sasquatch be a separate species of Homo, rather than a hybrid species or subspecies of *H. sapiens*? The authors seem strangely reluctant to consider the possibility that Sasquatch existed independently of Sapiens long before the era of interbreeding.

In the foregoing exchanges, it is clear the authors and reviewers differ over the sorts and sizes of inferences which they are willing to make based on the mtDNA data and apparent mito-nuclear discordance. The authors are eager to draw conclusions on the basis of evidence that the reviewers find suggestive, but inadequate without more extensive corroborating analyses of the nuclear DNA. Despite the above contention of Ketchum *et al*. (2013) that they have accounted for "the only two viable hypotheses," there is at least one more, mitochondrial introgression from Sapiens to Sasquatch, and it asserts that the Late Pleistocene hybridizing events indicated in the SGP mtDNA data were the start of a new mitogenome, but not a new species. This hypothesis also asserts that the pre-existing unknown primate is extant today in form which has changed little, if at all, as a result of this hybridizing (Liu and Wang *et al*. 2010). This unrecognized primate must be closely related to *H. sapiens*, but to know exactly how to characterize its relationship to humans and the other hominins, researchers should hold the mtDNA data in abeyance and seek answers

through analysis of the nuclear DNA (Stoeckle and Thaler 2018). Yet, given the difficulty in recovering nuclear material from the hair samples, and given the errors in identification of the whole genome nuclear sequences from other sample types, achieving this goal will probably require fresh samples and refinements in technique. Any new molecular studies, however, are likely to generate controversy that will not be settled until Sasquatch DNA can be studied in coordination with studies of the gross anatomy, organs, tissues, histology, etc., of the same physical specimen from which the DNA has been isolated.

3. HYBRIDIZATION AND SPECIATION

The human-hybrid young Sasquatch theory involves confusion of the near-term effects of hybridization on individual specimens, with the long-term, population-level process of speciation, the formation of a new species, which is always a process of genetic divergence, even in cases of hybrid species (Hochkirch 2013). In their 2014 article, "*How common is homoploid hybrid speciation?*" Schumer and Rosenthal *et al*. attest, "Homoploid hybrid speciation, or speciation via hybridization without a change in chromosome number, has historically been considered vanishingly rare." Hybridizing is not uncommon in nature, but, in the Animal Kingdom (where hybrids are homoploid) evolutionary biologists have tended to regard it as something which inhibits the formation of new species by disrupting reproductive isolation, enabling gene flow, and reducing genetic distance. Often, hybridizing has the effect of "reverse speciation" by bringing congener species together and producing intermediary forms (Seehausen 2006). If these hybrid intermediaries are fertile, and if the parent species and the hybrids have no aversion to pairing, distinct forms can soon be replaced by dull uniformity. Some few species have become recognized as naturally occurring hybrid species, most of them plants, but it is more common for hybridizing to result in extinctions and a loss of diversity (Seehausen 2006).

Hybridity in general must hold the explanation for the mysterious SGP mitochondrial data, but unfortunately, Ketchum *et al*. (2013) do not distinguish clearly between hybridization, and the appearance of a new hybrid species as one theoretically possible outcome of recurrent hybridizing. Hybridization (or hybridizing) begins with every successful reproductive pairing of members of distinct species, which are usually part of the same genus. Among mammals, for those inter-specific pairs which are able to reproduce, hybridizing usually culminates in first generation (F1) hybrid specimens ("hybrids") which are not fertile, or fertile but unable to find hybrid mates and form a new, reproductively isolated group. This outcome is due in part to the effect of interspecific hybridity known as Haldane's law (or Haldane's rule), after the work of J.B.S. Haldane from a century ago, "*Sex ratio and unisexual sterility in hybrid animals*" (1922), which explains that the heterogametic hybrid offspring of interspecific pairs are often missing or sterile. As it applies to mammals, Haldane's law affects males, the heterogametic sex (which has both sex chromosomes, X and Y) but does not affect females, the homogametic sex (which has two copies of the X chromosome). Haldane's law helps to explain why hybridizing rarely leads to the creation of new animal species, but often does lead to generations of backcrossing and mitochondrial introgression. Potential hybrid species are hampered by an extreme scarcity of mates, which must be limited to other hybrids, but the population of fertile hybrids is frequently limited to the homogametic sex.

Hybridization is widespread in nature, but not so with hybrid speciation. As Schumer and Rosenthal *et al*. (2014) explain, "Despite a surge in the number of studies that have proposed hybrid speciation, only a handful have presented strong evidence for a role of hybrid-

ization in speciation." The authors note that evidence of hybridization and speculation about its significance in the evolution of new species had become increasingly prominent over the preceding decade. Yet even in the professional literature there has been broad conflation of *hybridization* as a source of gene flow and genetic variation, which can provide raw material for evolutionary change in the longer term, and *hybrid speciation*, the appearance of a new species in addition to and distinct from the parent forms. As the authors explain, "Although genetic evidence of hybridization is an important part of demonstrating hybrid speciation, hybridization is common in the absence of hybrid speciation." I suggest that the Sapiens mtDNA and mito-nuclear discordance evident in DNA attributed to Sasquatch probably represents another ordinary case of hybridization in the absence of speciation.

Schumer and Rosenthal *et al*. (2014) propose three criteria to evaluate claims of hybrid speciation: "…(1) showing reproductive isolation from parental species, (2) documenting past hybridization, and (3) demonstrating that isolating mechanisms were derived from hybridization." The SGP genomic data alone are inadequate for application of these criteria. Nevertheless, the SGP data might be said to imply reproductive isolation of the hybridized form from the parent types (criterion 1), because the mtDNA lineages which should uniquely represent the non-human parent species have yet to be found. However, it is possible that the older mtDNA lineages have all been replaced through the process of mitochondrial introgression, so reproductive isolation and speciation is not a safe inference (Liu and Wang *et al*., 2010; Irwin and Rubtsov, *et al*., 2009). Regarding the second of the three criteria, the mito-nuclear discordance of the SGP DNA data could be said to provide evidence of past hybridization, but this inference is inadequate for the authors' requirement of documentation, in which the parent forms are known species. And the last of the three criteria is meaningless if reproductive isolation and speciation cannot be established.

Without a known species for each of the parent types, the suggestion that a new species has formed as a result of hybridizing, hybrid speciation, amounts to mere speculation. If the evidence of speciation is limited to mito-nuclear discordance, one would need to explain first why mitochondrial introgression, hybridization without speciation, is not a more likely explanation of the same limited picture of facts. Ketchum *et al.* (2013) also suggest, however, that the nuclear DNA data is consistent with the human-hybrid or hybrid species theory:

"Analysis of whole genome sequence and analysis of preliminary phylogeny trees from the Sasquatch indicated that the species possesses a novel mosaic pattern of nuclear DNA comprising novel sequences that are related to primates interspersed with sequences that are closely homologous to humans."

Sadly, the whole genome sequences mentioned here, and the phylogeny trees generated from them, have all been shown to be erroneous in the work of Hart (2016, 2020). But even if the nuclear whole genome sequences had been correctly produced and identified as an unknown primate, it would be impossible to know how to recognize mosaicism due to hybridizing when one of the sources of the mosaic elements is itself unknown and also closely related to the known source. Almost any sequence of nuclear DNA from the hypothesized hybrid species which appears to be "human" could be part of the common heritage of these two hominin species, the "persistence of ancestral variation" as Schumer and Rosenthal *et al*. (2014) put it:

"In most [unsuccessful] proposed cases of homoploid hybrid speciation, authors have

suggested that certain trait combinations were derived from hybridization and contributed to the emergence of reproductive isolation. However, . . . there are a number of explanations for mosaic phenotypes (persistence of ancestral variation or recent gene flow without the development of reproductive isolation)."

Ketchum *et al.,* however, do not give any discussion to ancestral variation in Sasquatch, nor do they seem to acknowledge any common ancestry of the "unknown progenitor" species and *Homo sapiens*.

Interspecific hybridizing is a common occurrence among some species, including some mammals and primates, but hybrid animal species are quite rare in nature, as Schumer and Rosenthal *et al*. put it in the Conclusions of their 2014 article:

"We argue that though hybridization is clearly an important evolutionary process, and may frequently contribute to evolutionary success through mechanisms such as heterosis and adaptive introgression, there are few cases that show a decisive role for hybridization in homoploid speciation. Only three proposed cases of homoploid hybrid speciation in plants and one in animals currently satisfy all three criteria set forth in this article (Fig. 4)."

