Conservation genetics of the Forbes' parakeet (*Cyanoramphus forbesi*) on Mangere Island, Chatham Islands

Chi-hang Chan, Kaye N. Ballantyne, Hilary Aikman,
Charles H. Daugherty and Geoffrey K. Chambers

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Assignment of Mangere Island and Rangatira Island parakeets using microsatellites, mtDNA and morphological markers 20

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Chi-hang Chan[1], Kaye N. Ballantyne[1], Hilary Aikman[2], Charles H. Daugherty[1] and Geoffrey K. Chambers[1]

[1] Institute for Molecular Systematics, School of Biological Sciences, Victoria University of Wellington, PO Box 600, Wellington 6140, New Zealand
Email: chihang_chan@yahoo.co.nz

[2] Wellington Conservancy, Department of Conservation, PO Box 5086, Lambton Quay, Wellington 6145, New Zealand

ABSTRACT

Genetic introgression from the Chatham Island red-crowned parakeet (*Cyanoramphus novaezelandiae chathamensis*) is currently the major threat to the survival of the endangered Forbes' parakeet (*C. forbesi*) on Mangere Island, in the Chatham Islands group of New Zealand. The culling of hybrids and Chatham Island red-crowned parakeets has been used in the past to control the interspecific hybridisation on Mangere Island, but the effectiveness of this practice in saving the Forbes' parakeet has not been assessed. Through the use of microchondrial and microsatellite genetic markers, we found that c. 81% of parakeets on Mangere Island have a history of hybridisation and over half of the birds with Forbes' parakeet morphology may be hybrids. Based on the genetic data obtained, we suggest that culling is no longer an effective method for controlling hybrids in the present population and that alternative management strategies should be considered.

Keywords: Chatham Islands, *Cyanoramphus forbesi*, *Cyanoramphus novaezelandiae chathamensis*, parakeets, hybridisation, microsatellite, mitochondrial DNA, crown plumage morphology

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1. Background

1.1 GENETIC INTROGRESSION THROUGH INTERSPECIFIC HYBRIDISATION

Genetic introgression, the introduction of new genetic variation from a different population or species, can lead to the ultimate extinction of a population or species by genetic assimilation (Rhymer & Simberloff 1996; Huxel 1999; Wolf et al. 2001). Conversely, the introgression of genes through hybridisation can be a source of genetic diversity that simulates diversification and rapid adaptive evolution of populations (Anderson & Stebbins 1954; Lewontin & Birch 1966; Dowling & Secor 1997). Therefore, careful considerations must be given to the management of hybridising populations.

Hybridisation is particularly common in bird species, with an estimated 9.2% of all known birds having bred with another species to produce hybrid offspring (Grant & Grant 1992). Some examples of New Zealand birds that hybridise include mallard (*Anas platyrhynchos*) and grey duck (*A. superciliosa*) (Haddon 1984, 1998; Gillespie 1985; Hitchmough et al. 1990), black stilt (*Himantopus novaezelandiae*) and pied stilt (*H. himantopus leucocephalus*) (Chambers & MacAvoy 1999; Greene 1999), and black robin (*Petroica traversi*) and tomtit (*P. macrocephala chathamensis*) (Ma & Lambert 1997). In this paper, we discuss the implications of genetic introgression to the survival of Forbes' parakeet (*Cyanoramphus forbesi*) and suggest future management directions for this species based on our recent genetic studies using mitochondrial and microsatellite DNA markers.

1.2 FORBES' PARAKEET POPULATION STATUS

Forbes' parakeet (*Cyanoramphus forbesi*) is classified by the Department of Conservation (DOC) as a Nationally Endangered parrot, with the qualifiers CD (Conservation Dependent), RC (Recovering), HI (Human Induced) and OL (One Location) (Hitchmough 2002). It is confined to Mangere and Little Mangere Islands in the Chatham Islands group. In contrast, the Chatham Island red-crowned parakeet (*C. novaezelandiae chathamensis*), which is classified as Range Restricted, with the qualifiers ST (Stable) and HI (Human Induced) (Hitchmough 2002), can be found on the main Chatham Island (Rekohu), Pitt Island, Rangatira Island (also known as South-East Island), Mangere and Little Mangere Islands (Fig. 1).

