

Highlights of the year

- In 2015 Centre for GeoGenetics published 98 publications, by far most of them peer reviewed papers of which six were in the journals *Nature* and *Science* and one in *Cell* (six with first and /or last authors from GeoGenetics; see Appendix H and H-1). The paper in *Nature* titled *Spatial and temporal distribution of mass loss from the Greenland Ice Sheet since AD 1900* has been viewed c. 10,000 times, and the paper *The ancestry and affiliations of Kennewick Man* had more than 64,000 page views/downloads in *Nature*.
- We published the largest ancient genome study to date sequencing low coverage genomes from 101 ancient Bronze Age individuals across Europe and Central Asia (*article, Nature*). The Bronze Age of Eurasia (around 3000–1000 BC) was a period of major cultural changes. However, there is a debate about whether these changes resulted from the circulation of ideas or from human migrations, potentially also facilitating the spread of languages and certain phenotypic traits.
We show that the Bronze Age was a highly dynamic period involving large-scale population migrations and replacements, responsible for shaping major parts of present-day demographic structure in both Europe and Asia. Our findings are consistent with the hypothesized spread of Indo-European languages during the Early Bronze Age. We also demonstrate that light skin pigmentation in Europeans was already present at high frequency in the Bronze Age, but not lactose tolerance, indicating a more recent onset of positive selection on lactose tolerance than previously thought.
- We discovered that close to 10 % of the Bronze Age individuals sequenced also contained DNA sequences of the bacteria *Yersinia pestis* (*article, Cell*). This is the etiological agent of plague and has caused human pandemics with millions of deaths in historic times. However, how and when it originated remains contentious.
By sequencing the genomes and plasmids of the ancient Bronze Age *Y. pestis* we could report the oldest direct evidence of *Y. pestis* identified by ancient DNA in human teeth from Asia and Europe dating from 2,800 to 5,000 years ago. We found that these ancient plague strains are basal to all known *Y. pestis*. We also found the origins of the *Y. pestis* lineage to be at least two times older than previous estimates. Additionally, we identified a temporal sequence of genetic changes that lead to increased virulence and the emergence of the bubonic plague. Our results show that plague infection was endemic in the human populations of Eurasia at least 3,000 years before any historical recordings of pandemics.
- We completed a long lasting study on the genetic history of Native Americans (*article, Science*). How and when the Americas were populated remains contentious.
Using ancient and modern genome-wide data, we found that the ancestors of all present-day Native Americans, including Athabascans and Amerindians, entered the Americas as a single migration wave from Siberia no earlier than 23 thousand years ago and after no more than an 8,000-year isolation period in Beringia. After their arrival to the Americas, ancestral Native Americans diversified into two basal genetic branches around 13 thousand years ago, one that is now dispersed across North and South America and the other restricted to North America. Subsequent gene flow resulted in some Native Americans sharing ancestry with present-day East Asians (including Siberians) and, more distantly, Australo-Melanesians. Putative “Paleoamerican” relict populations, including the historical Mexican Pericúes and South American Fuego-Patagonians, are not directly related to modern Australo-Melanesians as suggested by the Paleoamerican Model. The findings question a number of models

being put forward on early peopling of the Americas based on archaeological, linguistic, and genetic data.

- On a related note, we published the genome sequence of Kennewick Man – a c. 8,500 year old human skeleton from North America (*letter, Nature*). His population affinities have been the subject of scientific debate and legal controversy. Based on an initial study of cranial morphology it was asserted that Kennewick Man was neither Native American nor closely related to the Claimant Plateau tribes of the Pacific Northwest, who claimed ancestral relationship and requested repatriation under the Native American Graves Protection and Repatriation Act (NAGPRA). The morphological analysis was important to judicial decisions that Kennewick Man was not Native American and that therefore NAGPRA did not apply. Instead of repatriation, additional studies of the remains were permitted. Subsequent craniometric analysis affirmed Kennewick Man to be more closely related to circumpacific groups such as the Ainu and Polynesians than he is to modern Native Americans.

Comparing his genome sequence to worldwide genomic data including the Ainu and Polynesians, we find that Kennewick Man is closer to modern Native Americans than to any other population worldwide. Among the Native American groups for whom genome-wide data are available for comparison, several seem to be descended from a population closely related to that of Kennewick Man, including the Confederated Tribes of the Colville Reservation (Colville), one of the five tribes claiming Kennewick Man. We revisit the cranial analyses and find that, as opposed to genome-wide comparisons, it is not possible on that basis to affiliate Kennewick Man to specific contemporary groups. We therefore conclude based on genetic comparisons that Kennewick Man shows continuity with Native North Americans over at least the last eight millennia.

- We also investigated the spatial and temporal distribution of mass loss from the Greenland Ice Sheet since AD 1900 using old photos of Greenland shot from airplanes (*letter, Nature*). The response of the Greenland Ice Sheet (GIS) to changes in temperature during the twentieth century remains contentious, largely owing to difficulties in estimating the spatial and temporal distribution of ice mass changes before 1992, when Greenland-wide observations first became available. The only previous estimates of change during the twentieth century are based on empirical modelling and energy balance modelling. Consequently, no observation-based estimates of the contribution from the GIS to the global-mean sea level budget before 1990 are included in the Fifth Assessment Report of the Intergovernmental Panel on Climate Change.

We calculated spatial ice mass loss around the entire GIS from 1900 to the present using aerial imagery from the 1980s. This allows accurate high-resolution mapping of geomorphic features related to the maximum extent of the GIS during the Little Ice Age at the end of the nineteenth century. We estimate the total ice mass loss and its spatial distribution for three periods: 1900–1983 (75.1 ± 29.4 gigatonnes per year), 1983–2003 (73.8 ± 40.5 gigatonnes per year), and 2003–2010 (186.4 ± 18.9 gigatonnes per year). Furthermore, using two surface mass balance models we partition the mass balance into a term for surface mass balance (that is, total precipitation minus total sublimation minus runoff) and a dynamic term. We found that many areas currently undergoing change are identical to those that experienced considerable thinning throughout the twentieth century. We also reveal that the surface mass balance term shows a considerable decrease since 2003, whereas the dynamic term is constant over the past 110 years. Overall, our observation-based findings show that during the twentieth century the GIS contributed at least 25.0 ± 9.4 millimetres of global-mean sea level rise. Our result will

help to close the twentieth-century sea level budget, which remains crucial for evaluating the reliability of models used to predict global sea level rise.