Notice that "evolutionary success" in the quoted passage does not refer to the appearance of a new species; rather, evolutionary success means the endurance of the form of the pre-existing population among their descendants. Hybrid speciation may not require the extinction of one of the parent forms, but the development of the human-hybrid Sasquatch would require some yet-unexplained means of reproductive isolation of the hybrids from their parent forms. The Schumer and Rosenthal *et al*. criteria quoted above (page 89) have been criticized as overly restrictive, and too narrowly focused on reproductive isolation (Feliner and Alvarez *et al*., 2017). But for the sake of evaluating the theorized human-hybrid Sasquatch, reproductive isolation is an important yet unstated and unexplained aspect of the theory.

Although Ketchum *et al.* (2013) say it is unknown, we should also recognize that the pre-existing unknown "progenitor" species is a necessary part of any explanation of the SGP data which does not simply dismiss the possible existence of a non-Sapiens hominin species in North America. I suggest that each of the F1 hybrid offspring (at least 16 of which must have existed, but probably all at different times and places) should be regarded as an aberrant generation in the species represented by this male progenitor, as a local and temporary interruption of the older form, not as a founder of a new species. The matrilineal descendants of the hybrid offspring, who would carry the Sapiens mtDNA, should be regarded as later generations of the "progenitor" species. In comparison to Sasquatch individuals from other matrilines with no history of hybridizing, descendants of the hybrids would have been modified in an extremely subtle way, by the substitution of one hominin mitochondrial lineage for another—a difference which would probably not be evident to themselves or their conspecifics.

If we accept that the bio-samples identified as "Sasquatch" by the SGP contain mtDNA which is entirely homologous with that of "modern humans," we should also stipulate that species cannot be accurately inferred from the mtDNA—in fact, the former condition logically entails the latter. Instead of constructing an ambiguous scenario in which both conflicting identities might somehow be true (the human-hybrid Sasquatch theory), it makes better sense to reject the inference of species from the mitochondrial data, because several other lines of evidence—visual sightings, hair morphology, nuclear DNA analyses, trackways and foot impressions, etc.—point to a creature which is not *H. sapiens.* Regarding the inference of species from mtDNA, the log-

ical options are yes or no: Yes, the inference is valid; the species in question is *H. sapiens*, all of it, the mitochondrial and the nuclear DNA. Or, no, the inference is not valid; the species in question is not *H. sapiens*, even if the mtDNA is derived entirely from Sapiens.

New evidence of Sasquatch nuclear DNA will be needed to determine the extent of hybridization in its nuclear genome, but the mtDNA evidence presented by Ketchum *et al*. (2013), could be consistent with rare—isolated individual cases, few in total—but geographically widespread hybridizing of Sasquatch and Sapiens, which occurred tens of thousands of years ago, and extensive mitochondrial introgression which has accumulated since then. Therefore, neither the mtDNA data nor the apparent mito-nuclear discordance provides adequate reason to identify the Sasquatch as a hybrid or a hybrid species. However, the hypothesized reproductive capability of Sapiens and Sasquatch would strongly suggest that Sasquatch is a hominin of some kind and that the two species share a relatively recent common ancestry.

4. COMMON DESCENT OR SEPARATE CREATION?

So far, we have noted several instances (pages 77, 85, 87) in the article and in the authors' responses to peer reviews in which Ketchum *et al*. (2013) refer to separate "maternal" and "paternal" lineages of the human-hybrid Sasquatch species or subspecies. These statements are mistaken applications of the qualities of specimens to the species as a whole, and they indicate a core ideological problem concealed behind the scientific appearances of the Sasquatch Genome Project. Additional examples of these strange claims occur in the "Q & A" section of the SGP website, most prominently in reply to questions 1 and 2 of Part A. Compared to the limited claims and careful language of "*Novel North American Hominins*..." (Ketchum *et al*. 2013), here the unidentified author is more forthcoming:

"1. What are Sasquatch?

The Sasquatch are an indigenous, aboriginal people. Their maternal lineage is human and their paternal lineage is an unknown hominin. Their genetics reveal no relation to *Homo Neanderthalensis* (Neanderthal) or *Homo sapiens Altai* (Denisova). Despite their pop-culture image as "ape-men," they have no more genetic connection to apes than we do… The paternal lineage found in the nuclear DNA of Sasquatch suggests a distantly related hominin that evolved separately from humans, apes, and other primates but evolved to the point where it could interbreed with humans."

A number of problems are evident here. First, the author applies some over-simplifications which are popular heuristics for genealogical research, which relies heavily on mitochondrial DNA to represent one's exclusively maternal inheritance, and for men, in addition, Y-chromosome genes, which are part of the nuclear genome, to represent one's exclusively paternal inheritance. But these terms do not apply to a whole species, which is an entire population comprised of many closely related individuals, often dispersed over a large geographic area. Instead of the incoherent species-level claim that the Sasquatch maternal lineage is human (which implies that the Sasquatch is half human), one could coherently claim that the Sasquatch mitochondrial genome of the present has been acquired from Sapiens, but the Sasquatch species would have existed before this change, and nothing more can be attributed to *H. sapiens* based on the SGP data. As Section 5 will explain in more detail, hybridizing and gene flow could more easily account for the mito-nuclear discordance in Sasquatch DNA without the creation of a hybrid species.

The explanation quoted above concerning the "paternal lineage" of the human-hybrid young Sasquatch posits evolutionary trends

that are contrary to the ordering principle of taxonomy, which is common descent. No hominin could have "evolved separately from humans, apes, and other primates," because all hominins, including humans (Sapiens), are more closely related to each other than any of them are to the lower hominoids, the apes. That is what common descent means. The general trend of evolutionary development throughout the biological world is increasing diversity and increasing genetic differentiation or "genetic distance" between species over time. Species and groups of species diverge as they evolve, so the idea that the unknown progenitor species evolved separately from primates "but evolved to the point where it could interbreed with humans" is nonsense. The common ancestry of closely related species means that interspecific pairs are often capable of reproduction, even after their populations have separated permanently, until their divergent paths accumulate enough genetic distance to make hybridizing impossible. But species which have never been capable of interbreeding, because they belong to different genera or more distantly related groups, will never develop such a capacity by natural means. Separate species can evolve similar adaptations to similar environments, but this "parallel" or "convergent" development does not enable separate branches on the Tree of Life to grow together again.

Question 2 from Part A of the "Q & A" from the Sasquatch Genome Project website:

"2. Why don't we know more about the paternal lineage of the Sasquatch? Could the paternal species be *Homo heidelbergensis*? What about other recently discovered human ancestors?

Sasquatch is a recently developed species. Haplotype analysis within the mitochondrial (maternal) DNA indicates that the species is only about 15,000 years old. Only a very small percentage of human remains in their nuclear (paternal) DNA, which is primarily of the unknown hominin…*Homo heidlebergensis* is a more recent suggestion for a Sasquatch ancestor, but this human species died out at 400,000 years ago, long before Sasquatch came into existence."

I can find no justification for the assertion that "haplotype analysis" indicates the age of the species, rather than merely the ages of the haplogroups, a vast and profound difference in meaning. Ketchum *et al*. (2013) offer no other evidence to support the sudden appearance of a new hominin species only 15,000 years ago, which is far more recent than any hominin which has so far been recognized. Their pronouncements seem to be guided by the mistaken conviction that the Sasquatch or its "unknown progenitor" species shares no common ancestry with Sapiens, but the ability of interspecific pairs to produce fertile offspring would be clear indication that these species had been closely related before any hybridizing had taken place. Furthermore, it seems likely that the unknown species is older than *H. sapiens*, and *H. heidelbergensis* also, simply because these latter species are among the more recently evolved hominins, and a number of Sasquatch features (immense size and strength, thick hair covering most of the body, nocturnality, no use of fire…) suggest that it is older than most of its fellow hominins. As it appears to me, Dr. Ketchum's mistaken conviction that these two species share no prior ancestry has led her to emphasize, mistakenly, the hybrid nature, the Sapiens ancestry, and the recent beginning of the "Sasquatch."

To question 2, my answer would be: The Sasquatch does not have separate maternal and paternal ancestries, nor does any species. What Ketchum *et al.* (2013) refer to as the paternal lineage of the human-hybrid young Sasquatch was Sasquatch. The mtDNA data generated by the SGP provide no evidence for the appearance of a new species rather than merely the introgressive replacement of mtDNA in the unknown species with Sapiens

mitochondrial lineages. The mtDNA has been acquired from Sapiens, but the isolated prehistoric interbreeding which was necessary to produce such a mitogenome in the present-day North American Sasquatch population probably did not cause any lasting changes in the Sasquatch nuclear DNA, or in the species as a whole. This effect would be consistent with the process of mitochondrial introgression, which is common in a wide range of life forms, and known to occur in primates and among hominins. The true prevalence of completed mitochondrial introgression among recognized species is unknown, because it is not easily detected (Stoeckle and Thaler 2018).

