

# An Arctic Lens for American Migration: Integrating Genomics, Archaeology and Paleoecology

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## Introduction.

The original peopling of the Western Hemisphere consisted of both a period of isolation for the development of a recognizable Native American genome and a dispersal from an area of extreme Northwest North America or Northeast Siberia. Genetic and paleoecological data strongly suggest that Beringia was the point of origin for early American dispersals, although the archaeological record of a Beringian population during the Last Glacial Maximum (LGM) has, until recently, been lacking.

## Methods.

We use molecular genetic methods to document prehistoric diversity in both human and archaeofaunal material in coastal and interior Alaskan archaeological sites. The molecular data are merged with zooarchaeological analyses and new data on the paleoecology and archaeology of Beringia to infer multiple dispersals across northern latitudes in the Americas.

## Results.

Genetic analyses indicate that both Paleo- and Neo-Inuit derive from the same source population as the much earlier dispersal of Native American populations throughout the hemisphere. Moreover, mtDNA genomic analyses of the earliest human remains in the North American arctic are suggestive that the original Beringian population was characterized by greater diversity than is present in modern arctic populations, or in Paleo- or Neo-Inuit groups.

## Conclusions.

Coupled with new archaeological evidence of people in both Northwest and Northeast Beringia prior to 25kya, the molecular data support the hypothesis of a substantial population isolated in the south central portion of the Bering land bridge during the LGM. This population was genetically diverse, perhaps subdivided, and served as the source for both the early dispersal of Native American populations throughout the hemisphere between ~17-14kya, and the Paleo- and Neo-Inuit migrations at ~5kya and 800ya, respectively.

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## References (maximum three)

Hoffecker, J.F., S.A. Elias, **D.H. O'Rourke**, G.R. Scott and N.H. Bigelow (2016) Beringia and the Global Dispersal of Modern Humans. *Evol. Anthropol.* 25:64-78. DOI: 10.1002/evan.21478.

Tackney, J., B.A. Potter, J. Raff, M. Powers, S. Watkins, D. Warner, J.D. Reuther, J.D. Irish, and **D.H.O'Rourke** (2015) Two Contemporaneous Mitogenomes from Terminal Pleistocene Burials in Eastern Beringia. *Proc.Natl.Acad.Sci.,USA*, [www.pnas.org/cgi/doi/10.1073/pnas.1511903112](http://www.pnas.org/cgi/doi/10.1073/pnas.1511903112)

Tackney, J., J.B. Coltrain, J. Raff and **D.H. O'Rourke** (2016) Molecular Windows on Arctic Prehistory. In: Handbook of Arctic Archaeology. O. Mason and M. Friesen, eds. Oxford University Press: London.