About ten breeding Forbes' parakeet pairs were observed on Mangere Island by Taylor (1975). He also reported differences in feeding habits and territoriality between Forbes' parakeets and Chatham Island red-crowned parakeets: Forbes' parakeets seemed to be better adapted to forest habitat than to open vegetation, while Chatham Island red-crowned parakeets were seen to use habitats of scattered patches of grass, scrub and herbs more frequently. Forbes' parakeets are morphologically identified by a yellow crown with a red frontal band that

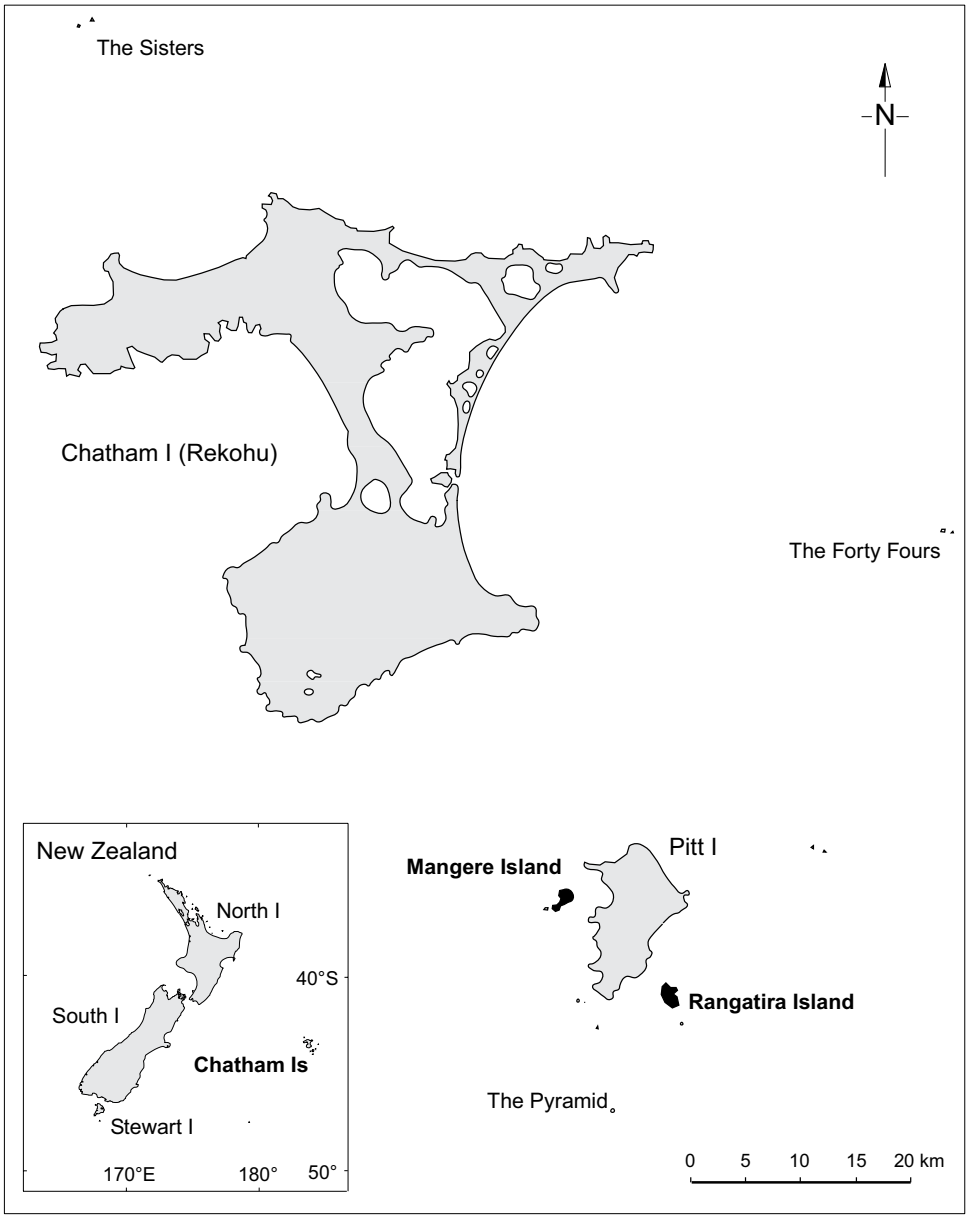

Figure 1. Map of the Chatham Islands group of New Zealand showing the location of the sampling sites: Mangere and Rangatira Islands.

does not extend to the eyes. In contrast, Chatham Island red-crowned parakeets have uniform red plumage on the crown with a red band extending to the eyes. Hybrids between the two species show a range of crown colourations intermediate between the two parental species (Nixon 1982).

Based on morphological identification (Nixon 1982), the Mangere Island parakeet population is made up of a mixture of Forbes' parakeets, Chatham Island red-crowned parakeets and hybrids, whereas the Rangatira Island population consists solely of Chatham Island red-crowned parakeets. The culling of hybrids and Chatham Island red-crowned parakeets on Mangere Island has been considered an urgent and essential measure to ensure the survival of Forbes' parakeets (Greene 2000). Hybrids were identified by crown morphology alone, using a scale developed by Nixon (1982) and Greene (2000). However, there has been no evidence to suggest that morphological features alone are a sufficient identifier of hybridisation. Consequently, it is unknown whether these culling practices are effective.

1.3 PAST GENETIC STUDIES OF FORBES' PARAKEET

Based on allozyme electrophoresis data, Triggs & Daugherty (1996) suggested the elevation of Forbes' parakeet from being a sub-species of yellow-crowned parakeet (*C. auriceps forbesi*) to full species status (*C. forbesi*). Further work with mitochondrial DNA sequences (Boon et al. 2001) supported the taxonomic arrangement as proposed by Triggs & Daugherty (1996) and identified three distinct groups of DNA sequences (haplogroups) within the control region of the maternally inherited mitochondria in morphological Forbes' parakeets on Mangere Island. Phylogenetically, haplogroups 