

# **Estimating the abundance and effective population size of Māui dolphins using microsatellite genotypes from 2015-2016, with retrospective matching from 2001 to 2016**

C. Scott Baker<sup>1</sup>, Debbie Steel<sup>1</sup>, Rebecca M. Hamner<sup>1,2,3</sup>, Garry Hickman<sup>4</sup>, Laura Boren<sup>4</sup>,  
Will Arlidge<sup>4</sup> and Rochelle Constantine<sup>2</sup>

<sup>1</sup>Marine Mammal Institute and Department of Fisheries and Wildlife, Oregon State University, 2030 SE Marine Science Drive, Newport, Oregon, 97365, USA

<sup>2</sup>School of Biological Sciences, University of Auckland, Private Bag 92019, Auckland 1142, New Zealand

<sup>3</sup>Department of Life Sciences, Texas A&M University-Corpus Christi, 6300 Ocean Drive, Corpus Christi, TX 78412-5800, USA

<sup>4</sup>New Zealand Department of Conservation, New Zealand

## **Summary**

Here we report on initial results from the continued genetic monitoring of the Māui dolphin subspecies in 2015-16, following methods reported previously for surveys conducted in 2010-11 (Oremus et al. 2012; Hamner et al. 2014b) and from 2001-2007 (Baker et al. 2013). Our primary objectives were to estimate the abundance and effective population size of Māui dolphins in 2015-16, as well as to document movements of individuals, including migrant Hector's dolphins, using DNA profiles derived from biopsy-dart samples. We also matched DNA profiles from biopsy samples collected during the 2015-16 surveys to those from previous surveys in 2010-11 and in 2001-07, as well as to necropsy samples from beachcast individuals. The integration of initial results from 2015-16 with previous results provides records of identification by DNA profiles of individuals, both living and dead, extending across 16 years.

Small-boat surveys dedicated to the collection of biopsy samples of Māui dolphins were conducted from south Kaipara in the north to the Mokau River, Taranaki in the south during the austral summers of 2015 and 2016: from 12 February – 1 March in 2015 and from 10 February – 5 March in 2016. A total of 92 biopsy samples were collected during these surveys from individual dolphins older than one year of age:  $n = 48$  in 2015 and  $n = 44$  in 2016. DNA profiles were completed for each sample, including genotyping of up to 25 microsatellite loci (average of 23.8 loci/sample), genetic sex identification and mitochondrial (mt)DNA control region sequencing.

Based on the microsatellite genotyping, we identified 40 individuals from the 48 samples

collected in 2015 and 28 individuals from the 44 samples collected in 2016. Seventeen individuals were sampled in both 2015 and 2016, providing a minimum census of 51 individuals (19 males, 32 females) alive at some point during the two-year study. Of this total, one male and one female were identified as Hector's dolphin migrants based on distinct mtDNA haplotypes and genotype-based population assignment procedures. The male Hector's dolphin was sampled in both 2015 and 2016. Since the previous report of the 2010-11 surveys, there has been only one sample of a beachcast individual; a female Māui dolphin found 13 September 2013, on Ripiro Beach, Dargaville.

Inference of individual movement from sampling locations was limited by the highly clumped distribution of encounters during 2015. In 2016, three individuals sampled north or south of the core distribution between Manukau and Raglan harbours (maximum distance 54 km over 21 days) were also identified in the primary aggregation within or between survey years. The evidence that some individuals move throughout much of the current range of Māui dolphins is consistent with the expectation of random intermingling for capture-recapture models.

For the 2015-16 surveys, excluding the Hector's dolphin migrants, the abundance of Māui dolphins was estimated to be 63 individuals of age 1+ (95% CL = 57, 75), using a two-sample, closed-population model. This estimate is comparable to, but slightly larger than the previous estimate of  $N = 55$  (95% CL = 48, 69) based on the genotype surveys in 2010-11. An effective population size of  $N_e = 34$  (95% CL = 24, 51) was estimated from the genotypes of the 49 Māui dolphins sampled in 2015-16, using the one-sample, linkage disequilibrium method. This estimate has declined compared to estimates for 2001-07 and 2010-11, although the confidence limits of the previous estimates were relatively large and overlap with those of the current estimate. The smaller size of  $N_e$  relative to the capture-recapture estimate is consistent with the expectation that  $N_e$  only represents the breeding individuals of the parental population. The apparent decline is consistent with the expectation that changes in  $N_e$  will lag behind a decline in the census population in the previous generation.

Retrospective matching of DNA profiles for all samples collected from 2001 to 2016 resulted in a total count of 115 individual Māui dolphins, 102 of which were sampled live, 13 sampled beachcast (dead) and one sampled alive and dead two years later. Three individuals (two females; one male) were sampled in both 2001 and 2016, confirming a minimum survival of

15 years. The complete 16-year capture record was made available for initial estimates of survival, recruitment and trends in abundance of Māui dolphins using the Pradel Survival and Lambda model, the Pradel Survival and Recruitment model and the POPAN model, implemented in the program MARK. The results of these analyses are reported in detail in Appendix 3 of this report.

Since 2001, and including the 2015-16 surveys with the previous records (Hamner et al. 2014), there have now been seven Hector's dolphins sampled live or dead on the west coast of the North Island (including Wellington Harbour). Three of these, two females and one male, were sampled alive among social aggregations of Māui dolphins. Despite the intermingling of the two subspecies, there is of yet no evidence of interbreeding between the Hector's and Māui dolphins, i.e., all subspecies identification has been consistent with a diagnostic difference in mtDNA and assignable differentiation of microsatellite genotypes.

Our results highlight the importance of individual identification and genetic monitoring using biopsy samples and DNA profiling. The 'register' of DNA profiles, now extending across 16 years, is providing new information on the life history parameters of Māui dolphins, their local movement, census abundance and effective population size, as well as the long-distance dispersal of Hector's dolphins into the range of the Māui dolphin.