



NOTE

# Critically low abundance and limits to human-related mortality for the Maui's dolphin

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**ABSTRACT:** The New Zealand endemic Maui's dolphin *Cephalorhynchus hectori maui* is characterized by several life history traits thought to be important predictors of extinction risk in marine mammals, including a slow rate of reproduction, small geographic range, small group size, and coastal distribution. We continued the genetic monitoring of the remnant population of Maui's dolphins using DNA profiles to identify 39 individuals from 73 skin biopsy samples collected during dedicated boat surveys in the austral summers of 2010 and 2011. Using a 2-sample, closed-population model with the genotype recapture records, we estimated the current abundance to be  $N = 55$  individuals approximately age 1+ (95% confidence limits = 48, 69; coefficient of variation = 0.15). The endangered species potential biological removal that would permit the recovery of the Maui's dolphin was calculated to be 1 dolphin every 10 to 23 yr. Despite this, the Maui's dolphin is not necessarily doomed to extinction. It appears to be maintaining an equal sex ratio and connectivity within its remnant range and has the potential for rescue by interbreeding with Hector's dolphin *C. h. hectori* migrants.

**KEY WORDS:** Abundance · Genotype mark-recapture · Potential biological removal · *Cephalorhynchus hectori maui* · Critically endangered · Cetacean · New Zealand

## INTRODUCTION

The risk of extinction for marine mammals is thought to be greater for those that have a slow rate of reproduction, small geographic range, small group size, and coastal or riverine distribution (Davidson et al. 2012). The baiji *Lipotes vexillifer* was characterized by all 4 of these life history traits and became the first cetacean to go extinct due to human activity (Turvey et al. 2007). Despite classification as Endangered in 1986 and Critically Endangered in 1996 by the International Union for Conservation of Nature

(IUCN 2012), little effort was made to mitigate the high rate of incidental fisheries-related mortality that drove the decline of the baiji. As a consequence, the last documented baiji sighting was in 2002, and the species is now considered extinct (Turvey et al. 2007, Committee on Taxonomy 2012).

The Maui's dolphin *Cephalorhynchus hectori maui* is also characterized by these 4 predictors of extinction as well as by the risk of fisheries-related mortality. The Maui's dolphin is one of 2 subspecies of the New Zealand endemic Hector's dolphin species *C. hectori*. It is classified as Critically Endangered by

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the IUCN (Reeves et al. 2008) and nationally critical under the New Zealand Threat Classification System (Baker et al. 2010). Stranding and sighting records suggest that Maui's dolphins were once widely distributed along the west coast of the North Island, and possibly parts of the east coast (the subspecies of the east coast records are unknown; Du Fresne 2010). Their current distribution has contracted to about 300 km along the west coast of the North Island, with the majority of sightings concentrated in a central distribution of approximately 140 km (Oremus et al. 2012). Population dynamic models suggested a substantial decline in the abundance of Maui's dolphins since the advent of nylon monofilament set nets in the late 1960s (Martien et al. 1999, Slooten et al. 2000). In 2001, the New Zealand government proposed fishing restrictions to reduce entanglement and has since implemented several sets of restrictions within the Maui's dolphin distribution (summarized by Baker et al. 2013). The West Coast North Island Marine Mammal Sanctuary was also established to restrict seismic surveys and mining activities (New Zealand Department of Conservation 2008).

Monitoring abundance is essential for evaluating the status of Maui's dolphins and strategies for conservation management. Estimates of abundance calculated from boat and aerial line-transect surveys since 1985 ranged from 75 to 140 (Table 1). More recently, Baker et al. (2013) used genotype recapture analysis to establish a census of known individuals and estimate an abundance of  $N = 69$  (95% confidence limits [CL] = 38, 125) for the midpoint of the study in 2003.

To aid with management considerations for exploited cetaceans, Wade (1998) developed the potential biological removal (PBR) method to calculate a threshold for human-related mortality. This method uses an estimate of abundance for the population subject to mortality and, for endangered species, a conservative recovery factor of 0.1, which was developed through simulations that will allow the population to recover at a rate close to its biological maximum ( $R_{max}$ ) without delaying the time to recovery (to the maximum net productivity level) by more than 10%. A default  $R_{max}$  of 0.04 has been recommended for cetaceans based on available observations and estimates from life history characteristics (Wade 1998) and is the value used under the US Marine Mammal Protection Act (Wade & Angliss 1997).