1 and 2 (HG1 and HG2 in Boon et al. 2001) sit respectively within and basal to the red-crowned parakeet clade. These were interpreted as cryptic hybrid birds in the Mangere Island population having red-crowned maternal ancestry (Boon et al. 2001). In contrast, haplogroup 3 (HG3 in Boon et al. 2001) sits basal to all other New Zealand parakeets, representing the ancestral Forbes' parakeet maternal lineage. The identification of the red-crowned related lineages represented by haplogroups 1 and 2 clearly suggested that interspecific hybridisation has occurred at the genetic level in the Mangere Island parakeet population.

1.4 NUCLEAR DNA MARKERS

Although Boon et al. (2001) have firmly established that genetic introgression has occurred from red-crowned parakeets into Forbes' parakeets, mitochondrial DNA (being maternally inherited) does not fully indicate the extent of this introgression. Instead, a bi-parentally inherited nuclear DNA marker, such as microsatellite DNA, is needed to assess the full extent of hybridisation in Forbes' parakeets.

Microsatellites are defined (following Chambers & MacAvoy 2000) as short segments of two to six nucleotides, that are repeated in more or less uniform tracts or arrays, with a minimum total length of eight nucleotides. They are widespread but non-randomly distributed in genomes (see Li et al. 2002, 2004). Their polymorphisms can be affected by their location and the presence of other linked genes (Slatkin 1995a; Thuillet et al. 2004). Repeat number mutations in microsatellite loci are considered as neutral mutations conferring no advantage or disadvantage with respect to natural selection (Tachida & Iizuka 1992; Michalakis & Veuille 1996; Schlötterer 2000), making them ideal nuclear DNA markers for population studies. Microsatellite DNA analysis is widely used in population genetics, especially in studies of population structure, breeding behaviour and kinship analysis (see Ellegren 1992; Chambers & MacAvoy 2000; Blouin 2003), due to the ease of the Polymerase Chain Reaction (PCR) (Saiki et al. 1985; Mullis & Faloona 1987) techniques involved. PCR allows large quantities of specific DNA product to be amplified from a small amount of DNA template (see Arnheim et al. 1990) such as feathers, thus allowing the use of non-invasive sampling methods that cause minimal disturbance to the organism (Taberlet et al. 1999).

