A genomewide catalogue of single nucleotide polymorphisms in white-beaked and Atlantic white-sided dolphins

The field of population genetics is rapidly moving into population genomics as the quantity of data generated by high-throughput sequencing platforms increases. In this study, we used restriction-site-associated DNA sequencing (RADSeq) to recover genomewide genotypes from 70 white-beaked (Lagenorhynchus albirostris) and 43 Atlantic white-sided dolphins (L. acutus) gathered throughout their north-east Atlantic distribution range. Both species are at a high risk of being negatively affected by climate change. Here, we provide a resource of 38,240 RAD-tags and 52,981 nuclear SNPs shared between both species. We have estimated overall higher levels of nucleotide diversity in white-sided ($\pi = 0.0492 \pm 0.0006\%)$ than in white-beaked dolphins ($\pi = 0.0300 \pm 0.0004\%$). White-sided dolphins sampled in the Faroe Islands, belonging to two pods ($N = 7$ and $N = 11$), showed similar levels of diversity ($\pi = 0.0317 \pm 0.0007\%$ and $0.0267 \pm 0.0006\%$, respectively) compared to unrelated individuals of the same species sampled elsewhere (e.g, $\pi = 0.0285 \pm 0.0007\%$ for 11 Scottish individuals). No evidence of higher levels of kinship within pods can be derived from our analyses. When identifying the most likely number of genetic clusters among our sample set, we obtained an estimate of two to four clusters, corresponding to both species and possibly, two further clusters within each species. A higher diversity and lower population structuring was encountered in white-sided dolphins from the north-east Atlantic, in line with their preference for pelagic waters, as opposed to white-beaked dolphins that have a more patchy distribution, mainly across continental shelves.

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