

# Distinctive mitogenomic lineages within populations of white-tailed eagles (*Haliaeetus albicilla*)

Charles Christian Hansen<sup>1</sup>, Sina Baleka<sup>1</sup>, Sólveig Gujónsdóttir<sup>1</sup>, Jacob Rasmussen<sup>2</sup>, Jesus Ballesteros<sup>2</sup>, Gunnar Hallgrímsson<sup>3</sup>, Robert Stefansson<sup>4</sup>, Menja von Schmalensee<sup>4</sup>, Kristinn Skarphéðinsson<sup>5</sup>, Aili Labansen<sup>6</sup>, Madis Leivits<sup>7</sup>, Kim Skelmose<sup>8</sup>, Christian Sonne<sup>9</sup>, Rune Dietz<sup>9</sup>, David Boettmann<sup>9</sup>, Igor Eulaers<sup>9</sup>, Michael Martin<sup>2</sup>, and Snaebjorn Palsson<sup>1</sup>

<sup>1</sup>University of Iceland

<sup>2</sup>Norwegian University of Science and Technology

<sup>3</sup>University of Iceland School of Engineering and Natural Sciences

<sup>4</sup>West-Iceland Nature Research Centre

<sup>5</sup>Iceland Institute of Natural History

<sup>6</sup>Greenland Institute of Natural Resources

<sup>7</sup>Estonian University of Life Sciences

<sup>8</sup>Natural History Museum of Denmark

<sup>9</sup>Aarhus Universitet

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## Abstract

Using whole mitochondrial DNA sequences from 89 white-tailed eagles (*Haliaeetus albicilla*) sampled from Iceland, Greenland, Norway, Denmark and Estonia between 1990-2018, we investigate the mitogenomic variation within and between countries. We show that there is a substantial population differentiation between the countries, reflecting similar major phylogeographic patterns obtained previously for the control region of the mitochondria, which suggested two main refugia during the last glacial period of Ice Age. Distinct mitogenomic lineages are observed within countries which divergence times exceeds the time since last glacial period of Ice Age ended. The lineages appear to have been maintained by natural selection. An excess of segregating amino acids in comparison with number of fixations, as revealed by the neutrality index suggests a load of deleterious mutations. The maintenance of mtDNA lineages within countries inflates our estimates of effective national population sizes and the times of their divergence.

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