This default is meant to be a reasonable value for most cetaceans; however, a species-specific estimate is recommended if available. For Hector's and Maui's dolphins, an  $R_{max}$  of 0.018 was estimated based on empirical survival rates, the most optimistic empirical parameters for age at first reproduction and calving interval, and marine mammal survivorship curves (Slooten & Lad 1991). Based on the 2004 Maui's dolphin abundance estimate of 111 from aerial surveys (Slooten et al. 2006), Slooten & Dawson (2008) calculated a PBR of 0.07 (1 dolphin every 14.3 yr) using the species-specific  $R_{max}$  of 0.018. For comparison, they also used the cetacean default  $R_{max}$  of 0.04 to calculate a PBR of 0.16 (1 dolphin every 6.3 yr). Here, we estimate the abundance of Maui's dolphins using genotype recapture records from more intensive sampling over a larger area and update the PBR as a guide to the limit of human-related mortality for Maui's dolphins.

## MATERIALS AND METHODS

Skin samples were collected from Maui's dolphins by dart-biopsy (Krützen et al. 2002) during 2 periods of dedicated small-boat surveys from 4 February to 2 March 2010 and from 14 February to 10 March 2011 (Fig. 1; see Oremus et al. 2012). The survey area along the west coast of New Zealand's North Island extended from Baylys Beach to New Plymouth, with effort concentrated primarily within 2 km of shore in accordance with the austral summer distribution of Maui's dolphins (Fig. 1; Oremus et al. 2012). Calves, approximately one-half or less the size of an adult (assumed to be <1 yr old; Webster et al. 2010), were excluded from biopsy sampling. Standard methods for DNA processing and individual identification based on DNA profiles (including 21 microsatellites) were

Table 1. Maui's dolphin *Cephalorhynchus hectori maui* abundance (N) estimates for 1985 to 2011 determined using a variety of methods. Associated 95% confidence limits (CL) and coefficients of variation (CV) are also included, unless not reported (nr) by the source

Method	Applicable year(s)	N	95% CL	CV	Reference
Boat line-transect	1985	134	nr	nr	Dawson & Slooten (1988)
Computer modeling	1985	140	46–280	nr	Martien et al. (1999)
Boat line-transect	1998	80	nr	nr	Russell (1999)
Aerial line-transect	2001/02	75	48–130	0.24	Ferreira & Roberts (2003)
Genotype recapture	2003	69	38–125	nr	Baker et al. (2013)
Aerial line-transect	2004	111	48–252	0.44	Slooten et al. (2006)
Genotype recapture	2010–11	55	48–69	0.15	Present study