At the televised press conference in Dallas, Texas, Oct. 1, 2013 (available on YouTube channel "Dr. Melba Ketchum") where the SGP results were first publicly presented, Dr. Ketchum explains some of the difficulties introduced by the species represented by the samples in the study. The nuclear DNA sequences did not match well with anything yet observed, and some geneticist colleagues were concerned by this "poor alignment" of the SGP nuclear DNA with that of any known species:

"…there is very little alignment, meaning: It doesn't match anything. It's novel. It's new. There's nothing to compare it with."…"So, we've got alignment that is not good. It doesn't fit well in the Tree of Life. And this is the problem that a lot of the scientists have. They expected that it's ancient, that it somehow branched off with evolution. But this creature does not follow the general rule. What it does do is, it's very different. We think it is a human hybrid. That is our theory."

Ketchum then explains what she sees as the two main reasons to favor the human-hybrid theory, the exclusively "human" (Sapiens) mtDNA haplogroups represented in the SGP data, and non-Sapiens nuclear DNA (insufficient reasons, as discussed in Section 3). A minute later Ketchum puts the matter a bit differently: "Since we don't fit in the Tree of Life with these animals, in a convenient way, scientists say 'Well, it has to be contaminated.'" But Dr. Ketchum reviews briefly the measures taken to eliminate contamination and degraded DNA, and asserts that the SGP extractions were pure and have produced high-quality DNA. Yet the composition of the nuclear DNA is without precedent:

"It's the first time that anybody has seen anything like this. And mainstream science has a problem with that, because we are all taught that evolution is very cut and dried. And 'This is how it is. It comes up the Tree of Life.' But what we have is the Tree of Life with a single branch coming up and crossing over to human."

Dr. Ketchum's press conference remarks make it clear that she holds some resistance to, or resentment of "evolution," but the conflict that the SGP data pose for evolutionary theory is not at all clear. The claim of "a single branch coming up and crossing over to human" seems to assert that the unknown progenitor species shares no ancestry with Sapiens, an impossible and unexplained proposition. To suggest that Sasquatch does not fit somewhere on the Tree of Life, or that Sapiens "don't fit in the Tree of Life with these animals, in a convenient way," is to deny the very concept of common descent, which is central to evolutionary theory. Somehow Dr. Ketchum came to these conclusions when only a tiny fraction of the purported Sasquatch nuclear genome had been analyzed, and not even a single specimen had ever been available for study. Under the circumstances, such pronouncements amount to a wholesale and cynical rejection of the Tree of Life and evolution.

Text on the home page of the SGP website expands on the perceived biases of many peers:

"We encountered the worst scientific bias in the peer review process in recent history. I am calling it the 'Galileo Effect'. Several journals wouldn't even read our manuscript when we sent them a pre-submission inquiry. Another one leaked our peer reviews. We were even mocked by one reviewer in his peer review."

I can believe that Ketchum *et al.* (2013) encountered scientific peers with prejudiced and dismissive views of Sasquatch. I know from personal experience that many established professionals in anthropology and other fields treat the topic as mere myth, or as little more than a joke, even though they should be capable of greater objectivity. However, I sense a deep irony in Dr. Ketchum's suggestion that the hostile reception of scientists to the SGP claims constitutes an example of the "Galileo Effect." The Church convicted Galileo of heresy for promoting a worldview based on empirical science, yet Dr. Ketchum seems to suggest that the SGP has found something which defies and exposes evolutionary science as another sort of religion, a false religion. Sadly, Science and the SGP have been talking past each other.

Ketchum *et al*. (2013) would have been more successful if they had sought a hypothesis which comports with all of their data and with evolution too, such as mitochondrial introgression from Sapiens to Sasquatch. Instead, the authors have asserted more than the evidence can explain, and then interpreted the criticisms and doubts of peers as an obligatory defense of evolution and evidence of bias in mainstream science. One might say that a scientifically plausible version of Sasquatch has been exchanged for a more complex human-hybrid version which seems to expose problems in evolutionary science, and which may validate the mysterious Biblical references to the ancient Nephilim, a special point of interest for many Creationists.

As some interpret it, *Genesis*, Chapter 6, verses 1-4, presents the Nephilim as the gigantic hybrid offspring of the "sons of God" and "daughters of Men," human females. It is believed that the sons of God, as angelic, supernatural beings, share no biological ancestry with humans, but the same assumption cannot apply to the Sasquatch, not if it is a natural species, accessible to science. Yet the theorized human-hybrid Sasquatch almost seems tailored to suit a Sasquatch-as-Nephilim thesis. Without additional evidence, however, there is no sufficient and valid reason to insist on the recent origin of the Sasquatch or its descent from an unknown progenitor. The human-hybrid young Sasquatch did not survive scientific peer review, nor should any future version of Sasquatch which requires for its origin some radical discontinuity with the world of organic life. Ketchum *et al*. must be comfortable with their nine-years-long ongoing disengagement from "mainstream science."

A more recent statement from Dr. Ketchum's personal Facebook account contains familiar and defiant claims. A post from September 17, 2020, features the headline of a linked article and a short accompanying note on Sasquatch from Dr. Ketchum:

"'Archaeology breakthrough: Major find rewrites 500,000-year-old extinct human understanding (express.co.uk).' [Dr. Ketchum:] An interesting article on ancient hominids for your enjoyment. Remember the Sasquatch aren't ancient. Modern humans were here well before they were. They had to be since their maternal lineage is modern human so the humans had to come first."

As this statement confirms, eight years after its doomed debut, Dr. Ketchum still mistakenly defines the "Sasquatch" by its discordant incorporation of Sapiens mtDNA. The three core elements of her theory remain unchanged: The Sasquatch is (1) a product of inter-species reproductive pairs, a hybrid, or

maybe a hybrid species; (2) partly "human," maybe as much as 50%, and descended as a species from *H. sapiens*; and (3) radically new, non-existent prior to the Late Pleistocene interbreeding. But without evidence of the unknown progenitor, there is no reason to take these claims seriously.

5. MITOCHONDRIAL GENE FLOW IN HYBRIDIZING HOMININS

In mistakenly assigning "maternal" and "paternal" lineages to whole species, the human-hybrid Sasquatch theory seems narrowly focused on the level of the individual and questions of genealogy or selective breeding. A better, more plausible explanation for the SGP mitochondrial data should approach the matter as a problem of population genetics and interspecific or "horizontal" gene flow, the movement of genes between populations in nature, across the usual boundary of species. Interspecific mitochondrial gene flow begins with each hybrid birth and continues for as long as the mother's matriline (her direct line of female descendants) exists apart from her species of origin. The mitochondrial lineage persists in this new context, as part of a different symbiotic host species, but the species itself is not new simply because it includes a mitogenome which has been newly acquired.

Let us consider hybridization and gene flow between Neanderthals and Sapiens as a model of Sasquatch-Sapiens hybridization and gene flow. As Mason and Short explain in their 2011 article, "*Neanderthal-human Hybrids*," a small percentage of Neanderthal nuclear DNA is reliably present in certain Sapiens groups, but Neanderthal mtDNA appears to be wholly absent from the Sapiens mitogenome. The authors also note that Neanderthal Y-chromosome genes, that part of the nuclear DNA which is transmitted only by males, are absent from the nuclear DNA which is shared with Sapiens. Theorizing about patterns of hybridization and gene flow which could have produced this set of facts, Mason and Short (2011) note the effects of sexual dimorphism and sexual selection in apes and humans:

"Sexual selection in humans and Great apes shows that males are physically bigger and stronger than females, hence allowing them to monopolize reproduction (26). Considering that Neanderthals were robust and humans were in comparison gracile, male Neanderthals may have had *le droit de seigneur* [French, "right of the lord," or, in context, reproductive priority imposed by force] in any matings."

