

Mitochondrial genome analysis revises view of the initial peopling of North America

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The initial peopling of North America from Asia occurred approximately 15,000-18,000 years ago, however estimations of the genetic diversity of the first settlers have remained inaccurate. In a report published online today in *Genome Research*, researchers have found that the diversity of the first Americans has been significantly underestimated, underscoring the importance of comprehensive sampling for accurate analysis of human migrations.

Substantial evidence suggests that humans first crossed into North America from Asia over a [land bridge](#) called Beringia, connecting eastern Siberia and Alaska. Genetic studies have shed light on the initial lineages that entered North America, distinguishing the earliest Native American groups from those that arrived later. However, a clear picture of the number of initial migratory events and routes has been elusive due to incomplete analysis.

In this work, an international group of researchers coordinated by Antonio Torroni of the University of Pavia in Italy performed a detailed mitochondrial [genome](#) analysis of a poorly characterized lineage known as C1d. [Mitochondrial DNA](#) (mtDNA) is passed down through the maternal lineage, and mtDNA sequence markers are extremely useful tools for mapping ancestry. Similar to other haplogroups that were among the first to arrive in North America, C1d is distributed throughout the continent, suggesting that it may have been also present in the initial founding populations. However, C1d has not been well represented in previous [genetic analyses](#), and the estimated age of approximately 7,000 years, much younger than the other founding haplogroups, was likely inaccurate.

To resolve these inconsistent lines of evidence, the group sequenced and analyzed 63 C1d mtDNA genomes from throughout the Americas. This high-resolution study not only confirmed that C1d was

one of the founding lineages in North America 15,000 to 18,000 years ago, but revealed another critical insight. "These first female American founders carried not one but two different C1d genomes," said Ugo Perego of the Sorenson Molecular Genealogy Foundation and primary author of the study, "thus further increasing the number of recognized maternal lineages from Beringia."

These findings raise the number of founding maternal lineages in North America to fifteen. Furthermore, this work emphasizes the critical need for comprehensive analysis of relevant populations to gather a complete picture of migratory events.

Alessandro Achilli of the University of Perugia, a coauthor of the report, suggests that the number of distinct mitochondrial genomes that passed from Asian into North America is probably much higher. "These yet undiscovered maternal lineages will be identified within the next three to four years," Achilli noted, "when the methodological approach that we used in our study will be systematically applied."

More information: Perego UA, Angerhofer N, Pala M, Olivieri A, Lancioni H, Hooshiar Kashani B, Carossa V, Ekins JE, Gómez-Carballa A, Huber G, Zimmermann B, Corach D, Babudri N, Panara F, Myres NM, Parson W, Semino O, Salas A, Woodward SR, Achilli A, Torroni A. The initial peopling of the Americas: A growing number of founding mitochondrial genomes from Beringia. *Genome Res.* [doi:10.1101/gr.109231.110](https://doi.org/10.1101/gr.109231.110)

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