

## 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  
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