The authors then spell out the implications: Given "…an understanding of interspecific hybridity, the available data leads to the hypothesis that only male Neanderthals were able to mate with female humans." This hypothesis, which suggests asymmetric introgressive mitochondrial gene flow from Sapiens to Neanderthals, would explain the lack of Neanderthal mtDNAs within the Sapiens mitogenome. It has been confirmed by later research, incorporating additional ancient mtDNA data, which finds Sapiens mtDNA pervading the Neanderthal mitogenome. Gene flow from African Sapiens of the Middle Pleistocene is now thought to be the source from which all of the known Late Pleistocene Neanderthal mitogenome is derived (Posth and Wißing *et al*. 2017). This research documents the completed replacement of one hominin species' mitogenome by Sapiens mitochondrial lineages, yet the authors of this study do not assert, as a consequence, the origin of a new hominin or hybrid species. Additional discussion of this research appears below in Section 6.

The same hypothesis, "only male Neanderthals were able to mate with female humans," might apply better to male Sasquatch, who would be even bigger and stronger vis-à-vis Sapiens females, and selection of mates in these cases assuredly took the form of hostile

abductions and long-term captivity. Because these women had been extracted from the society of *H. sapiens* to become the mothers of hybrid offspring which would be raised as Sasquatch, the inherited effects of inter-species mating would be confined to the latter species. Again, the same hypothesis, "only male Neanderthals were able to mate with female humans," seems to apply better to the SGP mtDNA data, which, it is claimed, include members of 16 different "human" (*H. sapiens*) haplogroups. Every such haplogroup represented in the mtDNA of the purported Sasquatch indicates an ancestral pairing with a Sapiens female. Ketchum *et al*. (2013) regard each of these inter-specific pairs as a point of origin for the human-hybrid young Sasquatch, but I argue that they mark the origins of the contemporary North American Sasquatch mitogenome, not the species itself. These points were spread out, unevenly, 13 of them across Europe and Asia, and three more which could have occurred in Asia or North America. (However, as discussed in Sections 7 and 8, Hart's 2020 revisions to the SGP haplogroups reduce the number of American haplogroups to two, or possibly only one). Ketchum *et al.* note that such a range suggests that "these hominins did not originate in a single geographic location," but the authors have no clear evidence of speciation, and one could argue that the hybrids had been too few and too widely separated for a new species to develop.

To have the best chance at producing a new hybrid species, the F1 hybrids would need to locate other, unrelated (not siblings) F1 hybrids, and, eventually, form a separate group of hybrid mates and their offspring which is reproductively isolated from both parent species. But, in addition to the overall scarcity of hybrids, the effects of Haldane's law (see page 89) would further reduce the chances that any of the rare hybrids could find reproductive success with hybrid mates. As Mason and Short (2011) explain, "If Haldane's Law applies to the offspring of Neanderthals and humans, we would expect to find female hybrids quite commonly, but male hybrids much more rarely." This effect appears to explain the absence of Neanderthal mtDNA in the Sapiens mitogenome, as well as the lack of Y-chromosome genes among the Neanderthal nuclear DNA sequences found in Sapiens, even if exclusively male Neanderthals had interbred with Sapiens. By contrast, mitochondrial introgression affects a pre-established species; it does nothing to limit or decrease the availability of mates. Instead, especially for any part of the Sasquatch population suffering from inbreeding "depression," which includes loss of fertility, it seems more likely that rare instances of hybridizing with congener species would enhance the availability of mates through the effects of heterosis and Haldane's law, which would tend to increase fertility and birth rates, and to increase the proportion of females.

Putting all of this together, we might hypothesize, as Mason and Short (2011) do about Neanderthal-Sapiens hybrids, that only inter-species matings of Sasquatch males and Sapiens females were likely to occur, and of the offspring that resulted, as Haldane's law suggests, it is likely that most or all of them were females, and that any males were sterile. Without hybrid males available, the hybrid females would have been claimed by unmixed males, "backcrossing" rather than continuing the process which, in theory, might produce a new hybrid species. Each hybrid female would thereby pass the mtDNA of her Sapiens mother to each of her Sasquatch children. These conditions could result, with the passage of many generations, in proliferation of the Sapiens mitochondrial lineages in the Sasquatch breeding population, the species. Each successive generation of matrilineal descendants would represent some additional transfer or "gene flow" of undiluted mtDNA from the Sapiens group of origin to the Sasquatch descendants and the Sasquatch gene pool. If

these hybridized matrilines were numerous enough, fertile and productive enough, and if the process of gene flow continued for long enough, the older mitochondrial lines could eventually be completely replaced by those acquired from Sapiens. Meanwhile the original Sapiens nuclear DNA would have been diluted away to negligible levels. After just ten generations of backcrossing, less than one-tenth of one percent of the Sapiens nuclear DNA would remain among the matrilineal descendants of the original inter-specific pairs.

6. MITOCHONDRIAL INTROGRESSION AND TAXONOMY

As the unseen effect of horizontal gene flow accumulated over many generations, mitochondrial introgression may seem mysterious, but it is not a rare phenomenon. It occurs in an enormous range of sexually reproducing plant and animal groups. Mitochondrial introgression has been documented, for just a few examples, in pine trees (Wang and Wang 2014) and spruce trees (Ran and Shen *et al*. 2015), in fruit flies (Powell 1983) and mosquitos (Mastrantonio and Porretta *et al*. 2016), in sharks (Corrigan *et al*. 2017) and salmon (Balakirev and Ayala *et al*. 2013), in frogs (Liu and Wang *et al*. 2010), in birds (Irwin and Rubtsov *et al*. 2009), in hares (Seixas and Melo-Ferreira *et al*. 2018), in bears (Hailer and Kutschera *et al*. 2012), in monkeys (Detwiler 2019), and in hominins (Posth and Wißing *et al*. 2017). For any species in which it occurs, mitochondrial introgression slowly obliterates the older mitochondrial lineages, which are of greater value for scientists seeking to establish the phylogeny, the evolutionary history, of that species, or its taxonomic status, how it is related to everything else in the Tree of Life.

Mitochondrial introgression is a kind of introgressive hybridization, meaning that certain foreign genes continue to spread among the descendants of hybrids even if the interspecies reproductive pairs were only a few isolated cases from long ago. Sometimes mitochondrial introgression is known as "ghost introgression," (Zhang and Tang *et al*. 2019) for cases in which the mtDNA of one species preserves the mitogenome of a related species which has become extinct. Completed mitochondrial introgression is sometimes called "mitochondrial capture," as in this reference to studies of three monkey species in the 2019 *International Journal of Primatology* special issue on primate hybridization (Cortez-Ortiz and Roos *et al*. 2019):

"In the case of the kipunji (*Rungwecebus kipunji*), mitochondrial capture (the replacement of the mitochondrial genome of one species with that of another as a consequence of rare hybridization events) has been considered to explain the presence of baboon-like mitochondrial genomes in one of the two kipunji populations and the presence of kipunji-like mitochondrial genomes in a small yellow baboon (*Papio cynocephalus*) population adjacent to the range of the other kipunji population (Roberts et al. 2010; Zinner et al. 2009a, 2018)."

Hybrid speciation is included among the possible effects of hybridization which are discussed in this special issue, but none of the contributors actually cites a known case of a hybrid primate species in the Ketchum *et al*. (2013) sense in which hybridizing produces a third species which is separate from the parent forms.

In their 2009 study of birds in the genus *Emberiza*, Irwin and Rubtsov *et al*. "…present a remarkable case in which highly phenotypically divergent species have almost no divergence in mtDNA." Sasquatch and Sapiens appear to present the same sort of case in which two species are radically different, physically and behaviorally (phenotypically), but all evidence so far compiled—by Ketchum *et al*. (2013) and other Sasquatch DNA sequencing efforts—seems to indicate minimal divergence

in mtDNA. Irwin and Rubtsov *et al*. continue:

"Yellowhammers (*Emberiza citrinella* Linnaeus) and pine buntings (*Emberiza Leucocephalos* S. G. Gmelin) differ noticeably in appearance and song but hybridize in some areas of contact. They share a variety of closely-related mtDNA haplotypes, with little divergence in frequencies, indicating a mitochondrial divergence time sometime during or after the last major glacial period. By contrast, nuclear DNA (amplified fragment length polymorphism markers and *CHD1Z* gene sequences) differs more strongly between the species..."

The nearly identical mtDNA implies a recent divergence of the two forms, but greater differences in the nuclear genomes seem to conflict with this conclusion. Given this mito-nuclear discordance, the authors "…argue that the evidence better supports another possibility: the two species are older and mtDNA has recently introgressed between them…" Likewise, I suggest that the Sasquatch species is older than the SGP mtDNA data might seem to imply, because mtDNA has recently introgressed from Sapiens to Sasquatch.

