

Genomic diversity and differentiation between island and mainland populations of White-tailed Eagles (*Haliaeetus albicilla*)

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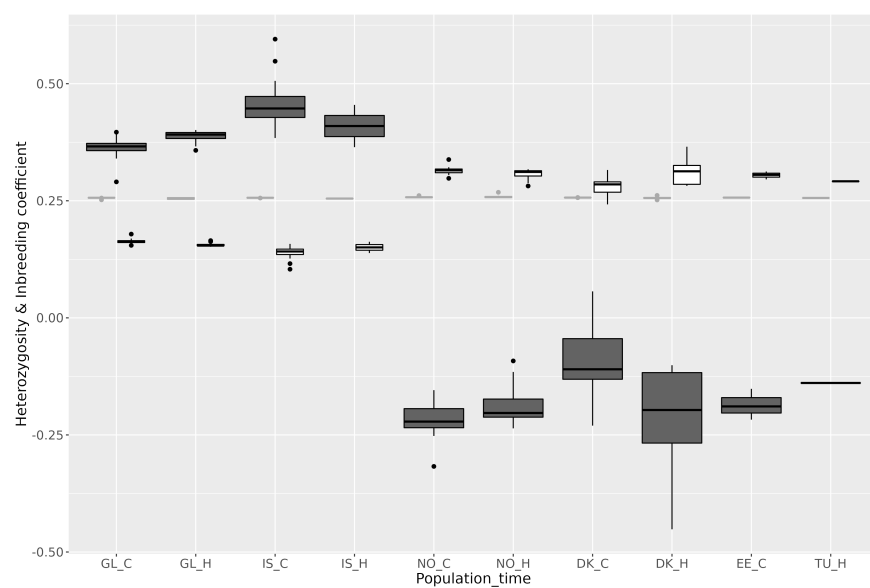
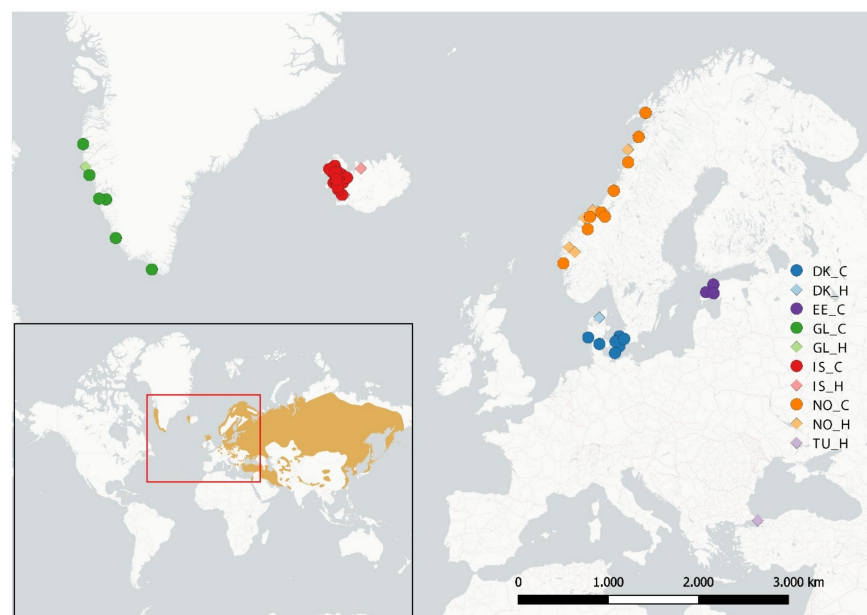
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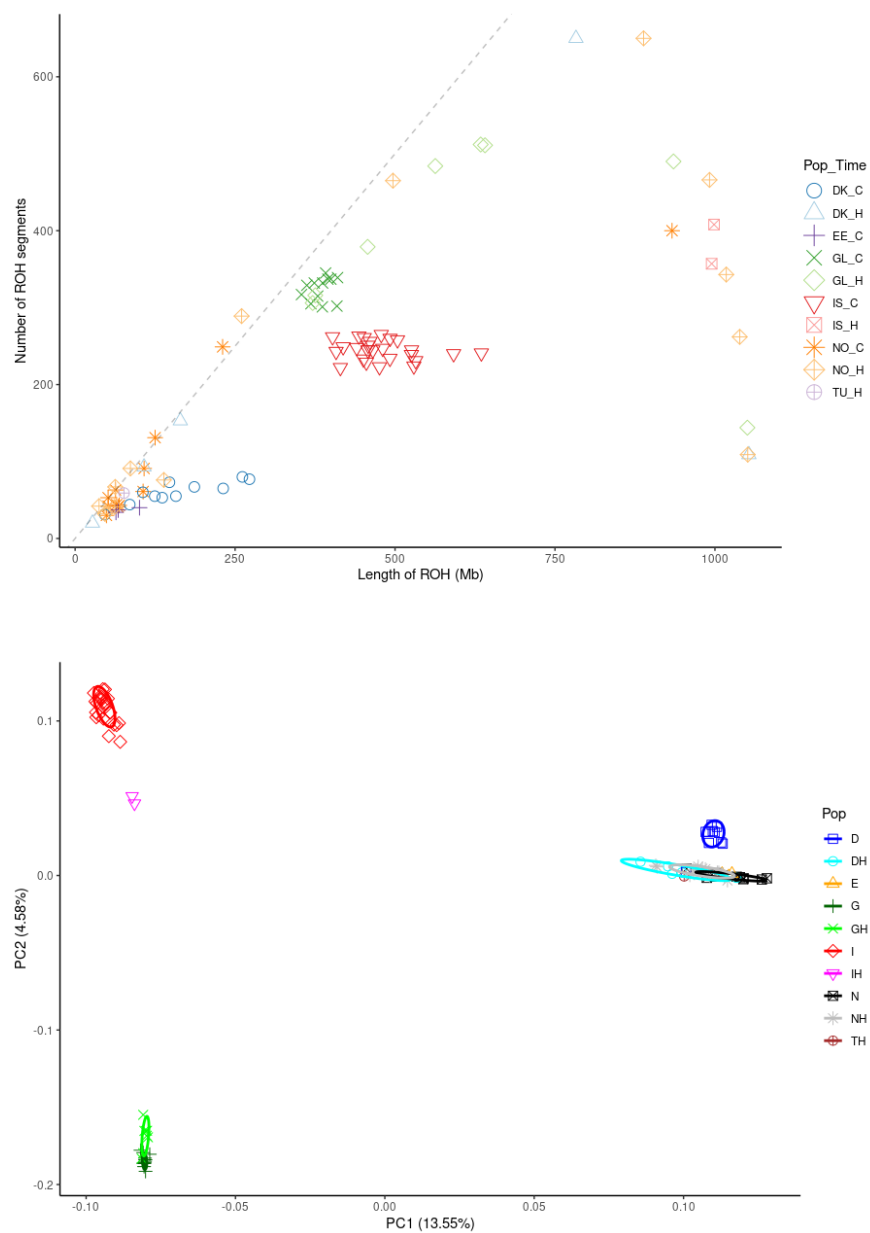
Abstract

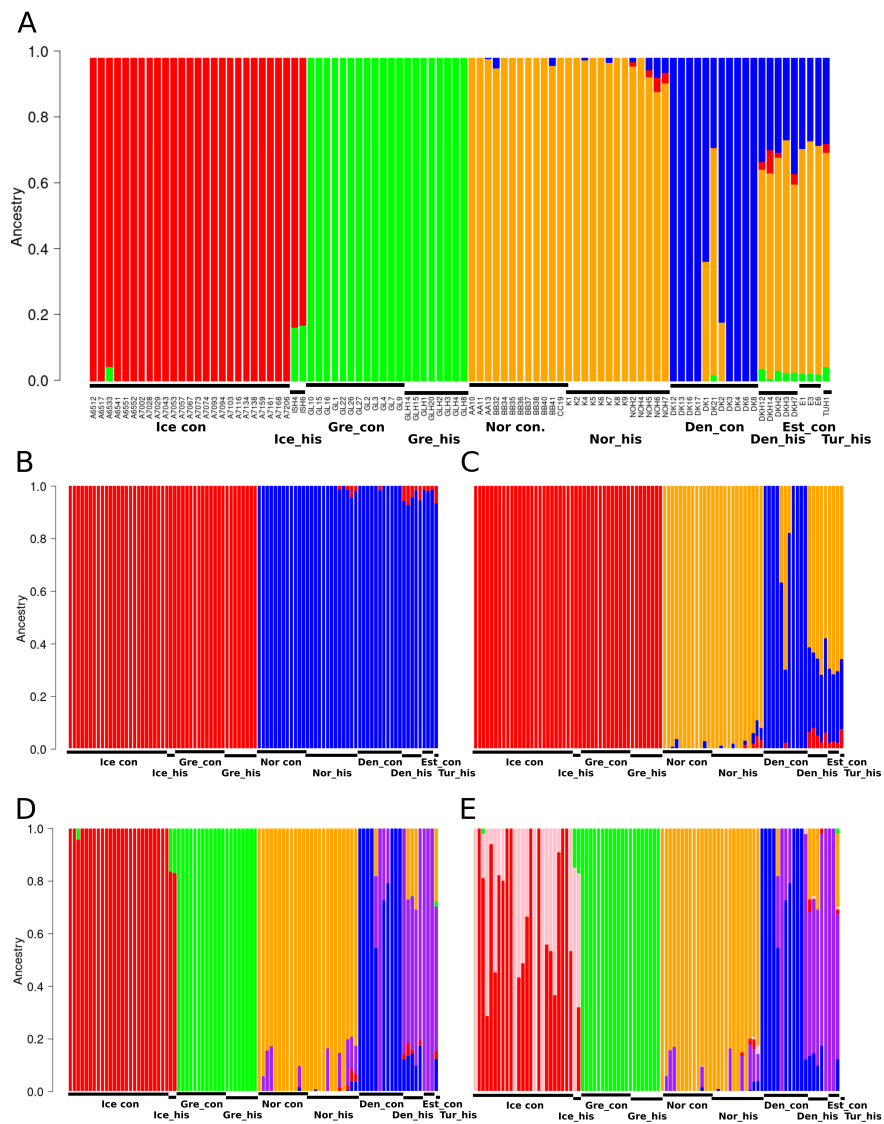
Divergence in the face of high dispersal capabilities is a documented but poorly understood phenomenon. The white-tailed eagle (*Haliaeetus albicilla*) has a large geographic dispersal capability and should theoretically be able to maintain genetic homogeneity across its dispersal range. However, following analysis of the genomic variation of white-tailed eagles, from both historical and contemporary samples, clear signatures of ancient biogeographic substructure across Europe and the North-East Atlantic is observed. The greatest genomic differentiation was observed between island (Greenland and Iceland) and mainland (Denmark, Norway and Estonia) populations. The two island populations share a common ancestry from a single mainland population, distinct from the other sampled mainland populations, and despite the potential for high connectivity between Iceland and Greenland they are well separated from each other and are characterized by inbreeding and little variation. Temporal differences also highlight a pattern of regional populations persisting despite the potential for admixture. All sampled populations generally showed a decline in effective population size over time, which may have been shaped by four historical events: I) isolation of refugia during the last glacial period 110-115,000 years ago, II) population divergence following the colonization of the deglaciated areas ~10,000 years ago, III) human population expansion, which led to the settlement in Iceland ~1,100 years ago, and IV) human persecution and exposure to toxic pollutants during the last two centuries.

