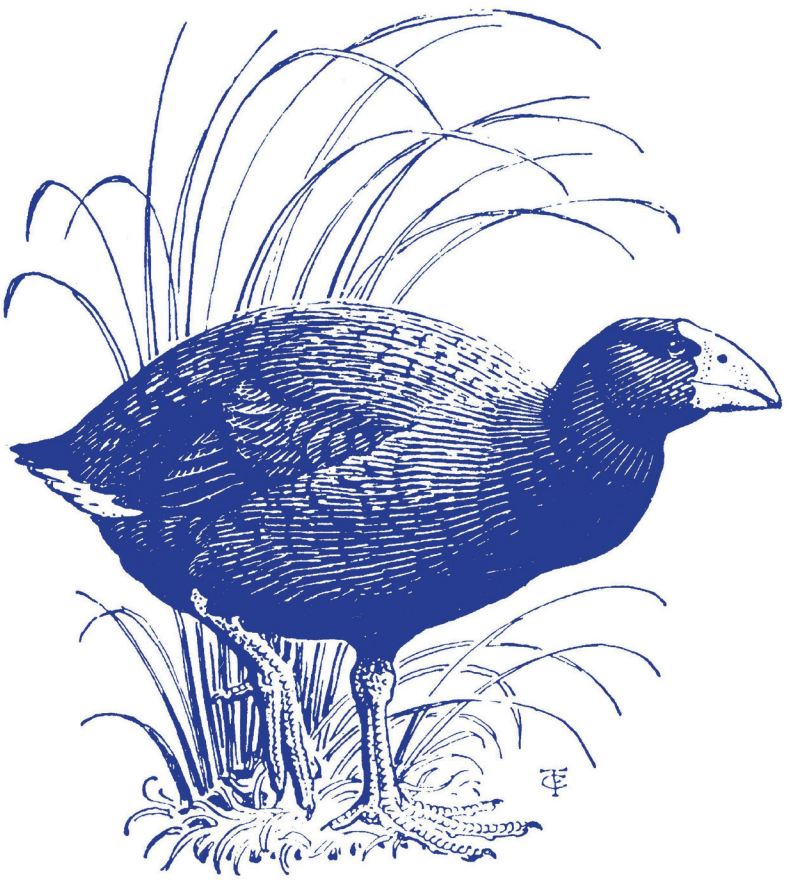
NOTORNIS

Ornithology of the Southern Pacific



ISSN 0029-4470

Volume 70 Part 1
March 2023
Journal of the Ornithological Society of New Zealand

NOTORNIS

Scope *Notornis* is published quarterly by the Ornithological Society of New Zealand Inc. The journal publishes original papers and short notes on all aspects of field or laboratory ornithology, and reviews of ornithological books and literature, student research, and reports of specialist ornithological events. *Notornis* concentrates on the birds of the ocean and lands of the Southern Pacific, with special emphasis on the New Zealand region. It seeks to serve professional, amateur and student ornithologists alike, and to foster the study, knowledge and enjoyment of birds.

Editor: CRAIG T. SYMES

Assistant Editor: VACANT

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Notornis, Vol. 4, No. 1 (July 1950) (ISSN 0029-4470)
In continuation of Reports and Bulletins (1939-1942) and New Zealand Bird Notes (1942-1950)

Vol. 70, No.1 (March 2023) (Published March 2023)

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Notornis, 2023, Vol. 70: 1-13
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The conservation status of Hutton's shearwater (*Puffinus huttoni*) at Shearwater Stream, Kaikōura, New Zealand: a small population at risk?

CHLOE PAULET CARGILL*
Puhi Peaks Station, Kaikōura 7371, New Zealand

DOUGAL TOWNSEND
GNS Science Te Pū Ao, 1 Fairway Drive, Avalon, Lower Hutt, Wellington 5011, New Zealand

NICKY R. McARTHUR
Puhi Peaks Station, Kaikōura 7371, New Zealand

REGINE MORGENSTERN
GNS Science Te Pū Ao, 1 Fairway Drive, Avalon, Lower Hutt, Wellington 5011, New Zealand

MIKE MORRISSEY
9 Grays Lane, Kaikōura 7300, New Zealand

GREG SHERLEY
14 Celtic Way, Paraparaumu 5032, New Zealand

MIKE BELL
Toroa Consulting Limited, L2, 1 Hutcheson Street, Mayfield, Blenheim, Marlborough 7201, New Zealand

Abstract: Hutton's shearwater (*Puffinus huttoni*) is a burrowing petrel endemic to the alpine zone of the Seaward Kaikōura Ranges, New Zealand. In November 2019, we accessed an understudied breeding colony at Shearwater Stream in the Puhi Peaks Nature Reserve for the first time since a M_w 7.8 earthquake struck the region in 2016. We measured population parameters and carried out a geomorphological assessment. We estimate that the Shearwater Stream colony supports approximately 3,000 breeding pairs. Ground deformation attributed to the 2016 earthquake did not explain the discrepancy between this estimate and the commonly cited (pre-quake) population estimate of ~8,000 pairs. We highlight the limitations of extrapolated population parameters and of using vegetation cover as a coarse proxy for colony area. We discuss how low burrow occupancy and long-term reductions in the availability of suitable habitat indicate a population at risk of decline. We highlight how stable long-term data for burrow density and breeding success may not be reliable indicators of population health at Shearwater Stream.

Cargill, C.P.; Townsend, D.; McArthur, N.R.; Morgenstern, R.; Morrisey, M.; Sherley, G.; Bell, M. 2022. The conservation status of Hutton's shearwater (*Puffinus huttoni*) at Shearwater Stream, Kaikōura, New Zealand: a small population at risk? *Notornis 70(1)*: 1–13.

Keywords: Hutton's shearwater, burrowing petrel, New Zealand, earthquake, population parameter, population trend

Received 19 August 2022; accepted 25 January 2023
*Correspondence: *chloe_cargill@hotmail.com*

INTRODUCTION

The effective conservation management for species with limited breeding range and fragmented conservation units requires the assessment of species health at the population level (Wilcox & Murphy 1985). For example, the adverse effects of predator-prey dynamics, in combination with demographic, genetic and environmental stochasticity, on the long-term viability of small populations are often disproportionately high (Shaffer 1981; Lyver *et al*. 1999). Conservation managers must implement mitigation measures to address progressive habitat fragmentation and insularity caused by anthropogenic factors and/or natural perturbation, at the population level. Such considerations have motivated the present study of a relict population of Hutton's shearwater (*Puffinus huttoni*) (Matthews 1912).

Hutton's shearwater is a burrowing petrel limited to two localities on the east coast of South Island New Zealand (Marchant & Higgins 1990; BirdLife International 2019), where breeding is confined to the alpine zone (1,200–1,800 m a.s.l.) of the Seaward Kaikōura Ranges. The two colonies comprise 94% and 6% of the total remaining population (Cuthbert 2019), in addition to one recently established lowland artificial colony of about 75 birds on the Kaikōura Peninsula (Rowe 2014, 2018; Rowe & Howard 2023). Historic range contractions for Hutton's shearwaters are primarily credited to habitat destruction by feral pigs (*Sus scrofa*) (Cuthbert 2002). Other factors considered to be involved include interannual declines in the seasonal availability of pelagic Euphausiid krill and Clupeid fish prey (Sherley 1992; Bennet *et al*. 2019), the destruction of burrows by browsing red deer (*Cervus elaphus*), chamois (*Rupicapra rupicapra*), and wild goats (*Capra hircus*) (Sherley 1992; Cuthbert 2002), and to a lesser degree predation by invasive stoats (*Mustela erminea*) (Cuthbert & Davis 2002a).

The smaller of the two remaining alpine colonies is located at Shearwater Stream in the Wharekiri Valley (42.10°S, 173.40°E), within the Puhi Peaks Nature Reserve. The terrain across the Shearwater Stream colony catchment consists of steep rock and scree slopes, which are difficult to access and traverse. The current classification (Endangered) of the species on the IUCN Red List, including the population trend (stable) (BirdLife International 2019) has been largely informed by long-term monitoring studies conducted at the larger and more accessible Kowhai Valley colony (42.16°S, 173.36°E) (Sommer *et al.* 2009), and supported by regional-scale population estimates derived from colour-mark-recapture studies of individuals foraging at sea (Rowe *et al*. 2018).

In November 2016, a shallow M_W 7.8 earthquake with a depth of about 14 km struck near Waiau, north-east Canterbury, propagating northwards towards Kaikōura. The Shearwater Stream colony is situated about 1.3 km from the Jordan Thrust, which underwent surface rupture during the earthquake (Litchfield *et al*. 2018) and was therefore within the high-shaking and high-damage zone surrounding the fault (Massey *et al*. 2018, 2020). Ground shaking in the area was modelled with peak ground acceleration (PGA) values exceeding 1 (gravity is overcome at PGA >1) over large parts of the region (Kaiser *et al*. 2017). In December 2017, an assessment of both the Shearwater Stream and Kowhai Valley colonies was commissioned by Fisheries New Zealand to assess the extent of habitat loss attributable to the earthquake (Cuthbert 2019). However, access on foot was not permitted at the Shearwater Stream colony due to the instability of the terrain at the time (Cuthbert 2019).

Prior to this study, the colony boundaries at Shearwater Stream were mapped once, in 1988, providing a planimetric colony area of 2.5 ha with a population estimate of 9,800 breeding pairs (Sherley 1992). Following the implementation of the burrowscope and standardized methodology for determining burrow occupancy in the late 1990s, the population at Shearwater Stream was thought to be more in the region of 7,750 breeding pairs (Cuthbert & Davis 2002b). The calculation used an average rate of burrow occupancy as measured over a ten-year period in the larger Kowhai Valley colony (Cuthbert & Davis 2002b), applied to the colony area as determined at Shearwater Stream the previous decade (Sherley 1992). The revised population estimate was never verified in the field. However, numerous studies, species assessments, and literature reviews have since reported the Shearwater Stream population of Hutton's shearwaters to be about 8,000 pairs (Cuthbert & Davis 2002a, 2002c; Sommer *et al.* 2009; Waugh *et al.* 2013; Rowe *et al.* 2018; BirdLife International 2019).

Up-to-date, site-specific population parameters are required to determine the conservation status of the smaller Hutton's shearwater colony and to inform appropriate management. The objectives of this study were, 1) to provide revised estimates of mean burrow density, mean burrow occupancy, breeding success, colony area, and population size for Hutton's shearwater at Shearwater Stream, and 2) to assess the underlying geomorphology of the colony catchment in order to better understand the extent of any damage to breeding habitat sustained during the 2016 earthquake. The current and long-term conservation status of the colony was inferred using longitudinal data derived from an in-depth review of primary and grey literature.

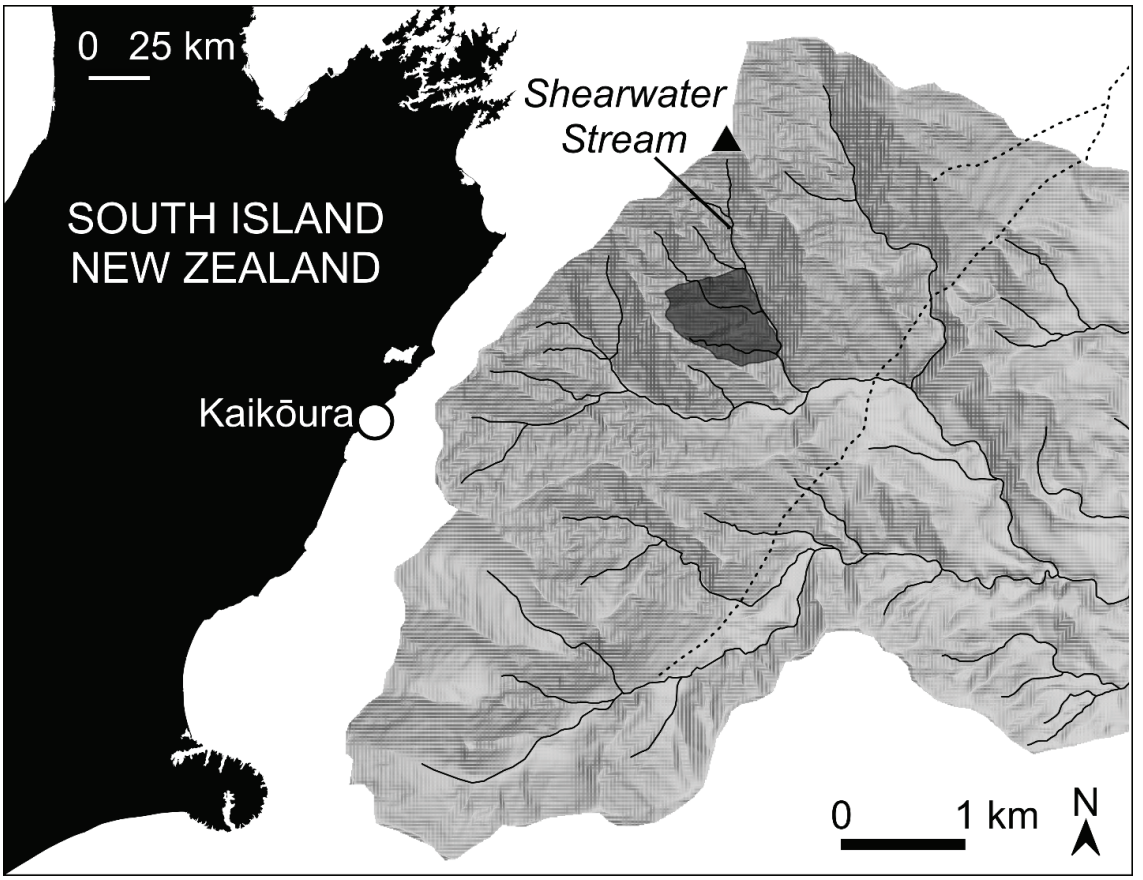

Figure 1. Location of the Hutton's shearwater (*Puffinus huttoni*) colony, darker shaded region south of Tarahaka Peak (2,283 m above mean sea level, black triangle), at Shearwater Stream in the Wharekiri catchment (white region to the north of the Kaikōura township) in the Seaward Kaikōura Ranges, New Zealand (42.2°S, 173.8°E), in relation to the local elevation (LINZ 2014), its nominal tributary of the Wharekiri watercourse (solid black lines, LINZ 2011a) and the Jordan Thrust (dashed black lines), which ruptured during the 2016 Kaikōura earthquake. Base map of New Zealand sourced from LINZ 2011b

MATERIALS AND METHODS

Study site

The rock substrate of the site of the Hutton's shearwater colony at Shearwater Stream (Fig. 1) is a mixture of argillite and sandstone dominated sequences of Torlesse (Pahau) terrane 'greywacke' (Rattenbury *et al.* 2006). The headwaters of the catchment drain from the main divide of the Seaward Kaikōura Ranges, from an unnamed peak (2,414 m) and Tarahaka (2,283 m), before joining with the larger Wharekiri Stream at 1,050 m elevation (Fig. 1).

The terrain is steep, with local relief >1,300 m, and comprises rocky slopes facing all directions. Chutes of shingle scree and thick colluvium (a mixture of grain sizes from clay to boulders indicative of down-slope movement and deposition of debris) separate the rock faces. Shearwaters burrow in areas of deeper soil associated with *Chionochloa* snow tussock (Cuthbert & Davis 2002c), in numerous small sub-colonies (Fig. 2). We were able to access sub-colonies 1, 2a and 5a in the 2019/20 and 2020/21 breeding seasons. Sub-colonies 2b-2d, 3a, 3b, 4 and 5b-5e were deemed inaccessible due to safety concerns.

Population parameters of the Hutton's shearwater

Measuring burrow density and burrow occupancy

The mean number of burrows per square metre, hereafter referred to as 'burrow density', was calculated using a plot sampling approach within sub-colony 1, sub-colony 2a, and sub-colony 5a

(sub-colonies labelled as per Fig. 2 in Sherley 1992). Sub-colonies were visited over two days 21–22 November 2019. Circular plots of 20 m^2 were constructed by describing a circle of radius (r) 2.52 m around a central aluminium pole using a length of rope with a marker at 2.52 m. The location of each non-overlapping plot was determined by sighting a plot centre at random, working uphill through each sub-colony in a zig-zag motion. One person walked the rope in an anti-clockwise direction beginning and ending at an azimuth of 270°. The same person counted all burrow entrances within the plot where ~1.26 m < r < 2.52 m. A second person walking behind the rope counted all burrow entrances located on the inside of the circle (0 m < r ≤ ~1.26 m). The rope was kept taut and lifted over tussock where required. Where it could be determined, a burrow with two or more entrances was recorded as a single burrow. Burrows at the edge of a plot were excluded where more than 50% of its entrance was beyond the 2.52 m marker. Burrows were counted by calling aloud consecutive numbers (starting at '1' with each new plot) and staking all entrances with 15 cm long, white pegs immediately after detection. The mean burrow density for each sub-colony was calculated as the sum of the burrow densities measured for each plot, divided by the total number of plots scored for burrow density within that sub-colony.

The rate of burrow occupancy (the proportion of burrows containing a nest chamber with both an egg and incubating bird at the time of detection) was determined for a subset (due to time limitations) of plots sampled for burrow density. A burrowscope (Sextant Technology Ltd, model "Taupe") was used to determine the contents of all tunnels and chambers within each burrow. Observers either had previous experience burrowscoping for Hutton's shearwater at Shearwater Stream (NRM, MM, MB, J. Kilgour) or were trained *in situ*. To reduce false negatives due to observer fatigue, observers were swapped out every 30 minutes from a team of five. Empty burrows were double-checked by a second observer. Occupied burrows were checked once. Observer initials were recorded against each burrow. Nesting material can be retained within burrows for consecutive years following a breeding attempt (A. Davis in Sherley 1992), therefore the sole presence of nesting material was not considered as adequate evidence of an occupied burrow. To prevent duplications, white pegs placed when scoring burrow density were removed immediately after scoping. In cases where the end of the burrow could not be located the burrow was excluded from further analysis. Burrows were first visited an average of 22 days after peak egg laying (around the second week of November, see Cuthbert & Davis 2002c). The mean burrow occupancy for each sub-colony was calculated as the sum of the burrow occupancies measured for each plot, divided by the total number of plots scored for burrow occupancy within that sub-colony.

Measuring breeding success

Breeding success, here defined as the proportion of chicks reared to late nestling or about 84 days old (Cuthbert & Davis 2002c), from a sample of incubating birds, was calculated for both the 2019/20 and 2020/21 breeding seasons. A subset of occupied burrows from sub-colony 5a were marked by inserting an upright metal pole of 1 m in length into the ground near the entrance of each burrow. These burrows were then checked for the presence of a live chick during the late chick-rearing stage (Table 1).

Table 1. Visit dates and sample sizes used to measure breeding success of Hutton's shearwater in sub-colony 5a at Shearwater Stream (see Fig. 1).

Season	1st visit	2nd visit	Difference	Number burrows
2019/20	24 November 2019	10 February 2020	79 days	60
2020/21	4 December 2020	22 February 2021	81 days	50

Burrowscopes are a reliable method for monitoring breeding success where occupancy can be confirmed (Cuthbert & Davis 2002c). The presence of down at the second check was not considered as sufficient evidence of a successful breeding attempt, as shed down feathers have been known to remain for at least one successive year in an unused burrow (A. Davis in Sherley 1992). All tunnels and chambers of 'failed' burrows were checked independently by two observers to prevent false negatives.

Delineating colony area

The boundaries of all known areas of burrowed ground at sub-colonies 1, 2a and 5a were recorded on foot using a hand-held GPS unit on 10 February 2020. The boundaries of inaccessible sub-colonies 2b–2d, 3a, 3b, 4, and 5b–5e were drawn by MM on 0.5 m resolution aerial photographs captured by drone on 10 February 2020. MM was able to assess the entire colony catchment by helicopter on 10 February 2020 and has considerable experience working within all sub-colonies both pre- and post-the 2016 earthquake.

Statistical and spatial analyses

Assessing spatial heterogeneity in burrow density and burrow occupancy

The following statistical analyses were carried out using the statistical software R v4.0.2 (R Core

Team 2020). Statistical significance was assumed at the 95% level where $\alpha = 0.05$. Factorial regression with Analysis of Variance (ANOVA) was first used to test for between-sub-colony variation in burrow density. Burrow density data were square root transformed to adjust for a positive skew in the observed distribution. Burrow occupancy was analysed as a function of sub-colony using binomial regression within a Bernoulli Generalized Linear Model (GLM), with a complementary-log-log link function to account for asymmetry in counts of successes and failures (occupied and unoccupied burrows). Models were sequentially relevelled and rerun to test for differences in burrow density and burrow occupancy against differing sub-colony baselines. A Pearson's chi-squared test was used to test the independence of count data between observer and sampling location, and a 5-sample two-sided test for equality of proportions was used to test for observer bias in determining burrow occupancy. Model assumptions and goodness of fit were verified by examining the distribution of either the standardised residuals (burrow density ANOVA) or the range of the deviance residuals (burrow occupancy GLM), by checking for unduly influential data points, and by plotting the residuals versus the fitted values and versus the covariates specified in the model.