Like the focus of the work of Irwin and Rubtsov *et al*. (2009), the Sasquatch may present a case of complete mitochondrial replacement, something which may frequently be missed even in well-documented, uncontroversial species:

"Cases of complete replacement might be much more common than presently thought because they are difficult to detect. When mtDNA has only partially introgressed, it is detectable because members of one species have two very divergent forms of mtDNA, one of which is similar to the other species (Plötner et al., 2008). When complete replacement has occurred, there are no surviving examples of the extinct haplotype group to reveal the presence of introgression; the remaining pattern is simply one of mtDNA similarity between the two species, which could be mistakenly interpreted as recent population splitting."

I suggest that Ketchum *et al*. (2013) have mistakenly interpreted the Sasquatch mitogenome as indicating a recent beginning to the species, whether as the result of population splitting or hybridizing. As explained in the Conclusions section of "*Novel North American Hominins* …":

"Though preliminary analysis supports the hybridization hypothesis, alternatively, it could also be hypothesized that the Sasquatch are human in origin, having been isolated in closed breeding populations for thousands of years. Nevertheless, the data conclusively proves that the Sasquatch exist as an extant hominin and are a direct maternal descendent of modern humans."

Unfortunately, that is all there is by way of alternate hypotheses in the paper, in which the leading theory and the alternative both assert a recent "human" role in the origin of Sasquatch! But if mitochondrial introgression better explains the mito-nuclear discordance, then the Sasquatch is certainly much older than its mitogenome, and the species itself is assuredly not descended from modern humans, even though its mitogenome at present could be descended entirely from 16-or-so Late Pleistocene Sapiens females.

As introduction to their 2010 study of mitochondrial introgression in frogs, Liu and Wang *et al*. explain: "Historical mitochondrial introgression often results in the mitochondrial genome of one species being replaced by that of another species without leaving any trace of hybridization in its nuclear genome." No trace of hybridization in the nuclear genome would mean that the species itself has not been significantly modified and that the individual specimens are not hybrids in any meaningful

sense. The same individuals that originally contributed the novel mitochondria also contributed half of the nuclear DNA, but unless there are additional interspecific or hybrid unions among the descendants, the exotic portion of the nuclear genome will be diluted with every subsequent generation, whereas the mitogenome will not change. Applying this to the hypothesis of Ketchum *et al.* (2013), consider some simple calculations: Figuring 20 years as the span of a generation, it has been 750 generations since the supposed birth of the human-hybrid Sasquatch about 15,000 years ago (one SGP estimate). In a first-generation hybrid, the mtDNA would be 100% Sapiens, and the nuDNA would be 50% Sapiens, 50% Sasquatch. After the first generation of "backcrossing" (unmixed Sasquatch paired with the hybrid F1 female, because hybrid males probably did not exist), the mtDNA would be 100% Sapiens, and the original Sapiens contribution to the nuDNA would be reduced by half to 25%. Every additional generation of backcrossing (no more Sapiens admixture) would further reduce the Sapiens nuclear DNA by half. After five generations of backcrossing, the mtDNA would be 100% Sapiens and the nuDNA would be 1.5625% Sapiens. After ten generations of backcrossing, less than one tenth of one percent of the original Sapiens nuclear DNA would remain (0.09765625%). Another 740 generations to go. How many more before the "hybrid" designation starts to feel misleading?

As Liu and Wang *et al*. (2010) explain further:

"Mitochondrial gene introgression can confuse the estimated genealogy of a species, because an introgressed genome will not reveal any history before the introgression events, and the mix of introgressed and original genomes within a species could lead to absurd inferences of the species history."

I suggest that mitochondrial introgression may well have confused the SGP view of the Sasquatch phylogeny, and the hypothesis that the Sasquatch is a human hybrid of recent origin appears to be an absurd inference resulting from such confusion. And without mtDNA from a Sasquatch fossil which is older than the human haplogroups so far identified, we have no information about the older Sasquatch mitogenome or how it differed from that of Sapiens, because "an introgressed genome will not reveal any history before the introgression events."

Mitochondrial DNA "barcoding" is one method of mitogenomic accession by which zoologists, wildlife biologists, and scientists of related fields define and distinguish eukaryotic species with reference to certain segments of the mtDNA molecule. It has been used successfully for over 15 years, and in those few cases in which mtDNA barcoding has produced ambiguous results, mitochondrial introgression has been the principal cause of confusion. As Stoeckle and Thaler explain in "*Why should mitochondria define species?*" (2018):

"In most well-studied cases of shared or overlapping barcodes, nuclear genome analysis demonstrates these anomalies are due to hybridization resulting in mitochondrial introgression from one species into the other. If recent, and complete across the whole population, introgression erases mitochondrial differences between species. Introgression events in the more distant past and those involving only part of a species produce more complex patterns, as illustrated by *Ursus* bears …"

From the work of Ketchum *et al*. (2013) and related studies, it seems likely that Sasquatch could be a species in which mitochondrial introgression is relatively recent and complete, and if so, the Sasquatch is a species whose identity cannot be accurately inferred from its mtDNA. Therefore, we should not conclude that the Sasquatch is a human hybrid, or a hy-

brid species, merely because it has a mitogenome of Sapiens origin. In making this faulty inference, Ketchum *et al*. have mistaken a new, Sapiens-sourced mitogenome for the appearance of a whole new hominin species. And because of this faulty inference, SGP principals and fans continue to mis-inform others with the dogmatic insistence that "Sasquatch" DNA shows it to be a human hybrid of recent origin, approximately 15,000 years ago, and that its non-human parent species (its "paternal lineage") is unknown, all of which is wrong.

In recent years, mitochondrial introgression has become a prominent part of evolutionary theory concerning species with DNA which exhibits deep mitochondrial divergence, or mito-nuclear discordance, or bio-geographic discordance—three terms used to denote apparent contradiction between the mitochondrial and nuclear genomes of a single species. Indeed, gene flow resulting in complete mitochondrial replacement has emerged as the best explanation for certain mysteries concerning the relationships of early *H. sapiens* and two of the fossil forms which are most closely related to us, Neanderthals and Denisovans. As Posth and Wißing *et al*. (2017) explain, hybridizing has complicated the phylogenies of these three groups:

"Nuclear DNA indicated Neanderthals as a sister group of Denisovans after diverging from modern humans. However, the closer affinity of the Neanderthal mitochondrial DNA (mtDNA) to modern humans than Denisovans has recently been suggested as the result of gene flow from an African source into Neanderthals before 100,000 years ago."

Such an explanation could make sense if the interbreeding were extensive enough, and if the introgressive gene flow continued for long enough to cause the dramatically changed mitogenome, but researchers needed a way to approximate the long-term effects of limited interbreeding:

"While genomic evidence showed that gene flow between lineages as divergent as modern humans and Neanderthals took place in both directions, it is unclear whether such small-scale phenomena were sufficient to explain the complete replacement of the initial Neanderthal mtDNA pool (found in Sima de los Huesos) ["Pit of the Bones," a cave in northern Spain] by a Middle Pleistocene human lineage from Africa."

Posth and Wißing *et al*. (2017) introduce the oldest mtDNA sequences yet recovered from Neanderthal remains, a femur from the Hohlenstein–Stadel cave in southwestern Germany, and employ a complex set of analytic tools to arrive at an estimate of the time needed for complete mitochondrial replacement to occur. Their conclusions support the hypothesized interbreeding and mitochondrial introgression from African Sapiens to Neanderthals: "The African introgression hypothesis suggests that Late Pleistocene Neanderthal mtDNAs originated through gene flow from an African source, which we constrain taking place more than ~270 ka." Remarkably, the mitochondrial haplogroups which have long been identified with Neanderthals of the Late Pleistocene appear to have originated with *H. sapiens*:

"Our analytical calculations show that this event is plausible even if the introgressing lineage represented a minimal proportion of the initial gene pool. This scenario reconciles the discrepancy in the nDNA and mtDNA phylogenies of archaic hominins and the inconsistency of the modern human–Neanderthal population split time estimated from nDNA and mtDNA. Under this demographical model, the Denisovan mtDNA type was common among early Neanderthals in Eurasia (for example, Sima de los Huesos) and was then largely replaced by an introgressing African

mtDNA that evolved into the Late Pleistocene Neanderthal mtDNA type."

