

What we can learn from ancient genetics and genomics

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Next generation DNA sequencing has had a large influence on many aspects of genetic research, but arguably among the most profound impact has been in the field of ancient DNA. From the retrieval of just a few fragmented sequences of mitochondrial DNA, it is now feasible sequencing entire nuclear genomes from the past. Likewise, while ancient DNA retrieval directly from environmental samples were restricted by the practicalities of cloning it is now possible conducting exhaustive surveys of past animal and plant diversity using in depth sequencing of tagged amplicons. In this talk, I present some of the recent technical breakthroughs and challenges in my groups work with ancient genomics and environmental DNA. The presentation will showcase our recent sequencing of the first ancient human genome (a 4000 year old Paleo-Eskimo), the genome of an historical Aboriginal Australian, the oldest genome sequenced to date (a 700,000 year old horse) using the 3rd generation Helicos platform, the Clovis genome from the Americas (from a 12,600 year old human), the oldest human genome published to date (from a 24,000 year old child from southern central Siberia). Analyses of these genomes have changed our view of human migration and admixture in the past. I will also present some environmental DNA data, which includes evidence of the earliest humans in North America, refugia of spruce in ice covered Scandinavia, and vegetation changes in the northern hemisphere over the past 50 thousand years and its impact on the extinction of the ice age megafauna.