Estimating colony area and population size

The boundaries of all occupied areas were manually digitized in QGIS v3.10.11 (QGIS Development Team 2020) using a New Zealand Transverse Mercator 2000 (NZTM2000) projection (LINZ 2008). Sub-colony areas were overlaid against aerial photographs captured February 2020 (0.5 m^2 resolution) to identify and remove areas of scree and bare rock. The boundary polygons representing each sub-colony were buffered by the hypotenuse of the raster resolution prior to further analysis to mitigate for edge effect negative bias during surface area calculations (see Jenness 2004). The total 3D surface area of the colony was estimated from post-2016 raster elevation data (digital surface model, 1 m resolution (Aerial Surveys 2017) using the tool *r.surf.area* (Brown *et al*. 1994–2011) available in the Geographic Resources Analysis Support System v7.8 plugin (GRASS Development Team 2020). This tool estimates the 3D surface area of a region by employing the following method: for every cell within a polygon, eight three-dimensional triangles were generated connecting the cell centrepoint with the centrepoint of the eight surrounding cells, and the areas of the portions of each triangle that lay within each cell-boundary were calculated and summed.

Population size, given in breeding pairs, was calculated as the summed product of colony area, burrow density, and burrow occupancy using sub-colony specific parameters. Appropriate values for burrow density and burrow occupancy were assigned to unvisited sub-colonies based on detailed descriptions provided by MM following both aerial assessment and a qualitative comparison of these sites to those where burrow density was measured (see RESULTS). A 95% confidence interval (CI) around the population estimate was calculated using the lower and upper 95% confidence intervals around the mean values for burrow density and rate of burrow occupancy calculated in R using a nonparametric bootstrap with replacement over 100,000 simulations.

Literature review

Longitudinal data for population parameters specific to the Shearwater Stream colony were sourced from all available primary and grey literature. Where required, raw data values were sourced from archived material provided by the Hutton's Shearwater Charitable Trust, formerly the Hutton's Shearwater Recovery Group, and the New Zealand Department of Conservation. Long-term averages and 95% confidence intervals around the mean were calculated where appropriate.

Quantifying habitat loss attributed to the 2016 Kaikōura earthquake

A detailed survey of the colony catchment was carried out on 10 February 2020. Cracks, faults, damage, and joint defects observed in sub-colonies 1, 2a, and 5a were recorded and measured *in situ*, and the general stability of the landscape was assessed across the catchment. Aerial photographs of all sub-colonies were taken the same day using a drone. See Townsend & Morgenstern (*In prep.*) for detailed methodology and full results of the geomorphological assessment conducted across the Shearwater Stream catchment.

RESULTS

Population parameters

Burrow density and burrow occupancy

Burrow density ranged from 0.15 to 1.5 burrows m^{-2}, with a colony mean of 0.565 burrows m^{-2} (number of plots = 39, 0.476–0.661 95% CI; Table 2). The rate of burrow occupancy ranged from 0% to 88% per plot, with a colony mean of 33.8% (number of burrows = 225, 22.8–45.4 95% CI; Table 2). Burrow density was significantly lower in sub-colony 1 compared to sub-colony 5a (ANOVA, $df = 36$, $t = -2.623$, $P = 0.0127$).

For the purpose of estimating population size, sub-colonies inaccessible on the ground were pooled into categories for burrow density according

to common visual descriptions provided during an aerial survey of the colony catchment. Inaccessible sites that were observed to have a relatively good cover of burrows were assigned the mean burrow density value measured at neighbouring colonies with similar slope angle, soil type, and underlying rock type. Where this was not possible, inaccessible sub-colonies were divided between two categories. The categories were 'good' or 'mostly destroyed' and were assigned a value for burrow density that was either equal to the colony average, or a lower, fixed value of five burrows per 20 m^2 plot, respectively (Table 2). The colony mean for burrow occupancy was assigned to all inaccessible sub-colonies (Table 2). Whilst burrow occupancy in the sub-colonies visited was found to be lower in sub-colonies with lower burrow density, and *vice versa*, we felt that this observation alone did not justify lowering the rate of burrow occupancy for unvisited sites. Overall, the summed area of the inaccessible sub-colonies accounted for 20% of the total colony area.

Each observer sampled a mean of 43.8 ± 25.3 *sd* burrows for burrow occupancy. Observers were correlated with sub-colony (Pearson's Chi-squared test, df = 8, χ^2 = 111.74, $P < 2.2^{-16}$), and spatially auto-correlated with sampling plot (Pearson's Chi-squared test, df = 80, χ^2 = 335.08, P < 0.001). However, no observer recorded any more or less occupied burrows than expected under an assumption of equal detection probability (5-Sample Two-Sided Test for Equality of Proportions, χ^2 = 7.56, df = 4, P = 0.109).

Breeding success

Breeding success for the 2019/20 and 2020/21 breeding seasons was 0.53 (number of burrows monitored = 60) and 0.50 (n = 50), respectively. Observations of note recorded at failed burrows included single, intact eggs within the nest chambers of three separate burrows, one depredated chick found at a burrow entrance, and one burrow containing four eggs.

Table 2. Summary of parameters for the Shearwater Stream sub-colonies of Hutton's shearwater. Sub-colonies, denoted 'Site', are grouped by the method of assessment (either estimates obtained in the field or by aerial survey in February 2020) and then, for inaccessible sites, by qualitative score. A cross † denotes where specific values for burrow density ('Density') and burrow occupancy ('Occupancy') were assigned to inaccessible sub-colonies based on qualitative assessment. 'Samples' refers to the total number of plots or burrows scored for burrow density and burrow occupancy in the following format, 'plots for burrow density: plots for burrow occupancy, *total burrows for burrow occupancy*'. Areas given are three-dimensional values calculated for each sub-colony or set thereof (summed where appropriate). Corresponding population estimates are given in terms of breeding pairs ('Pairs'). Asterisks * mark the pair of sub-colonies for which the difference in burrow density between sub-colonies was statistically significant (P < 0.05). Boot-strapped 95% confidence intervals are given in parentheses where appropriate.

Site	Samples	Density (m^{-2})	Occupancy (%)	Area (ha)	Pairs
1	12:6, *57*	0.43* (0.33–0.53)	24.4 (11.2–36.7)	0.40	410 (150–770)
2a–b	13:7, *74*	0.52 (0.41–0.65)	35.3 (17.4–45.0)	0.34	620 (240–1,190)
2c–d, 3a–b, 5b	-	0.25†	33.8 (22.8–45.2)†	0.19	150 (99–196)
4	-	0.57 (0.48–0.66)†	33.8 (22.8–45.2)†	0.17	320 (180–510)
5a-e	14:8, *94*	0.73* (0.54–0.92)	39.6 (19.1–60.8)	0.53	1,530 (540–2,980)
Total				**1.62**	**3,030 (1,210–5,640)**

Colony area and population estimate

The total occupied area across the entire Shearwater Stream catchment was calculated to be 1.62 ha (Table 2), supporting an estimated 3,030 breeding pairs (1,210–5,640 95% CI, Table 2). Colony areas were sited on moderate slope angles (30–60°). There were many slopes similar in both angle and aspect that did not have nesting sites and burrowed ground across the colony was considerably fragmented (Fig. 2). Sub-colonies 1 and 2a comprised the largest continuous regions of utilised habitat and many burrowed areas comprised isolated patches of less than 0.1 ha.

Long-term colony status

Longitudinal data for population parameters specific to the Shearwater Stream shearwater colony were scarce. We observed negligible long-term change in burrow density (Fig. 3a). Mean burrow occupancy appears to have decreased, although the long-term trend was not statistically significant (Fig. 3b). Breeding success was punctuated by years with low or near-total breeding failure. Breeding success was lower post-quake than in previous years, but was generally as expected for the species at this location (Fig. 3c).

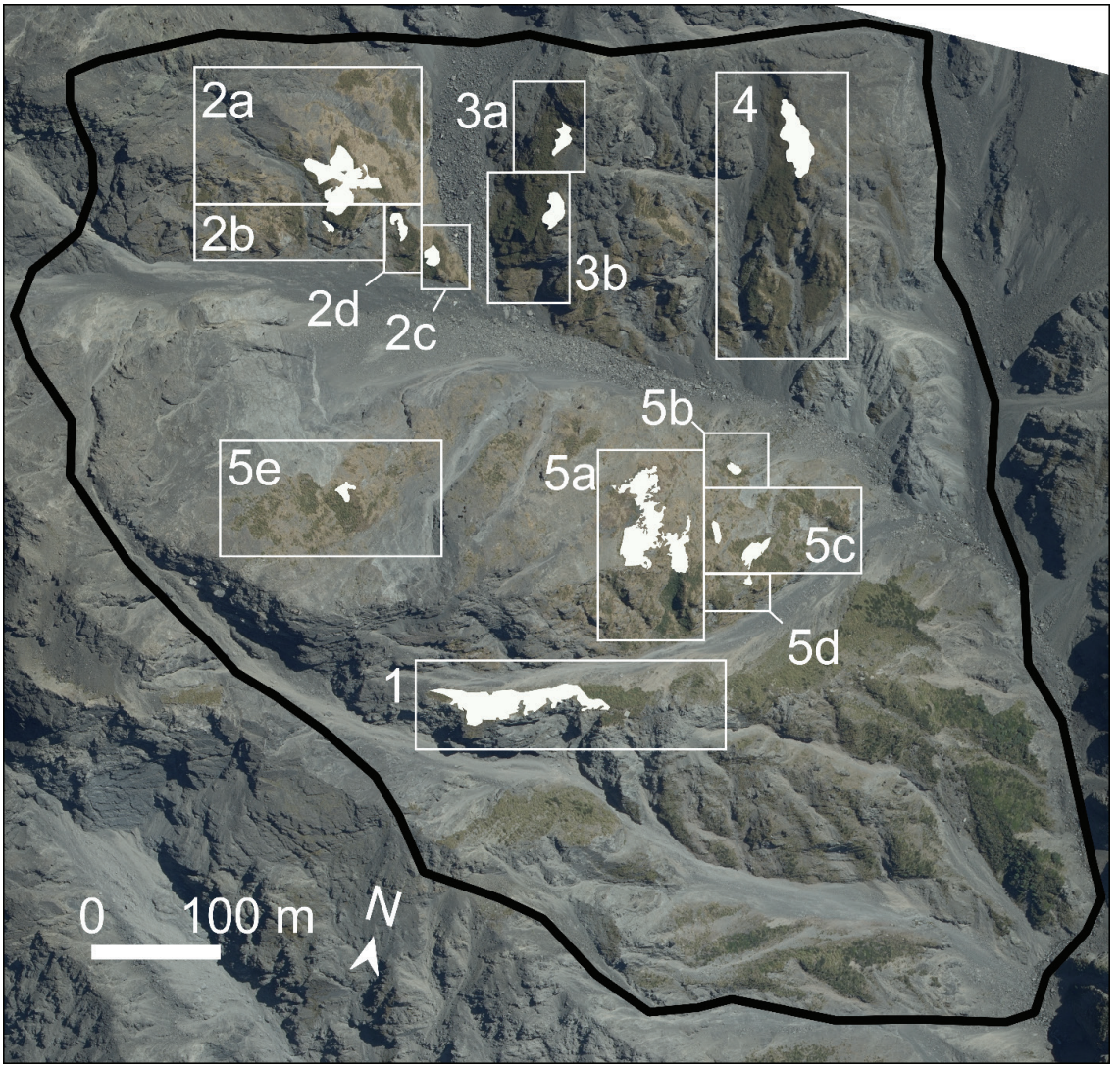

Figure 2. Hutton's shearwaters breed in numerous small sub-colonies associated with *Chionochloa* snow tussock (vegetated areas) at scattered sites across the Shearwater Stream colony catchment (delineated here by the solid black line; shown as the darker shaded region south of Tarahaka Peak in Fig. 1) in the Wharekiri Valley, Puhi Peaks Nature Reserve. The general locations of the sub-colonies (white boxes) are delineated and labelled as per Sherley 1992 for consistency. Areas occupied by Hutton's shearwaters across the Shearwater Stream colony catchment in November 2019 are indicated by the solid white polygons. Total occupied area: 1.62 ha. Aerial photograph captured by RM in February 2020.

Habitat loss attributed to the 2016 Kaikōura earthquake

Burrowed ground in sub-colony 1 was intersected by three cracks, the largest of which was associated with >2 m of southwards displacement. We also noted evidence of minor ravelling or toppling of the cliff edge at the southern edge of the sub-colony. A 1 m approximate scarp and an approximate 15 m wide area of shallow slumping was noted on the north face of the sub-colony where a large boulder and the surrounding soil has pulled away from the ridge. A collapse was also recorded cutting into an area of vegetated ground to the west of sub-colony 5a. Deformation within the sub-colony proper was limited to minor cracking (about 20 cm vertical) and disruption and jostling of *in situ* blocks or boulders along the ridgeline to the southeast at the colony edge. Evidence of fresh rockfalls sourced from the

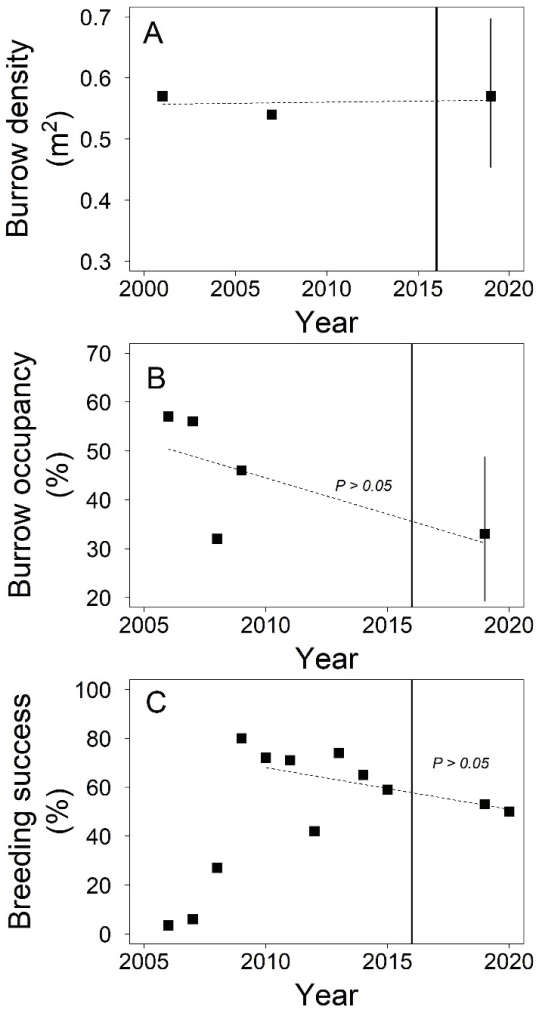

Figure 3. Colony-level means for burrow density (A), burrow occupancy (B) and breeding success (C) for the Hutton's shearwater at Shearwater Stream. Dashed lines indicate the direction of the long-term trends. Note that these were not statistically significant ($P > 0.05$). Linear regression models for burrow density and occupancy were informed by all available and comparable data, whereas we provide a decadal trend for breeding success. Error bars in panels A and B represent 95% confidence intervals around the mean for data collected over the 2019/20 breeding season. Data for burrow occupancy and breeding success prior to the 2005/06 breeding season were not included due to positive bias incurred from the field methods used. Vertical lines indicate the 2016 earthquake event. Data sourced from this study, Bell (2007 *unpubl. data*, 2008 *unpubl. data*), Sommer *et al.* (2009), Cuthbert (2019) and the New Zealand Department of Conservation.

cliff faces above were observed in two gullies within sub-colony 5a. Only minor damage was observed in sub-colony 2a, limited to fresh and unweathered minor cracks (about 5 cm) on a structure parallel to the slope. No cracking or soil separation was observed at the base of the exposed rock faces at the upper edges of either sub-colony 5a or sub-colony 2a, as would be expected if there had been shallow sliding of the soil and vegetation (e.g. Massey *et al*. 2018).

DISCUSSION

The current population of Hutton's shearwaters at Shearwater Stream is estimated to be about 3,000 breeding pairs. This figure is substantially lower than both the 1988 population estimate of 9,800 pairs (Sherley 1992) and the commonly cited 2002 recalculation (~8,000 pairs) (Cuthbert & Davis 2002a, 2002b, 2002c; Sommer *et al*. 2009; Waugh *et al.* 2013; Rowe *et al*. 2018; BirdLife International 2019). We did not find evidence to suggest that this difference was attributable to damage incurred during, nor in the aftermath of, the 2016 earthquake. Instead, the current population status of the Shearwater Stream colony is a likely consequence of, 1) improved methodology for measuring colony area, 2) lower burrow occupancy than expected for the species, and 3) long-term declines in the availability of suitable habitat. We address these in turn.

This study reports the first time that the colony boundaries have been mapped in the field for over three decades. We found the colony considerably fragmented, nested within larger areas of tussock-covered ground and only occupying a total of 1.62 ha (three-dimensional surface area). In 1988, the total colony area was estimated at 2.65 ha (planimetric) (Sherley 1992). In 2002, the corresponding population estimate was revised using the same estimate of colony area, despite this figure being over a decade old (Cuthbert & Davis 2002b). More recently, in 2019, the groundcover of snow tussock (*Chionochloa* sp.) was used as a proxy for estimating the area of burrowed ground at Shearwater Stream from aerial photographs (Cuthbert 2019). We suggest that the use of snow tussock cover as a proxy for burrowed ground is not an appropriate method in terrain with high heterogeneity of topography, soil structure, and tussock development, such as occurs across the Shearwater Stream catchment. We observed that the best soil development (up to 80 cm thick in gullies) appeared to coincide with patches of snow tussock and spear grass (*Aciphylla* sp.) on moderately dipping, relatively stable slopes. These were also the densest areas of shearwater burrows, which concurs with records from the Kowhai Valley colony (Cuthbert & Davis 2002c). Other areas, however, had smaller tussock and generally

thinner soils (<20 cm), which did not contain as many burrows. Burrow diameters of about 10–15 cm were noted, therefore there must be a minimum soil thickness to enable burrowing. Whatever the threshold, it is clear that not all areas of tussock-covered ground comprise suitable habitat at the Shearwater Stream colony. Unfortunately, it is not possible to retrospectively measure the sub-colony boundaries from the preceding decades, nor is it appropriate to recalculate the 1988 area estimate using contemporary methods (digital surface models). Nevertheless, we highlight the potential for previous estimates of colony area and population size to be inflated.

The rate of burrow occupancy used to estimate the population size at the Shearwater Stream colony has been assumed to be equal to that measured over ten years at the larger Kowhai Valley colony: 70.5% (61.8–77.4% CI, Cuthbert & Davis 2002b). In contrast, burrow occupancy measured in the 2019/20 breeding season at the Shearwater Stream colony was 33.8% (22.8–45.4% CI). Burrowscopes are not infallible and require some experience to use effectively. We took steps to prevent false negatives by training and swapping-out observers, and by double-checking all burrows initially recorded as empty. It is likely that, compared to the Kowhai Valley colony, the rate of burrow occupancy is generally lower at Shearwater Stream; the maximum rate of burrow occupancy measured at the Shearwater Stream colony prior to this study was 57% (Sommer *et al*. 2009). Further, the rate of occupied burrows also appears to be lower than expected for the species at this location (Fig. 3). We discuss predation by stoats as a possible driver.

Predation by stoats is not considered to be responsible for population decline in an otherwise "healthy" colony (Cuthbert & Davis 2002a). However, it is not a novel suggestion that the Shearwater Stream sub-colonies are likely to be disproportionately affected due to their relatively small sizes (see Sommer *et al*. 2009), and the propensity of the stoat to systematically destroy all accessible prey beyond their immediate needs for sustenance (King *et al.* 2021). Cuthbert's previous assertion in relation to stoat predation is relevant: 'there will be a threshold colony size beyond which the impact of predation is less than the [Hutton's] shearwaters' population growth rate, and predation therefore becomes non-regulatory. Below this threshold, predator control is needed if the population is not to decline to extinction' (Cuthbert 2002, p.75).

