Understanding the peopling of the Americas from ancient genomics

Eske Willerslev

University of Copenhagen

Studies of ancient genomes have transformed our understanding of the early peopling of the Americas. They reveal people coming from northeastern Siberia into Alaska in multiple waves. These started in the late Pleistocene, as early as 24 thousand years ago, and continued well into the Holocene. Some of the groups involved were genetically unknown, as they have no currently known direct descendants, while others gave rise to contemporary indigenous Americans. In contrast with traditional beliefs, ancient environmental genomics questions whether North America's interior ice-free corridor was in fact the entrance route of the first Americans moving from Alaska to the lower 48 states. Nevertheless, once south of the continental ice sheets, ancient human genomic analyses show that early Americans spread rapidly and widely, quickly adapting to distinct climates and environments. In some areas there is long-term continuity of these early inhabitants into the present, while in other cases first arrivals are replaced by newcomers. Notably, all ancient individuals in the Americas, except for later-arriving Arctic peoples, are more closely related to contemporary Indigenous Americans than to any other present-day populations, challenging claims based on anatomical or lithic evidence that there was an early, non-Native American population in the Americas.