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ADDED INFO

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REVIEW

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PEQ = 4.3 / 5

Peer reviewed by 5 Peers.

Introduction

This manuscript attempts to demonstrate that between-breeding season dispersal of [REDACTED] is common, and that each [REDACTED] is composed of a mixture of breeders that bred elsewhere in one of the two previous years. The authors use their conclusion to highlight that [REDACTED], which has been genetically demonstrated for this species by previous studies, is likely a result of this high degree of dispersal.

Merits

score: 4.2 / 5

The manuscript builds on a sizeable data set of feather samples collected over a wide region. The data clearly demonstrate that there is large isotopic variation among the feathers collected within a given breeding region.

Critique

score: 4.8 / 5

Based on the preliminary information provided (L. 64-68, 99-100; [REDACTED] are highly mobile), the collected feathers cannot be treated as of 'known origin', which unfortunately renders all geographical analyses flawed, because they assume that samples are of known origin. The authors acknowledge that they do not know when a collected feather was moulted (1, or 2 years previously, L. 135-137), but they fail to acknowledge that they also do not know where the feathers were grown. They state that "isotopic signatures in the feathers of birds returning to breed at a given [REDACTED] should reflect the local environment on the breeding grounds in which that feather was grown" (L. 138-140). The feathers collected in a given [REDACTED] can therefore only be considered of 'known

origin' if the birds [REDACTED] display 100% breeding site fidelity for at least 2 years. This critical assumption underpins the entire geographic assignment analysis of this study. Unfortunately, this assumption is almost certainly violated. If this assumption would be met then the goal of the study (to find out whether birds disperse between breeding regions) would be moot.

At each colony (or in each region) the feathers collected consist of an unknown mixture of birds that moulted in various regions in the 1-2 years previously (the only exception may be [REDACTED]). Treating the isotope ratios of all these feathers as representative of the [REDACTED] where they were collected will lead to bias, because any local isotopic signal is contaminated by the inclusion of feathers that were actually grown elsewhere, and may therefore have a different isotopic signature.

In L. 227-228 the authors describe actions they took to improve assignments by using only 'correctly assigned' feathers. This statement indicates that the authors are aware that their feather collections at any given [REDACTED] are a mixture of feathers of different origins, and thus must be separated into 'local' and 'immigrant' feathers. However, the posterior 'correct' assignment will not offer a robust and unbiased way to do that: if all feathers were used to train the model initially, then the feathers that are 'correctly assigned' are those that reflect the mixture of isotope values from local and immigrant feathers, and not necessarily the true local feathers. Thus, it seems both circular and unreliable to use the 'correct assignments' to identify (and exclude) the immigrant feathers.

The lack of truly 'known origin' feathers also renders the latitudinal gradient analysis problematic (L. 196-201). The authors use GLMMs to test for latitudinal gradients in d2H, d13C and d15N in isotope ratios, but such a gradient analysis is only valuable if the feathers are of known origin. In addition, these analyses seem very speculative for d15N and d13C, for which in my opinion no plausible biological hypothesis exists why there should be a latitudinal gradient in [REDACTED] feathers.

Discussion

score: 4.0 / 5

The large variation in feather isotope ratios in each region is valuable and informative, and would be indicative of birds from various origins even without the sophisticated geographic assignment analysis. A geographic assignment analysis would only be possible with isotope data of 'known origin'. Unless there are certain characteristics in the collected feathers that could be used to unambiguously determine their origin, disentangling the 'locally grown' from the 'immigrant' feathers for each of the [REDACTED] will be challenging (or impossible). A far simpler analysis that would overcome the problem of not having truly 'known origin' samples would be to pool all feathers [REDACTED], and conduct a hierarchical cluster analysis (e.g. see [1] and [2]) to split the data set into 5 isotopic clusters (tentatively representing the 5 regions, under the assumption that they differ isotopically - an assumption that is more likely to be valid than the current assumption that feathers were grown locally). Based on the number of represented clusters in each region, inference could be drawn about the number of other regions from where breeders 'immigrated' to a given target region. The downside of this analysis is that it would be difficult to unambiguously associate isotope clusters with a given region (with the possible exception of [REDACTED]).

Even if isotope clusters could not be unambiguously assigned to geographic regions, there should be supporting evidence to suggest that regions may differ isotopically (such as those outlined for the colony in [REDACTED], L. 343-351). In conjunction with that assumption, the results (which would presumably assign feathers from each geographic region to >1 isotopic cluster) could be used to argue that [REDACTED] do indeed disperse between breeding regions, and thus support the findings from genetic studies which indicate a [REDACTED]. This simplified analysis would provide more credible evidence than a geographic assignment analysis that relies on an almost certainly invalid assumption.

High dispersal that [REDACTED] has been demonstrated in other species as well. For example, King Eiders (*Somateria spectabilis*) do not show any spatial genetic structure across much of the Arctic [3], which is most likely due to the high dispersal of breeding males. King Eiders exhibit diffuse migratory connectivity, and because males pair up with females on wintering grounds and follow philopatric females back to breeding areas [4-7], there is a high rate of dispersal between different breeding populations.

References

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