Prior to the 2016 earthquake, baited trap lines were regularly maintained throughout the Shearwater Stream catchment and likely played an important role in reducing predation pressure on the colony. No predator control was implemented during the three years following the earthquake and preceding this study. Upon accessing the colony, we observed one live stoat above ground in sub-colony 5a (November 2019), in addition to a stoat cache (see King *et al*. 2021) of shearwater eggs and a predated chick at a burrow entrance (February 2021). However, we note that the long-term trend for breeding success at Shearwater Stream appears relatively stable (Fig. 3), an observation which seems contrary to that expected within a colony hypothesised to be experiencing an increase in predation pressure. We suggest the following explanation: Stoats with 'ermine' (mainly white) winter coats have historically been seen in the snow-covered Shearwater Stream sub-colonies during the early breeding season (GS, September 1987). The stoat is an opportunistic, voracious predator with the ability to efficiently kill large animals relative to its size (King *et al.* 2021). At Shearwater Stream, stoats likely predate and cache adult shearwaters during courting and burrow clearing, and before eggs and chicks become available. Such behaviour has been well documented in the Kowhai Valley colony, where incidence of egg predation by stoats was rare, and of chicks, low (12% of study burrows) (Cuthbert & Davis 2002a).

An important consideration for the long-term viability of the Shearwater Stream colony is the deterioration of the remaining habitat. Reports of progressive loss of vegetation in the colony catchment and the negative impacts of ungulates on the colony date from January 2003 (Hutton's Shearwater Charitable Trust, *unpubl. data*). 'Considerable numbers of deer and chamois' were observed in the colony during the 2008/09 season, 'with some evidence of damage to burrows and certainly to vegetation' (Sommer *et al*. 2009, p.149). Deer tracks and live deer and chamois were also observed throughout the colony catchment in both 2019/20 and 2020/21 (this study). Feral pigs were not able to access the colony prior to the 2016 earthquake, however, important physical barriers were destroyed during the 2016 earthquake (NRM, MM, & J. Kilgour *pers. obs.*) and the species is considered an important factor in the contraction of the Hutton's shearwater's historic breeding range (Cuthbert 2002).

Ground deformation attributed to the 2016 earthquake was mainly surface deformation and slumping of the shallow soil and regolith, in addition to rockfalls, shallow slides, toppling, and a few large block failures in greywacke. The Torlesse greywacke comprises variably bedded sandstone and mudstone (or argillite) and is highly deformed. The argillite sequences are inherently dominated by small-scale fractures (cleavage), whereas the sandstone is dominated by widely spaced fractures that define large blocks. The different rock types

responded differently to shaking during the earthquake: the largest failures seated in sandstone were likely influenced by the pre-existing structure and defects and were consistent with the styles of slope failure observed throughout the wider region (Massey *et al*. 2018; Townsend & Morgenstern *In prep*.). The main geological hazards to the colony at Shearwater Stream are rock fall or inundation from above, and cliff collapse or retreat from below, triggered by earthquake shaking, intense or long-duration rainfall, and freeze-thaw processes (Townsend & Morgenstern *In prep*.). A gully in sub-colony 2a had a collapsed soil-pipe/tunnel gully structure, open to the rock surface below for about 1 m, which was related to ongoing erosion of the soil rather than earthquake damage. In many places there was very little soil, possibly having been stripped off in previous landslide/avalanche events. Thick deposits of colluvium in the 'chute' that separates sub-colony 1 from the main hillslope also indicate that there is a history of inundation by debris in this area.

Burrow density is often cited as a useful indicator of fluctuations in population size and/or habitat availability in seabirds (Rodway & Lemon 2011; Sutherland & Dann 2012). The fine, sandy aeolian soil in which the shearwaters burrow is extremely friable and vulnerable to collapse, thus population decline is expected to be reflected by decreasing burrow density over time (Sommer *et al*. 2009). This reasoning can be applied at the sub-colony level within the Shearwater Stream colony: Here, slumping and shallow sliding of the vegetation and soil attributable to the 2016 earthquake occurred within sub-colony 1. Mean burrow density in sub-colony 1 was found to be lower than sub-colony 2, and significantly lower compared to sub-colony 5 (Table 2). This did not influence mean burrow density at the population level because the loss of suitable habitat in sub-colony 1 was offset by an increase in burrow density in sub-colony 5, which was markedly higher than the long-term mean recorded for the species at this colony. The results of this study concur with Sommer *et al.* (2009), who identified negligible change in population-level burrow density at the Shearwater Stream colony over the last forty years. However, we reject the corresponding hypothesis of long-term population stability and suggest that the small population of Hutton's shearwaters occupying this catchment is at high risk of, if not already undergoing, long-term decline. We note that this hypothesis contrasts with the conclusion of Sommer *et al*. and offer the following explanation: Inferences using longitudinal burrow density data require the use of consistent methodology including sampling effort which should be equal and unbiased over time. The use of fixed plots across years has been a feasible method at the Kowhai Valley colony (Sommer *et al*. 2009), whilst the sampling approach at the Shearwater Stream colony has been less structured, with no fixed reference plots retained between breeding seasons (see Sommer *et al*. 2009). Although plots were sampled at random across sub-colonies (Sommer *et al*. 2009; this study), the boundaries of the sub-colonies at Shearwater Stream are not marked in the field, save for the natural separation of tussock by scree slopes (all authors *pers. obs*.). The definition of 'sub-colony' therefore equates to 'an area of tussock seen to contain burrows'. Estimates of burrow density cannot be indicative of population trends if the areas sampled are targeted because of the presence of burrows. Rather, the estimates will be positively biased. We recommend that all previous burrow density data available for the Shearwater Stream colony are treated with extreme caution if used to infer a population trend.

Populations of a long-lived species are highly sensitive to the loss of breeding adults from a population, either by mortality, reduced recruitment, or emigration (Sæther & Bakke 2000). Both the Shearwater Stream and Kowhai Valley colonies suffered highly reduced breeding success, and therefore downstream recruitment to the breeding population, in the 2007/06 and 2007/08 breeding seasons. This was attributed to poor at-sea feeding conditions (Sommer *et al*. 2009). Sommer *et al.* (2009) also suggested that fluctuations in natal recruitment at the Shearwater Stream colony might be offset by the immigration of birds from the larger Kowhai Valley colony. Alternatively, the Kowhai catchment may act as a net sink, drawing birds prospecting for breeding sites and/or partners away from Shearwater Stream because they are attracted by the larger numbers of established birds (Brown & Rannala 1995), their calls (Major & Jones 2011; Oro *et al*. 2011), and public information such as breeding success (e.g. Danchin *et al*. 1998). This scenario is consistent with the finding of Hale *et al*. (2015), who reported no genetic differentiation between colonies, indicating some level of long-term connectivity. Thus, while recognizing the limitations of comparing demographic parameters between the two populations due to differences in methodologies, the possible drift of Hutton's shearwaters from the Shearwater Stream colony to the Kowhai Valley colony could be a factor in population depensation at Shearwater Stream and a contributor to the stable/increasing population trend reported for the Kowhai Valley prior to the 2016 earthquake (Sommer *et al*. 2009).

If a population of a long-lived species is made small enough through a series of additive or interacting events, such as habitat loss, breeding failure, predation, and low recruitment, it loses the ability to recover from the adverse effects

of, for example, environmental variation and demographic stochasticity (Gilpin & Soule 1986). It is a priority that throughout at least the next decade, standardized monitoring methodology using fixed plots is carried out on an annual basis at the Shearwater Stream Hutton's Shearwater colony. This will enable a robust assessment of the long-term population trend and colony viability once sufficient data become available. A clear priority is also to review the impact of stoats. We recommend fencing any points that might provide access into the colony for feral pigs, and a review of the methods employed to control ungulates in the catchment. Serious consideration should be given towards establishing a new colony or facilitating the recolonization of a former alpine colony within the flight path. Alpine catchments with similar environmental characteristics to existing colonies are preferable to lowland areas because the comparatively low agricultural value of the surrounding land provides space for colony establishment and expansion. Proposals to establish a new alpine colony should certainly consider in detail the underlying geomorphology, including rock type, soil structure, and pre-existing faults.

ACKNOWLEDGEMENTS

Funding for fieldwork was provided equally by Puhi Peaks Station and the New Zealand Department of Conservation (Grant number DOCCF5-117). The geomorphological survey was part-funded by the EILD Program (MBIE Endeavour Fund); we thank Chris Massey, GNS Science for enabling this work. Many thanks to James Kilgour, Stock Manager Puhi Peaks Station April 2017–2019, for his logistical expertise during the planning and execution of fieldwork. Kaikōura Helicopters Limited facilitated access to the colony. Many thanks to James Kilgour, Harry McArthur, Peter Fay, Henry White, Heath Melville, and Wayne Nelson, who assisted with scoring plots for burrow density and burrow occupancy. Orthophoto mosaics and digital surface models were produced by Katie Jones, GNS Science. This paper contains data sourced from Toitū Te Whenua Land Information New Zealand under CC-By. Our thanks go out to Simon Litchwark, New Zealand Department of Conservation, for providing historic data pertinent to the colony at Shearwater Stream, to Sam McArthur for his contributions towards improving the quality of maps and figures, and to Richard Cuthbert, Grant Ellis, Alec Burslem, Craig Symes, and a further anonymous reviewer for their thorough and helpful critiques of earlier drafts of this manuscript.

Author contributions: CPC: author of first and subsequent drafts, statistical and spatial analyses and data collection and management relating to the breeding biology of the Hutton's shearwater. DT: contributions to the first draft and subsequent drafts, statistical and spatial analyses, and data collection and management relating to the geomorphological assessment of the Shearwater Stream catchment. NRM: study design, contributions to the first draft and subsequent drafts relating to the history of land management at Shearwater Stream, data collection and management relating to the breeding biology of the Hutton's shearwater. RM: drone operation, data collection and management relating to the geomorphological assessment of the Shearwater Stream catchment, feedback provided on manuscript drafts. MM: study design, data collection and management relating to the breeding biology of the Hutton's shearwater, feedback provided on manuscript drafts. GS: scientific guidance, feedback provided on manuscript drafts. MB: study lead, data collection and management relating to the breeding biology of the Hutton's shearwater, feedback provided on manuscript drafts.

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Notornis, 2023, Vol. 70: 14-30
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Hutton's shearwater (*Puffinus huttoni*) at Te Rae o Atiu, Kaikōura Peninsula South Island east coast, New Zealand: a colony established by translocations – 16 years progress

LINDSAY K. ROWE*
T198 24 Charles Upham Drive, Rangiora 7400, New Zealand

TED HOWARD
Hutton's Shearwater Charitable Trust, PO Box 58, Kaikōura 7740, New Zealand

Abstract: A new colony of the endangered Hutton's shearwaters (*Puffinus huttoni*) has been established at Te Rae o Atiu on the Kaikōura Peninsula, South Island east coast, New Zealand to provide insurance against catastrophic events at the high-altitude natural colonies in the Kōwhai River and Shearwater Stream, Seaward Kaikōura Range. The translocation of 495 chicks from the Kōwhai River colony was carried out in six operations from 2005 to 2013. Of the 473 fledglings, 97 have been recorded back at Te Rae o Atiu. Chick selection criteria, fledgling mass, fledgling wing length, days present before fledging, and days of emergence before fledging had no bearing on whether chicks returned from their post-fledging migration to Australian waters or not. One hundred and twelve Te Rae o Atiu bred chicks have fledged up until 2020–21. The Te Rae o Atiu fledglings had similar mass and wing lengths, and days emerged prior to fledging, to the translocated fledglings. There were no differences between the groups of Te Rae o Atiu bred birds that returned or did not. At 2020–21, 21 of the 112 second-generation chicks have returned from their initial migration, and the earliest have bred successfully. The colony has grown to about 75 birds producing about 30 eggs, 24 chicks, and 22 fledglings annually. Future growth of Te Rae o Atiu will be reliant on these home-bred chicks as the oldest translocation birds will soon be approaching the end of their breeding lives. Acoustic attraction of birds flying over Te Rae o Atiu from the sea towards the Kōwhai River natal colony has been mostly unsuccessful with only two birds attracted.

Rowe, L.K.; Howard, T. 2023. Hutton's shearwater (*Puffinus huttoni*) at Te Rae o Atiu, Kaikōura Peninsula: a colony established by translocations – 16 years progress. *Notornis 70(1)*: 14–30.

Keywords: Hutton's shearwater, *Puffinus huttoni*, Te Rae o Atiu, Kaikōura Peninsula, translocations, chick transfer, endangered species, conservation management

INTRODUCTION

Hutton's shearwater (*Puffinus huttoni*) is a small black and white shearwater (length 36–38 cm; mass 365 g; Marchant & Higgins 1990) currently classified by BirdLife International (2021) as "Endangered" and as "Threatened – Nationally Vulnerable" under the New Zealand Threat Classification system (Robertson *et al*. 2021). Hutton's shearwater was first described by Mathews (1912), and Brooke (1990) considered it to be one of seven close relatives to Manx shearwater (*P. puffinus*). Before the 1900s, Māori (Ngati Kuri) knew of shearwaters nesting in the mountains, and used them as a food source. In

Received 26 June 2021; accepted 24 July 2022
*Correspondence: *lindsay.jan.rowe@xtra.co.nz*

1965, following anecdotal reports of "muttonbird" burrows high in the Seaward Kaikōura Range, Geoff Harrow found carcases that were confirmed as Hutton's shearwaters in the headwaters of the Kōwhai River (42.261°S, 173.603°E) at altitudes between 1,200 and 1,800 m a.s.l. (Harrow 1965). At these altitudes, Hutton's shearwater breed at the highest altitudes of the Manx related shearwaters, only the Newell's shearwater (*P. newelli)* breeding close to 1,200 m a.s.l. (BirdLife International 2021).

Extensive searching in the Kaikōura Ranges led to the confirmation of other populations, but only two remain today – in the Kōwhai River and Shearwater Stream (42.167°S, 173.727°E) (Marchant & Higgins 1990; Cuthbert 2001; Sommer *et al*. 2009). The reasons for the decline in population to the current two colonies are not definitive. The effects of trampling by deer (*Cervus elaphus*), goats (*Capra hircus),* and chamois (*Rupicapra rupicapra*) breaking through the shallow friable soils into burrows and nest chambers have been observed (Harrow 1976) and these are regularly controlled by the Department of Conservation (DOC). Stoats (*Mustela erminea*), although present in the colonies, were not considered to be in sufficient numbers to be a threat (Cuthbert 2001; Cuthbert & Davis 2002a). Cuthbert (2002) noted accessibility for, and evidence of, pigs (*Sus scrofa*) in the colonies that had recently become extinct, and the relative inaccessibility to pigs of the Kōwhai River and Shearwater Stream breeding sites. Thus, he concluded predation and habitat destruction by pigs was likely to be the main cause of the population decline. A pig trap built in 2009 at 1,180 m a.s.l. in the Kōwhai River at one of the few points that could provide access to the colony is still operating. This has likely proved beneficial as more than ten pigs were trapped in 2013 (L. Armstrong & M. Morrissey *pers. comm*. April 2013) indicating this colony, at least, is still extremely vulnerable to pig predation. A new, potential threat at the Kōwhai River colony follows the sighting of a cat (*Felis catus*) at 1,200 m a.s.l. in November 2020, and subsequently, evidence of cat predation was seen in March 2021 (TH *pers. obs*.).

Another major threat to the continued existence of the mountain colonies is devastation by natural processes such as debris avalanches/ rock falls resulting from tectonic activity and snow avalanches. Sherley (1992) observed that two sub-colonies had slipped away between 1986 and 1992 and that erosion could cover burrows with alluvium. Magnitude 5.7 (April 2015) and 6.2 (February 2016) earthquakes, about 50 km deep centred near St Arnaud 50 km to the northwest, did not produce any obvious landsliding in the Kōwhai River area (LR *pers. obs*.). However, the 7.8 magnitude Kaikōura earthquake on 14 November 2016 resulted in about 12% of the colony area being lost through landslides, a reduction in burrow density of about 29% in the remaining areas, and a reduction of about 40% of breeding pairs (Cuthbert 2019). As this earthquake struck at the peak of laying and at 0002 h, burrows with breeding birds that collapsed or were buried by landslides would have resulted in the loss of an egg and at least one adult. A minimum of 40,000 breeding Hutton's shearwaters were lost in landslides and potentially another 80,000 from burrow collapse (Cuthbert 2019). Prior to the Kaikōura earthquake, the Hutton's shearwater population had been expanding at about 2%/year (Sommer *et al*. 2009; Rowe *et al*. 2018) despite recorded losses up to 0.3% of fledglings to fallout around Kaikōura (Deppe *et al*. 2017).

Hutton's shearwaters spend the non-breeding season in Australian waters (Imber & Crockett 1970; Halse 1981; Warham 1981; Rowe & Taylor 2020). The adults are absent from New Zealand waters from mid-February/March to late August/ September (Falla 1965; Harrow 1976; Marchant & Higgins 1990). Juvenile specimens are only found on New Zealand beaches during March and April and have been reported from Australia during the breeding season (Halse 1981; Rowe & Taylor 2020).

The Department of Conservation (DOC) identified Hutton's shearwater as a threatened species requiring medium term action for recovery (Molloy & Davis 1992). A departmental meeting in June 1997 recommended the formation of a recovery group and discussed the option that a third colony be established at a lowland site as insurance against unforeseen occurrences in the two mountain colonies. A draft recovery plan (Paton & Davis 1997) further explored the option of a third, lowland colony, and a review of the status of Hutton's shearwater by Cuthbert (2001) also recommended a site be found for a third colony. A number of investigations were undertaken before selecting the site – productivity assessments (DOC *unpubl. data*), a population estimate of birds present in the Kaikōura region by colour marking birds at the Kōwhai River colony and resighting them at sea (Rowe *et al*. 2018), and the determination of flight paths to and from the Kōwhai colony to the sea (G.A. Taylor, DOC, *unpubl. data*). Early in 2005, an agreement was reached between DOC and Whale Watch Kaikōura for a new colony (now called Te Rae o Atiu) to be established on Whale Watch land on the Kaikōura Peninsula (42.429°S, 173.703°E) (Fig. 1). Vehicle access to the site, the colony being under the Hutton's shearwater flight path to the Kōwhai River colonies and seaward facing, and being able to have a predator-proof fence established around the site were major determinants in the site selection even though it is near sea-level.

Successful translocations of chicks to establish

new colonies of endangered seabirds have been undertaken in New Zealand since the mid-1980s (Miskelly *et al*. 2009). One of the first projects was a transfer of black petrels (*Procellaria parkinsoni*) at Little Barrier Island (Imber *et al*. 2003), and the largest number of birds moved prior this study was 334 fluttering shearwaters (*P. gavia*) from Long Island to Maud Island over six continuous seasons (Bell *et al*. 2005). Thus, there was a wealth of New Zealand expertise available to establish a new colony by translocation at Te Rae o Atiu. In March 2005, an initial trial translocation of Hutton's shearwater to Te Rae o Atiu was undertaken by DOC (Knevel 2005).

At the instigation of Geoff Harrow, the Hutton's Shearwater Charitable Trust (HSCT) was established in October 2008 with the initial task to obtain funds to erect a predator-proof fence around an extended colony site. Funding was obtained by June 2009 and the fence completed in February 2010, five years after the initial translocation. The site is surrounded by a stock fence at least 5 m from the predator-proof fence to protect it from damage by cattle trampling over the buried skirt or rubbing against the mesh (Fig. 1).

This paper summarises aspects of the translocation process, the progress of the Te Rae o Atiu colony development to April 2021, and pitfalls in the process.

Figure 1. Hutton's shearwater (*Puffinus huttoni*) colony (Te Rae o Atiu) on the Kaikōura Peninsula, South Island east coast, New Zealand (42.429°S, 173.703°E). The predator-proof fence completed in February 2010 is protected from stock damage by a deer fence at least 5 m away. The original colony is the outlined area in the lower centre of the colony and the original nestboxes were the six rows delineated by the tussocks below the hut. (Photograph: Andrew Spencer).

METHODS

The area initially selected for Te Rae o Atiu was 0.3 ha of farmland enclosed by a standard farm fence (Fig. 1). The area was extended to 2 ha in 2010 when the predator-proof fence was erected. The altitude range is 55–80 m a.s.l. with the slopes predominantly facing the sea; there is a 35° slope below the colony to the sea. In 2005, 30 artificial burrows (nestboxes) of treated timber and plywood were dug into the soil and connected by a length of 110 mm slotted drainage pipe to the surface (Fig. 2). Access to the nest chamber for helpers was via a removable lid which was insulated to avoid the nestbox overheating. Pea gravel was placed in each nestbox to aid drainage and dry grass was added for nest material. Another 78 nestboxes were installed in summer 2005–06. A few weeks prior to each translocation, a pest control programme was instigated at Te Rae o Atiu to remove as many cats, rats (*Rattus* sp.), mice (*Mus musculus*), stoats (*Mustela*

erminea), and ferrets (*Mustela furo*) from the area as possible (Knevel 2005); the predator-proof fence was not in place until after the translocations were completed. After a cat killed roaming pre-fledgling chicks in March 2007, fish netting was placed over the fence and pegged down in an attempt to reduce their access to the colony.

