

## SHORT NOTE

### DNA sequencing detects an additional museum specimen of the Chatham Island taiko (*Pterodroma magentae*)

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The Chatham Is taiko (*Pterodroma magentae*) or tchaik in the Moriori language, is one of the world's rarest seabirds. The taiko is critically endangered with a population size of approximately 120-150 individuals including just 8-15 breeding pairs (G. A. Taylor, *pers. comm.*). The taiko is thought to have only ever bred on the main island of the Chatham group (Rēkohu/Wharekauri; Aikman *et al.* 2001). Current issues affecting the recovery of the taiko population include predation by introduced species (Johnston *et al.* 2003) and possibly the excess of unpaired males present at the colony (Lawrence *et al.* 2008a).

Very few museum specimens of the Chatham Is taiko exist. The type specimen (called the magenta

petrel) is held in the Turin Regional Natural Science Museum in Italy (Giglioli & Salvadori 1869; Crockett 1994). No other taiko specimens are known to be held by any other overseas museum. Te Papa Tongarewa Museum of New Zealand holds 1 adult study skin (NMNZ OR.25209; Imber *et al.* 1998) and 1 mounted juvenile (NMNZ OR.27098; A.J.D. Tennyson, *pers. comm.*). We report the discovery of a mounted taiko specimen that had been misidentified as a Tahiti petrel (*Pseudobulweria rostrata*) at the Canterbury Museum.

We extracted DNA from a feather sample taken from the specimen labelled Tahiti petrel (Old registration number O1013.0, catalogue number AV14948; Fig. 1). DNA extraction and Polymerase Chain Reaction (PCR) set-up were carried out in a dedicated ancient DNA laboratory. Three regions of the mitochondrial cytochrome-*b* gene were amplified using PCR. Target region 1 was amplified and sequenced 3 times in 1 direction. Target regions

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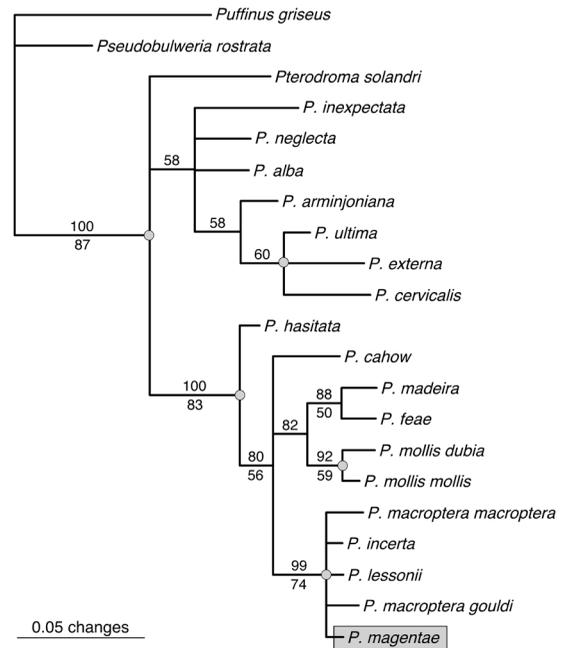


**Fig. 1** Mounted taiko (*Pterodroma magentae*) specimen held by the Canterbury Museum, initially misidentified as a Tahiti petrel (*Pseudobulweria rostrata*). Note the posture is not typical. Photo: Paul Scofield.

2 and 3 were each amplified twice and sequenced in both directions. These 3 regions of the mitochondrial cytochrome-*b* gene totalled 311 base pairs (bp; Genbank accession number FJ463404; methods as in Lawrence *et al.* 2009). When compared, these DNA sequences from the Canterbury Museum specimen were identical to 1 of the most common haplotypes found in the modern taiko population and in ancient taiko bones (Lawrence *et al.* 2008b; Lawrence *et al.* 2008c).

We aligned a section of DNA sequence from the Canterbury Museum specimen with 150 bp of cytochrome-*b* sequence available on Genbank from Tahiti petrels (accession numbers U70482 and U70493; Bretagnolle *et al.* 1998). The 2 Tahiti petrel sequences from Genbank were identical and alignment revealed 16 nucleotide substitutions between these sequences and that of the Canterbury Museum specimen (11% of the total sequence was different).

We next performed phylogenetic analyses of the 150bp of cytochrome-*b* data (with Bayesian inference, maximum likelihood and maximum parsimony methods as in Lawrence *et al.* 2009). These analyses showed that the Tahiti petrel diverged close to the outgroup (sooty shearwater/tītī, *Puffinus griseus*, Genbank accession number U74353). However, the Canterbury Museum specimen sequence was identical to that of *Pterodroma magentae* and fell within a separate clade with a Bayesian probability of 100% and maximum likelihood bootstrap value of 87 (Fig. 2). These results reveal that the Canterbury Museum specimen is not a Tahiti petrel, but a Chatham Is taiko.



**Fig. 2** Phylogenetic relationship of the Chatham Is taiko Canterbury Museum specimen (*Pterodroma magentae*; highlighted) to other *Pterodroma* petrels and the Tahiti petrel (*Pseudobulweria rostrata*), based on mitochondrial cytochrome-*b* sequence (150 bp). The Bayesian inference consensus tree (shown) was constructed with the HKY-I model of sequence evolution. Bayesian inference posterior probabilities of clades have been converted to percentage of trees with that topology and are presented above the branch; maximum likelihood bootstrap values are shown below the branch. Bayesian inference and maximum likelihood trees concurred. Grey circles indicate nodes that also occurred in maximum parsimony trees. (Methods and Genbank accession numbers of sequences are in Lawrence *et al.* 2008a).

Subsequent morphological examination of the Canterbury Museum specimen also confirmed that the specimen is a taiko. The specimen has a pale chin, streaked under-tail coverts and flanks typical of a taiko – all features that the Tahiti petrel lacks (Onley & Scofield 2007). Measurements are all within the range of those published for taiko (Table 1). The specimen's culmen and tarsus measurements are shorter than those published for Tahiti petrel (Villard *et al.* 2006).

The only information available on provenance of the specimen is that it was collected in the Pacific Ocean. It has been in the Canterbury Museum collection since at least 1910. Display of this specimen will help to increase the public profile of New Zealand's most endangered seabird species.

**Table 1** Standard measurements (range in millimetres) of the Canterbury Museum specimen, Tahiti petrel (*Pseudobulweria rostrata*) and Chatham Island taiko (*Pterodroma magentae*).

	Canterbury Museum Specimen	Tahiti Petrel <sup>a</sup>	Taiko <sup>b</sup>	Taiko Type Specimen <sup>c</sup>	Te Papa Taiko Specimen <sup>d</sup>
Culmen	31.2 mm	32.25 – 39.9	30.3 – 35.1	32	32.1
Bill depth	13.9 mm	12.7 – 16.5	13.1 – 17.4	15	16.3
Wing	306 mm	274 – 318	284 – 316	306	300
Tail	c. 129 mm	112 – 133	116.5 – 139	127	129
Tarsus	41.2 mm	43.3 – 52.95	38.0 – 45.0	42	41.5
Mid-toe claw	59.2 mm	-	53.0 – 62.0	54	58.5

<sup>a</sup> Villard *et al.* 2006<sup>b</sup> Marchant & Higgins 1990; Crockett 1994<sup>c</sup> Bourne 1964<sup>d</sup> NMNZ OR.25209; Imber *et al.* 1998

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