SMBE 2017

Population genomics of ancient DNA

POB-429

PALEOGENOMES SHED LIGHT ON THE ROLE OF THE BERING LAND BRIDGE ON MIGRATIONS OF LATE PLEISTOCENE CABALLINE HORSES

Alisa Vershinina [1,*], Peter Heintzman [2], Grant Zazula [3], Mathias Stiller [4], Joshua Kapp [1], Ludovic Orlando [5], Cristina Gamba [6], Russell Corbett-Detig [1], Beth Shapiro [1]

[1]University Of California Santa Cruz, Santa Cruz, United States, [2]Tromsø University Museum, Tromsø, Norway, [3]Government of Yukon Department of Tourism and Culture, Whitehorse, Yukon Territory, Canada, [4]Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, [5]Centre for GeoGenetics, University of Copenhagen, Copenhagen, [6]Biomatters ApS, Silkeborg , Denmark

Poster: Climate change drives rapid and extreme fluctuations in habitat availability and Arctic mammals are most vulnerable to these effects. Shifts in habitat availability have potentially broad evolutionary consequences by both creating and destroying barriers to dispersal for many species. Here, we explore the influence of shifting barriers to gene flow on the evolution and diversification of horses, *Equus caballus,* during the Pleistocene ice ages. We use four high-coverage, complete paleogenomes, including a new paleogenome that we isolated and assembled from a ~30,000-year-old horse metapodial found in the placer mines of Canada's Yukon Territory; the first ancient horse paleogenome from North America. Using a set of genome-wide SNPs called from this and other ancient North American and Eurasian horse genomes, we infer the demographic history of North American horses and explore the timing and nature of connectivity between horse populations on these two continents. The Bering Land Bridge allowed dispersal between Eurasia and North America during periods of cold climate and low sea level, however, a formation of mesic steppe and shrub tundra along the bridge may have obstructed migration of large grazing mammals even when the bridge was present. Our results provide new insights into the role of connectivity and barriers to gene flow in shaping genetic diversity and mitigating extinction risk.

Disclosure of Interest: None Declared

Keywords: None