The source areas for the chicks were sub-colonies near the research hut in the Kōwhai River at about 1,250 m a.s.l. The main constraint when sourcing chicks was accessibility to the nest chambers in the natural burrows that are up to 2 m in length and twist up, down or sideways, with stones and bedrock present. The nominal criteria for chick selection was mass ≥450 g and wing length 195–215 mm on the day of transfer (Williams 2006). Except for 2005 when unavoidable delays prevented collection until early April, at which time fledging was well underway at Kōwhai River, the collection took place late February to early March before chicks began exiting burrows and receiving visual signs of their home colony (Table 1). Chicks were banded and weighed, wing length measured, and transferred into cardboard "cat boxes" with dry grass on the base; two birds were in each box separated on the diagonal by a cardboard divider. They were flown 20 km by helicopter to Te Rae o Atiu.

At Te Rae o Atiu they were hand-reared and monitored following protocols in Miskelly *et al*. (2009). On arrival, they were checked, given 10 ml of water to reduce dehydration via a syringe fitted with a crop tube, and placed one in each nestbox. Netting gates placed at the tunnel exits prevented chicks from leaving immediately; they were held for at least two, but usually five, days. Every day from the second day until near fledging they were fed sardine "smoothies" (one tin of New Brunswick™ sardines in soya oil blended with 50 ml of water [Miskelly *et al*. 2009]) via crop tubes. Chick mass was measured daily with Pesola™ spring balances or electronic scales, the chicks being in bags or sleeves; wing lengths were measured every second day as flattened chords using stop end rules

Figure 2. Clockwise from top left: View of part of Te Rae o Atiu Hutton's shearwater (*Puffinus huttoni*) colony; a closed nestbox with PIT tag reader; the first egg laid at Te Rae o Atiu; interior of a nestbox with adult and chick. (Photographs: L. Rowe)

(Melville 2011). At Te Rae o Atiu, chicks from the 2012 and 2013 cohorts also had passive integrated transponders (PIT tags) placed in the back of their necks. From 2012–13 onwards, PIT tags were inserted into returned adults from the 2006 to 2008 translocations when they were found in nestboxes, and into Te Rae o Atiu bred chicks.

In 2011–2012, the HSCT made up 100 PIT tag reader systems using DOC made loggers similar to those used by Taylor *et al*. (2012) to study Chatham Island taiko (*Pterodroma magentae*). Each logger was attached to an antenna coil placed around the nestbox tunnel about 20 cm above the exit (Fig. 2; see Rowe [2014] for details). Placing the coil away from the exit reduced the collection of excess records when birds sat at the tunnel exits for extended periods. When a tagged bird passed through the antenna coil, the logger identifier, date, time, and bird transponder number were recorded.

An acoustic sound system was installed at Te Rae o Atiu next to the hut in the middle of the colony (Fig. 1). Hutton's shearwater calls recorded at the Kōwhai River colony were beamed via loudspeakers soon after dark to near dawn between August and March in an attempt to attract additional shearwaters to the colony over and above those translocated.

Apart from PIT tag recordings, Te Rae o Atiu was monitored at about weekly intervals, usually during mornings. Movement of three pins at the tunnel entrance was a guide to which nestboxes may have had birds return since the last inspection and worth inspecting. Movement of three more pins placed in the nestbox at the entrance to the tunnel was considered evidence of the nestbox chamber being visited. No movement of the inside pins was probably an indication of birds searching for food or other shearwaters disturbing the outer pins. HSCT site protocols prevented us undertaking night visits that might disturb any returning birds; it was considered that birds seen and/or handled during the day would have settled by nightfall. Band numbers of the birds found in nestboxes were verified and, up until 2010, white correction fluid (Twink™) was applied to their heads as an identifier to reduce repeat handling.

Reports were produced after each translocation (Knevel 2005; Williams 2006; McGahan 2007, 2008; Williams 2012; WMIL 2013) but the data in them were not always comparable so information reported here has been recalculated from the original datasheets. Calculated averages are given with 95% confidence limits. Other statistics and tests were performed using methods in Freese (1967) or Sokal & Rolfe (1981) and the calculated values for t, F, and χ^2 are given relative to published 95% (P = 0.05) significance levels; calculated test statistics < tabulated values are not significant and *vice versa*.

Birds translocated in any cohort are referred to by the year of transfer; i.e. 2006 for March 2006. The breeding season in New Zealand is from August through to the following March and, for example, August 2005–March 2006 is denoted 2005–06. A bird arriving back in its n^{th} year after hatching is deemed to be n-years-old as it will pass by its n^{th} birthday in late December/early January (Brooke 1990). With the exception of some late fledging birds, laying through to fledging occurs within New Zealand Daylight Saving Time (NZDST). The PIT tag readers are programmed in NZDST to reduce the possibility of errors in setup, so all times given here are in NZDST. The sexes of many returned birds were determined by outsourcing analysis of feather samples. Where feathers were not available, the sex has been inferred from that of their mates.

RESULTS

Translocation

In total, 495 chicks were translocated from Kōwhai River to Te Rae o Atiu (Table 1). The first ten birds were transferred as a trial in early April 2005. That transfer was atypical as it was delayed by inclement weather (Knevel 2005). Those chicks were at a much later stage of development than the other years and many birds had already fledged. These pre-fledglings may have already imprinted on the Kōwhai River site; none returned to Te Rae o Atiu and have, therefore, been excluded from further analysis although Table 1 includes this information for completeness. The 2006–2013 translocations all took place during 27 February – 9 March.

On arrival at Te Rae o Atiu, the 2006–2013 chicks had an average mass of 485 g (range 205–650 g, SD = 67 g, CL = ± 6 g, n = 485) and an average wing length of 212 mm (range 175–231 mm, SD = 11 mm, CL = ± 1 mm, n = 485) (Table 1). The mass selection criterion was met for 73% (355) of the chicks, 50% (243) met the wing length criterion, and only 36% (175) both met criteria.

ANOVA tests showed there were significant differences between translocations for arrival mass ($F = 33.1 > F_{P=0.05} = 2.39$, df = 4,480); annual average mass varied by ± 8% about the overall average. There was no significant difference between translocations for wing lengths ($F = 2.24 < F_{P=0.05} = 2.39$, df = 4,480). The significant relationship between wing length and mass at transfer, wing length = 199 + 0.0262 x mass (Fig. 3; $F = 12.7 > F_{P=0.05} = 3.86$, df = 1,461; COD = 0.0268), showed a wide scatter of points and only explained 2.7% of the variance in the data; other unknown variables, therefore, contribute to the variance.

Table 1. Summary of Hutton's shearwater (*Puffinus huttoni*) translocations from Kōwhai River to Te Rae o Atiu, 2005–2013. The 2005 data are not included in the final column. Averages are presented with 95% CLs.

	2005	2006	2007	2008	2012	2013	2006–13
Arrival date	2 Apr	8 & 9 Mar	7 & 9 Mar	5 & 6 Mar	7 & 8 Mar	27 & 28 Feb, 8 Mar	
Number of chicks transferred	10	86	95	100	101	103	485
Average mass at transfer (g)	435 ± 20	495 ± 13	525 ± 11	460 ± 12	445 ± 12	510 ± 11	485 ± 6
Mass range (g)	375–480	275–595	385–640	275–610	205–620	385–650	205–650
Standard deviation	31	63	54	61	62	56	67
Average wing length at transfer (mm)	222 ± 2	215 ± 2	211 ± 2	211 ± 2	212 ± 2	211 ± 1	212 ± 1
Wing length range (mm)	217–229	183–231	187–230	175–229	178–229	187–227	175–231
Standard deviation	3	10	11	12	11	11	11
Chicks fledged and left	10	79	83	98	100	103	463
Probable losses by cats	0	2	11	1	0	0	14
Probable losses by swamp harrier	0	5	0	0	0	0	5
Losses from natural causes	0	0	1	1	1	0	3
Nights stayed after arrival	5 ± 2	15 ± 1	21 ± 1	22 ± 1	19 ± 1	18 ± 1	19 ± 1
Nights stayed range	2–8	3–26	8–30	3–38	1–35	7–32	1–38
Standard deviation	3	6	5	7	8	4	6
Date first chick fledged	4 Apr	11 Mar	15 Mar	8 Mar	8 Mar	6 Mar	6 Mar
Date last chick fledged	10 Apr	4 Apr	6 Apr	13 Apr	11 Apr	31 Mar	13 Apr
Average mass at fledging (g)	410 ± 17	425 ± 7	435 ± 7	415 ± 8	400 ± 7	400 ± 7	415 ± 3
Mass range (g)	375–445	350–515	380–550	315–500	295–485	300–550	295–550
Standard deviation	28	34	35	34	34	36	36
Average wing length at fledging (mm)	224 ± 2	226 ± 1	228 ± 1	227 ± 1	225 ± 1	226 ±1	226 ± 1
Wing length range (mm)	221–229	214–237	217–238	200–238	214–237	212–237	200–238
Standard deviation	3	5	4	6	4	5	5
Wing growth rate (mm/day)	0.37 ± 0.25	0.85 ± 0.11	0.79 ± 0.09	0.66 ± 0.08	0.58 ± 0.08	0.80 ± 0.08	0.73 ± 0.04

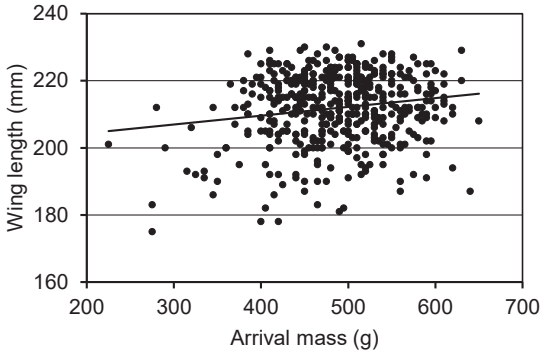

Figure 3. Relationship between wing length and mass of translocated Hutton's shearwater (*Puffinus huttoni*) chicks on arrival at Te Rae o Atiu.

Fledging

Of the 495 chicks brought down from the Kōwhai River, we believe 473 fledged on the basis that we know 22 birds were lost: 14 to cats, five to swamp harrier (*Circus approximans*) or cats, and three from undefined natural causes (Table 1).

Chicks were at Te Rae o Atiu 19 days on average (SD = 6 days, CL = ± 1, n = 463) (Table 1) and stayed between 1 and 38 days; 74% of chicks were present between 11 and 25 days (Fig. 4a). The number of days chicks were present varied significantly between translocations (ANOVA, $F = 20.4 > F_{P=0.05} = 2.39$, df = 4,458). The earliest date translocated chicks fledged was 6 March (2013) and the last chicks left each season between 4 (2006) and 13 (2008) April.

There was a significant relationship between the number of days translocated chicks spent at Te Rae o Atiu before fledging and their arrival mass (Fig. 4b), days = 13 + 0.014 x mass ($F = 9.6 > F_{P=0.05} = 3.9$, df = 4,461, COD = 0.02), but this only explained 2% of the variance in the data. Wing length at arrival was a better predictor of the number of days birds would stay. The relationship, days = 91 – 0.337 x wing length ($F = 201 > F_{P=0.05} = 3.9$, df = 4,461, COD = 0.30) (Fig. 4c) was highly significant and explained 30% of the variance in the data. It is, however, of limited value for estimating how long individual birds will stay until fledging as Fig. 4c shows there is a scatter of about ± 12 days birds could stay for any given arrival wing length.

Birds fledged at an average mass of 415 g (range 295–550 g, SD = 36 g, CL = ± 3 g, n = 463) and wing length of 226 mm (range 200–238 mm, SD = 5 mm, CL = ± 1 mm, df = 463) (Table 1). A regression analysis indicated there was a significant relationship between chick mass and wing length immediately prior to fledging, wing length = 214

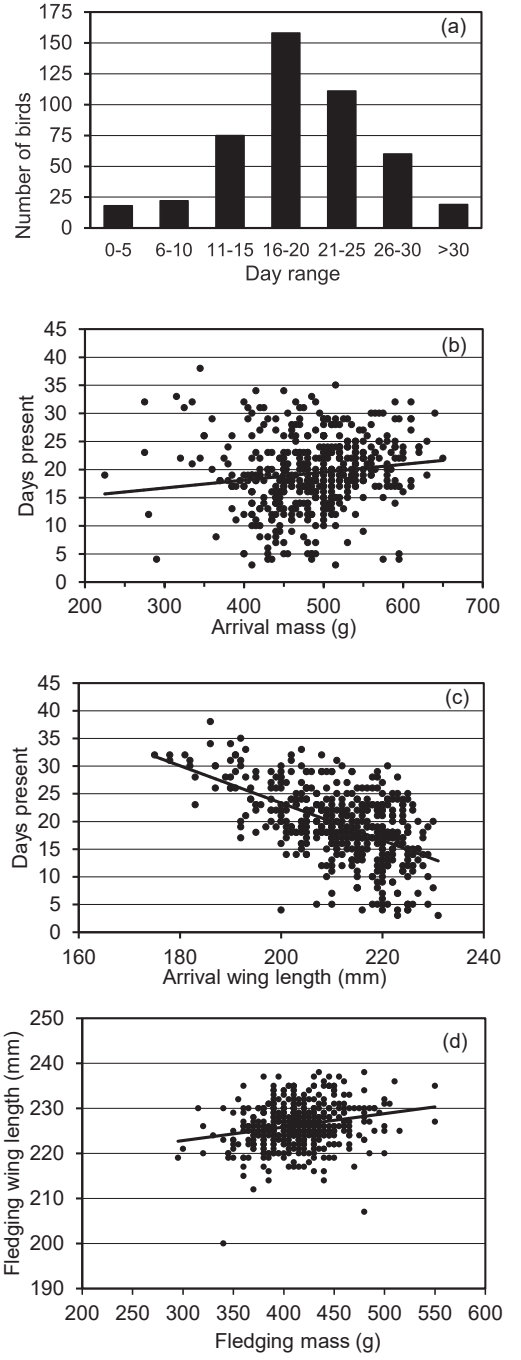

Figure 4. Translocated Hutton's shearwater (*Puffinus huttoni*) chicks at Te Rae o Atiu near fledging. (a) the number of days chicks were present before fledging; (b) the relationship between arrival mass and days present; (c) the relationship between arrival wing length and days present; (d) the relationship between mass and wing length near fledging.

Table 2. Known returns to Te Rae o Atiu of Hutton's shearwaters (*Puffinus huttoni*) from translocations undertaken in 2006 to 2013.

	2006	2007	2008	2012	2013	Total
Fledged	79	83	98	100	103	463
Birds seen	11	12	23	8	30	84
Birds noted from PIT tags only	–	–	–	5	8	13
Total birds returned	11	12	23	13	38	97
% returned	14	14	23	13	37	21
Birds present in 2020–21	3	8	12	6	25	54
Losses of returned birds	8	4	11	7	13	43

+ 0.030 x mass ($F = 24.7 > F_{P=0.05} = 3.9$, df = 1,461, COD = 0.051) but there was a wide scatter of points (Fig. 4d) and the relationship only explained 5.1% of the variance in the data.

The average rate of wing growth of the translocated chicks was 0.73 mm/day (SD = 0.42, CL = ± 0.04, n = 463), ranged up to 1.78 mm/day, and averaged between 0.58 and 0.85 mm/day on a translocation basis (Table 1); these rates were significantly different (ANOVA $F = 6.3 > F_{tab} = 2.39$, df = 4,458). Using the average growth rate, and arrival and fledging wing length differences, the discrepancies in the calculated and actual number of days to fledging for individual birds averaged 9 days and were in the range 25 days too few to 39 days more than observed.

Returns of translocated birds

The earliest confirmed return of a translocated bird from Australian waters was a 2006 bird in its third year and the only bird identified back in the 2008 season. Unfortunately, it was killed in a DOC250 trap set for predators. A cat, eventually tracked to the scrub below the colony, killed three returned birds in one night in November 2009. Two of these were 3rd and 4th year birds that had not been sighted previously; no band could be found to identify the third bird. Indirectly, cats were also responsible for the deaths of another two 4th year birds early in the 2009–10 season when they were caught in the fishing net draped over the stock fence in an attempt to keep cats out. After the predator-proof fence was erected, there have only been two more

Table 3. Numbers of translocated Hutton's shearwater (*Puffinus huttoni*) chicks that met or did not meet the selection criteria, and that returned to Te Rae o Atiu or did not return after fledging. Percentages are in parentheses.

	Mass criterion ≥450 g		Wing length criterion 195≤215 mm		Both criteria	
	Did not return	Returned	Did not return	Returned	Did not return	Returned
Not met	98 (27)	26 (27)	186 (51)	41 (42)	236 (70)	55 (57)
Met	268 (73)	71 (73)	180 (49)	56 (58)	130 (30)	42 (43)
χ^2	0.00		2.24		1.99	
$\chi^2_{P=0.05}$, df=1	3.84		3.84		3.84	

Table 4. Hutton's shearwater (*Puffinus huttoni*) fledging mass and wing lengths, days present until fledging, and days of emergence for those Hutton's shearwater chicks translocated to Te Rae o Atiu that returned from Australian waters or did not return.

	Mass (g)		Wing length (mm)		Days present		Days of emergence	
	Returned	Did not return	Returned	Did not return	Returned	Did not return	Returned	Did not return
Number	97	366	97	366	97	366	25	39
Average	410	415	227	226	20	19	8.8	7.2
Std dev	34	37	4	5	5	7	3.6	3.4
CL	7	4	1	1	1	1	1.4	1.1
t	0.70		1.49		0.98		0.08	
t, P= 0.05	1.97 (df = 461)		1.97 (df = 461)		1.97 (df = 461)		2.00 (df = 62)	

deaths when birds struck the fence as they were leaving the colony.

Of the 463 fledglings, 21% (97) have now been seen or noted from PIT tag records at Te Rae o Atiu (Table 2). The known returns for the five main translocations were variable ranging between 13% and 37% of birds that fledged. Observations from 2012 and 2013 translocations show that 13 of 51 birds (25%) that returned were only recorded by PIT tag readers. Thus, there was probably a numbers of birds from the early translocations not seen, perhaps as many as 12 birds.

There were no significant differences between the proportions of birds that met or did not meet the selection criteria (mass, wing length, or both) and returned or did not (Table 3). Fledging mass, fledging wing length, the number of days chicks stayed until fledging, and the number of days from first emergence to fledging (2013 translocation birds only) were determined for birds that returned to Te Rae o Atiu and the birds that did not (Table 4); unpaired sample t-tests did not indicate any significant differences between the two groups.

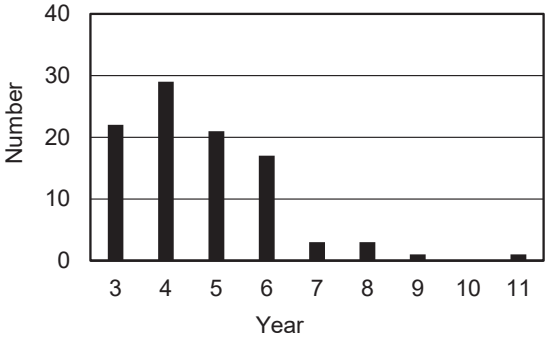

Figure 5. Ages at which translocated Hutton's shearwaters (*Puffinus huttoni*) were first noted returning to Te Rae o Atiu (includes up to 2020–21).

Similarly, χ^2 tests of the frequency distributions of those values for the two groups indicated no significant difference between them: mass $\chi^2 = 4.31 < \chi^2_{P=0.05} = 11.07$, df = 5; wing length $\chi^2 = 3.13 < \chi^2_{P=0.05} = 9.49$, df = 4; days present $\chi^2 = 4.27 < \chi^2_{P=0.05} = 11.07$, df = 5; emerged days $\chi^2 = 3.43 < \chi^2_{P=0.05} = 7.81$, df = 3). Thus, there is no reason to believe that any of these parameters had a significant influence on whether birds returned from their first migration or not.

Birds translocated to Te Rae o Atiu that fledged and returned from their first migration to Australia were seen or recorded from PIT tags the earliest in their 3rd year, at least 23% (22) of the 97 returned birds (Fig. 5); 92% were first noted up to their 6th year and one bird was first seen in its 11th year. It is probable that some birds from earlier translocations may have been back sooner but were not seen in nestboxes nor PIT-tagged. The returned birds comprised 43% males and 56% females; the difference was not significant ($\chi^2 = 1.46 < \chi^2_{P=0.05} = 3.84$, df = 1). From 2012 and 2013 translocations only for which we have better records (all birds were PIT-tagged), the timing of first male and first female returns were not significantly different (unpaired sample t-test: $t = 0.52 < t_{P=0.05} = 2.02$, df = 43).