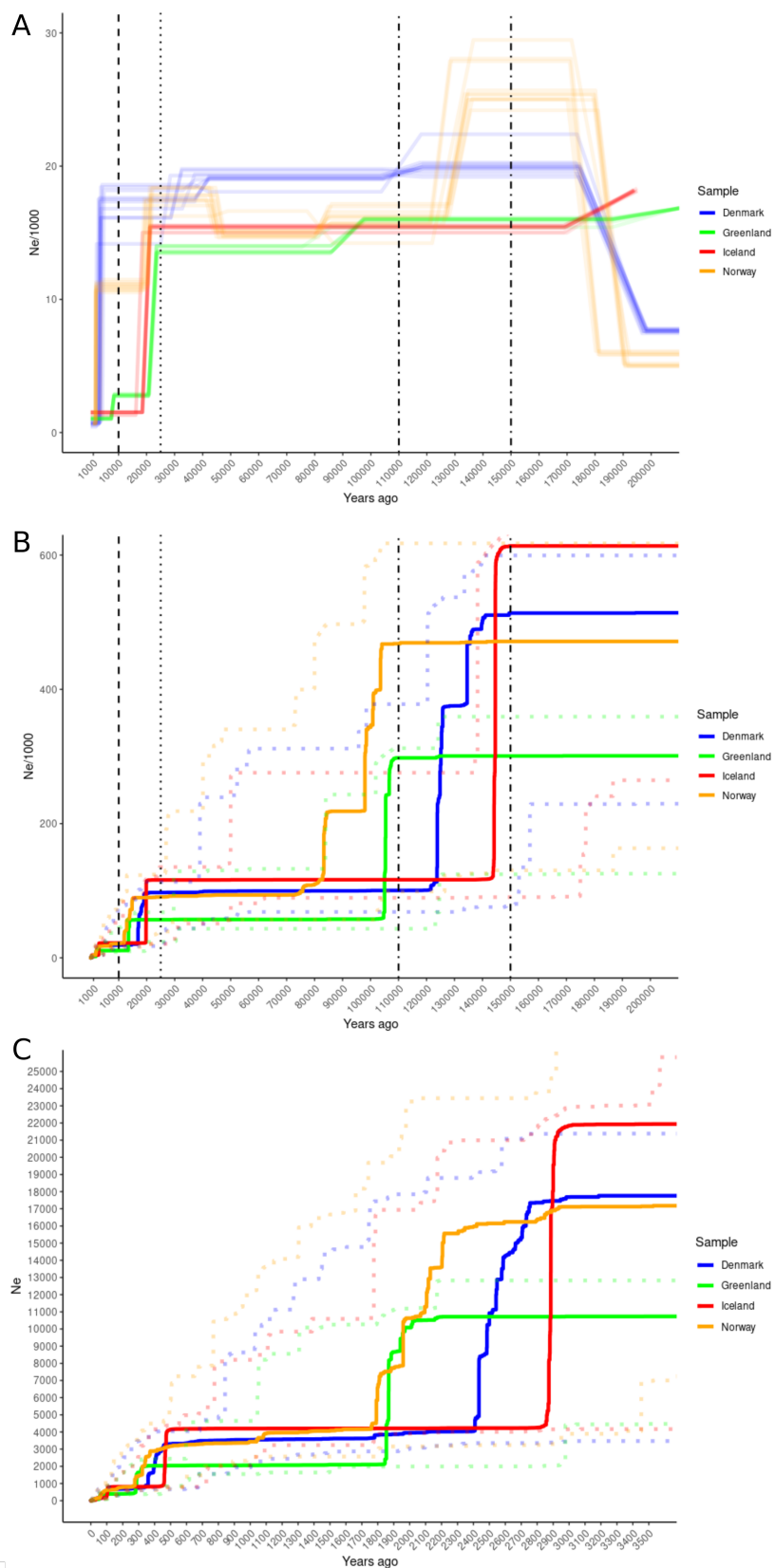
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