

## Demographic reconstruction from ancient DNA supports rapid extinction of the great auk

The great auk was once abundant and distributed across the North Atlantic. It is now extinct, having been heavily exploited for its eggs, meat, and feathers. We investigated the impact of human hunting on its demise by integrating genetic data, GPS-based ocean current data, and analyses of population viability. We sequenced complete mitochondrial genomes of 41 individuals from across the species' geographic range and reconstructed population structure and population dynamics throughout the Holocene. Taken together, our data do not provide any evidence that great auks were at risk of extinction prior to the onset of intensive human hunting in the early 16th century. In addition, our population viability analyses reveal that even if the great auk had not been under threat by environmental change, human hunting alone could have been sufficient to cause its extinction. Our results emphasise the vulnerability of even abundant and widespread species to intense and localised exploitation.

**Forfatter:** Jessica E Thomas ; Gary R Carvalho ; James Haile ; Nicolas J Rawlence ; Michael D Martin ; Simon YW Ho ; Arnór P Sigfússon ; Vigfús A Jósefsson ; Morten Frederiksen ; Jannie F Linnebjerg ; Jose A Samaniego Castruita ; Jonas Niemann ; Mikkel Holger Strander Sinding; Marcela Sandoval-Velasco ; André ER Soares ; Robert Lacy ; Christina Barilaro ; Juila Best ; Dirk Brandis ; Chiara Cavallo ; Mikelo Elorza ; Kimball L Garrett ; Maaïke Groot ; Friederike Johansson ; Jan T Lifjeld ; Göran Nilson ; Dale Serjeanston ; Paul Sweet ; Errol Fuller ; Anne Karin Hufthammer ; Morten Meldgaard; Jon Fjeldså ; Beth Shapiro ; Michael Hofreiter ; John R Stewart ; M Thomas P Gilbert ; Michael Knapp **Type:** Article | Artikel **Årstal:** 2019 **Emner:** Evolutionary biology; Genetics and genomics; Seabird exploitation; 19th century extinction; Paleogenetics; Hunting; Ancient DNA **Titel på tidsskrift:** eLIFE **DOI nummer:** 10.7554/eLife.47509

### [Åben publikation](#)

## Population genomics of grey wolves and wolf-like canids in North America

North America is currently home to a number of grey wolf (*Canis lupus*) and wolf-like canid populations, including the coyote (*Canis latrans*) and the taxonomically controversial red, Eastern timber and Great Lakes wolves. We explored their population structure and regional gene flow using a dataset of 40 full genome sequences that represent the extant diversity of North American wolves and wolf-like canid populations. This included 15 new genomes (13 North American grey wolves, 1 red wolf and 1 Eastern timber/Great Lakes wolf), ranging from 0.4 to 15x coverage. In addition to providing full genome support for the previously proposed coyote-wolf admixture origin for the taxonomically controversial red, Eastern timber and Great Lakes wolves, the discriminatory power offered by our dataset suggests all North American grey wolves, including the Mexican form, are monophyletic, and thus share a common ancestor to the exclusion of all other wolves. Furthermore, we identify three distinct populations in the high arctic, one being a previously unidentified "Polar wolf" population endemic to Ellesmere Island and Greenland. Genetic diversity analyses reveal particularly high inbreeding and low heterozygosity in these Polar wolves, consistent with long-term isolation from the other North American wolves.

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### [Åben publikation](#)

## The evolutionary history of dogs in the Americas

Dogs were present in the Americas before the arrival of European colonists, but the origin and fate of these precontact dogs are largely unknown. We sequenced 71 mitochondrial and 7 nuclear genomes from ancient North American and Siberian dogs from time frames spanning ~9000 years. Our analysis indicates that American dogs were not derived from North American wolves. Instead, American dogs form a monophyletic lineage that likely originated in Siberia and dispersed into the Americas alongside people. After the arrival of Europeans, native American dogs almost completely disappeared, leaving a minimal genetic legacy in modern dog populations. The closest detectable extant lineage to precontact American dogs is the canine transmissible venereal tumor, a contagious cancer clone derived from an individual dog that lived up to 8000 years ago.

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## Greenland sled dogs at risk of extinction

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