Acoustic attraction

In 12 years of operation of the sound system, only two unbanded birds were found at the colony (X19101 in 2010; X17347 in 2013). These two birds, both female, may have been attracted to the site by the broadcast sounds, but they did become an integral part of the breeding population.

Losses to the Kōwhai River natal colonies

We know that seven PIT-tagged birds that were brought down to Te Rae o Atiu as part of the translocation programme in 2012 and 2013 returned to the Kōwhai River natal colonies in their 3rd and 4th years (Rowe 2018). Two, as 3rd year birds, had

Table 5. Numbers of Te Rae o Atiu bred Hutton's shearwater (*Puffinus huttoni*) chicks that have returned from Australian waters up to 2020–21.

Cohort	2011–12	2012–13	2013–14	2014–15	2015–16	2016–17	2017–18	2018–19	2019–20	2020–21	Total
Fledged	1	2	8	7	6	12	17	15	21	23	112
Bird returned	0	2	6	3	4	3	2*	1**	–	–	–
% returned	0	100	75	43	68	25	–	–	–	–	–
Present 2020–21	0	1	6	3	4	3	2	1	–	–	–
Losses	1	0	2	4	2	0	–	–	–	–	–

*Chicks returned as 3-year-olds only; **chick returned as a 2-year-old. More birds are expected back from 2016–17 on cohorts.

Table 6. A comparison of near departure mass (g) and wing lengths (mm), and days of emergence for Te Rae o Atiu bred Hutton's shearwater (*Puffinus huttoni*) fledglings that returned or did not return from Australian waters. Data for fledglings from 2011–12 to 2016–17.

	Mass (g)		Wing length (mm)		Days of emergence	
	Returned	Did not return	Returned	Did not return	Returned	Did not return
Fledged	18	18	18	18	13	15
Average	385	415	222	223	8.0	9.3
Std dev	49	61	6	8	3.4	5.3
CL	23	28	3	4	1.9	2.7
Maximum	455	525	233	233	15	20
Minimum	265	280	211	203	2	1
t	1.50		0.54		0.78	
$t_{P=0.05}$	2.03 (df = 34)		2.03 (df = 34)		2.06 (df =26)	

Table 7. A comparison of Hutton's shearwater (*Puffinus huttoni*) near departure mass (g) and wing lengths (mm), and days of emergence of translocated and Te Rae o Atiu bred fledglings.

	Mass (g)		Wing length (mm)		Days of emergence	
	Translocation	Te Rae o Atiu	Translocation	Te Rae of Atiu	Translocation*	Te Rae o Atiu
Fledged	463	101	463	89	64	100
Average	415	410	226	226	7.8	8.1
Std dev	36	49	5	7	3.5	3.6
CL	3	10	1	1	0.9	0.7
Maximum	550	565	238	237	16	20
Minimum	295	260	200	203	1	1
t	0.54		0.14		0.57	
$t_{P=0.05}$	1.97 (df = 562)		1.97 (df = 550)		• df = 162)	

* 2012-13 birds only

spent a night at Te Rae o Atiu in early November before being recorded in late December at Kōwhai River. No earlier translocation birds have been physically sighted or recorded in the Kōwhai River by researchers undertaking projects at the natal sub-colonies.

Te Rae o Atiu bred chicks

The first chick bred at Te Rae o Atiu to fledge was in the 2011–12 season; a further 111 fledged up until the 2020–21 season (Table 5). By the end of the 2016–17 season, 18 of the 36 chicks that fledged have come back; this 50% return rate is over twice that of the translocated birds, and there may be more if others return as 5-year-olds or older. Seventeen of the 18 returned birds were still present in 2020–21. On the basis of the 2011–12 to 2016–17 returns, we might expect 38 of the 76 chicks that fledged from 2017–18 to 2020–21 to return and for about 36 to remain medium term.

The mass and wing length near fledging, and the days between first emergence and fledging of the Te Rae o Atiu chicks that returned from their Australian migration were not significantly different from those that did not return, i.e. they were not from different populations (Table 6).

The youngest Te Rae o Atiu bred birds seen back at the colony were in their 2nd year (two) and a further ten birds first returned in their 3rd year. The limited time span since breeding commenced at Te Rae o Atiu means there is little data with which to determine trends or to make comparisons with translocation birds.

Translocation chicks and Te Rae o Atiu chicks

A comparison of the mass and wing lengths at near departure, and the number of days birds emerged before fledging of Te Rae o Atiu bred chicks and translocation chicks showed no significant differences (Table 7). This suggests that the birds

Table 8. Hutton's shearwater (*Puffinus huttoni*) breeding success (fledglings/egg laid) at Te Rae o Atiu. The number of breeding pairs per season is assumed to be equal to the number of eggs laid.

Season	Breeding pairs	Chicks hatched	Fledged	Breeding success (%)
2009–10	0	-	-	-
2010–11	2	0	0	0
2011–12	4	1	1	25
2012–13	16	3	2	13
2013–14	15	8	8	53
2014–15	16	8	7	44
2015–16	16	8	6	38
2016–17	23	14	12	52
2017–18	25	20	17	68
2018–19	31	15	15	48
2019–20	29	24	21	72
2020–21	33	26	23	70
Total	210	127	112	53

could be from the same populations despite the different feeding regimes – translocation feeding vs parental feeding.

Te Rae o Atiu colony growth

Colony growth to date has been mostly from returning translocated and Te Rae o Atiu bred chicks. There have only been two unbanded birds brought in by, possibly, acoustic attraction; these two females have had chicks fledge. We can now identify nearly all the birds at the colony as, from 2014–15 on, most birds present have been recorded by PIT tag readers.

At 2020–21, it is probable that all translocated birds that will return have done so. Numbers of each cohort peaked at about age five to six years old and were steady until a slow decline from about age 10 years with the loss of older birds (Fig. 6). Unlike for translocations, the Te Rae o Atiu plot reflects only the younger birds from the first few Te Rae o Atiu breeding seasons; older returning birds and those fledglings yet to return from their first Australian migration will enhance those numbers.

The breeding success (fledged/eggs laid) at Te Rae o Atiu has been about 62% from 2016–17 through 2020–21 (Table 8). There has been an increase in the number of fledglings with bursts in 2013–14 reflecting the increased breeding success with older birds, and 2016–17 with the second batch of translocated birds and Te Rae o Atiu bred birds starting to contribute to the colony.

The growth of the Te Rae o Atiu colony is shown in Fig. 7. At 2020–21 there was about 75 birds present producing about 20–25 fledglings/season.

DISCUSSION

Operational procedures

Before the predator-proof fence was installed at the Te Rae o Atiu colony, it was necessary to undertake

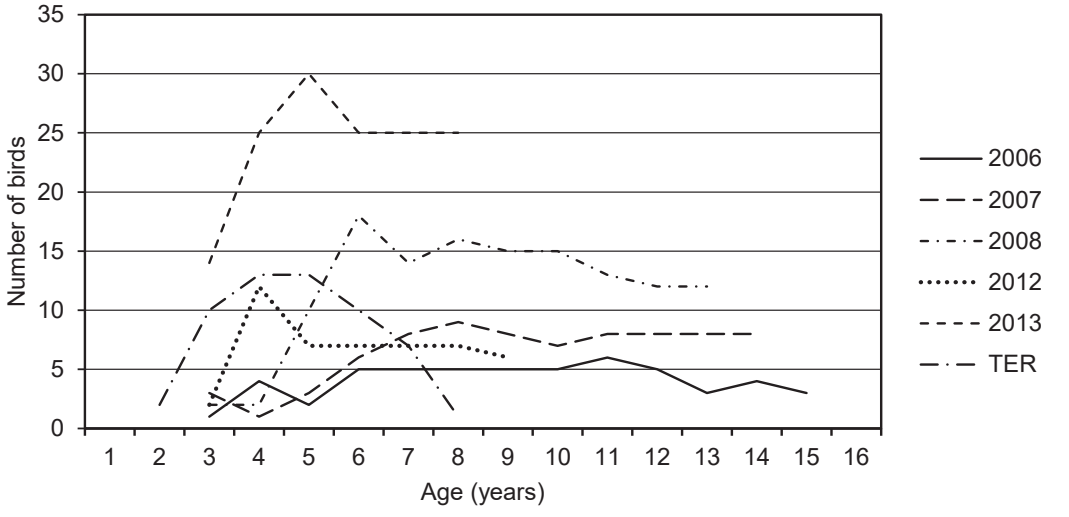

Figure 6. Number of Hutton's shearwaters (*Puffinus huttoni*) by age and cohort noted at Te Rae o Atiu. The Te Rae o Atiu graph will change significantly with time as more chicks fledge and return from their first migrations to Australian waters. Data to 2020–21.

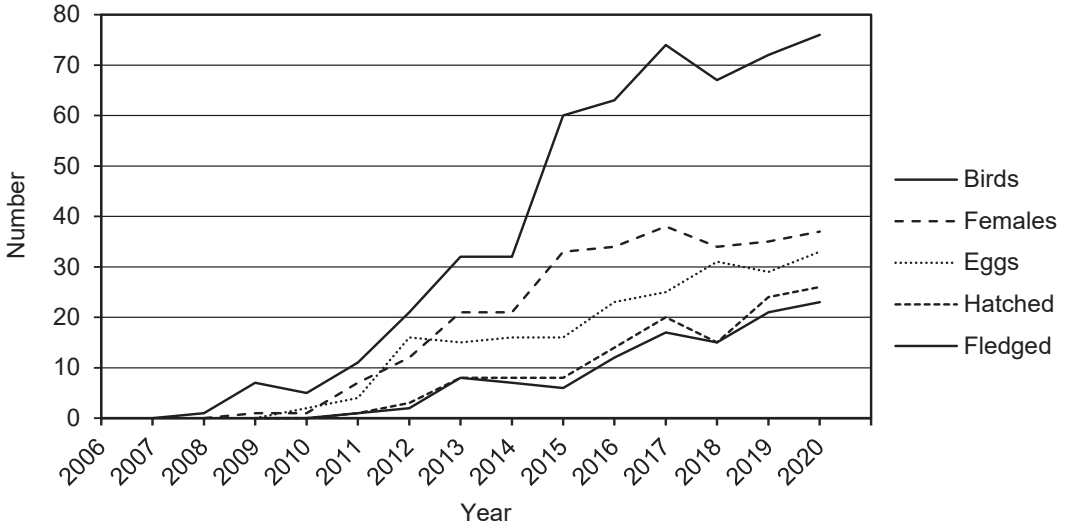

Figure 7. Growth of the Te Rae o Atiu Hutton's shearwater (*Puffinus huttoni*) colony. 2006 represents the 2006–07 season, and so forth.

predator control as the new site was located on farmland which was home to cats, rats, stoats, etc. One control measure was the use of DOC250 predator traps laid out around the new colony site. Unfortunately, the first known translocated Hutton's shearwater to return from its maiden migration was killed in a trap inside the standard farm fence; the bird triggered the trap when it put its head through the opening (M. Morrissey, DOC Kaikōura, *pers. comm*.). The openings of all traps were then made smaller by fitting small battens across the top of the entrance holes but leaving the openings large enough for mustelids to enter; there were no more fatalities associated with the traps, but we do not know if they have been tested.

There were significant losses of pre-fledging chicks at Te Rae o Atiu during 2006–2008 by cats and swamp harriers despite substantial control work of the former in the area surrounding the translocation site. On the worst night seven roaming chicks were taken. Once birds started to return from their first migrations the problem continued with three birds killed in one night and two more dying in the fishing net placed over the farm fence in an attempt to reduce cat access. That was the major drawback of trying to establish a new colony on farmland with the Kaikōura township less than 1 km distant, and it highlighted the need for a predator-proof fence that would exclude cats. Those losses may have been a prime factor that persuaded funders the fence was necessary. Without a predator-proof fence this colony would not have prospered as the relatively small number of returning birds would have been wiped out by cats. Since the fence was erected, there were no further losses to predators.

Two returned birds are known to have died when they flew into the bottom predator-proof fence when leaving the colony. Shrubs planted a few metres inside the fence may have prevented further fatalities because no more fatalities have been recorded to date.

The simple Twink™ marking system used to identify which bird of a pair was present without extracting it from the nestbox and reading the band, proved not to be foolproof. Birds seen together and marked in a nestbox very early in the season were sometimes found later breeding in other boxes with different partners. In some cases, both birds of the new pairing had the same twink patterns, i.e. both horizontal or both vertical marks. Thus, this simple system was abandoned after two seasons because of the uncertainty created in individually identifying birds. We now know adult shearwaters range widely; for example, one bird triggered 22 PIT tag readers beyond its own nestbox in one season (LR *unpubl. data*).

The movement of three pins placed at the external entrance of each nestbox tunnel to give a record of when chicks emerged from, and adults visited, nestboxes proved to be an unreliable measure for three reasons. Firstly, before the predator proof fence was erected, rabbits (*Oryctolagus cuniculus*) seen in nestboxes (LR *pers. obs.)* had knocked over the pins. Secondly, pins were moved by song thrushes (*Turdus philomelos*) prospecting for snails in the tunnels thus negating the reliable interpretation of the movements.

Thirdly, PIT tag records obtained during the 2013 translocation showed that pre-fledging chicks could move up to 25 m away from their home nestbox visiting up to four nestboxes in one night (Rowe 2014), a phenomenon also observed at the natal Kowhai River colony (Rowe 2018), and in fluttering shearwaters at Mana Island (Gummer & Adams 2010). These roaming chicks knocked over pins outside nestboxes other than their home nestbox up to 13 days before the incumbent chick triggered the logger for the first time (Rowe 2014). As a consequence of the chick and adult movements, the three pins were only useful in indicating which nestboxes may have been visited since the last check, and thus worth inspecting. To solve the problem, an additional three pins were placed at the exit of the nest chamber but the movement of these pins only indicated if a bird entered the nestbox, not which bird nor at what times.

It is highly likely we missed some returning birds each year up until, at least, 2013 because we did not make night visits when birds would be present. The daytime visits at about weekly intervals did not often find birds present unless on eggs or very small chicks. At that time the early birds were not PIT-tagged, and the value of PIT tagging was demonstrated in the 2015–16 season when 61 birds were recorded but only 34 were seen. The other 27, mainly young birds from the 2013 translocation, were known to have been at Te Rae o Atiu only from PIT tag reader records.

Contrary to some other studies, e.g. common diving petrels (*Pelecanoides urinatrix*) at Mana Island (Miskelly & Taylor 2004), the acoustic system calls at night has not been very successful in attracting new birds to the colony. Only two unbanded birds have been caught and banded, and became part of the breeding population. This rate of attraction is similar to that for the closely related fluttering shearwater which also had limited acoustic attraction to new sites. Two unbanded birds were seen prospecting near loudspeakers at Mana Island (Gummer & Adams 2010), and at Maud Island eight unbanded fluttering shearwaters were found at the translocation site, possibly attracted by the sound system (Bell *et al*. 2005). There does, however, seem to be some response by Hutton's shearwaters to the playbacks here because the majority of the nestboxes used are in a vee-formation below the speakers and not at the upper corners of the nestbox array. We know that the site is under the flight path to the Kōwhai River colony (G. Taylor; F. Barber, *unpubl. data* presented to OSNZ Conference 1 June 2003), and complaints from the public 1.5 km from the loudspeakers suggests that there was a lot of noise emitted. Why acoustic attraction has not been very successful here remains to be investigated, but the reason may be as simple as Hutton's shearwaters flying past not being attracted to that particular recording.

Translocation

With 495 Hutton's shearwater chicks translocated from the Kōwhai River, the Te Rae o Atiu experience is possibly the largest seabird translocation carried out since the 1970s—1980s when Atlantic puffin (*Fratercula artica*) chicks were translocated 1,600 km to Eastern Egg Rock (954 chicks, 1973–86) and Seal Island (950 chicks, 1984–89) in the Gulf of Maine, USA (Kress 1997; Jones & Kress 2012). While it may not be the longest continuous translocation project, it may well have been the first to carry out top up transfers a few years after the first set (M. Bell *pers. comm*. 2020), a procedure since followed at Mana Island where 200 fairy prion (*Pachyptila turtur*) chicks were moved in 2015 and 2016 to enhance the colony established from 240 chicks translocated in 2002–04 (Gummer *et al*. 2015, 2016).

Chicks for translocation need to be selected so that they have not emerged from their natal burrows and imprinted on the natal site, and to have sufficient time to imprint on the new site before fledging (Miskelly *et al*. 2009), about 2–5 weeks before fledging. Wing length is usually considered the best predictor of age with heavier birds often preferred to optimise fledging (e.g. Miskelly *et al*. 2009; Gummer & Adams 2010). Bell *et al*. (2005) confined their selections to fluttering shearwater chicks in full down with primaries half grown as more advanced chicks may already have begun imprinting on the natal site, and they noted that returning chicks had mean fledging weights greater that those that did not return. In this project the selection of chicks was based on wing length and mass but difficulties in retrieving the required number of chicks necessitated taking many chicks outside the guidelines. The wing length range, 195–215 mm, corresponded to chicks 23–15 days before fledging (from a wing length growth curve in Cuthbert & Davis [2002b]) which should have provided adequate time to imprint on the Te Rae o Atiu site and are within the time line suggested by Gummer & Adams (2010) and Miskelly *et al*. (2009). From a body mass growth curve (Cuthbert & Davis 2002b), chicks meeting the minimum mass criteria, >450 g, could be aged from about 42 days before fledging, through the peak mass of 530 g at about 18 days to fledging, through to fledging. Thus, mass is not as useful as wing length to estimate the days chicks stayed until fledging. Although potentially the best predictor of how long birds would stay, wing length was also not particularly useful in a practical sense as, for any given value, the translocated chicks showed a range of 24 days about the predicted value of how long a bird would stay.

Of the 495 chicks translocated, only three (0.6%) were recorded as having died of unidentified natural causes before fledging. This high level of survival was similar to that for many other translocations of small petrels: 100% for 240 fairy prions transferred to Mana Island in 2002–2004 (Miskelly & Gummer 2013) and 200 in 2015–2016 (Gummer *et al*. 2015, 2016), Gould's petrel (*Pterodroma leucoptera leucoptera*) 100% (Priddel & Carlile 2001), Chatham petrel (*Pt. axillaris*) 99% (Miskelly *et al*. 2009), Bermuda petrel (*Pt. cahow*) 97% (Carlile *et al*. 2012), and Pycroft's petrel (*Pt. pycrofti*) 98% (Miskelly *et al*. 2009). The survival rate was better than for the closely related fluttering shearwater, 82% at Maud Island (Bell *et al*. 2005) and 83% at Mana Island (Miskelly *et al*. 2009). The high survival rate of translocated Hutton's shearwater chicks at Te Rae o Atiu suggests that the collection procedures, transporting to, and housing at Te Rae o Atiu, and the feeding regimes using sardine smoothies were adequate despite there being four different lead contractors for the six translocations, each following their own, unpublished, guidelines as to a chick's feed requirements prior to fledging.

The criteria used to select chicks for translocation appear not to be definitive but provide a suitable guideline for which birds may survive the translocation process and fledge. Also, they were not factors that determined whether the birds returned to Te Rae o Atiu or not. The same parameters at fledging did not appear to influence returns. While fledging mass has been shown to have an effect for some species, e.g. for diving petrels and fluttering shearwaters where returned birds averaged 7% heavier at fledging than those that did not return (Miskelly & Taylor 2004, Bell *et al*. 2005), it was not a factor determining Hutton's shearwater returns. Unknown environmental factors while on migration, possibly weather, sea conditions, and food supplies, may be the important determinants for Hutton's shearwaters returning or not.

There were marked differences in the returns, 13 to 38%, from each translocation cohort which is not unusual. For example, returns of early translocations of fairy prions ranged between 2–29% (Miskelly & Gummer 2013), 11–23% for diving petrels (Miskelly & Taylor 2004), and fluttering shearwaters 4–32% (Bell *et al*. 2005). The average return to Te Rae o Atiu, 21%, is higher than at other translocation studies: 8% for fairy prions (Miskelly & Gummer 2013), 17% for diving petrels (Miskelly & Taylor 2004), and 12% for fluttering shearwaters (Bell *et al*. 2005). One reason may be that Te Rae o Atiu is a relatively small, defined site within a predator proof fence with the shearwaters only using nestboxes, and does not need the extensive search effort required at some natural release sites which may not find all returns.