1.5 A GENETIC AND MORPHOLOGICAL STUDY IN PARAKEET HYBRIDISATION

We have successfully isolated nine microsatellite DNA loci from Forbes' parakeet (Chan et al. 2005), and have also developed a rapid and cost-effective system for screening parakeet mitochondrial DNA haplogroups on Mangere Island (Ballantyne et al. 2004). Using these new genetic techniques and crown morphology data, in a recent study (Chan et al. 2006) we investigated in depth the status and effects of interspecific hybridisation in the Mangere Island parakeet population.

2. Objectives

Building on the framework of a recently completed genetic and morphological analysis of the Forbes' parakeet population on Mangere Island (Chan et al. 2006), we summarise and discuss the implications of these findings for future management strategies to save the Forbes' parakeet from extinction.

3. Methods

3.1 SAMPLES

During the field seasons between 1999 and 2003, parakeet blood and/or feather samples were collected from individual birds on Mangere Island ($n = 250$) and Rangatira Island ($n = 35$). DNA was extracted from the samples for the molecular analyses (Chan et al. 2005). Microsatellite genotype data were collected from all samples. However, mitochondrial DNA data were only collected from 203 Mangere samples and 34 Rangatira samples due to difficulties in amplifying the mitochondrial control region in the remaining samples. Among these genetically analysed samples, morphological data were also available for 169 Mangere parakeets and 34 Rangatira parakeets.

3.2 CLASSIFICATION

To distinguish between morphological, mitochondrial control region DNA haplogroup and microsatellite DNA categories, the prefixes MP (morphology), MT (mitochondrial DNA) and MS (microsatellite DNA) are used before numbers in each class.

On the morphological scale, MP1 denotes a Forbes' parakeet, MP5 denotes a Chatham Island red-crowned parakeet and MP2–MP4 denote hybrids, with higher numbers indicating increasing amounts of red feathers in the crown (after Nixon 1982).

For mitochondrial control region DNA haplogroups, the original HG prefixes of Boon et al. (2001) have been substituted by MT prefixes. Thus, the ancestral Forbes' parakeet mitochondrial DNA lineage is MT3, the Chatham Island red-crowned parakeet lineage is MT4, and hybrids with red-crowned parakeet maternal ancestries are MT1 (within red-crowned parakeet clade) and MT2 (basal to red-crowned parakeet clade).

Microsatellite DNA assignments for Forbes' parakeets, hybrids (or unable to assign) and Chatham Island red-crowned parakeets are denoted by MS1, MS2 and MS3, respectively (after Chan et al. 2006).

Using this three-part classification system, a pure Forbes' parakeet would be designated 'MP1, MT3, MS1' and a pure Chatham Island red-crowned parakeet would be 'MP5, MT4, MS3'. All other combinations are considered to be hybrids, with the exception of a proportion of birds that could not be assigned with confidence by the microsatellite tests.

3.3 MORPHOLOGICAL IDENTIFICATION

The parakeets sampled were classified morphologically on a scale of MP1–MP5 based on crown plumage patterns as explained above, and as described in Nixon (1982) and Greene (2000). The classification was done for 169 Mangere Island and 34 Rangatira Island parakeet samples.

3.4 SCREENING FOR MITOCHONDRIAL CONTROL REGION HAPLOTYPES

The method developed by Ballantyne et al. (2004) was used to score the parakeet samples for mitochondrial control region haplotypes. To assign an individual parakeet sample to its haplogroup, the mitochondrial control region was PCR amplified from DNA samples and the products were digested with the restriction enzymes *Cla*I, *Hae*III, *Hin*dIII or *Rca*I. The resulting DNA fragments were electrophoretically separated on an agarose gel and haplogroups were scored based on the banding patterns observed on the gels. A total of 203 Mangere Island birds and 34 Rangatira Island birds were successfully scored using this method.

