**Supplemental text 1. Genetic analyses**

The sample was first decontaminated with a 6% household bleach solution for 10 min and rinsed with molecular grade water. The tooth was ground with a dental drill and 250 mg of the resulting powder was decalcified and digested in 1mL of 0.5 M EDTA and 1mg of proteinase K at 56º C while incubating with mild rocking for 24 h. DNA was subsequently recovered from the supernatant using the Wizard SV kit PCR Clean-Up System (Promega). The extraction procedure was carried out twice.

Hypervariable Region I (HVRI) of the mitochondrial DNA was PCR-amplified using the following three sets of overlapping sets of primers to obtain sequence for a 400-bp region (Raff et al., 2010): P1F (16023-16043) 5’ GTTCTTTCATGGGGAAGCAG 3’ and P1Rb (16182-16160) 5’ TTTGATGTGGATTGGGTTTTT 3’; P2Fb (16163-16182) 5’ AAAACCCAATCCACATCAAA 3’ and P2R (16296-16278) 5’ GGGTGGGTAGGTTTGTTGG 3’; and\_P3F (16266-16288) 5’ CCCACTAGGATACCAACAAACC 3’ and P3R (16422-16402) 5’ ATTGATTTCACGGAGGATGG 3’. PCR products were visualized by acrylamide: bisacrylamide gel electrophoresis and sent for purification and sequencing (both strands) to Macrogen (Seoul, Korea). The sequences were manually edited, then aligned and compared with the revised Cambridge Reference Sequence (rCRS; Andrews et al. 1999) using Sequencher 5.3 (Gene Codes Corporation). Haplogroup was assigned using estimates from the web application HaploGrep 2.0 (Kloss-Brandstaetter et al. 2011; http://haplogrep.uibk.ac.at/), based on PhyloTree (Build 17; van Oven and Kayser, 2009).

Sex was estimated by PCR amplification of the amelogenin gene with the primers Forward 5’ CCCTGGGCTCTGTAAAGAATAGTG 3’ and Reverse 5’ ATCAGAGCTTAAACTGGGAAGCTG 3’ (Sullivan et al., 1993). The sizes of the PCR product were analyzed by polyacrylamide gel electrophoresis. Male sex is assigned when fragments of both the X (106 base pairs) and Y (112 base pairs) chromosomes are observed, while female sex is given when only the X chromosome fragment is amplified.

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