If the SGP mtDNA data are valid, they could be evidence of precisely the same process, asymmetric introgressive mitochondrial gene flow and replacement, which is now recognized as having occurred between Sapiens and Neanderthals starting about 270,000 years ago. Importantly, Posth and Wißing *et al*. (2017) do not assert the origin of a hybrid species as a result of the hybridizing which is theorized, nor do they suggest that the Late Pleistocene Neanderthal species is any more closely related to *H. sapiens* despite extensive mitochondrial introgression from Sapiens to Neanderthals. Rather, Neanderthals and Denisovans are more closely related to each other than to Sapiens, and completed mitochondrial introgression from Sapiens to Neanderthals has obscured but has not changed these facts of their evolutionary history.

7. MASSIVE MITOCHONDRIAL INTROGRESSION OF HUMAN HAPLOGROUPS

In the first-round peer review of "Novel North American Hominins…" (Ketchum *et al.* 2013), *Nature* Referee 3, sounding somewhat exasperated and incredulous, articulates the most challenging aspect of the SGP mtDNA data:

[Referee 3] "The mtDNA results are hardly explainable unless one believe that American woman of Caucasian descent (within the last 200-300 years as its America) runs around in the forest having sex with a undiscovered hominin and leaving the baby to their care take of the new hominin (as the rest of us have not heard about such hybrid babies yet the baby must be send of) [*sic.*]."

The mention of American women of Caucasian descent refers to the presence of a dozen samples representing H haplogroups in this data set. The implication is that the ultimate source of these Caucasian mitochondrial lineages must be modern American society, because the H haplogroup is known to have originated in the Old World, and it is not represented among Native American haplogroups. I think Referee 3 is mistaken here, only because no consideration is given to the possibility that minimal interbreeding tens of thousands of years ago could result in extensive mitochondrial introgression, which could explain the exclusive presence of Sapiens haplogroups in the SGP mtDNA data.

In reply to this point from Referee 3, Ketchum *et al*. (2013) reiterate one of their most absurd claims:

[Authors' response] "As far as when this species arrived in the United States, we do not know, however due to H haplotypes in their mitochondrial DNA, the age of these hominins is less than 15,000 years. However, they could have arrived in the United States before Native American peoples according to the Solutrean Theory now added as a reference in this manuscript."

Although the H haplogroup is less than 15,000 years old, Ketchum *et al*. cannot justify the inference that the age of the Sasquatch species is limited by the age of its youngest or most numerous or most discordant mitochondrial lineages. The authors mistakenly assume that the discordant presence of exclusively Sapiens haplogroups in the purported Sasquatch mtDNA constitutes strong evidence of a recently emerged hybrid species, and Referee 3 suggests, incorrectly, that (if true) it would constitute evidence of hybridizing in the present era, but mitochondrial introgression provides a simpler and more likely explanation of the same data than either of these alternatives.

Though it is not well understood nor easily detected, field researchers have encountered mitochondrial introgression so frequently in so

many species that it seems to defy explanation (Currat and Ruedi *et al*. 2008; Toews and Brelsford 2012). Even so, a cogent general theory has been part of the discussion since the mid-twentieth century. Hybridizing in nature usually results from the movement of members of one species (often described as "exotic," "rare," "invading," "advancing," or "colonizing") into a range already occupied by a closely related "local," "native," or "established" species. As Currat and Ruedi *et al.* (2008) explain:

". . . it has been suggested that introgression of neutral genetic markers should affect mostly the advancing taxon as compared to the already established one (e.g., Baker 1948; Moran 1981; Barton and Hewitt 1985; Buggs 2007)…This type of explanation appears rather intuitive: as the wave of advance spreads forwards, neutral alleles or traits will flow in the opposite direction, into the invading population, and the frequency of introgressed alleles will steadily increase behind the advancing wave front, until introgression is complete."

In the article quoted here, "*The Hidden Side of Invasions: Massive Introgression by Local Genes*," the authors report on their use of simulations to evaluate a suite of variables affecting hybridization between local and invading species: "Here we show by spatially explicit simulations that massive introgression of neutral genes takes place during the invasion of an occupied territory if interbreeding is not severely prevented between the invading and the local species." "Neutral" in this context means evolutionarily neutral, not favored or disfavored by natural selection. Researchers have sought to make more sense of mitochondrial introgression by tying its effects to selection pressure, but this link has not yet been elucidated. Among their conclusions, Currat and Ruedi *et al*. explain at least part of the answer:

"First, our simulations show that it is not necessary to invoke selection (Ballard and Whitlock 2004; Rieseberg et al. 2007), unusual behaviors (Wirtz 1999), or differences in relative species abundance (Cianchi et al. 2003) to explain massive levels of introgression from a local to an invading species. Distribution shifts can also explain why introgression can be detected beyond current areas of sympatry, which is otherwise difficult to explain without invoking positive selection (Evans et al. 2006)."

Having investigated an array of factors affecting patterns of hybridization, Currat and Ruedi *et al.* (2008) find that massive introgression of neutral genes, including mtDNA, is the most likely result when locally established species encounter invasions of rare congener cousins: "We therefore propose that massive introgression in an invading species should not be considered as a sign of selection or disassortative mating but as the null expectation for neutral genes." The further implication for Sasquatch is that its (introgressed) mitogenome may be more indicative of rare hybridizing from tens of thousands of years earlier, on the far edges of its range or beyond, than of its true phylogeny or core geographic range. Its older, "native" mitogenome should have been more distinct from that of Sapiens, but it has probably been completely replaced with introgressed Sapiens mitochondrial lineages, and these probably do not indicate any significant adaptation or division within the species.

Recall that the Abstract of Ketchum *et al*. (2013), explains that the 16 mitochondrial haplogroups identified in the purported Sasquatch samples are consistent with modern humans, and their diversity suggests "these hominins did not originate in a single geographic location." This statement implies with good reason that the bride-stealing abductions and F1 hybrid births probably occurred in dif-

ferent times and places for each of the haplogroups, and, except for those belonging to American haplogroups (A, C, and D), these must have been Old World locations. But it is not good reason which authorizes the suggestion that these hybridization events represent the origin of a new hominin species (or subspecies, or hybrid species). In the Discussion section of their article, Ketchum *et al*. remark on the variety of human haplogroups, and imply something further, though ambiguous, about the relationship of the haplogroups to the time and route of their movement to North America:

"Of the 16 haplotypes, most were European or Middle Eastern in origin. African and American Indian haplotypes were also observed… With the wide variety of haplotypes in the study and especially with the majority of the haplotypes being European or Middle Eastern in origin, migration into North America by these hominins may have occurred previous to the migration across the Bering land bridge. This previous migration is supported by the Solutrean Theory.[41-42]"

The reasoning in this statement is unclear to me. Why the suggestion that Sasquatch migration would adhere to the timing and route of Sapiens migrations? It is true that the one proven pre-historic route of overland travel for Sapiens, from eastern Siberia through Beringia and into Alaska, was open for a limited time before rising sea levels covered the isthmus and separated the Asian and North American land masses about 11,000 years ago. But couldn't Sasquatch have crossed into North America by this route earlier than Sapiens did?

Regarding the movement of the SGP mtDNA human haplogroups from locations across Europe and Asia to North America, either theory has the same basic problem to overcome. For each of the Old-World human haplogroups represented in the contemporary North American Sasquatch population, it is necessary that an absolute minimum of one female carrier of childbearing capacity completed the journey to North America from the region in which that haplogroup was acquired by her ancestral matriline—a journey which had to be accomplished prior to the inundation of the Beringia isthmus about 11,000 years ago. For such an achievement, the human-hybrid Sasquatch theory suggests a more tenuous, less likely scenario than does mitochondrial introgression, because, as Ketchum *et al*. (2013) claim, an entirely new species had to coalesce in the Late Pleistocene, and some sizable portion of that population, including individual women belonging to each of the SGP haplogroups, had to migrate to North America. But without a pre-existing population base anywhere, as the human-hybrid young Sasquatch theory suggests, it would have been extremely difficult for any F1 hybrids to find unrelated hybrid mates. If a pair of hybrids did manage to find each other and did manage to reproduce, the prospects for their offspring would probably be even more challenging. It is more likely that the F1 hybrids would be claimed by un-mixed Sasquatch, and "backcrossing" between the would-be hybrid species and their parent form would bring them into the process of mitochondrial introgression and destroy the prospects for a hybrid species to develop. If the Sasquatch species were established in North America prior to the arrival of these human haplogroups, the process of mitochondrial introgression and replacement could have proceeded through this population *in situ*, and the minimum of about 11,000 years since the arrival of these mitochondrial lineages to North America could be enough time for this process to affect the entire continental population. Such a scenario comports with the research on mitochondrial introgression, especially those cases which are surprisingly extensive.