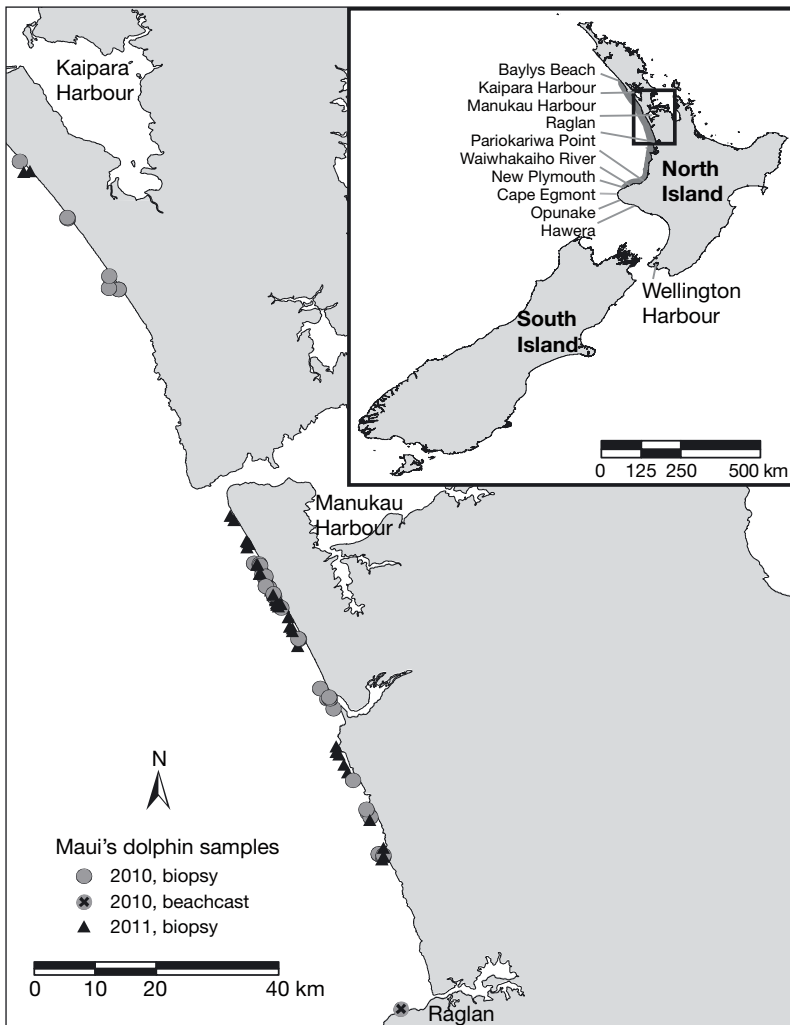


Fig. 1. Maui's dolphin *Cephalorhynchus hectori maui* sample locations and the coastline along the North Island of New Zealand covered by the 2010 and 2011 surveys (shaded dark grey in inset; Oremus et al. 2012)

applied to the 73 skin samples that were collected, as described by Oremus et al. (2012) and Hamner et al. (2014). Based on a low probability of identity ( $P_{(ID)} = 8.5 - 10^{-8}$ ) and probability of identity for siblings ( $P_{(ID)sib} = 4.4 - 10^{-4}$ ), 39 Maui's dolphin individuals were identified, 11 of which were sampled in both years (Table 2; Oremus et al. 2012, Hamner et al. 2014). The 73 samples also included 5 samples from 2 individual Hector's dolphins *Cephalorhynchus hectori hectori* that were identified by mitochondrial DNA control region haplotypes and microsatellite genotype assignment (Hamner et al. 2014). These 2 Hector's dolphins were excluded from the analyses presented here.

Using the Maui's dolphin individuals sampled in 2010 and 2011, we estimated abundance with the Chapman-corrected Lincoln-Petersen estimator

(Chapman 1951). This method assumes that: the population is geographically and demographically closed; all animals are equally likely to be sampled in each occasion; and genotypes are read correctly. Chao's (1989) method for sparse data was used to calculate log-normal 95% CL.

We calculated the potential biological removal (PBR) for Maui's dolphins according to Wade (1998) using the 2010–2011 abundance estimate and a recovery factor value of 0.1. Following Slooten & Dawson (2008), 2 values of  $R_{max}$  were used:  $R_{max} = 0.04$ , the default value recommended for cetacean populations (Wade & Angliss 1997, Wade 1998), and  $R_{max} = 0.018$ , as estimated for Maui's and Hector's dolphins (Slooten & Lad 1991).

## RESULTS AND DISCUSSION

### Abundance

We used annual recapture histories for the 39 Maui's dolphins to calculate an abundance of  $N = 55$  individuals approximately age 1+ (95% CL = 48, 69). This application of genotype-recapture confirmed the extremely low abundance of the subspecies with higher precision than methods previously implemented (Table 1).

