The origin of American Indian populations

With interest I have read the 2012 paper by Evenboer and Terborg[1]. The authors refer to the study by Moraga *et al*.[2] This paper presents information regarding mitochondrial DNA sequences (mtDNA) as observed in remains of prehistoric American Indians. Moraga *et al*.[2] mention that four haplotypes do not typically belong to four reference groups A, B, C and D. They suggest that artefacts could have been produced as a result of the analysis (PCR error or sequencing error) as well as contamination (DNA of people involved in the research). Alternatively, they suggest "these may be Native American haplogroups that were possibly infrequent in the past and that vanished".

The exclusive notion that four samples (025, 042, 608, and 715) do not fit a presupposed pattern, however, is no justification for the following remark by Evenboer and Terborg[1]:

> "The mtDNA of prehistoric Amerindians of the Andes clearly demonstrates a high frequency of non-classical haplogroups (A–D), which can *certainly* be interpreted as the fingerprint of non-Asian migrations [emphasis added]."

To me it remains unclear why the authors use the word 'certainly'. Where does this certainty come from? On the contrary, there are no arguments to conclude that these four samples would originate from non-Asian people.

My first objection against Evenboer and Terborg results from the dendrogram published by Moraga *et al*.[2]. The dendrogram shows clearly that the four disputed items (see figure below, disputed samples are indicated in red by me) fit the topology of the dendrogram (figure 1). The four samples cluster nicely along with both prehistoric and

extant Indian people. The samples are not placed close to the six non-American samples which were included as outgroup.

My second objection relates to how serious the observation is that the four samples cannot be fitted along with the grouping A–D. The dendrogram shows a fairly nice clustering of samples in groups A–D, but a number of crossovers can be observed as well. Crossovers of samples that were named as belonging to one group of A–D, but nevertheless do not cluster with other members in their group. On the basis of previous research a nomenclature was based on diagnostic mtDNA polymorphisms to classify samples into groups A–D. The dendrogram displays that for the remainder of the polymorphisms a sample (e.g. 017), in spite of having the C identity, shows higher similarity to the body of A samples. Therefore the A–D criteria for haplotype nomenclature cannot be viewed as an absolute criterion among the bona fide samples. Therefore, if the presence of such a diagnostic character cannot be used as a hard criterion for clustering, then the absence of such a diagnostic polymorphism cannot be used as a hard criterion for the conclusion of Evenboer and Terborg on a non-American identity.

My third objection is that Evenboer and Terborg did not refute the arguments by Moraga *et al.*[2] that "these may be Native American haplogroups that were possibly infrequent in the past and that vanished".

The next sentence of Evenboer and Terborg is equally remarkable:

> "Unfortunately, the authors *did not further elaborate* on the origin of these 'alien' haplogroups, but rather chose to *explain away* these interesting findings—since the data point to the East, i.e. Europa and Africa [emphasis added]."

In my opinion there is no reason to suggest that Moraga *et al.*[2] have downplayed any of the information provided by these four samples. Moraga *et al.* mention the usual explanations and continue to present also for these four samples every detail. Moraga *et al.*[2] only say that the four do not fit the standard A–D nomenclature, and refrain from further conclusions for obvious reasons. There is no further conclusion to be drawn.

However, if these four samples were indeed highly remarkable and make the basis for their own paper, then I would have expected Evenboer and Terborg to perform those analyses. Evenboer and Terborg accuse Moraga *et al.*[2] for their lack of further elaboration, but Evenboer and Terborg made no effort either to demonstrate the value of these samples for their conclusions. Since Moraga *et al.*[2] in 2005 and the paper by Evenboer and Terborg[1] in 2012, a lot of new data on mtDNA haplotypes have become available. Perego *et al.*[3] already showed a much larger number of American founder haplotypes. I conclude that Evenboer and Terborg made no effort to re-analyse the data of Moraga *et al.*[2] to arrive at a *de novo* identification of the origin of these four mtDNA haplotypes, although this was possible in 2012. Indeed others elaborated on mtDNA haplotypes as shown by the publication of Behar *et al.*[4] almost simultaneously in 2012. Behar *et al.*[4] provide the information we need.

