Review of taxonomy and development of a genetic assignment test for Northern Buller's Albatross (*Thalassarche bulleri platei*)

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Overall Objective(s):

The overall aim of this study was to develop a species specific genetic "toolkit" for Buller'sAlbatross

Specific Objective(s):

The specific aims of this study were to: 1) determine levels of genetic variation between Northern and Southern Buller's Albatross, and 2) develop a genetic marker for determining the provenance of individuals.

Summary of methods used and key findings

To resolve the degree of differentiation between two subspecies of Buller's Albatross, Northern (*Thalassarche bulleri platei*) and Southern (*Thalassarche bulleri bulleri*), a total of 73 blood samples were obtained from chicks and nesting adults between 1996 and 2007. Twenty-six samples are representative of *Thalassarche bulleri platei* (22 = Motuhara, 4 = Rangitatahi) and an additional 47 samples are representative of *Thalassarche bulleri bulleri* (24 = North East Island, 23 = Solander Island). Liver samples from a further 97 individuals were harvested during routine necropsy of bycatch between July 1999 and June 2016. Analysis of a 221 bp fragment of the mitochondrial DNA control region Domain II revealed high levels of diversity similar to those previously reported for Domain I of the control region in other seabirds (*add reference*).

Regional differentiation was difficult to assess due to the high variation within Northern Buller's Albatross (percent pairwise differences ranged from 0 – 6.4%). However, pairwise comparisons among colonies demonstrated high levels of differentiation between colonies from different regions (pairwise Φ_{ST} = 0.586 - 0.703, $p < 0.00001$). Regional population structure was further examined without *a priori* assignment in BAPSv6.0 (Bayesian Analysis of Population Structure) as suggested by Corander *et al.* (2008); Corander and Tang (2007), and Maltagliati *et al.* (2010). BAPS identified three haplogroups; Haplogroups I & II were only found in the Northern Buller's Albatross, and Haplogroup III was found only in Southern Buller's Albatross. All but two individuals from samples of known provenance were able to be assigned to the population of origin with maximum probability (P =1.00). These two individuals from Motuhara shared the genetic characteristics of all 3 haplogroups, but were most strongly associated with Haplogroup III. This suggests that there may be additional haplogroups not represented within the current sample set and increased colony sampling may resolve this uncertainty.

Despite the presence of this one ambiguous haplotype, all 97 samples collected from bycatch were able to be assigned to their population of origin with maximum probability. A total of 19 bycatch individuals were representative of Northern Buller's Albatross (Haplogroup I: n = 8, Haplogroup II: n = 11), while the remaining 78 bycatch samples were

assigned to Southern Buller's Albatross (Haplogroup III). This method did not permit assignment back to distinct colonies or sites. This may be because there is genetic homogeneity between colonies within regions. Our findings were similar to previous work on the Southern Buller's Albatross which reported finding no differentiation among two southern colonies (van Bekkum *et al.* 2006). However, these new findings support the conclusion that Northern and Southern Buller's are genetically differentiated populations, and show that assignment to source is possible using short CRII sequences as a tool.

Recommendations

The mtDNA assay appears to be able to determine whether a Buller's Albatross is from the Northern or Southern group. However, the level of certainty for this mtDNA-based identification approach does need to be tested further. It can be gradually phased in as a potential stand-alone method for assigning individuals to their population of origin as the level of certainty improves. It is recommended that more samples of known Northern and Southern Buller's albatross are collected and DNA typed to increase the sample sizes and help improve the statistical power of the method. Increasing the number of samples of known provenance should enable the ambiguity of the haplotype shared by 2 *Thalassarche bulleri platei* individuals sampled from Motuhara to be resolved. This will also enable a better assessment of the diversity within the observed haplogroups and precisely define all of the haplogroups.

Citations

Corander J, Marttinen P, Siren J, Tang J (2008) Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. *Bmc Bioinformatics* **9**.

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