3.5 MICROSATELLITE SCORING AND ANALYSES

All 250 parakeet DNA samples from Mangere Island and 35 samples from Rangatira Island were screened for allele size variations at six polymorphic microsatellite loci (*Cfor0809*, *Cfor1415*, *Cfor1617*, *Cfor2021*, *Cfor2829* and *Cfor3031*) (Chan et al. 2005). Three other loci that were isolated from the same genomic library screening experiments (*Cfor1819*, *Cfor2223* and *Cfor2627*) were not used in further analyses: *Cfor1819* showed size homoplasy (some alleles exhibit different repetitive motifs but of the same size) in the parakeet populations; *Cfor2223* was monomorphic (no detectable size variations between individuals); and *Cfor2627* had at least one allele that did not amplify.

Assignment tests were run using the software NewHybrids (version 1.1b3) (Anderson & Thompson 2002) as described in Chan et al. (2006). These tests use a Bayesian algorithm to differentiate between individuals in a population based on their microsatellite genotypes (see Anderson & Thompson 2002). Since the Mangere Island population is already a mixed population, it is difficult to define a Forbes' parakeet genotype. However, parakeets in the Rangatira Island population can be used to define Chatham Island red-crowned parakeet genotypes. Thus, in these tests, Forbes' parakeets can be taken as those birds that have genotypes most distant from those of Chatham Island red-crowned parakeets. The assignment tests calculate the probabilities of being a parental individual, *P*(Forbes') and *P*(red-crowned). Samples with *P*(Forbes')$\geq$0.95 were scored as MS1, those with *P*(red-crowned)$\geq$0.95 were scored as MS3, and all others were scored as MS2. Using six loci, this type of assignment test would typically result in 70%–97% correct assignments (Cornuet et al. 1999; Berry et al. 2004). More robust assignments could possibly be obtained by using a larger number of loci. However, this objective is limited by the technical difficulties involved in isolating a large number of microsatellite loci from parrots (Hughes et al. 1998; Robertson et al. 2000; Russello et al. 2001, 2005; Caparroz et al. 2003; Sainsbury et al. 2004), which may be due to a generally low abundance of microsatellites in birds (Primmer et al. 1997).

We also analysed microsatellite genetic distances between individuals based on the proportion of shared alleles statistic (Bowcock et al. 1994). A genetic distance matrix was constructed using the Microsatellite Analyser (MSA) software (version M3.15) (Dieringer & Schlötterer 2002). The matrix was analysed through Principal Coordinates Analysis (Gower 1966) by the PCO software (Anderson 2003), which plots the distances over a two-dimensional area.

Population genetic differentiation between the Mangere Island and Rangatira Island populations was also calculated from the microsatellite genotype data. Estimators of F_{ST} (Weir & Cockerham 1984) and R_{ST} (Slatkin 1995b) were estimated using MSA software and the GENEPOP software (version 3.4) (Raymond & Rousset 1995) respectively. The inbreeding coefficient F_{IS} was also calculated using the MSA software. Genetic differentiation between the populations was assessed by Analysis of Molecular Variance (AMOVA) (Excoffier et al. 1992) as implemented in the GeneticStudio software (version 2.01) (Dyer & Sork 2001).

4. Results

4.1 HYBRIDISATION STATUS IN FORBES' PARAKEET

A large majority ($n = 136$; 80%) of the 169 Mangere Island parakeets with available data for crown colouration had Forbes' parakeet crown morphology (MP1), 10 birds (6%) showed MP2 morphotype, 11 birds (7%) had MP3 morphotype, 9 birds (5%) had MP4 crowns, and only 3 birds (2%) appeared as typical Chatham Island red-crowned parakeets (MP5). In contrast, all the Rangatira Island birds ($n = 34$) were recorded as having Chatham Island red-crowned parakeet morphology (MP5).

