

From: Jim Wilson

To: Mark Thomas and David Balding

Date: 30/8/2012

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Dear David and Mark

Thank you for your emails.

BritainsDNA is committed to the highest standards of interpretation of ancestry, based on peer-reviewed literature and also using newer, as yet unpublished markers, e.g. from the 1000 Genomes project or sequencing we have carried out. I reject utterly your published claims of BritainsDNA being a “fraudulent commercial enterprise”. I think this is defamatory. We do not peddle genetic nonsense for profit.

One of the main reasons for being involved in BritainsDNA is to facilitate public understanding of science. I have contributed to many documentaries over the last five years, two of which won Irish Film & Television Academy awards, and which bring genetics to the public. BritainsDNA provides further opportunities in this area. For instance we run events which educate people about DNA and genetic history – there is nothing that fires people up more than learning about their own DNA. Inevitably some things must be simplified in order to get the message across. That is the nature of explaining things to lay people.

You take issue with the pricing of ancestry tests. I note that BritainsDNA’s prices are considerably lower than those provided by other UK-based companies, one of which offers testing of the Y chromosome and mtDNA for £369, almost double the price at BritainsDNA.

You hope that there are research spin offs and I am also happy that BritainsDNA is engaged in research through, among other things, whole Y chromosome sequencing to identify new markers which increase the resolution of the Y chromosome genealogy, and using deep pedigrees to derive better estimates of the mutation rate. There will be further opportunities arising from the largest database of well provenanced, high resolution Y chromosome and mtDNA haplotypes from the British Isles, and in the future autosomal variation as well.

While it is true that the Y chromosome and mtDNA only represent a small proportion of our ancestral lineages, they are the ones about which we can learn the most information. A focus on the Y chromosome is popular with the public, probably for the same reasons that traditional genealogy often focusses on the surname – the custom in western countries that the surname is inherited from the father, just as the Y chromosome is; people identify themselves with this particular lineage. The Y chromosome is also special because of its length, which of course is inherited whole from father to son. Two individuals sharing a Y chromosome share a similar amount of DNA to a pair of third or fourth cousins. It is in most cases the single largest block of DNA a man inherits from any ancestor eight or more generations ago.

With regard to Alistair Moffat’s live interview on the Today programme I am afraid I disagree with a number of the points in your letter to him and was particularly disappointed in what appeared to be an intemperate, misconceived and insulting approach to what he had said.

The claim that Adam and Eve really existed, as you suggest, refers to the most recent common ancestors of the mtDNA and non-recombining part of the Y chromosome. I don't agree that there is nothing special about these individuals: there must have been a reason why mitochondrial Eve was on the front cover of Time magazine in the late 80s! You will be aware that it would take the best part of a one hour documentary to explain the variation in time to most recent common ancestor at different genetic loci, differences in effective population size between the Y, X and autosomes, and all the other subtleties you list. As stated above, in the material returned to BritainsDNA customers it is made clear that these are only two lineages among many others.

The effect of the Toba event is much argued about and we provide both sides of the debate in the text customers are given.

Phylogeography is a well-accepted approach in population genetics of humans and other species. As you will know phylogeographic inference formed one of the first main planks of evidence for the recent African origin of modern humans. There are papers in the American Journal of Human Genetics using this approach almost every month.

With regard to the Berber ancestry, I find it amusing that you consider that an ancient Scottish migrant enjoying reproductive success in the Sahara could explain the distribution of the M81 Y chromosome lineage in North Africa. In some Berber villages, over 80% of the sampled men carry this marker. Neither do I find it likely that the sharing of this haplotype between some modern day Scots and Berbers is due to descent from a common ancestor in some other part of the world, given published work inferring the origin of M81 about 5600 years ago in the Maghreb (Cruciani et al Am J Hum Genet 74: 1014-22, 2004; Semino et al Am J Hum Genet 74: 1023-34, 2004; Arredi et al Am J Hum Genet 75: 338-45, 2004).

Alistair acknowledges that he used the wrong word, mutations, rather than branches, when referring to the L1b1a1 mtDNA. The figure for the frequency of the Cohen Modal Haplotype among Cohanim was misstated, as was any specific claim about the Queen of Sheba's DNA, however I disagree that we cannot know if there were HV lineages present in the relevant region 3000 years ago.

It would of course be better if these small errors had not slipped in, but your other points are simply differences in opinion or inference. Alistair Moffat is a historian and as such is able to form his own opinions and interpretations of the evidence. As you know I was not on the programme.

It must always be borne in mind that in five minute radio interviews time is very short and when live the words are "as spoken" – a person might not use identical words if given the time to write out a text of the same length.

There is also simply no time to put across all the nuances; this is not the same as misleading the public. As you will also be aware I have no control over what the BBC decide to feature in their shows – and neither can Alistair Moffat.

It appears that you reject the notion we can learn anything about our ancestry from our DNA and thus the entire genetic ancestry testing industry, including 23andMe, FTDNA, the National Geographic project and others are without a basis in science. I think you will find that many others disagree with you, including Dr Joanna Mountain, Dr Spencer Wells, Dr Doron Behar and Prof Mike Hammer, whom I see from the relevant websites are closely associated with the named companies.

Encouraging your colleagues to expose misleading claims made by some companies can only be a good thing – I know of one company which sells a “Tribes of Britain” test which appears to simply assign men carrying Y chromosome haplogroup R1b to “Celtic”, those carrying an I haplogroup to “Anglo-Saxon” and those carrying the R1a group to “Viking”!

Indeed I recall a programme called 100% English on Channel 4 in November 2006 which it appears Mark Thomas was the consultant for (<http://www.imdb.com/title/tt0907295/fullcredits#cast>), and which used a deeply flawed ancestry test with 8 people who considered themselves to be 100% English. When I first saw this I thought it was a spoof, the celebrities appear to have been chosen for their strong views that they are “purely” English and the tests apparently contradicted this. However, tests using large numbers of autosomal markers and model-based inference of either the proportions or probabilities of ancestry in different clusters (Structure-like programmes) generally find typical English people to be of ~100% European ancestry, and not to have significant components of West Asian or South Asian, as claimed in the programme. Either the contributors to the programme were chosen from the extremes of the distribution of ancestry or the test was not accurately inferring ancestry. There is in fact evidence that the (now discontinued) DNAPrint test which was used is inaccurate – and this was available before the programme came out (e.g. <http://www.kerchner.com/cgi-bin/dnaprint.cgi>). The small number of markers used and poor representation of global populations in the reference panel probably contribute to the inaccuracy. While the programme participants’ ideas of racial purity are clearly bunkum, it appears that analysis with many unlinked autosomal markers can differentiate some populations rather well. I don’t know that the reasons are well known, but it is probably due to endogamy within Europe and in many other smaller populations or subpopulations over the last few hundred years or longer. This must have been sufficient to generate small allele frequency differences at many markers, the sum of which is then picked up by these tests. It’s a pity that these subtleties could not be addressed even with an hour’s airtime.

I am fully committed to improving the genetic ancestry products available to customers and also to increasing public understanding of science in this area and feel that I have already contributed to this ideal in no small way through the establishment of BritainsDNA, giving many public talks and contributing to television and radio broadcasts.

With best wishes

Jim

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