May 4th 2021

To: the Editor-in-Chief, Vicent Devictor,

UMR CNRS-UM2 5554 cc065,

Institut des Sciences de l'Evolution de Montpellier,

Montpellier,

France

Dear Vicent Devictor,

We are pleased to submit our article titled ‘Quantifying a wildlife conflict: estimates of seabird predation by recovering fur seals across southeastern Australia’ for publication with Biological Conservation.

Our paper provides critical quantitative information to enable progress in managing a contentious wildlife conflict first at a local scale in southern Australia, between two species of conservation concern – recovering long-nosed fur seals and the culturally important little penguin. This conflict is resulting in largely unfounded calls for culling the predator (seals) when extremely little data exist to quantify their impacts to the prey (penguins). Importantly, advances in frameworks for processing DNA metabarcoding data (here for the 12sa/hRNA gene for little penguins) enabled us to identify up to 7 individual penguin haplotypes, representing a total of 21 little penguins consumed across 100 predator samples. Our results indicate that seabird and particularly little penguin predation may be a relatively important individual foraging strategy for some long-nosed fur seals, with potentially negative impacts for local penguin populations. However, we posit that predator impacts need to be considered and managed within an up-to-date cumulative impacts assessment for threats to little penguins in southern Australia. In conclusion to our study, we recommend that practitioners develop targeted assays for identifying individuals among predator and prey species, in order to determine the prevalence of this foraging strategy among long-nosed fur seals and to obtain more accurate estimates of predation abundance.

Ultimately, our paper presents a valuable and modular mutli-assay method that can be applied very broadly across systems and wildlife conflict scenarios for identifying and quantifying predation. We combine the use of a traditional morphological and a modern DNA metabarcoding assay to estimate the prevalence of predation events among predator samples - whereby we corroborated and expanded on previous estimates of predation. We contribute the following significant advances both to our local context and to the broader conservation biology community: (i) a multi-assay method for comparison of target species identification, and (ii) a reproducible protocol for DNA metabarcoding analyses for identifying target prey species from predator scat samples, lastly (iii) haplotype analyses for genetic diversity and probable abundances of target species within and between samples using shorter base-pair target DNA. Both in this system and elsewhere, we highlight developments of cost-effective assays tailored to the needs of specific wildlife conflict scenarios in order to better quantify these conflicts.

We present original work carried out by the authors and acknowledge the following requirements for publication in Elsevier’s Biological Conservation. All authors agree with the contents of the manuscript and its submission to the journal. We acknowledge that no part of the research has been published or submitted in any form elsewhere. Any research in the paper not carried out by the authors is fully acknowledged in the manuscript. All sources of funding are acknowledged in the manuscript, and authors have declared any direct financial benefits that could result from publication. All appropriate ethics and other approvals were obtained for the research and for research protocols, and we include reference codes in our Acknowledgement section.

Sincerely,

Natasha Hardy