

Genomics of white-tailed eagle (*Haliaeetus albicilla*) in the North-Atlantic islands reveal low diversity and substantial inbreeding in comparison with the mainland populations

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Abstract

Using whole genome shotgun sequences from 92 white-tailed eagles (*Haliaeetus albicilla*) sampled from Greenland, Iceland, Norway, Denmark, Estonia, and Turkey between 1885-1950 and after 1990, we investigate the genomic variation within countries over time, and between countries. Clear genetic differentiation is observed between samples from the different countries, with the largest differences between the island and mainland populations, and indications that the island populations share the most recent ancestry with the Norwegian population. We find signs of strong inbreeding in the island populations. Further, temporal differences are observed in some populations, for example, replacement of the Danish gene pool following its population's extinction in the early 20th century, as well as a change in the genetic diversity of the Icelandic population following a severe bottleneck during the last century, all of which could warrant a further conservation effort in Iceland. More generally, all populations show a decline in effective population size, which may have been shaped by I) distinct refugia during the last glacial period, II) population divergence following the colonization of the deglaciated areas ~10,000 years ago, III) human population expansion and e.g., settlement in Iceland ~1,100 years ago, and IV) human persecution and toxic pollutants during the last two centuries.

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