Some studies, e.g. fluttering shearwaters moved from Long Island to Maud Island (Bell *et al*. 2005) and fairy prions from Takapourewa to Mana Island (Miskelly & Gummer 2013) have shown a number of birds returned to the natal colonies. There has been no systematic survey of the natal colonies in the Kōwhai River to determine how many Hutton's shearwaters may have returned. Annual limited scale productivity surveys, and captures for banding, determining migration patterns, and food source studies have not found any returns (LR *unpubl. data*) but, incidental to another project, Rowe (2018) found seven PIT-tagged Hutton's shearwater chicks had returned to the Kōwhai River. This was in spite of them being at Te Rae o Atiu for 1–18 days prior to fledging, long enough for other birds to imprint there and return to breed. Two of these birds had previously spent a night at Te Rae o Atiu on their return from Australian waters. Before returning to the colonies at night, Hutton's shearwater raft off the Kaikōura coast and it is possible that the birds that returned to the Kōwhai River were caught up in the movement of these birds which was strong enough to overcome any imprinting on Te Rae o Atiu. This small loss to the Kōwhai River, 1.5% of the translocation birds, is unlikely to have had a significant impact on the new colony.

Te Rae o Atiu colony growth

Breeding success (fledglings/egg laid) at Te Rae o Atiu has increased to about 70% by 2020–21 as the number of experienced breeders present increased. This success rate is encouraging as it is above that reported for the Kōwhai River colonies between 2009 and 2015, 63% calculated from Cuthbert (2019). It is similar to that for fluttering shearwaters at Maud Island which averaged 72% rising to over 80% in the last two years reported (Bell *et al*. 2005), but is lower than at Mana Island where it is now usually above 82% (Gummer 2020). Returns of locally bred birds have contributed to the recent steady growth of the Te Rae o Atiu colony which had previously been boosted greatly in 2015–16 by returns from the second set of translocations. Half of the early Te Rae o Atiu bred chicks have returned and these second-generation birds have bred and contributed to fledgling numbers from 2018–19. We await this third generation to return and contribute to the colony growth as future growth will soon depend on the Te Rae o Atiu bred birds returning from Australia and breeding.

Birds at Te Rae o Atiu are the only known age breeding Hutton's shearwaters and the oldest of these are three 15-year-olds (2 male, 1 female) from the 2006 translocation. Although DOC records

have about 775 birds banded as pulli and juveniles at Kōwhai River, only 14 have been recaptured alive, ranging in age from 6.6 to 19.0 years, and their breeding status was not known when recaptured. Eleven birds banded as adults have been recaptured at minimum ages of 19–23 years old and one at 32 years (Rowe & Taylor 2020) but it is not known if these birds were still breeding. Thus, there is insufficient data to produce reliable life tables for Hutton's shearwaters and their potential breeding span. BirdLife International (2021) lists the generation length of Hutton's shearwater at 19.5 years and for the seven other Manx related shearwaters to be between 15 and 18.3 years; individual Manx shearwaters have been recovered at over 50 years old (Robinson 2005) and fluttering shearwaters 27 years (M. Bradshaw, DOC *pers. comm.*). This limited information suggests that Hutton's shearwaters could breed to about 20 years, so the older birds may be nearing the end of their reproductive lives. There are indications here that there is a gradual decline in numbers of a given cohort at Te Rae o Atiu from about age 10. There will soon be a need for replacements for the natural losses of the translocated birds as they cease being part of the breeding stock. Additional birds may be necessary to expand the colony further and to diversify the gene pool which is limited through lack of new birds being attracted to the site. While the current and future breeding stock may provide sufficient replacements, a third set of translocations to Te Rae o Atiu, perhaps 300 chicks over two or three years, is desirable to ensure another boost to the growth of the colony as was seen after the 2012 and 2013 translocations.

There is a lot of space for potential growth at Te Rae o Atiu. During 2020–21, Hutton's shearwaters were found in 49 burrows and eggs in 33, suggesting the present 108 wooden nestboxes will be adequate for a number of years to come. Shearwaters have not dug their own burrows to date but have dug around the back of nestboxes and dug tunnels up to 0.5 m deep out the back of chambers where there were gaps in the woodwork. At the density of the nestboxes already installed, there is a potential for about 4,000 breeding pairs at Te Rae o Atiu. The potential numbers could be as high as 10,000 pairs at the density reported for areas at Kōwhai River by Cuthbert (2019). This does not include any birds that might burrow outside the predator-proof fence. Thus, there is no real limit on the number of birds that can be resident at the Te Rae o Atiu colony. It need not be a token insurance colony in the event of more catastrophic events at the Kōwhai River and Shearwater Stream colonies, nor be of a limited size where it could be vulnerable to avian diseases or other events.

Conclusions

This study has shown that for translocation birds that returned or did not return from their first migration to Australia, the two groups had similar wing lengths and mass at collection, at fledging, and emerged for a similar number of days before fledging. The translocation chicks and locally bred chicks also had similar parameters at fledging. Fledging parameters for Te Rae o Atiu chicks that returned or did not were also similar. This suggests that for birds that are adequately provisioned by the translocation teams or parents, man might have little influence over returns. Weather and sea parameters including food sources whilst the birds are on migration probably control the numbers of birds that return.

The colony numbers have been relatively stable over the last four years of the study at about 75 birds. With the numbers of older breeding birds declining slowly it is hoped that chick production will be adequate to replace those. Warming sea temperatures may be a factor influencing future colony expansion as birds have to travel further than at present, around and south of Banks Peninsula (Bennet *et al.* 2019, 2022) to find food as sources move south to cooler waters. Further translocations may be necessary to boost Te Rae o Atiu colony growth.

ACKNOWLEDGEMENTS

This project would not have been possible without the efforts of a huge number of people and funding agencies. Our thanks go to: Whalewatch and Tukete Charitable Trust (formerly The Kaikōura Charitable Trust) for making the Te Rae o Atiu site available at the Kaikōura Peninsula; Geoff Harrow and the Hutton's Shearwater Recovery Group for driving the 2005–08 translocations, and the HSCT for overseeing the 2012 and 2013 translocations; DOC funded the logistics and management of the 2005–08 translocations; DOC, Geoff Harrow and Encounter Kaikōura provided logistics and funding for the 2012 and 2013 translocations; the Canterbury Community Trust, New Zealand Lottery Board, Pub Charity, Eureka Trust, World-Wide Fund for Nature New Zealand, The Lions Club of Kaikōura, the North Canterbury and Kaikōura branches of the Royal Forest and Bird Protection Society of New Zealand, and many individual donors made the installation of the predator proof fence and site enhancements possible; the New Zealand Lottery Board, The Mohamed bin Zayed Species Conservation Fund, Sistema Plastics, and Reid Technology funded the PIT tags and the tag reader equipment; The HSCT for managing and funding the continuing operations of the Te Rae o Atiu colony; The Sargood

Bequest for funding equipment facilitating the ongoing monitoring; and, finally but not least important, the many volunteers from the Kaikōura and wider community who have assisted with feeding the translocated chicks and monitoring at the colony. The work was performed under permits and authorities issued by the New Zealand Wildlife Service and Department of Conservation and carried out using DOC protocols. Comments from the editor and anonymous referees are appreciated and have contributed to improvements in this paper.

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Notornis, 2023, Vol. 70: 31-38
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A PCR-based assay for screening substrates for *Aspergillus fumigatus* for application in kiwi hatcheries

STEPHEN P. ROWE*
Manaaki Whenua – Landcare Research, PO Box 69040, Lincoln, New Zealand
University of Canterbury, School of Biological Sciences, Christchurch, New Zealand

MATTHEW B. STOTT
University of Canterbury, School of Biological Sciences, Christchurch, New Zealand

BETHANY BRETT
Willowbank Wildlife Reserve, Christchurch, New Zealand

MANPREET K. DHAMI
Manaaki Whenua – Landcare Research, PO Box 69040, Lincoln, New Zealand

Abstract: Captive facilities across New Zealand strive to mimic natural conditions for captive animals as closely as possible. In the case of the kiwi (*Apteryx* spp.), captive habitats are augmented with natural stimuli such as soils, leaf litter, bark, plants, logs, and mosses. Interaction with these introduced stimuli has been shown to encourage normal foraging behaviour and is speculated to aid in inoculating young animals with healthy microbial communities. However, introducing non-sterile natural stimuli into the captive environment also carries the risk of exposing kiwi to diseases such as aspergillosis, coccidiosis, and candidiasis. Aspergillosis is of particular concern to rearing facilities – the disease is most commonly attributed to exposure to *Aspergillus fumigatus*, an opportunistic fungal pathogen. Here we present a PCR-based screen to qualitatively detect the presence and/or absence of *A. fumigatus* in soils. Soil samples collected from nesting sites of rowi (Ōkārito brown kiwi, *Apteryx rowi*) in the Ōkārito region of the West Coast were screened for *A. fumigatus* using a species-specific primer set coupled with a basic DNA extraction. Willowbank Wildlife Reserve soil and substrate samples were also screened as a baseline comparison representing captive rearing facilities. Results from the assays showed that the extraction technique was effective at isolating *A. fumigatus* DNA at detectable levels from a variety of soils, and that Ōkārito soils did not harbour a higher abundance of *A. fumigatus* than those found at Willowbank. This preliminary screening method could be used by facilities in New Zealand to quickly and cheaply screen soils and substrates for *A. fumigatus* before introducing them to captive enclosures.

Rowe, S.P.; Stott, M.B.; Brett, B.; Dhami, M.K. 2023. A PCR-based assay for screening substrates for *Aspergillus fumigatus* for application in kiwi hatcheries. *Notornis 70(1)*: 31–38.

Key words: *Aspergillus fumigatus*, aspergillosis, kiwi, hatcheries, Ōkārito, soils

INTRODUCTION

Captive rearing of endangered species is the cornerstone of conservation programs in New Zealand. For the rarest of the rare, such as rowi (Ōkārito brown kiwi, *Apteryx rowi*) and kākāpō (*Strigops habroptilus*), captive rearing efforts have helped to dramatically improve survivability and stabilise populations (Colbourne *et al.* 2005; Holzapfel *et al*. 2008). However, the sensitivity of these species to captive conditions remains a challenge. In the case of kiwi (Family Apterygidae),

Received 23 May 2022; accepted 26 January 2023
*Correspondence: *stephenp.rowe@pg.canterbury.ac.nz*

a nocturnal, territorial ground-dwelling forager, these challenges include restricted foraging spaces, disruptions to their chronobiology, unnatural diets, and exposure to foreign microbes and antimicrobials (Taborsky & Taborsky 1992, 1995; Dickens *et al.* 2006; Becker *et al.* 2014; Pan & Yu 2014; Waite *et al.* 2014). The extent to which these factors affect the long-term survivability of captive-bred kiwi in the wild is not yet fully known. While some variables, such as territory size, are inherently unavoidable, efforts have been made by rearing facilities to carefully recreate a "wild" environment for kiwi in captivity. Captive diets are often supplemented with live invertebrates to teach young kiwi how to forage and enclosures are filled with a wide variety of stimuli such as deep soils, rocks, plants, logs, mosses, leaf litter, and hutches to encourage exploratory behaviour in birds that would be roaming several hectares in search of food in the wild (Fraser *et al.* 2009). Studies have shown that including a variety of natural stimuli for captive animals to interact with not only helps with behavioural development but also with the establishment of a properly attuned microbiome – the collection of bacteria, fungi, protists, and other microorganisms that form a symbiotic community with kiwi as their host (Colston & Jackson 2016; Berg *et al.* 2020). Louden *et al.* (2014) and Becker *et al.* (2014) showed that including an "environmental reservoir" of relevant symbiotic organisms in the form of introduced soils or substrates in captive environments established a more favourable microbiome in amphibians (Becker *et al.* 2014; Loudon *et al.* 2014). Further, San Juan *et al.* (2021) showed that soil bacteria comprised a vast proportion of the gut microbiome in wild kiwi, stressing the importance of these soil organisms. However, care must be taken when adding these stimuli – not all microorganisms present are symbiotic, and introducing diseases into habitats remains a major risk. One such disease that is carefully guarded against in captive facilities, hatcheries, and wildlife sanctuaries across New Zealand is aspergillosis (Fraser *et al.* 2009; Glare *et al.* 2014; Tell *et al.* 2019; Hauck *et al.* 2020). This disease is caused by the inhalation of conidia (spores) of species in the fungal genus *Aspergillus* and their subsequent proliferation in the lungs (Bossche *et al.* 1988; Fischer *et al.* 2018; Arné *et al.* 2021). The majority of worldwide aspergillosis cases are attributed to one species in particular, *Aspergillus fumigatus* (Bossche *et al.* 1988; Fischer *et al.* 2018; Arné *et al.* 2021). Recent studies have highlighted that *A. fumigatus* is omnipresent in most soil types in many kiwi sanctuaries, either in hyphal or conidial form (Glare *et al.* 2014). The disease is often fatal for young or immunocompromised birds and can cause long-term damage to animals that do survive infection (Ainsworth & Rewell 1949). Captive facilities employ multiple strategies to reduce the likelihood of aspergillosis cases in the animals in their care. These include the regular replacement of soil, leaf litter, and substrates in enclosures, spore counts by external laboratories, daily cleaning and aeration of bedding materials and proper storage of these materials in dry, well-ventilated spaces (Fraser *et al.* 2009). Aspergillosis was responsible for 24 kiwi deaths since 2003 and a recent outbreak in captive kākāpō (*Strigops habroptilus*) at a sanctuary on Codfish Island (Whenua Hou) resulted in 21 cases of infection and a total of 9 deaths (Gartrell 2021). These statistics demonstrate the importance of preventing aspergillosis in captive habitats, especially those of rare and endangered species. Given the tenuous stability of kiwi populations, it is critical that any modifications to their habitat, including soils in enclosures and as probiotic food additives as well as substrates for bedding are screened for the presence of *A. fumigatus* to minimise the risk of exposure for captive birds. However, regular screening is currently not undertaken due to limitations of available methods. Current methods of *Aspergillus* detection include culturing the pathogen from soils or samples of infected tissue and performing colony and spore counts for quantification, as well as Polymerase Chain Reaction (PCR) and sequencing to confirm taxonomic identification (Glare *et al.* 2014). This is a time-consuming process and requires taxonomic expertise. Commercial testing is also available to captive facilities in the form of multiplex quantitative PCR (qPCR) testing of soils and tissues (D. Tisnall, *pers. comm.* 2022). These quantitative assays are thorough and provide accurate results of both the numbers of *Aspergillus* colony forming units (CFU) per gram of sample as well as genotyping to determine the species of *Aspergillus* present. However, due to the cost per sample these tests are deployed only when disease-onset occurs and can have long turnaround times. We provide a test-case for a simple species-specific PCR based assay that could be deployed to routinely screen substrates from kiwi habitats to proactively minimise exposure to *Aspergillus fumigatus*. This study describes the optimisation and testing of a simple qualitative PCR assay to specifically detect *A. fumigatus* in soil samples. Soil and other substrates such as peat moss from Willowbank Wildlife Reserve, and soil from the Ōkārito Reserve, a natural habitat of rowi, were tested and compared in this study. A primer set developed by Serrano *et al.* (2011) was used to selectively amplify *A. fumigatus* DNA found in samples. The two sets of soil samples, from the captive rearing facility and a native reserve were tested to understand the differences in the baseline levels of *Aspergillus fumigatus* in the two habitats.

METHODS

Sample collection and DNA extraction

All field sampling from the Ōkārito Reserve and Willowbank Wildlife Reserve (WWR) was carried out using sterilised equipment (autoclaved, 121°C, 15 psi, 60 minutes) and with permission from the relevant authorities of each site. The Ōkārito Reserve was chosen as a suitable native habitat that best represents the types of soils and flora that wild kiwi might be exposed to – the region comprises around 90km^2 of beech (Fuscospora), rimu (*Dacrydium cupressinum*) and mānuka (*Leptospermum scoparium*) forest as well as extensive wetlands and is home to the only wild population of rowi. Willowbank is a major kiwi captive rearing facility in New Zealand, receiving a large proportion of rowi chicks each year for rearing via Operation Nest Egg (Colbourne *et al*. 2005). The facility provided an accurate representation of the typical conditions of captive kiwi habitats, maintained to the National Kiwi Husbandry Standard (Fraser *et al*. 2009). From the Ōkārito Reserve, soils were collected by field teams from the field teams from the Department of Conservation at five different egg-collection sites throughout the Reserve, for a total of 5 kg. Samples were stored at 4°C and transported to Manaaki Whenua Landcare Research (MWLR) in Lincoln for processing. Five-gram subsamples (n = 36) were collected from the total and stored at -18°C. From Willowbank, multiple samples of soil (n = 17, 5 g each) and bedding materials such as peat moss (n = 17, 5 g each) and straw (n = 17, 1 g each) were collected from rowi enclosures. To extract and suspend environmental DNA, 50 mL of sterile water (Milli-Q) was added to each sample in an autoclaved flask. Flasks were shaken on a Ratek Orbital Mixer (Ratek Instruments, Boronia, Australia) at 160 RPM for 30 minutes. One mL was then extracted into a clean microcentrifuge tube, heated at 95°C to lyse microbial cells, centrifuged at 11,000 RPM in a 5145-D benchtop centrifuge (Sigma-Aldrich, Darmstadt, Germany) for four minutes and the supernatant transferred into new 1.7 mL microcentrifuge tubes.

Assessment of DNA extraction efficiency using PCR with broad fungal ITS primers

To test the efficacy of the rapid DNA extraction technique, ITS1-F_KYO1 forward (5′-CTHGGTCATTTAGAGGAASTAA-3′) and ITS2_KYO1 reverse (5′-CTRYGTTCTTCATCGDT-3′) primers developed by Toju *et al*. (2012) were used to broadly amplify fungal DNA in a random selection of extracted soil and substrate samples (n = 16). DNA from an isolate of *A. fumigatus* (conc. 2 ng/μL) was extracted at the MWLR laboratory in Auckland (ICMP accession number 23465) to be used as a positive control. The 15 μL PCR mix consisted of 7.50 μL of 2× KAPA Plant PCR Buffer (KAPABiosystems, Wilmington, MA), 0.60 μL of each primer (10 μM), 0.12 μL of 3G KAPA DNA polymerase (KAPABiosystems), 5.18 μL of PCR-grade water (Milli-Q) and 1.00 μL of sample DNA. The PCR protocol was as follows – denaturation at 95°C for 2 minutes, then 34× cycles of 95°C for 20 seconds, 50°C for 20 seconds, 72°C for 30 seconds and a final extension of 1 minute. Gel electrophoresis with a standard 2% agarose gel and 5 μL of PCR product per lane was used to visualise PCR products and confirm expected fragment sizes of 300–350 bp.

Optimisation of species-specific *A. fumigatus* RodA primers

Annealing temperature

The rodlet A region of *A. fumigatus* DNA was targeted using RodA forward (5′-ACATTGACGAGGGCATCCTT-3′ and reverse (5′-ATGAGGGAACCGCTCTGATG-3′) primers (Integrated DNA Technologies, Auckland, New Zealand) as described by Serrano *et al*. (2011). RodA primers were optimised for specificity to *A. fumigatus* using a gradient PCR with annealing temperatures ranging from 50–65.8°C. Pure *A. fumigatus* DNA samples were used (n = 16) in two dilution series, 1:10 and 1:100, to assess differences in signal strength. The 15 μL PCR mix used for this protocol was the same as above, but with the ITS1-F_KYO1 and ITS2_KYO1 primers replaced with RodA forward and reverse primers. PCR products were visualised using the same gel electrophoresis method as above.

Efficiency & species-specificity

RodA primers were tested for specificity to *A. fumigatus* compared to DNA from a closely related species, *Aspergillus niger*. DNA from a culture of *A. niger* (conc. 2 ng/μL) (ICMP accession number 2523) was obtained to act as a negative control for this test. Additionally, primers were assessed for efficiency in the presence of soil-based inhibitors. Random soil and substrate samples were chosen (n = 4) and spiked with equal amounts of either *A. fumigatus* or *A. niger* DNA. The same PCR and gel electrophoresis method as above was used, but with the optimised annealing temperature.

Detection of *A. fumigatus* in Ōkārito and WWR soils and substrates using optimised RodA primers

The optimised assay was employed to screen for the presence of *A. fumigatus* in samples collected from soils, and other substrates within the captive

rearing facility, as well as soil samples collected in the natural habitat of rowi, i.e the Ōkārito Reserve (n = 85). Assay results were assessed via gel electrophoresis, with bands detected at ~320 bp considered positive for *A. fumigatus*. Data were recorded in an Excel spreadsheet and analysed as below.