Table 2. Maui's dolphin *Cephalorhynchus hectori maui* individuals identified from samples collected during small-boat surveys along the west coast of New Zealand's North Island from 4 February to 2 March 2010 and 14 February to 10 March 2011 (Oremus et al. 2012)

	2010	2011	Genotype recaptures	Total recaptures
Number of surveys	12	11		23
Distance travelled (km)	2117	1893		4010
Samples <sup>a</sup>	37	36		73
Maui's dolphin ind.	24	26	11	39
Females	14	15	6	23
Males	10	11	5	16

<sup>a</sup>Includes 5 samples representing 2 individual Hector's dolphins *C. hectori hectori* that were excluded from the current work (Hamner et al. 2014)

We consider our abundance estimate for the Maui's dolphin to be generally robust to the assumptions of the Lincoln-Petersen model, listed above (Williams et al. 2002). Individual identification by multi-locus genotypes provides a universal permanent tag, but genotyping error has the potential to negatively bias the estimate if an error causes a genotype to match that of another individual, or to positively bias the estimate if an error creates a false new genotype. A sufficiently low  $P_{(ID)}$  and  $P_{(ID)sib}$ , along with our use of controls and rigorous error checking, minimize the potential for incorrect identification of individuals (see Oremus et al. 2012, Hamner et al. 2014).

The assumption of demographic and geographic population closure would be violated by (1) the loss of individuals between the 2010 and 2011 sampling occasions by death or emigration, or (2) the addition of individuals between the 2 occasions by recruitment (i.e. calves born in 2010 growing large enough to be sampled in 2011) or immigration. If either only losses or only additions occurred, a negligible clarification of the time of reference, to 2010 or 2011 respectively, would result. If both removals and additions occurred between the 2 occasions, the abundance estimate of the living population would be positively biased, and the true PBR would be lower than the estimate presented below; however, our study was designed to minimize such bias by considering the life history characteristics and population structure of the Maui's dolphin. Therefore, in a strict sense our abundance estimate applies to the population of Maui's dolphins alive and approximately age 1+ at some point during the study period.

Although the strict assumption of a demographically closed population is violated for most studies of wild populations, the short 1 yr interval between our 2 sampling occasions and the 2 to 3 yr calving interval of these dolphins (Slooten & Lad 1991) minimizes the recruitment of individuals for sampling in the second occasion. During our study period, the death of 1 male Maui's dolphin was documented from a carcass that was found floating and recovered off Raglan in 2010 (NZ Department of Conservation incident code: H202/10). There was no obvious cause of death and the individual was not known from previous genotyping (New Zealand Department of Conservation 2012). As this individual was found dead in the interval between the 2 sampling occasions, it was not available for recapture and was excluded from the abundance estimate.

The potential for violation of geographic closure was considered unlikely given the extent of the surveys, the limited remnant range of Maui's dolphins,

and the absence of local population structure (Pichler 2002, Hamner et al. 2012, Oremus et al. 2012). The genetic identification of 2 immigrant Hector's dolphins among the Maui's dolphins was unexpected (Hamner et al. 2014) and would have contributed to a positive bias in the estimate if undetected. However, these Hector's dolphins were identified and excluded from the analyses presented here, and there was no evidence of interbreeding at the time of our study.

The assumption that all individuals are equally likely to be sampled within each occasion can be violated if individuals exhibit transience, trap (sampling) response, or other characteristics that create individual differences in their sampling probability. Transience or temporary emigration seem unlikely for Maui's dolphins given the reasons discussed above regarding geographic closure. A trap-shy response to sampling would positively bias the abundance estimate; however, no evidence for this was observed, as dolphins remained in the vicinity of the boat following sampling. By focusing our sampling into approximately 1 mo during each of 2 austral summer seasons, we allowed for the randomization of individuals within the Maui's dolphin distribution between the sampling occasions. This is reflected by the movement of individuals up to 80 km and between areas with high sighting densities (Oremus et al. 2012). A few Maui's dolphin sightings have occurred beyond the offshore boundary of the surveys (New Zealand Ministry for Primary Industries and Department of Conservation 2012), but if the movements are occurring at random, then the abundance estimate would not be biased, only less precise (Kendall 1999). An offshore stratification preventing the randomization of individuals between the sampling years seems unlikely, and our abundance estimate has high precision (coefficient of variation [CV] = 0.15). Finally, although our 2-occasion sampling design does not allow for statistical tests of heterogeneity in individual sampling probabilities, no significant evidence for violation of this assumption was found by a previous genotype recapture study of Maui's dolphins, which included less systematic sampling effort distributed over 5 summer sampling occasions from 2001 to 2007 (Baker et al. 2013).

