


Letter

Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans

J. Víctor Moreno-Mayar, Ben A. Potter, Lasse Vinner, Matthias Steinrücken, Simon Rasmussen, Jonathan Terhorst, John A. Kamm, Anders Albrechtsen, Anna-Sapfo Malaspinas, Martin Sikora, Joshua D. Reuther, Joel D. Irish, Ripan S. Malhi, Ludovic Orlando, Yun S. Song, Rasmus Nielsen, David J. Meltzer & Eske Willerslev 

Nature **553**, 203–207 (11 January 2018)

doi:10.1038/nature25173

Download Citation

Biological anthropology

Next-generation sequencing Population genetics

Received: 29 March 2017

Accepted: 26 November 2017

Published online: 03 January 2018

Abstract

Despite broad agreement that the Americas were initially populated via Beringia, the land bridge that connected far northeast Asia with northwestern North America during the Pleistocene epoch, when and how the peopling of the Americas occurred remains unresolved^{1,2,3,4,5}. Analyses of human remains from Late Pleistocene Alaska are important to resolving the timing and dispersal of these populations. The remains of two infants were recovered at Upward Sun River (USR), and have been dated to around 11.5 thousand years ago (ka)⁶. Here, by sequencing the USR1 genome to an average coverage of approximately 17 times, we show that USR1 is most closely related to Native Americans, but falls basal to all previously sequenced contemporary and ancient Native Americans^{1,7,8}. As such, USR1 represents a distinct Ancient Beringian population. Using demographic modelling, we infer that the Ancient Beringian population and ancestors of other Native Americans descended from a single founding population that initially split from East Asians around 36 ± 1.5 ka, with gene flow persisting until around 25 ± 1.1 ka. Gene flow from ancient north Eurasians into



Native Americans took place 25–20 ka, with Ancient Beringians branching off around 22–18.1 ka. Our findings support a long-term genetic structure in ancestral Native Americans, consistent with the Beringian ‘standstill model’⁹. We show that the basal northern and southern Native American branches, to which all other Native Americans belong, diverged around 17.5–14.6 ka, and that this probably occurred south of the North American ice sheets. We also show that after 11.5 ka, some of the northern Native American populations received gene flow from a Siberian population most closely related to Koryaks, but not Palaeo-Eskimos¹, Inuits or Kets¹⁰, and that Native American gene flow into Inuits was through northern and not southern Native American groups¹. Our findings further suggest that the far-northern North American presence of northern Native Americans is from a back migration that replaced or absorbed the initial founding population of Ancient Beringians.

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Acknowledgements

The Upward Sun River excavations and analysis were conducted under a Memorandum of Agreement (MOA) signed by the State of Alaska, the National Science Foundation, the Healy Lake Tribal Council and the Tanana Chiefs Conference. We appreciate the cooperation of all parties. We thank M. Allentoft, S. Gopalakrishnan, T. Korneliussen, P. Librado, J. Ramos-Madrigal, G. Renaud and F. Vieira for discussions, and the Danish National High-throughput Sequencing Centre for assistance with data generation. GeoGenetics members were supported by the Lundbeck Foundation and the Danish National Research Foundation (DNRF94) and KU2016. J.V.M.-M. was supported by Conacyt (Mexico). Samples were recovered during excavations by B.A.P. supported by NSF Grants 1138811 and 1223119. Research was supported in part by NIH grant R01-GM094402 (M.St., J.T., J.A.K. and Y.S.S.) and a Packard Fellowship for Science and Engineering (Y.S.S.). Y.S.S. is a Chan Zuckerberg Biohub investigator. D.J.M. is supported by the Quest Archaeological Research Fund. A.-S.M. is supported by the Swiss National Science Foundation and the ERC.

Author information

J. Víctor Moreno-Mayar, Ben A. Potter & Lasse Vinner

These authors contributed equally to this work.

Affiliations

Centre for GeoGenetics, Natural History Museum of Denmark, University of Copenhagen, 1350 Copenhagen, Denmark

J. Víctor Moreno-Mayar, Lasse Vinner, Anna-Sapfo Malaspinas, Martin Sikora, Ludovic Orlando, Rasmus Nielsen, David J. Meltzer & Eske Willerslev

Department of Anthropology, University of Alaska, Fairbanks, Alaska 99775, USA
Ben A. Potter & Joshua D. Reuther

Department of Biostatistics and Epidemiology, University of Massachusetts, Amherst, Massachusetts 01003, USA

Matthias Steinrücken



Department of Ecology and Evolution, University of Chicago, Chicago, Illinois 60637, USA

Matthias Steinrücken

Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark, 2800 Kongens Lyngby, Denmark

Simon Rasmussen

Department of Statistics, University of California, Berkeley, California 94720, USA
Jonathan Terhorst, John A. Kamm, Yun S. Song & Rasmus Nielsen

Department of Statistics, University of Michigan, Ann Arbor, Michigan 48109, USA
Jonathan Terhorst

Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, UK

John A. Kamm & Eske Willerslev

The Bioinformatics Centre, Department of Biology, University of Copenhagen, 2200 Copenhagen, Denmark

Anders Albrechtsen

Department of Computational Biology, University of Lausanne, Lausanne, Switzerland
Anna-Sapfo Malaspinas

Swiss Institute of Bioinformatics, 1015 Lausanne, Switzerland

Anna-Sapfo Malaspinas

Research Centre in Evolutionary Anthropology and Palaeoecology, Liverpool John Moores University, Liverpool L3 3AF, UK

Joel D. Irish

Department of Anthropology, University of Illinois at Urbana-Champaign, Urbana, Illinois 61801, USA

Ripan S. Malhi

Carle R. Woese Institute for Genomic Biology, University of Illinois at Urbana-Champaign, Urbana, Illinois 61801, USA

Ripan S. Malhi

Computer Science Division, University of California, Berkeley, California 94720,



Yun S. Song

Chan Zuckerberg Biohub, San Francisco, California 94158, USA

Yun S. Song

Department of Integrative Biology, University of California, Berkeley, California 94720, USA

Rasmus Nielsen

Department of Anthropology, Southern Methodist University, Dallas, Texas 75275, USA

David J. Meltzer

Department of Zoology, University of Cambridge, Downing Street, Cambridge CB2 3EJ, UK

Eske Willerslev

Contributions

The project was conceived by E.W. and B.A.P. and headed by E.W. L.V. processed ancient DNA. J.V.M.-M. and S.R. assembled datasets. J.V.M.-M., M.St., J.T., J.A.K. and A.A. analysed genetic data. B.A.P. led the USSR field investigation and B.A.P. and D.J.M. provided anthropological contextualization. B.A.P., J.D.R. and J.D.I. conducted archaeological and bioanthropological work. R.N., Y.S.S., M.Si., A.-S.M., and L.O. supervised bioinformatic and statistical analyses. B.A.P. engaged with indigenous communities. J.V.M.-M., B.A.P., D.J.M. and E.W. wrote the manuscript with input from L.V., A.-S.M., M.Si., R.S.M., L.O., Y.S.S, R.N. and the other authors.

Competing interests

The authors declare no competing financial interests.

Corresponding author

Correspondence to Eske Willerslev.

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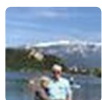
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Patricia Birch • 9 days ago

Very interesting paper. But please edit the abstract: "Inuits" is not a word: Inuit ("the people") is already plural, the singular being Inuk.

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John Ensminger • 2 days ago

This comment may only be appropriate for certain of the authors of this paper who are associated with the excavations at Sun River. I would appreciate any information as to whether there is any evidence that there may have been dogs at the Sun River site. I do not see any