Statistical analysis

To determine whether there was a significant difference in *A. fumigatus* presence between the two sample groups (Ōkārito vs WWR), a general linear model (GLM) was used. Samples positive for *A. fumigatus* were labelled with a 1, and negatives with a 0, to create a presence absence matrix which was exported to RStudio (version 1.4) for analysis. RStudio packages Hmisc (Harrell Jr & Harrell Jr 2019) (version 4.6-0) and lme4 (Bates *et al.* 2007) (version 1.1-27.1) were used to run a GLM for binomial data. Ōkārito soil samples, as baseline in the natural habitat, were compared against all other soil types, with soil groups retained as a random effect in the model and using the formula, *Aspergillus.presence ~ samples + (1/sample.type).*

RESULTS

Optimal PCR mix and protocol of the assay for screening

15 µL PCR mix – 7.50 µL of 2× KAPA Plant PCR Buffer (KAPABiosystems), 0.60 µL of each primer (10 µM), 0.12 µL of 3G KAPA DNA polymerase (KAPABiosystems), 5.18 µL of PCR-grade water (Milli-Q) and 1.00 µL of sample DNA.

Protocol – denaturation at 95°C for 2 minutes, then 34× cycles of 95°C for 20 seconds, 65.8° for 20 seconds, 72°C for 30 seconds, final extension 1 minute.

Detection of *A. fumigatus* DNA in soil and substrates and statistical analysis of Ōkārito vs WWR groups

RodA primers were used to amplify *A. fumigatus* DNA from environmental DNA extracted from Ōkārito soil and WWR soil and substrate samples. A faint band of ~320 bp indicated the presence of *A. fumigatus* DNA and therefore a positive sample. It was expected that any amount of extracted and amplified fungal DNA in samples would be very low, due to the resistance of fungal conidia to lysis. Therefore, samples positive for *A. fumigatus* may have only shown a faint band that could be mistaken for a negative. To mitigate this, all samples displaying even a faint band would be counted as positive. Figure 1 shows the gel electrophoresis output with positive samples highlighted, and Table 1 shows a summary of positive and negative results. Overall, Ōkārito soils had a positive rate of 2.9%. WWR run soils had a rate of 5.8%, and WWR peat moss and straw a rate of 17.6% and 5.8% respectively. After being split into two groups (Ōkārito vs WWR) a GLM (lme4) with a fit of maximum likelihood found no significant difference between the positive rates of the two groups (Ōkārito vs WWR, p = 0.254). Table 2 shows a summary of the GLM results.

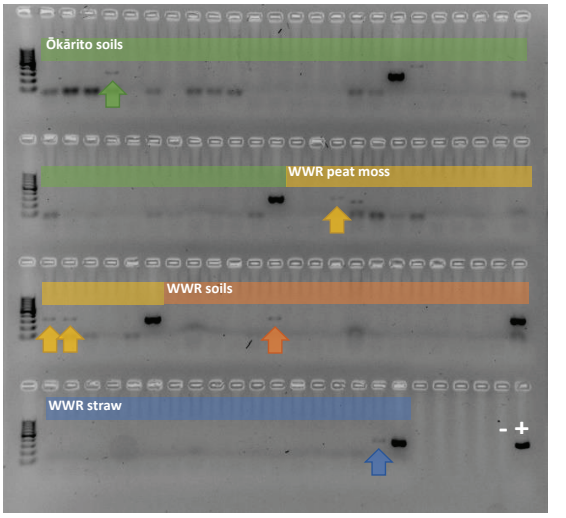

Figure 1. Gel electrophoresis image of Ōkārito natal soil samples compared against Willowbank Wildlife Reserve peat moss, soils and straw, coloured as green, yellow, orange, and blue from left to right. Arrows highlight samples positive for *Aspergillus fumigatus* for each substrate type. Dark bands represent positive controls, faint bands positive samples.

Assessment of DNA extraction efficiency

PCR amplification of samples post-extraction using broad fungal ITS primers showed positive results across all samples. Gel electrophoresis visually confirmed the presence of amplified DNA from a variety of fungal species. These results confirmed the ability of the extraction method to adequately isolate and suspend fungal DNA from soil and substrates.

Optimal annealing temperature for RodA primer set

A gradient PCR confirmed specificity of the primers at higher temperatures as stated by Serrano *et al.* (2011). Clear bands of ~300 bp (the target amplicon size) in the gel electrophoresis output showed the highest specifity to target *A. fumigatus* DNA at an annealing temperature of 65.8°C.

Table 1. Total counts for each soil/substrate type positive for detectable *Aspergillus fumigatus* content and their percentage (WWR is Willowbank Wildlife Reserve).

Soil/substrate	Positive counts	Total counts	Percentage positive
Ōkārito soil	1	34	2.9
WWR soil	1	17	5.8
WWR peat moss	3	17	17.6
WWR straw	1	17	5.8

Table 2. Generalised linear mixed model output comparing both soil groups against each other. Soil type (natal, run, peat moss, straw) was included as a factor.

	Standard Error	z-value	p-value
Intercept	0.4709	-4.713	2.44e-06
Natal vs WWR	1.1189	-1.142	0.254 ^{ns}

Fainter bands were visible in different size ranges as the temperature decreased. 65.8°C was used as the annealing temperature for all further PCR amplification protocols that used RodA primers in this study.

Primer cross-specificity to closely related species and efficiency in the presence of potential PCR inhibitors

The RodA primer set showed no cross-specificity to close relatives of *A. fumigatus* such as *A. niger*. Purified *A. fumigatus* DNA amplified strongly, whereas no amplification was reported for purified DNA of *A. niger* at comparable concentrations. It was also clear that soil samples spiked with *A. fumigatus* had an equal level of amplification to pure DNA samples, indicating that any PCR inhibitors present in the soil and substrate extracts did not sufficiently inhibit amplification.

DISCUSSION

We provide an optimised PCR-based rapid screening method for *A. fumigatus* and test its application at a captive-rearing facility, Willowbank Wildlife Reserve (WWR), that houses rowi. We find that background levels of *A. fumigatus* in soils from the participating captive-rearing facility are comparable to those in the natural habitat of the rowi. Below we discuss the applicability of this method, especially proactive use in kiwi captive-rearing facilities, and its limitations.

Detection of *A. fumigatus* in soils and substrates

Aspergillus fumigatus is a common soil-borne fungus that is well-known to hatcheries and captive-rearing facilities as the largest contributor to cases of aspergillosis. As such, all soils and substrates used in rowi enclosures at Willowbank were screened to provide an accurate overview of the presence of *A. fumigatus*. While we found no significant difference between numbers of positive samples of natal soils compared to WWR soil, peat moss and straw, peat moss from the brooder boxes of young kiwi exhibited the highest proportion of positive samples.

Peat Moss

Peat moss is an ideal substrate for fungal growth, with a high humidity and nutrient content and a supportive matrix structure (Gorham & Rochefort 2003). WWR peat moss is stored in dry environments to minimise fungal growth.

Straw

The straw used as bedding material in hutches was suspected to be the highest risk substrate for *A. fumigatus* by WWR keepers (B. Brett, *pers. comm.* 2020). As such, straw is regularly inspected and replaced by staff to minimise the risk of fungal growth. However, straw is often obtained as whole bales from local agricultural providers, with little record of its storage conditions before arriving at WWR – it has been found that an important determinant of *Aspergillus* levels in substrates is age of the substrate and storage condition (Glare *et al.* 2014). However, our screen only detected a contamination rate of 5.8%, much lower than that of peat moss and comparable with general WWR soils. This may have been due to the fact that we only collected ~1g of straw per sample due to its bulk.

Soils

Soils at WWR that are used in outdoor habitats are sourced from multiple local areas. *A. fumigatus* is known to have a ubiquitous presence in soils, and so we suspected a high rate of contamination from WWR soils. However, WWR soil had the same number of positive samples as straw, with a rate of 5.8%. This may have been due to a lack of nutrients or humidity in these high-turnover agricultural soils, as well as efforts by WWR keepers to regularly replace soil to ensure it does not stagnate.

Ōkārito soil

Ōkārito soil samples were collected from five different egg collection sites, 1 kg from each. These

samples were then subsampled and statistically pooled to form the "Natal soil" group. Ōkārito soils had the lowest level of *A. fumigatus*, at 2.9%, despite samples including a large proportion of dead plant material such as roots and a high moisture content. Heterogenous soils from old growth forests are typically rich in fungal diversity (Jansson & Hofmockel 2020). As a result, the high species diversity observed in such soils may reduce the proliferation of a few dominant species and thereby reduce the load of *A. fumigatus.*

Advantages and applications of the assay

This assay was developed to quickly and accurately screen substrates for *A. fumigatus* in an effort to ensure their introduction to rowi enclosures did not exascerbate the risk of aspergillosis for birds in captivity. While commercial testing options through veterinary clinics are often available for this purpose, we sought to develop a faster protocol that could provide a simple positive or negative result without the need for extensive laboratory testing. This assay does not require a typical DNA extraction kit, can be used with a wide variety of substrates, and DNA sequencing is not necessary due to the specifity of the primers used. Large numbers of samples can be screened in a matter of hours using minimal equipment at any moderately equipped PC2 laboratory. Furthermore, this assay does not rely on a clinical case of aspergillosis to arise before being implemented – it can be used as a preventative method to reduce the risk of aspergillosis in captive environments. Regular application of the assay, especially when new captive habitats are established, could help monitor contamination levels over time and determine when soils and substrates should be replaced.

Limitations of the assay

While we developed an assay that could be used proactively to limit exposure of *A. fumigatus* containing substrates to kiwi in captivity, confirmation of highly contaminated samples via sequencing is recommended. Our rapid DNA preparation method may allow 'leaking' of PCR inhibitors which may vary across soils and substrate types (Schrader *et al.* 2012). In our tests, while this was not an issue, this may be problematic in other sample types such as high humic acid containing soils. Our method could be further improved by employing a DNA extraction kit specifically optimised for the sample type. These kits efficiently remove PCR inhibitors present in a sample (Whitehouse & Hottel 2007), but can be expensive and time consuming for large numbers of samples. Further, our DNA preparation method may not efficiently lyse conidial cells – the predominant disease causing agent in aspergillosis (Fischer *et al.* 2018). Fischer *et al.* (2018) demonstrated that *A. fumigatus* conidia can suvive temperatures of up to 60°C (Vallejo-Cardona *et al.* 2017). As such, we chose a temperature of 95°C to ensure complete degradation of spores. Even so, no chemical additions were made to the extraction solution that could have helped to degrade conidial cells. Again, these agents are found in commercial extraction kits, which would further optimise this step in future. Aspergillosis can also be caused by other species of *Aspergilli*, such as *A. niger* or *A. flavus* (Serrano *et al.* 2011). However, discussions with the Department of Conservation and WWR keepers determined that a focus on *A. fumigatus* specifically was imperative for this study since this species is responsible for the majority of aspergillosis cases in New Zealand (K. McInnes, *pers. comm.* 2021). Moving forward, further primers targeting these alternative species could also be applied to this screen in a multiplexed fashion (Xu *et al.* 2000; San Juan *et al.* 2021).

CONCLUSIONS

Aspergillosis is a significant contributor to the mortality rates of captive avian species in New Zealand wildlife sanctuaries. Efficient and thorough testing of captive environments for *A. fumigatus* remains an important component of captive rearing. The purpose of this study was to demonstrate a simple yet effective PCR-based method for qualitative testing of substrates for *A. fumigatus* in captive habitats. A primer set was optimised for specificity to *A. fumigatus* and efficiency in the presence of soil-based contaminants. Findings indicated that this screen is useful in the context of qualitatively detecting the presence or absence of *A. fumigatus* in various soil and substrate types, and could be applied as a cost-effective routine screen for wildlife sanctuaries concerned about aspergillosis.

ACKNOWLEDGEMENTS

We would like to thank the following people and organisations for their contributions to this project: Laurie Keller at the West Coast Wildlife Centre for helping with the groundwork and for facility access, Tracey Dearlove (Department of Conservation, DOC) and the Franz Josef DOC Office for sample collection, and Kai Tahu Makaawhio runaka and Kate McInnes (DOC) for their support of this study. Ian Dickie at the University of Canterbury for statistical support. The GEM laboratory team at Manaaki Whenua Landcare Research for their knowledge and expertise. SPR was supported

by the Birds New Zealand Marj Davis Fund for postgraduate study and MKD is supported by a Marsden Fund grant (MFP-LCR-2002) with further research funding from the MBIE Strategic Science Investment Fund.

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Notornis, 2023, Vol. 70: 39-41
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SHORT NOTE

Longevity record for common diving petrel (kuaka, *Pelecanoides urinatrix*) in New Zealand

COLIN M. MISKELLY*
Museum of New Zealand Te Papa Tongarewa, PO Box 467, Wellington 6140, New Zealand

GRAEME A. TAYLOR
Department of Conservation, PO Box 10420, Wellington 6143, New Zealand

Common diving petrels (kuaka, *Pelecanoides urinatrix urinatrix*) have been monitored on Mana Island, Wellington, since a colony was established there following translocations of chicks in 1997–99 (Miskelly & Taylor 2004; Miskelly *et al.* 2009). In addition to the 118 translocated chicks that fledged, 229 parent-reared chicks and 183 adult diving petrels were banded on Mana Island between 1997 and 2022 (Miskelly & Taylor 2004; authors, *unpubl. data*). During these 26 years, up to 20 breeding pairs per annum have been monitored at the main colony at Shearwater Point, south-west Mana Island, with occasional monitoring of isolated pairs and sub-colonies elsewhere on the island (e.g. Miskelly *et al.* 2004). This monitoring programme has revealed that few diving petrels survive longer than 15 years. Of 246 adult diving petrels handled on Mana Island, only three have exceeded this age to date (Table 1). These three birds comprise 3.1% of the 98 birds handled or recaptured as adults before 2008 (birds that would potentially be 16 years or older by 2022).

Table 1. Brief histories of the three longest-lived common diving petrels (kuaka, *Pelecanoides urinatrix urinatrix*) recorded on Mana Island, Wellington. Ages are based on an estimated October hatch date, with a minimum age of first return of 10 months. D-154390 & D-154392 were both translocated to Mana Island from North Brother Island the day after they were banded. D-178698 raised a chick to fledging in 2022.

Band no.	Sex	Date banded	Banded as	Last recorded	Age
D-154390	Male	26 Nov 1998	Chick	21 Oct 2020	22 y 0 m
D-154392	Female	26 Nov 1998	Chick	16 Nov 2015	17 y 1 m
D-178698	Male	17 Mar 2005	Adult	5 Dec 2022	19 y 2 m +

Received 19 August 2022; accepted 25 January 2023
*Correspondence: *colin.miskelly@tepapa.govt.nz*

The longest-lived individual was a male (band number D-154390) that was translocated as a chick from North Brother Island on 27 November 1998, and which fledged from Mana Island on the night of 16 December 1998. He was first recorded back on Mana Island on 26 February 2000, and remained faithful to the same burrow for 21 consecutive breeding seasons. For the first 16 years he was paired with D-154392 from the same cohort of translocated chicks (Table 1). These two long-lived birds raised ten chicks together, five of which were recorded back at the colony as adults. Following loss of his first mate, D-154390 paired with three different females over the following five years, and last raised a chick in 2019, when 21 years old. He was last recorded at the colony on 21 October 2020 (at 22 years old), when his final breeding attempt failed at the egg stage when a pair of sooty shearwaters (*Ardenna grisea*) took over the breeding burrow.

During his lifetime, D-154390 incubated an egg in 21 consecutive years, cared for 16 chicks, and fledged 13 of them. Six of his offspring were recorded back on Mana Island as adults, with five of them known to have bred (two of them bred at least 11 times each). His total number of descendants known to have fledged by the end of 2022 was 43 (F1 x 13, F2 x 19, F3 x 11). At least five of his descendants were present and bred in the colony in 2022. These figures are minima, as not all diving petrel burrows on Mana Island are monitored. All petrel species produce a maximum of one chick per annum, and so the major determinant of an individual's lifetime reproductive success is its lifespan (Ollason & Dunnet 1988; Wooller *et al*. 1989; Brooke 2004).

The previous oldest age for a common diving petrel that we are aware of in New Zealand was a bird banded as an adult on Motuotau Island, Bay of Plenty, on 24 May 1994, and found dead on nearby Waihi Beach on 22 July 2011, at a minimum age of 18.5 years old (Te Papa specimen OR.029576). After submitting this note, we were informed of a common diving petrel (subspecies *chathamensis*) recaptured on Whenua Hou / Codfish Island in October 2022, nearly 19 years after it was banded as an adult in November 2003, making it at least 20 years old (Johannes Fischer, *pers. comm*.). The oldest common diving petrel recorded in the French bird banding scheme was a bird of subspecies *exsul* recovered on Île Mayès, Îles Kerguelen, in February 2019, 29 years after it was banded there as a likely juvenile in April 1990 (Karine Delord & Aymeric Fromant, *pers. comm*., 29 November 2022), making it at least 29 years old. The next oldest birds in the Southern Seabird Demographic Database, Chizé, were recaptured 22 and 20 years after they were banded as adults; these three long-lived birds represent 0.09% of the 3,283 common diving petrels banded on the island, of which 2.5% reached a minimum 16 years of age (Karine Delord, *ibid*).

Compared to other petrel species, diving petrels start breeding at a young age, and have comparatively short lives. Most diving petrels on Mana Island breed at 2-years-old, and several have bred at 1-year old (Miskelly & Taylor 2007; authors, *unpubl. data*). In contrast, most genera of procellariids start breeding when four or more years old (Croxall 1981; Warham 1990; Brooke 2004), and many species have been recorded at more than 36 years of age (Table 2). The longevity of procellariids requires long-term commitment to demographic monitoring programmes to reveal their lifespans, often exceeding the working careers and funding streams of individual scientists (Ollason & Dunnet 1988; Wooller *et al*. 1989, 1992).

Table 2. Longevity records from nine genera of procellariid petrels. Birds listed with '+' ages were banded as adults or independent juveniles, and so their estimated ages are minima based on minimum ages of return for each species. ABBBS 2022 = Australian Bird & Bat Banding Scheme (https://www.environment.gov.au/cgi-bin/biodiversity/abbbs/abbbs-search.pl), accessed: 25 November 2022.

Common name	Scientific name	Max. age (years)	Reference
Northern giant petrel	*Macronectes halli*	40[1]	ABBBS 2022
Northern fulmar	*Fulmarus glacialis*	40+	G.M. Dunnet *in* Brooke 1990
Cape petrel	*Daption capense*	40+	Sagar 2022
Grey-faced petrel	*Pterodroma gouldi*	41+	Taylor 2022
Fairy prion	*Pachyptila turtur*	24+[2]	Graeme Loh, *pers. comm.*
Westland petrel	*Procellaria westlandica*	37+	Waugh & Bartle 2022
Short-tailed shearwater	*Ardenna tenuirostris*	38[3]	Szabo 2013
Manx shearwater	*Puffinus puffinus*	55+	Clark *et al*. 2004
Common diving petrel	*Pelecanoides urinatrix*	29+	Karine Delord, *pers. comm.*

[1]Banded as a chick; Amelia Cook, ABBBS, *pers. comm*. 25 November 2022.
[2]Likely an underestimate, as at least six birds from the same (initial) cohort of 86 birds were alive in 2022.
[3]ABBBS has a bird recovered 48 years after it was banded; however, as it was a skeleton/dried out corpse, its date of death is uncertain.

ACKNOWLEDGEMENTS
We thank the Department of Conservation and the Friends of Mana Island for supporting and facilitating our access to Mana Island, and are grateful to Karine Delord and Aymeric Fromant (Institut Polaire Français Paul-Émile Victor – projects 109 P.I. Christophe Barbraud, 394 P.I. Charles-André Bost, and the Zone Atelier Antarctique (CNRS-INEE)), Amelia Cook (Australian Bird & Bat Banding Scheme), Graeme Loh, and Johannes Fischer for information on long-lived petrels. This note was improved by comments received from Johannes Fischer and Craig Symes.

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Keywords: longevity, lifetime reproductive success, diving petrel, *Pelecanoides urinatrix*

Notornis, 2023, Vol. 70: 42-44
0029-4470

SHORT NOTE

Kākā (*Nestor meridionalis*) investigate and depredate kakaruai (South Island robin *Petroica australis australis*) eggs

MANAIA PEARMAIN-FENTON*
Department of Zoology, University of Otago, Dunedin, New Zealand

ANNE SCHLESSELMANN
SUSAN WALKER
Manaaki Whenua – Landcare Research, Dunedin, New Zealand

During routine nest checks as part of a research project focusing on a kakaruai (South Island robin *Petroica australis*) population inside Te Korowai o Mihiwaka/Orokonui Ecosanctuary, Aotearoa/New Zealand (14°13′51″E, 49°28′41″N), we witnessed two kākā (*Nestor meridionalis*) approach a kakaruai nest and one kākā destroy the eggs. The observation was made on 12 October 2022, roughly halfway through the kakaruai breeding season. Located approximately 20 km from Ōtepoti/Dunedin, the 307 ha fenced ecosanctuary consists of both regenerating and indigenous podocarp and broadleaf forest. Here we describe the circumstances of this observation and acknowledge that this is the first recorded case, to our knowledge, of such an interaction.

