Agreement on the Conservation of Albatrosses and Petrels

Seventh Meeting of the Population and Conservation Status Working Group

Edinburgh, United Kingdom, 18 - 19 May 2023

Population genomics of Shy and White-capped Albatross: understanding management units and developing tools for bycatch identification

Anna J MacDonald, Julie C McInnes, Mike Double, Jonathon HS Barrington, Sheryl Hamilton, Barbara Wienecke, Andrea Polanowski

A **password is required** to view the full text document

SUMMARY

Seabirds face multiple threats, including fisheries-associated mortality. To effectively conserve threatened species, it is important to define appropriate management units for each species and to understand the precise nature of the threats faced by each management unit. Here we used population genomics to investigate relationships among populations of *Thalassarche cauta* (Shy Albatross) and *Thalassarche steadi* (White-capped Albatross), to review management units for each species and with the aim of identifying species-specific genetic markers. These two species can be distinguished using microsatellite markers, but microsatellites are more difficult to analyse and interpret than diagnostic DNA sequences. One mitochondrial sequence marker is available, but this has a 3% error rate. We used a genotyping-by-sequencing method, DArTseq, to simultaneously identify and genotype thousands of Single Nucleotide Polymorphism markers for samples from three colonies of each species.

Our results provide clear evidence of genetic divergence between the two species, confirming that the species should be managed separately. Low levels of genetic differentiation among the three largest breeding sites of White-capped Albatross suggest management of this species as a single unit is appropriate. There is evidence of genetic structure among Shy Albatross colonies, especially between Pedra Branca and other breeding sites, indicating that these may be considered separate management units. Future management approaches would benefit from incorporating these genomic data along with data from other sources, to ensure that factors such as population-specific foraging behaviours and distributions are also considered. We identified no markers with 100% fixed differences between the two species, which may not be unexpected given their recent divergence. However, we identified several thousand loci with private alleles within one species or breeding site. These may provide opportunities for future development of species- or population-specific panels of SNP markers that could be applied to improve identification of bycaught seabirds.