Behar *et al.*[4] also released tools at www.mtdnacommunity.org to allow every individual to compare any mtDNA relative to all known haplotypes. So I have searched for sample 608 (in Moraga *et al.*[2]) the A16293C as well as the T16311C polymorphism, but found no hit. So at these two nucleotide positions never ever before a mutation

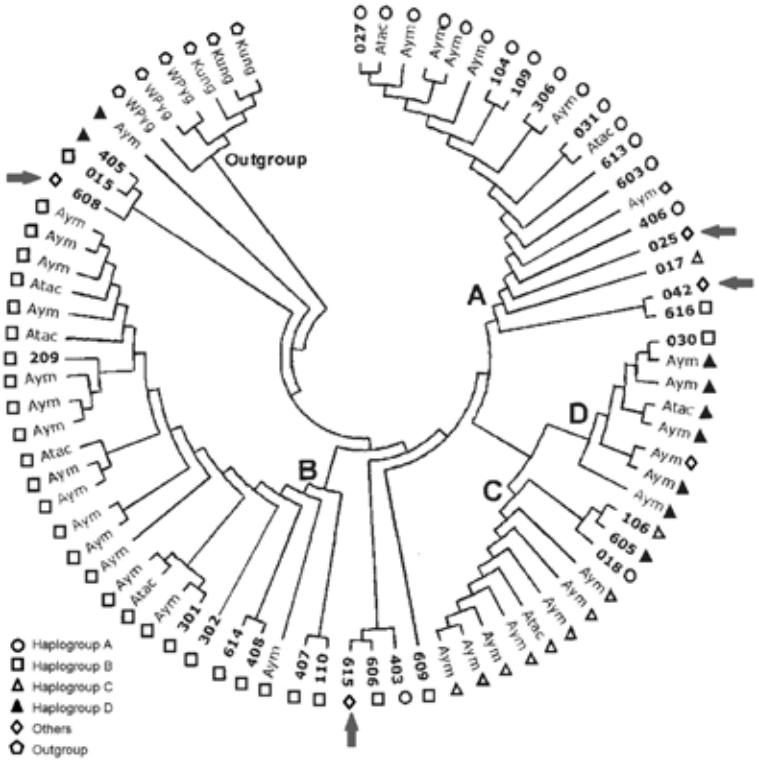

Figure 1. Dendrogram modified after Moraga *et al.*[2] showing variability in the mtDNA hypervariable region I, among prehistoric and extand individuals of desert valleys of northern Chile. Numbers represent sample identification codes. Arrows indicate four deviating samples that were interpreted by Evenboer and Terborg[1] as migrants of non-American origin. However, these individuals nicely cluster along with samples having American haplogroups. The four deviating individuals certainly do not cluster within or near non-American outgroup samples.

was found across a global sample of all currently known mtDNA samples. This makes the earlier explanation of a PCR artefact much more likely. Further analysis for the remaining four samples did not allow me to find evidence for a non-American origin of these samples.

In conclusion, so far I have not been able to see any reason for Evenboer and Terborg to suggest a non-American origin of mtDNA in the Moraga *et al.*[2] data. Furthermore their conclusion for pre-Columbian migrations from the East to America is utterly without evidence.

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» Peer Terborg and Tjarko Evenboer reply:

Before commencing our rebuttal, we would like to note that in the Netherlands an uncompromising dispute is ongoing between the neo-Christians, better known as theistic evolutionists, and Christians who still believe God created through his Word as it is written in Genesis. It is a pleasure, therefore, to see that Dutch theistic evolutionists, such as Dr Van Eck, are reading creation science journals. We really appreciated his comments and we are happy to reply to his critiques.

In his letter, Van Eck states:

> "Moraga *et al.* mention that four haplotypes do not typically belong to four reference groups A, B, C, D. They suggest that artefacts could have been produced as result of the analysis (PCR error or sequencing error) as well as contamination (DNA of people involved in the research)."

We agree that artefacts can never be completely excluded. However, the possibility of contamination was excluded by the authors, who wrote:

> "The precautions taken with respect to these issues (see Material and Methods) make this explanation unlikely. Moreover, only one of us (M.M.) was in direct contact with the samples. He belongs to haplogroup C, and its HVR I sequence is different from the sequences obtained for the two specimens classified as C."

Therefore, we fully agree with the Moraga *et al.* suggestion that

> "… these [haplotypes] may be Native American haplogroups that were possibly infrequent in the past and that vanished ... ."

Of course, the origin of these haplotypes is unknown, but their existence supports the hypothesis of additional pre-Columbian migration unrelated to migrations from Asia. A low frequency of non-classical haplotypes (and loss through genetic drift) is what might be expected if the founder population from Europe and/or North Africa mixed with ancient Amerindians already living on the South American continent.

Our argument was a strong one, since we focused on mtDNA isolated from *pre-Columbian* bones, so admixture with mtDNA that arrived after Columbus reached the continent could be excluded. In the samples of pre-Columbian mtDNA, >20% did not fit the haplogroups we *currently* observe in Amerindian populations (A–D). Therefore, we wrote:

> "The mtDNA of prehistoric Amerindians of the Andes clearly demonstrates a high frequency of non-classical haplogroups (A–D), which can certainly be interpreted as the fingerprint of non-Asian migrations."

