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Invited reply

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Response to Edward and Barnett

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We appreciate notification of the error in Sykes *et al.* [1], where we matched mitochondrial 12S RNA sequence recovered from two ‘yeti’ hair samples found in Ladakh, India (no. 25025, >40 years old) and Bhutan (no. 25191 >10 years old) with GenBank accessions recovered from the jawbone of a Pleistocene polar bear *Ursus maritimus* described in Lindqvist *et al.* [2]. The matches were instead to a modern specimen of *U. maritimus* from the Diomed Islands in the Bering Sea reported in the same paper. The error was caused by an incomplete GenBank search linking the sample to the paper rather than to the individual isolate. Although the error is certainly unfortunate, it does not change the conclusion that the sequences recovered from the ‘yeti’ hairs connect to *U. maritimus* nor does it invalidate any of the possible explanations discussed in the paper. Importantly, for the thrust of the paper as a whole, the conclusion that these Himalayan ‘yeti’ samples were certainly not from a hitherto unknown primate is unaffected.

For clarification and in response to the well-known technical issues of DNA degradation painstakingly elaborated by Edwards and Barnett, we can confirm that the raw data from each of the two samples in question was of excellent quality. Both samples amplified extremely well, giving DNA yield equal to that of the positive HL60 control. Sample no. 25191 was about 10 years old, well within the age range of samples typically tested in the laboratory. At more than 40 years, sample no. 25025 was considerably older than no. 25191, but gave equally good amplification products. In our experience, damaged DNA sites appear where there is low copy template in samples of advanced age, but we saw no sign of this in either sample. Sanger data were unambiguous, with no evidence in either sample of any mixture at position 1751 or any other position. Each sample underwent thorough cleaning prior to extraction, all negative controls associated with the samples were free of contamination, and each sample was analysed individually. We have no reason to doubt the accuracy of these two sequences any more than the other 28 presented in the paper, each of which showed 100% matches to a known mammalian species.

We stressed in the original paper that the true identity of this intriguing animal needs to be refined, preferably by sequence data from fresh tissue samples derived from a living specimen where DNA degradation is no longer a concern.

References

1. Sykes BC, Mullis RA, Hagenmuller C, Melton TW, Sartori M. 2014 Genetic analysis of hair samples attributed to yeti, bigfoot and other anomalous primates. *Proc. R. Soc. B* **281**, 20140161. (doi:10.1098/rspb.2014.0161)
2. Lindqvist C *et al.* 2010 Complete mitochondrial genome of a Pleistocene jawbone unveils the origin of polar bear. *Proc. Natl Acad. Sci. USA* **107**, 5053–5057. (doi:10.1073/pnas.0914266107)

The accompanying comment can be viewed at <http://dx.doi.org/10.1098/rspb.2014.1712>.