Although a sampling design including more than 2 occasions would have been preferable in some regards, it was not desirable or necessary for this particular case. Due to the Critically Endangered status of the Maui's dolphin, it was preferable to minimize our interaction by constraining the sampling to 2 occasions. By concentrating our dedicated survey effort into two 1 mo sampling occasions 1 yr apart, we

were able to achieve extensive coverage of the distribution of Maui's dolphins and high capture probabilities ( $p$ ) within each of the occasions ( $p_{2010} = 0.44$ ;  $p_{2011} = 0.47$ ). These showed great improvement over the capture probabilities (range  $p = 0.037$  to  $0.243$ ) estimated from open-population models used in the previous multi-year study (Baker et al. 2013). Furthermore, the high precision ( $CV = 0.15$ ) achieved by our 2-occasion abundance estimate meant that the additional resources and interaction with Maui's dolphins required for additional occasions were not justified for the small increase in precision that might have resulted.

### Potential biological removal

Using our abundance estimate and the default value of  $R_{\max} = 0.04$  for cetaceans (Wade 1998), we calculated the PBR for Maui's dolphins to be 0.10, or 1 dolphin every 10 yr. Using  $R_{\max} = 0.018$ , as estimated for Hector's dolphins (Slooten & Lad 1991), the PBR was 0.044, or 1 dolphin every 23 yr. This suggests that the remnant population of Maui's dolphins is not likely to show recovery if anthropogenic mortality causes 1 or more dolphin deaths every 10 to 23 yr. Given that the PBR calculation is implicitly deterministic, and thus does not account for the increased threat of extinction through stochastic processes or depensation, it does not represent a threshold above which extinction is certain, or below which survival is assured (Wade 1998). A population viability analysis could provide further insight into the probability of events outside the control of management (Wade 1998).

### Conservation implications

The results presented here were reported first to the New Zealand government and contributed to accelerating the review of the Maui's Dolphin Threat Management Plan (New Zealand Ministry for Primary Industries and Department of Conservation 2012). Additionally, the deaths of 2 dolphins in 2012 near Cape Egmont – south of the set net and trawling bans implemented in 2008 – confirmed the presence of Hector's (Hamner et al. 2014) and perhaps Maui's dolphins in this area. These deaths led to an extension of commercial and recreational set net restrictions out to 7 nautical miles (n miles) from the former boundary at Pariokariwa Point south to the Waiwhakaiho River, and extending further south to Haw-

era out to 2 n miles from shore, with observers required for commercial set netting between 2 and 7 n miles (New Zealand Ministry for Primary Industries 2012, New Zealand Department of Conservation & Ministry for Primary Industries 2013). This decision will reduce entanglement risk to Maui's dolphins utilizing the southern part of their distribution, as well as any Hector's dolphins that disperse north into that area (see Hamner et al. 2014).

Despite its critically low abundance, we do not consider the Maui's dolphin to be doomed to extinction. The population appears to be maintaining an equal sex ratio and connectivity across the remaining distribution by individual movements of up to 80 km (Oramus et al. 2012). Although there is currently no evidence of interbreeding between the 2 subspecies, the documentation of Hector's dolphins naturally dispersing to the North Island (Hamner et al. 2014) provides the potential for enhancing the low genetic diversity of the Maui's dolphin and preserving the species as part of the west coast North Island ecosystem.

*Acknowledgements.* This work was funded by the New Zealand Department of Conservation and completed under UniServices Contracts 17095 and 30642. Thanks to: all involved with sample collection, especially C. Duffy, K. McLeod, G. Hickman, B. Williams, S. Watts, C. Lilley, D. Patterson, K. Hillock, E. Carroll, D. Heimeier, and E. Brown; S. Lavery and the University of Auckland Molecular Ecology Lab. We also thank local iwi and Department of Conservation Area Offices of Auckland, Kauri Coast, Maniapoto, Taranaki, Waikato, and Warkworth for supporting this work. Samples were collected under permit RNW/HO/2009/03 from the Department of Conservation and University of Auckland Animal Ethics Protocol AEC/02/2008/R658 to CSB. The manuscript was improved by comments provided by 4 anonymous reviewers.

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