To Van Eck it remains unclear why we use the word *certainly* and he argues, based on the additional research of Moraga *et al.*, that there are no arguments to conclude that these four samples would originate from non-Asian people. He argues that the dendrogram of mtDNAs (see figure) of both modern and pre-Colombian mtDNAs reveals:

> "… the pre-Columbian samples cluster nicely along with both prehistoric and extant Indian people. The samples are not placed close to the six non-American samples which were included as outgroup."

A careful reading of Moraga *et al.* demonstrates that the non-American outgroup consists of Kung (Koi San) and Western African Pygmy mtDNAs. It is hardly surprising, therefore, that the non-classical Amerindian mtDNA do not cluster with this outgroup: Kung and Pygmy mtDNAs would also serve as outgroup for European and/or North African mtDNA sequences. Interestingly, the dendrogram also shows that the pre-Columbian mtDNA (608) forms a small *sister group* with mtDNA samples (015 and 405) to the classical haplotypes (A–D). Although this indicates that non-classical pre-Columbian Amerindian mtDNAs are still present in extant populations, it does not reveal the origin of these haplotypes (which could still be Europe and/or North Africa as argued in our paper).

Van Eck's second objection relates to how serious the observation is that the four samples cannot be fitted along with the grouping A–D. We would like to point out here, that the dendrogram (the figure included by Van Eck) not only shows a fairly nice clustering of

samples in groups A–D, as he rightfully asserts, but it also demonstrates a novel non-classical sister group including the pre-Columbian haplotype, confirming our hypothesis of non-Asian admixture (as discussed above).

Furthermore, Van Eck argues that a number of crossovers can be observed that "in spite of having the C identity shows higher similarity to the body of A samples". The problem here is that crossovers of different haplotypes to form 'hybrids' is merely a theoretical justification for mixed ('unexpected') observations. We would like to ask him: How and where do mtDNAs of C and A haplotypes meet to engage in crossovers? Our answer would be: nowhere. MtDNA are inherited only via the female germ line cells, can only be of one haplotype, and crossovers between two haplotypes will simply never occur in real biology. Therefore, the correct explanation for the observed 'hybrids' may rather be found in non-random mutations, a phenomenon also observed for mtDNA sequences. Non-random mutations, i.e. hot-spot mutations, will arrange for sequence characteristics that are indistinguishable from common descent and/or crossovers.[1]

Van Eck's third objection is that we have not refuted the argument that "these may be Native American haplogroups that were possibly infrequent in the past and that vanished". Here, we agree that we did not refute this observation, rather we elaborated on it. As explained above, the origin of these haplotypes is unknown—they may be Native American—but considering the data presented by Van Eck (see dendrogram) their presence as a sister group to the A–D haplotypes still supports our hypothesis of additional pre-Columbian migrations unrelated to migrations from Asia. Then, Van Eck seems to suggest that we would reproach Moraga *et al.* for downplaying information provided in his studies and argues:

> "Moraga *et al.* mention the usual explanations and continue to present also for these four samples every detail. Moraga *et al.* only say that the four do not fit the standard A–D nomenclature, and refrain from further conclusions for obvious reasons. There is no further conclusion to be drawn."

The problem here lies in "the usual explanations". We are fully aware of the usual explanations and assumptions of these types of studies. One of the explanations that will never be considered is: Maybe there was an ancient gene flow unrelated to the Asian, probably from Europe and/or North Africa towards the Americas. Another explanation never considered is: Maybe the accumulation of mutations in mtDNA sequences is not entirely random. The ruling paradigms regarding origins ('evolution') prohibit these explanations. Ruling paradigms will hardly ever be openly questioned. As demonstrated by Moraga *et al.*, the possibility of a non-Asian admixture is not even mentioned, because the ruling paradigm is that Amerindians stem from Asia. Let alone non-random mutations that give an impression of common descent and/or mtDNA crossovers, which would overturn a lot of Darwinian 'justifications'.

Our whole world and world view has to adapt to 'ruling paradigms' which, as history shows, have always been wrong. So why adapt to ruling paradigms, which will eventually be false anyway? As Christians, we better rethink what science is; what it really shows us, and whether we choose to adapt to the Darwinian, but false paradigm, or do research ourselves and put forward novel hypotheses and models that are consistent with the observations *and* our world view.

Finally, we are grateful and thank Herman van Eck for providing some interesting links regarding this interesting topic, although they do not shed further light on the origin of Amerindians. We would also like to draw his attention to the fact that recently more genetic evidence (mtDNA and chromosomal) was uncovered linking the genetics of Amerindians to Europe *and* East Asia.[2,3] So, a non-Asian genetic fingerprint in native Amerindians is now undisputable. That this is uncovered only now, after the sequencing of ancient genomes, may communicate that we cannot comprehend the origin of genomes from DNA data obtained from living organisms. Christian scientists should therefore be cautious about adapting to Darwinian interpretations.

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