The kakaruai nest (~10 cm in diameter) was located about 1.8 m above ground on a semi-exposed platform within the trunk of a dead ponga/silver fern (*Cyathea dealbata*). The female began nest building on 9 September, and eggs were laid nine days later on 18 September, making the eggs 24 days old when our observation was made. It is worth noting that the average incubation period for kakaruai is 18 days (Powlesland 1997).

Received 21 November 2022; accepted 30 January 2023
*Correspondence: *manaia.pearmain@postgrad.otago.ac.nz*

The nest was observed from the public path about five metres away every three to four days since nest-building commenced. Flagging tape was attached to a tree adjacent to the ponga (~1 m away) when the nest was built to help with future observations. On 12 October 2022 at 1230 h, when the female left the nest, an observer (MP-F) walked directly up to the nest to inspect the eggs and check whether they had hatched. We had not realised two kākā had been in the vicinity, and when we left the nest tree to take notes from the path, they immediately proceeded to climb up to the nest. One of them inspected the contents of the nest, then held one egg in its beak and promptly crushed it open. It picked away the eggshell and manipulated the embryo for a couple of seconds, then returned the egg to the nest and climbed down the tree. The other kākā, which had been watching the whole time, then followed. A minute later, both climbed back up the nest, and the same kākā that had crushed the first egg returned and crushed the second of the two eggs. In both instances, the embryo was not eaten. After a few seconds of inspecting this second egg, both kākā left. We monitored the nest for an additional five minutes but neither kākā returned. The interaction between the kākā and the nest took less than three minutes. During this process, the male and female kakaruai remained close to the nest and observed the kākā destroy the eggs. Neither of them attempted defensive strategies to protect the nest.

It was possible that the embryos were deceased before the depredation event. One week before this observation, an uncharacteristically cold two days in combination with spring snow had caused six other kakaruai nests of a similar developmental stage to fail. On the days of 6–7 October average daily temperature was 1°C compared to the 10°C average over the month of October 2022 (National Institute of Water and Atmospheric Research [NIWA] 2022).

To our knowledge, there are only two other known observations of kākā destroying the eggs of other birds. The first was made in 1999 at Nelson Lakes National Park, where a radio-tagged female kākā preyed on a riroriro (grey warbler *Gerygone igata*) nest. The kākā removed the top section of the nest and ate two or three eggs (L. Moran *pers. comm.*, 24 October 2022). The second instance of this behaviour was made in 2002, also within an ecosanctuary (Karori; now known as Zealandia). A pair of kākā removed eggs from a Eurasian blackbird (*Turdus merula*) nest (roughly 3–4 m above ground) and dropped them only to watch them smash (Batcheler & Batcheler 2002). The same bird did this three times. The nest was located on an accessible fork of a tree and was highly conspicuous. Only in the Nelson observation was the kākā recorded eating the embryo. This kākā behaviour has also been suspected as the cause of multiple nest failures in the closely related toutouwai (North Island robin *P. longipes*) population in Zealandia (R. Shaw *pers. comm.*, 9 November 2022).

Kākā are sequential specialist foragers (O'Donnell & Rasch 1991), meaning they move between different resources throughout the year to account for seasonal differences in food availability. Their usual diet consists of wood-boring invertebrates (a major protein source being the larvae of kanuka longhorn (*Ochrocydus huttoni*), scale insects (consuming both the insect and the honeydew they produce, for example *Ultracoelostoma assimile;* Beggs & Wilson 1991), as well as seeds, nectar, fruits, and sap (Beggs & Wilson 1991). Kākā primarily feed from Podocarpaceae canopy species, including rimu (*Dacrydium cupressinum*), miro (*Prumnopitys ferruginea*), and Hall's totara (*Podocarpus laetus*). They also utilise species within the family Myrtaceae, including southern rātā (*Metrosideros umbellata*; O'Donnel & Dilks 1994). In a study focusing on a population with a similar ecosystem as Orokonui (broadleaf forest in South Westland), kākā spent most of their foraging time collecting wood-boring insects (O'Donnell & Dilks 1994). They do this only when alternative sources of protein and fat, like those found in seeds and fruit, are unavailable (Beggs & Wilson 1991). Kākā are considered more neophobic than the closely related kea (*Nestor notabilis;* Diamond & Bond 2004). Unlike kākā, opportunistic kea are also known to consume meat from sources other than invertebrates (Schwing 2010), including carrion (deer, chamois, tahr, and sheep carcasses) throughout their range, as well as prey on Hutton's shearwater (*Puffinus huttoni*; Cuthbert 2003), whio (*Hymenolaimus malacorhynchos;* Whitehead *et al*. 2008), and tokoeka (southern brown kiwi *Apteryx australis*; Checklist Committee 2022; Tansell *et al.* 2016). However, juvenile kākā have demonstrated innovation and flexibility in their explorative behaviour (Loepelt *et al.* 2016), showing higher persistence and exploratory diversity than adults.

Although our observation was only the third recorded incident, kākā likely employ these exploratory tactics more often than has been documented. Kākā spend a significant proportion of their foraging time high in trees (O'Donnell & Dilks 1994) where other bird species are likely to build nests, so it is not surprising that they would come across these novel food resources and have no choice but to give in to their explorative nature and investigate them. It is worth acknowledging that both kākā and kakaruai are thinly dispersed outside the safety of ecosanctuaries. Outside of these areas, predation webs are often dominated by introduced species (see Carpenter *et al*. 2021) as opposed to native species.

The two native parrot species in Aotearoa/New Zealand described here (those belonging to the order Psittaciformes; see Checklist Committee 2022) are unusual in their consumption of animal matter in comparison to the strictly herbivorous diets of many of the other world's parrots (Higgins 2001). The more general diets of these parrots in Aotearoa may be partly due to the different evolutionary pressures experienced in an island ecosystem lacking mammalian predators and competitors in combination with high levels of cognitive abilities and playfulness (Huber & Gajdon 2006). This observation contributes to the list of behaviours that make Aotearoa/New Zealand birds unique. In addition, it adds to our understanding of species' interactions in ecosystem restoration projects.

ACKNOWLEDGEMENTS

We would like to acknowledge the mana whenua of Te Korowai o Mihiwaka, Kati Huirapa Runaka ki Puketeraki. We want to extend our thanks to Orokonui Ecosanctuary staff, in particular, Elton Smith as well the Orokonui Knowledge Group, for allowing us to conduct our research within the beautiful sanctuary. This project was made possible through funding from the Ministry of Business and Innovation under contract C09X1805 'More Birds in the Bush' to Manaaki Whenua – Landcare Research and from the University of Otago. All nest monitoring was conducted under DOC authorisation 97675-FAU, and Animal Ethics permit AUP-22-39. Thank you to Colin Miskelly, Ron Moorhouse, Les Moran, and Rachael Shaw for directing us to and providing help with previous observations, and Jo Monks for editorial support. Lastly, I wish to acknowledge two kakaruai parents that lost their tamariki that day. Kua whetūrangitia kōrua (*return, and take your place amongst the stars along with your ancestors that adorn the sky*).

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Keywords: kākā, *Nestor meridionalis,* South Island robin, *Petroica australis,* predation, mesopredation, foraging behaviour, nesting, exploration, Orokonui, ecosanctuary

Notornis, 2023, Vol. 70: 45-48
0029-4470

SHORT NOTE

First and second breeding of Australian gull-billed tern (*Gelochelidon nilotica macrotarsa*) in New Zealand

SEAN JACQUES*
46C Theodore Street, Bluff 9814, Southland, New Zealand

GLENDA REES
10B Onslow Street, Gore 9710, New Zealand

PHIL RHODES
8 Regent Street, Heidelberg, Invercargill 9812, New Zealand

JOE BLISS
15 Oreti Street, Kingswell, Invercargill 9812, New Zealand

JOSEPH ROBERTS
137 Paterson Street, Grasmere, Invercargill 9810, New Zealand

PETE McCLELLAND
237 Kennington-Roslyn Bush Road RD2, Invercargill 9872, New Zealand

The gull-billed tern (*Gelochelidon nilotica*) is a cosmopolitan wetland species, patchily distributed across the Americas, Europe, Asia, and Australia. Seven sub-species are recognised, including nominate *nilotica* breeding sparsely through Eurasia and NW Africa, *affinis* in SE Asia, *addenda* in coastal China, *aranea* in E. USA and Caribbean islands, *vanrossemi* in S. California to W. Mexico, and *grönvoldi* in South America from Guyana to Argentina (Higgins & Davies 1996). In Australia two sub-species occur, overlapping in their ranges: *affinis* is a regular non-breeding visitor predominantly to coastal areas in the north of the country, while the widespread breeding population belong to the sub-species *macrotarsa* (Rogers *et al.* 2005). Having marked physiological, ecological, and behavioural differences from other gull-billed tern taxa (Rogers *et al*. 2005), *macrotarsa* is regarded as a full species by some authorities and was admitted to the IOC

Received 14 August 2022; accepted 29 January 2023
*Correspondence: sean.recg@googlemail.com

world bird list 9.2 as Australian tern (Gill & Donsker 2019). The taxon is considered a sub-species in the checklist of the birds of New Zealand; Australian gull-billed tern (*Gelochelidon nilotica macrotarsa*) (OSNZ checklist committee, 2022).

Gull-billed tern is a vagrant to New Zealand, with the first record being of two birds at Invercargill airfield (46°41′S, 168°31′E) in winter 1955 (McKenzie 1955). Since then, the species has occurred sporadically, with records from coastal or near-coastal locations scattered through both main islands, and from a number of inland lakes (Southey 2019). Many of these records are of multiple birds, with the largest groups seen following an influx in 2011, when up to 16 birds were present on the Manukau Harbour (37°03′S, 174°72′E), up to 15 at Lakes Forsyth (43°80′S, 172°75′E) and Ellesmere (43°77′S, 172°48′E), with numerous smaller groups around the country. Birds reaching New Zealand can stay for extended periods; one individual in the Hawkes Bay region was recorded annually between 1982 and 1996 (Southey 2019). Records to date are known only to be of *macrotarsa*; *affinis* could occur as a non-breeding straggler but is as yet unconfirmed in New Zealand (Southey 2019).

Following the 1955 record, gull-billed tern was not reported in Southland until one at Waituna lagoon (46°56′S, 168°60′E) in November 1985, with a further 14 sightings provided to the local recorder prior to the recent breeding records (P. Rhodes, *pers. comm*). Of these 14, five records were submitted to, and accepted by, the Birds New Zealand Records Appraisal Committee (RAC) (C. Miskelly, *pers. comm.*).

All but one Southland observation has come from either the New River estuary (46°46′S, 168°33′E) or the Awarua-Waituna complex (46°57′S, 168°53′E), two sites separated from one another by a narrow isthmus of agricultural land, and together forming around 21,500 ha of Ramsar designated wetland of international importance. This protected landscape is one of New Zealand's largest remaining coastal wetland complexes (DOC 2022) and provides vital refuge for a wide range of birds, from breeders including Australasian bittern (*Botaurus poiciloptilus*) to short-range migrants such as wintering southern New Zealand dotterels (*Charadrius obscurus obscurus*) and global travellers like bar-tailed godwit (*Limosa lapponica*). The area is frequently visited by birdwatchers, and co-ordinated counts of the main wader roost sites have occurred three times annually since at least 1983 (Riegen & Sagar 2020).

A roving pair of adult gull-billed terns (and on two occasions three birds) were reported by birders each year between 2015 and 2019 from a number of sites within the wetlands. Although not confirmed during this period, breeding was suspected; for example, GR observed two adults alarm calling, one showing breast staining which may have resulted from food spillage while chick rearing, at Tiwai Bridge sandspit (46°57′01″S, 168°43′35″E) in December 2018.

Re-visiting the spit on 21 December 2019, GR again observed two adult gull-billed terns, and was able to watch and photograph the pair attending a nest with clutch of three eggs (Fig. 1A). The scrape was located amongst mounded shells beside a clump of yellow flowering *Senecio*, close to a small number of nesting white-fronted terns (*Sterna striata*), one pair of Caspian terns (*Hydroprogne caspia*), and adjacent to a large southern black-backed gull (*Larus dominicanus*) colony. The record was submitted to the RAC (as Unusual Bird Report UBR 2019-094), and accepted as New Zealand's first confirmed breeding record for this species (Miskelly *et al*. 2021). Although not assigned to sub-species at the time, the birds are clearly identifiable as Australian gull-billed tern (*Gelochelidon nilotica marcrotarsa*) based on diagnostic characters (I. Southey, *pers. comm.*). These features include pale silvery-grey upperparts in adult plumage, and heavy bill with strongly decurved upper mandible (Rogers *et al*. 2005).

The nest was still active on 27 December 2019 with an adult seen sitting when PR and SJ visited to make brief observations from distance. When GR returned on 04 January 2020 however, she found the tern colony deserted except for the Caspian tern pair, and signs of heavy disturbance including tyre tracks close to the now unoccupied gull-billed tern nest location. One of the adult birds was seen hovering briefly around a kilometre from the former nest site, but it was clear that the breeding attempt had been unsuccessful. Despite searches, there have been no further reports of the species from the Tiwai Bridge sandspit to date. Terns in general are sensitive to disturbance (Wu *et al*. 2020), and gull-billed tern is no exception, with Sears noting that his research visits to an American colony (sub-species not named) over three summers affected the distribution of nests, including abandonment of parts of the site (Sears 1978).

On 24 February 2021, SJ and JB visited the New River estuary shellbanks (46°48′03″S, 168°34′37″E) to undertake the Birds New Zealand wader census. The banks, separated from the mainland by a tidal channel, cover approximately one hectare, consisting of several low islands of mounded shells and an area of saltmarsh. Breeding birds include Caspian and white-fronted tern (*c.* 30 and *c.* 4 pairs respectively in 2021), southern black-backed gull and royal spoonbill (*Platalea regia*) (authors, *pers. obs.*). Whilst counting roosting waders in strong westerly wind and light rain, the observers found an adult and dependent juvenile gull-billed tern,

and were able to make detailed observations. The record was submitted to and accepted by the RAC (as UBR 2021-022), the committee agreeing with the sub-specific identification as *macrotarsa.*

Brown scalloping in the upperparts, short wings and bill all suggested that the young bird had recently fledged. It was reluctant to fly, showed no signs of foraging for itself and begged regularly from the adult. The adult encouraged flight by making short trips around the saltmarsh and banks, landing and calling to coax the juvenile to follow, which it was seen to do several times. At one stage the adult left on a long flight down river, returning with an unidentified food item that it provided to the juvenile which had remained huddled amongst the roosting waders. The parent was defensive and wary. Despite the distance of SJ and JB from the birds, and efforts made to minimise disturbance, it circled overhead on two occasions giving a distinctive bleating alarm call. JB recorded this call using a mobile phone and uploaded the sonogram to eBird for reference along with the species checklist (eBird 2022). The begging calls of the juvenile were also clearly audible at times, a thin, mewling cry.

The weak flight behaviour of the juvenile coupled with the exposed nature of adjoining habitats and the local scarcity of, and distance to, other suitable tern breeding sites, all suggested that nesting had occurred on the shell-banks rather than the birds having dispersed from elsewhere. This site would seem to suit many of the defensive characteristics that Sears (1978) noted gull-billed terns preferred in nesting locations, most notably its isolation offering protection from disturbance and mammalian predation.

The birds were still present on 28 February 2021 (Fig. 1B) when SJ and JB returned with PM and photographer JR, with the young bird appearing more mobile and stronger on the wing than on 24 February (possibly also aided by improved weather). On several occasions the juvenile took flights around the banks with the adult protectively describing wide circles above it, alarm calling at times. The young bird was still not observed foraging for itself, and frequently begged for food. SJ returned to the site on 5 March, when there was no sign of the gull-billed terns and very few Caspian terns remained.

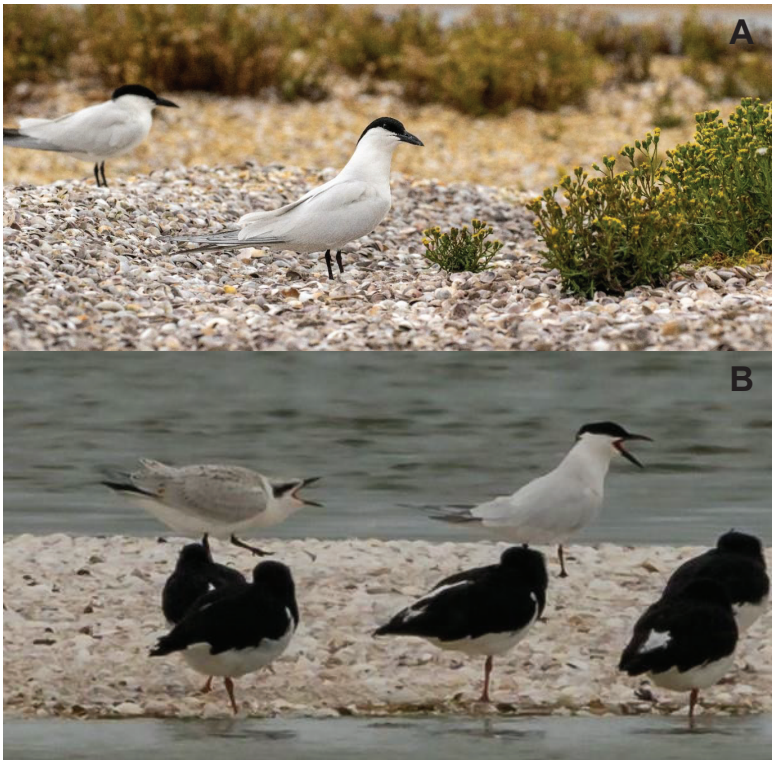

Figure 1. A) Australian gull-billed tern (*Gelochelidon nilotica macrotarsa*) breeding pair, Tiwai Bridge sandspit, Southland 21 December 2019. The nest scrape and eggs are located close to the *Senecio* clump at the right of the image. Photograph: Glenda Rees. **B)** Adult and dependent juvenile Australian gull-billed tern, New River estuary shellbanks, Invercargill 28 February 2021, South Island pied oystercatchers (*Haematopus finschi*) in the foreground. Photograph: Joseph Roberts.

The two New Zealand breeding sites described here differ from those typically used by *macrotarsa* in their core range. The Southland birds chose coastal locations, bars or banks of mounded pea gravel and shells at the edge of extensive estuarine areas. In Australia, nesting also occurs on low banks, spits, or similar features; however, these are usually inland on large and often ephemeral lakes and swamps, and are rarely on near-coastal wetlands (Higgins & Davies 1996).

This ability to exploit new opportunities in the local absence of preferred habitat may be a function of the adaptability of this taxon. Australian gull-billed tern has adopted a high degree of plasticity in breeding and moult strategies to cope with an unpredictable climate (Rogers *et al.* 2005). In Australia it can be strongly nomadic, though there remains a broadly latitudinal and seasonal pattern to movements. Most breeding occurs in the south during September–January, and most of the population winters in the north; however, *macrotarsa,* in common with many Australian waterbirds, can breed at any time of the year if water levels are suitable (Higgins & Davies 1996; Rogers *et al*. 2005).

By contrast, gull-billed tern taxa elsewhere in the world include long-distant migrant populations (*affinis* for example), with tightly scheduled annual cycles (Rogers *et al*. 2005). Given the opportunism shown already in terms of choice of nesting habitat, it seems reasonable to speculate that were Australian gull-billed tern to establish as a regular breeding bird in New Zealand, some adaptation of movement patterns, breeding and perhaps moult strategies might be expected in response to the more strictly seasonal climate of this country.

Of additional note over the course of Southland *macrotarsa* gull-billed tern sightings is an observation of diet. Two birds that were hawking over the Tiwai Bridge sandspit on 20 April 2019 were seen to catch a number of common redpoll (*Acanthis flammea*) amongst a large flock of that species (P. Rhodes *pers. obs.*). This foraging behaviour matches that reported in Canterbury and further demonstrates the ability of this broadly carnivorous species to exploit novel food sources (Crocker 2014).

A large white-fronted tern colony formed on the New River estuary shellbanks late in 2021 (SJ, *pers. obs.)*. Despite searches, however, no further sightings of gull-billed tern were made here or reported from elsewhere in Southland over the course of the 2021/22 summer breeding season.

ACKNOWLEDGEMENTS

Many thanks to the birders and photographers whose diligent observations and commitment to recording have allowed these events to be documented. Comments received on a draft of this note from Ian Southey and an anonymous reviewer were greatly appreciated.

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Keywords: Australian gull-billed tern, *Gelochelidon nilotica macrotarsa*, Southland, breeding, New River estuary, Awarua-Waituna wetlands

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NOTORNIS
Journal of the Ornithological Society of New Zealand Inc.
Volume 70, Part 1, March 2023

CONTENTS