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BARCODING: DNA-BARCODING OF BARF YIELDS INSIGHTS INTO SEABIRD FORAGING ECOLOGY

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Morphological identification of digested prey remains from a generalist forager can be a challenge, especially to species level. DNA techniques, whereby prey is sequenced and matched to large public nucleotide sequence databases, are increasingly being used to augment traditional morphological identification. To identify highly-digested prey items from Christmas (Chocolate) shearwater (*Puffinus nativitatis*) regurgitations from Kure Atoll, we used two DNA approaches that target the cytochrome *c* oxidase subunit I (COI) mitochondrial gene. First, we individually sequenced prey items from five regurgitations retrieved from birds tagged with time depth recorders in 2017, pairing dive behavior with diet. Second, we used “metabarfcoding” to bulk-process 92 water samples from regurgitations collected from 2009-2017 to get an overview of their diet. The prey items identified from tagged birds spanned a diverse range of taxa, including three reef-associated families, four pelagic-oceanic families, and a meso-pelagic family. The integration of diet and diving data provided insights into the vertical distribution of the prey, particularly regarding mesopelagic and nocturnal species. The metabarfcoding technique identified 94 unique taxa from 31 families of fish and squid. Overall, 45% percent of the families detected in the contemporary diet were previously documented in historical Chocolate shearwater diets from the Northwestern Hawaiian Islands dating back to the 1970s (Harrison *et al.* 1983). Rare species (occurring \leq 5% of the samples) constituted 70% of the species richness. Our results indicate that the COI region is successful in identifying a wide range of taxa from highly digested seabird regurgitations.