In their 2012 meta-analysis, "*The Biogeography of Mitochondrial and Nuclear Discord-*

ance in Animals," Toews and Brelsford explain, "Mitochondrial DNA has been shown to heavily introgress between interbreeding animal species that meet in new sympatric areas and, often, asymmetric introgression from local to the colonizing populations has been observed." The authors address a surprising pattern encountered in many of these studies:

"For those cases where foreign mtDNA haplotypes are found deep within the range of a second taxon, data suggest that those mtDNA haplotypes are more likely to be at a high frequency and are commonly driven by sex-biased asymmetries and⁄or adaptive introgression."

This pattern could be consistent with the mitochondrial introgression re-interpretation of the SGP mtDNA data: The range of haplogroups identified by Ketchum *et al.*, most of which (12 of 16) are incongruous with the North American sample collection sites, could be interpreted as an example writ large of foreign (Old World Sapiens) haplotypes found deep within the range of another species, the North American Sasquatch (the H-family haplogroups, representing Caucasian *H. sapiens*, the most prominent example). This pattern is yet more stark if we refer to Hart's (2020) revisions (discussed further below), established using *mtDNAble* software, to the SGP list of haplogroups, in which 14, or possibly 15, of the 16 haplogroups (accounting for 25 or 26 of the 27 corrected total Sasquatch mtDNA sample identifications) are incongruous with their North American collection sites. In the limited number of data so far collected, these foreign haplogroups do seem to be present at high frequency, given the fact that the "native" Sasquatch mtDNA remains unidentified.

In light of this research (Currat and Ruedi *et al*. 2008; Toews and Brelsford 2012) into biogeographic patterns of mitochondrial introgression, let us further hypothesize that the Sasquatch-Sapiens interbreeding was always the result of isolated younger Sasquatch males, with no mates and no prospects, acting alone, abducting Sapiens women as a natural recourse in times of necessity. And let us further hypothesize that these events occurred outside of the core Sasquatch range, on the periphery or frontier of its geographic distribution, where the solitary male would assume the character of an "invading" or "colonizing" species. These a-typical relations likely played out where the conspecific Sasquatch population was non-existent. In those times and places where Sapiens and Sasquatch core ranges meet or overlap, certain factors must inhibit inter-species pairing which are weakened or removed for the isolated Sasquatch male on the frontier, chiefly the potential availability of conspecific females. Young males coming of age would aspire to finding mates of their own kind, and if Sasquatch follows the pattern of social monogamy evident in other solitary mammals and primates (Lukas and Clutton-Brock, 2013), they would compete with any other males for exclusive access to one individual female. Those individuals who are unsuccessful in this competition would be pushed out of the territory of one male after another until either, (1) successfully attaching to the range of a single female and defending as their own territory an area encompassing her home range, or, (2) finding themselves beyond the range of all conspecific females and their male defenders or suitors. And in the latter scenario, the selection of mates would take on a new form and character more consistent with that of an invading or colonizing species.

8. HAPLOGROUP REVIEW

Haskell Hart (2020), as part of his analysis of the mutations in the SGP mtDNA data (discussed in Section 1) also reviews the set of SGP haplogroups using *mtDNAble* software. Table 1 incorporates Hart's corrected and revised list of the SGP Sapiens-Sasquatch hap-

logroups. They are listed in descending order of the estimated age plus one standard deviation, according to Behar *et al*. (2012); the age ranges represent one standard deviation above and one below the given estimates. The age estimates in this source are data-driven and generally more conservative (low) than estimates from other sources. The Behar *et al*. age estimates are likely to be revised higher in time, as additional data are introduced, especially for those haplogroups which have been identified most recently. Hart's revisions of the SGP Sasquatch-Sapiens mtDNA haplogroups improve the plausibility of these data by assigning corrected older groups and diversifying the set, but age estimates from Behar *et al*. which are too young also erode the plausibility of about seven samples.

Notes on Hart's (2020) revisions of the SGP mtDNA haplogroups: Sample 39b, originally identified as haplogroup T2 by Ketchum *et al*. (2013), has been corrected to R2'JT, which is estimated to be 37,000 years older. Sample 33, originally identified as H, is corrected to U5, which is about 32,000 years older. Sample 11, originally identified as A6L2c, has been corrected to haplogroup L2c3 containing allele A6, which is more than 9000 years older than haplogroup A6. None of these samples (39b, 33, and 11) seemed to be in conflict with the 11,000-years-ago closing of the Bering "land bridge" before revision of the haplogroups. However, four other samples with revised haplogroups (44, 26, 24, and 28) do appear to be in conflict, or possibly so, with the estimated ages given in Behar *et al*. (2012). Sample 44, originally identified as H2a2, has been corrected to the more plausible T2, which is estimated to be more than 10,000 years older. For Sample 26, Hart has identified two equally likely haplogroups, one of which, H5e, is nearly 3000 years older, and thus more plausible than the other, original identification, H1a. Samples 24 (originally H1s) and 28 (originally H1) are both revised to H1ba, which makes Sample 24 over 4800 years older, and therefore more plausible, but it renders the estimate for Sample 28 about 900 years younger than before. Whereas Ketchum *et al*. originally identify 12 samples representing seven different H haplogroups, Hart's revision includes only 10, in six or possibly only five different subgroups, and estimates for three of these samples (24, 26, and 44) are significantly improved in plausibility as noted above, whereas only Sample 28 is slightly weakened.

Referring to Table 1, it is clear that even the conservatively low age estimates of the haplogroups for 14 samples (39b, 140, 168, 33, 71, 117, 118, 81, 41, 42, 43, 44, 11, 95, 1, 2, 12, and 36) including the oldest lineages of the H haplogroup, are old enough that they could have been acquired in Europe or Asia thousands of years in advance of the inundation of the Bering isthmus. Haplogroup T2b, (represented by Samples 1, 2, 12, and 36) is the first one, chronologically, with an estimate from Behar *et al*. (2012) that post-dates the submergence of the land bridge, although 11,000 ybp (years before present) is well within one standard deviation. Four more samples (26, 28, 46, and 138), all representing H haplogroups, might be called borderline cases with 11,000 ybp barely within one standard deviation of the Behar *et al*. (2012) estimates. Samples 4 and 37, representing haplogroup H3, are two of the most problematic samples, with their estimated ages more than 2000 years and nearly two standard deviations too young to have crossed the Bering land bridge by about 11,000 ybp.

Recall that Sample 31 (the only representative of haplogroup L0d2a1) is one of the three samples (26, 31, and 140) with "next generation nuclear whole genome sequences" which Hart (2016, 2020) has shown to be mistakenly identified. For Sample 31, the nuclear DNA matches an un-mixed Sapiens, which is consistent (not discordant) with the mtDNA identification as Sapiens. So, as Hart (2020) suggests, the mtDNA for Sample 31 is probably

correctly identified, and therefore I think it can be removed from consideration as representing Sapiens DNA only. For Sample 140 (representing haplogroup D, one of the few Native American identifications), Hart maintains the nuclear DNA data match best with Canis, and therefore the mtDNA data is probably the result of human contamination on a canine sample. Like Sample 31, Sample 140 can be removed from consideration because it likely represents no Sasquatch DNA.

But the situation with Sample 26 is more complicated. Although the American black bear identification for the nuclear DNA of Sample 26 is well established in Hart (2016, 2020), Dr. Hart has also included the mtDNA of Sample 26 among the five samples which are most likely to represent authentic Sasquatch specimens (see page 82), a conclusion based in part on the presence of two mutations which it shares with the other four samples, mutations which are rare in humans but more common in other primates. As Hart acknowledges, this interpretation assumes that the mtDNA isolated from Sample 26 must have been present as Sasquatch contamination on a black bear tissue sample.

The original set of SGP haplogroups included only three Native American groups represented by a total of four samples: A (Sample 11), C (81), and D (140 and 168). Dr. Hart's (2020) revisions eliminate Sample 11 as erroneous, and for Sample 81, Hart introduces a second equally likely African haplogroup. If we also omit Sample 140 (as Sapiens mtDNA but not from Sasquatch), the data indicate a total of only two samples (81 and 168), or possibly only one (168), which represent American haplogroups in the remaining total of 27 SGP mtDNA samples identified as Sasquatch (29 field samples minus Samples 31 and 140). Referee 3 (to extend his or her quotation from the previous section, page 102) notes:

"It is also sticking that the entire mtDNA lineages of this new hominin is poorly human. One would expect at least some mtDNA genomes coming out as being accordance with this being a new hominin or if nothing els some of the mtDNA being Native American (everything being equal they have been in America more than 10,000 years) [*sic*]."

From the present vantage point, however, this peculiarity in the distribution of mtDNA lineages appears to extend and intensify the pattern in the overall set of SGP mtDNA haplogroups, a pattern consistent with the findings of Currat and Ruedi *et al*. (2008), in which "introgression can be detected beyond current areas of sympatry," and the findings of Toews and Brelsford (2012), in which "foreign mtDNA haplotypes are found deep within the range of a second taxon."

Finally, regarding the revisions of the most recent haplogroups, Hart (2020) notes: "There are discrepancies in some haplogroups. For samples 28, 31, 35, and 38 the addition of a suffix letter may just be that new haplogroups were determined since the Ketchum *et al.* references were published." This observation may help to explain the inadequate ages of the four remaining samples, identified as haplogroups H1ba (Samples 24 and 28), V2c (38), and H10e (35). These newly designated haplogroups are probably not yet represented by enough data to give accurate estimates of their true ages.

CONCLUSIONS

The present-day geographic distribution of "human" (Sapiens) mtDNA in the North American Sasquatch population could be the result of a long-term pattern of introgressive gene flow which began with rare hybridizing on the frontiers of the Sasquatch range, probably during times of population growth and range expansion. Sudden population decline and severe range contraction could have halted the process of mitochondrial replacement

for some mtDNA lineages, but it would be less likely to stop the introgression of all foreign mitochondrial lineages at once, because they had been initiated at different times and places over a long period and vast area. If the mitochondrial genome of the North American Sasquatch is the result of massive mitochondrial introgression, the success and distribution of the Sasquatch population probably depends *not at all* on the proliferation of any particular haplogroup within it. It is likely that some number of introgressive mtDNA lines died out before becoming established in the larger population, perhaps even a majority of them, but massive mitochondrial introgression appears to act independently of natural selection.

We are now better in position to grasp the enormous difference between two conditions which are consistently conflated in Ketchum, *et al*. (2013), on the SGP website, in Dr. Ketchum's social media posts and radio interviews, etc. Hybridizing which results, after many generations of backcrossing, in the proliferation of new mtDNA lineages throughout the gene pool or population of an invading species is known as mitochondrial introgression (or "massive" mitochondrial introgression, or "mitochondrial capture") and it does not by itself indicate the appearance of a new species. Nor does it present any good reason to modify the taxonomic status of the species involved, although the introgressed mitochondrial lineages may appear to present such a reason if one ignores the contrary implications of the nuclear DNA, which is unchanged. It seems likely that all evidence of an original or native mitogenome in the living Sasquatch population has been erased by completed mitochondrial introgression.

However, hybridizing which results in the creation of an entirely new hybrid species, distinct from both parent forms, is called "hybrid speciation," and Shumer and Rosenthal *et al*. (2014), distinguishing carefully between hybridizing and hybrid speciation, explain that, although the former is common in nature, hybrid speciation is quite rare among animals. Further, such a thesis could not be taken seriously on the basis of molecular evidence without type specimens and genomic data for each of the parent forms. Without such certain knowledge of the pre-existing "progenitor" species, there is no evidentiary basis for claims of hybrid speciation. Yet Ketchum *et al*. (2013) claim that the Sasquatch is a hybrid species without explaining why the more common phenomenon of mitochondrial introgression (hybridization without speciation) cannot be the correct interpretation of the same data. For Sasquatch, we do not yet possess the contemporary nuclear DNA nor the fossil evidence and ancient DNA which might confirm one or the other of these conflicting hypotheses. But hybrid speciation is extremely rare among mammals, whereas Currat and Ruedi (2008) argue that massive introgression of neutral genes into the exotic species is the most likely result of hybridizing between an established local species and a rare, colonizing or invading relative.

Mitochondrial introgression resulting from asymmetric interspecific gene flow could explain the SGP mitochondrial data more simply and fully than the human hybrid hypothesis advanced in Ketchum *et al*. (2013). Samples purported to be Sasquatch mtDNA could match Sapiens parameters and sequences without indicating the appearance of a new species, and so long as we lack mtDNA yielded from fossil evidence of Sasquatch which is older than the interbreeding events, we have no way of identifying Sasquatch mtDNA as it appeared in the Late Pleistocene prior to the initiation of gene flow.

Since the presence of Sapiens mitochondrial DNA has confounded efforts to identify "Sasquatch DNA" from the very beginning, understanding of these results has taken on two conflicting forms: (1.) The Sapiens mtDNA is evidence of error and/or misidentification, and therefore it constitutes accumu-

lating support for the non-existence of Sasquatch, which nevertheless remains the focus of a fanatically delusional subculture, and (2.) Sasquatch mtDNA is completely human, and therefore Sasquatch is substantially human, but how human is it? If the mitochondrial introgression hypothesis is correct, we can interpret the SGP mtDNA data as evidence of Late Pleistocene Sapiens-Sasquatch hybridizing, and yet understand that such limited hybridization need not have compromised the distinctness of either species. Instead it would be consistent with their distinctness at that time and in the present, as well as indicative of their common ancestry in an earlier period of hominid evolution. The Late Pleistocene interbreeding suggested by the SGP mtDNA data should not be understood to indicate the end of a species or the start of another. Rather, it is more likely that these data indicate a common pattern of massive mitochondrial introgression from a local, established species, into an invasive or colonizing cousin.

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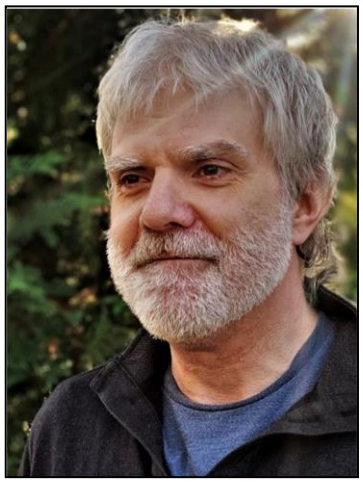

Kevin L. Harter is a 1991 graduate of Duke University, where he completed majors in Philosophy and Anthropology. After college he learned to play old-time string band music and then devoted most of 1993 and ’94 to graduate study with the UNC-Chapel Hill Curriculum in Folklore. From 1995 to ’98, he taught courses in folklore and Appalachian cultures for the James Madison University Dept. of Anthropology. From 2001 to 2019, Mr. Harter taught courses in Humanities for the JMU General Education Program and the Dept. of History. His mainstay course, “Great Works,” satisfied the Literature requirement for undergraduates, with content representing multiple periods, genres, and fields. Some core texts featured in Kevin’s syllabi included *Genesis*, Plato’s *Republic* and the early Socratic dialogues, Dante’s *Comedy*, More’s *Utopia*, Darwin’s *Descent of Man*, Freud’s *Civilization and Its Discontents*, and Margaret Atwood’s *Oryx and Crake.* As a fan of Plato, Kevin respects Academia and the Ph.D., and he may yet pursue a Doctoral degree himself, but doubts that he would have been led to write the present essay as a practicing Doctor of Philosophy. He hopes this work will foster greater mutual respect between Folklore and Science and help address the charge that no DNA evidence of Sasquatch exists. Kevin is fascinated with the covert co-existence and selective interaction of Sasquatch and Sapiens in rural and suburban environments. He plans to continue efforts to document such relationships among the Old Order Anabaptist farm families in the Shenandoah Valley of Virginia.

Table 1. Revised SGP mtDNA haplogroups in descending order of age plus one standard deviation.

SGP Samples	mtDNA Haplogroup Ketchum (2013)	Hart (2020)	Age of Revised Haplogroups ± one SD; Behar *et al*. (2012)
39b	T2	R2'JT	59,490—48,052
140, 168	D	D	43,172—33,695
33	H	U5	35,578—24,917
(71, 117, 118)	L3d	L3d	29,768—21,709
(81)	C	C	28,693—19,131
(71, 117, 118)	L3d	L3e4	22,748—10,965
41, 42, 43	T2	T2	21,861—16,771
44	H2a2	T2	
11	A6L2c	L2c3	20,325—10,811
(81)	C	L3e1b	16,004—8460
95	H	H	13,619—12,072
1, 2, 12, 36	T2b	T2b	11,679—8459
(26)	H1a	H5e	11,088—4263
29, 46, 138	H2a2	H2a2	11,000—7252
31	L0d2a	L0d2a1	10,340—3122
4, 37	H3	H3	9981—7856
24, 28	H1s, H1	H1ba	9870—2355
38	V2	V2c	8790—3683
(26)	H1a	H1a	8127—4487
35	H10	H10e	6952—2425