Among 203 samples screened for mitochondrial control region haplotypes from Mangere Island, 136 (67%) had the ancestral Forbes' parakeet haplotype (MT3), 22 (11%) had the ancestral Chatham Island red-crowned parakeet haplotype (MT4), and 26 (13%) and 19 (9%) had MT1 and MT2 haplotypes, respectively (see Appendix 1 for full dataset). Among 34 Rangatira Island samples screened, 30 (88%) of these parakeets had the ancestral Chatham Island red-crowned parakeet haplotype (MT4) and 4 (12%) had the haplotype MT2.

Using the criteria set by Chan et al. (2006) described above, the NewHybrids assignment tests assigned 67 of the 250 Mangere Island parakeets (27%) as Forbes' parakeets (MS1), 12 birds (5%) as Chatham Island red-crowned parakeets (MS3), and 171 birds (68%) as hybrids or unassigned (MS2). In the Rangatira Island population, 13 parakeets (37%) were assigned as Chatham Island red-crowned parakeets (MS3) and 22 were assigned as hybrids or unassigned (MS2; 63%).

Combining these data, totals of 169 Mangere Island parakeets and 34 Rangatira Island parakeets could be scored with respect to hybridisation status (Appendix 1). On Mangere Island, 30 parakeets were assigned as Forbes' parakeets (18%), meeting the criteria set by all genetic and morphological tests described above, 2 parakeets were assigned as Chatham Island red-crowned parakeets (1%), and 137 parakeets were hybrids or unassigned (81%). The Rangatira Island population sampled was made up of 12 Chatham Island red-crowned parakeets (35%) and 22 hybrids or unassigned (65%).

A Principal Coordinates Analysis plot of microsatellite genetic distances between individuals showed a large hybrid swarm with intermediate microsatellite genotypes and fairly well-separated but diffuse parental groups (Chan et al. 2006). Mapping NewHybrids, mitochondrial DNA and morphological assignments on this plot revealed that the Chatham Island red-crowned parakeets formed a more closely associated cluster than the Forbes' parakeets. This situation strongly suggests that Forbes' parakeets have hybridised extensively with Chatham Island red-crowned parakeets in the past.

A moderate level of genetic differentiation between the Mangere Island and Rangatira Island populations was indicated by $F_{ST} = 0.12$, $R_{ST} = 0.20$ and a molecular variance of 0.18 (AMOVA: $P = 0.01$). This suggested that there are genuine genetic differences between the two populations. A moderate level of inbreeding in the Mangere Island population was also suggested by $F_{IS} = 0.15$.

4.2 RELAXING NEWHYBRIDS ASSIGNMENT CRITERIA

Using the *P*(red-crowned)≥0.95 criteria set by Chan et al. (2006), 18 of the 30 MT4 parakeets sampled on Rangatira Island were assigned as hybrids. These 18 birds had *P*(red-crowned) assignment scores ranging from 0.17 to 0.94; among them, 11 (61%) had *P*(red-crowned)≥0.75. If birds with *P*(red-crowned)≥0.75 are recognised as Chatham Island red-crowned parakeets, then 23 birds (68% of the sampled population) on Rangatira Island would fall into this category.

Similarly, if the cut-off point between Forbes' parakeets and hybrids for microsatellite assignments is changed to *P*(Forbes')≥0.75, then 24 (18%) of the birds originally classified as hybrids in the Mangere Island samples are recognised as Forbes' parakeets. The Mangere Island population composition changes to 32% Forbes' parakeets, 67% hybrids or unassigned, and 1% Chatham Island red-crowned parakeets. Parakeets classified as hybrids or unassigned still dominate the Mangere Island population under this cut-off level.

4.3 CROWN MORPHOLOGY AND UNDERLYING GENETICS

The majority (80%) of birds sampled from Mangere Island showed Forbes' parakeet crown morphology. However, 29% of these morphological Forbes' parakeets did not descend from an MT3 Forbes' parakeet maternal lineage and 71% were not classified as MS1 by microsatellite DNA assignments (Fig. 2). This suggests that Forbes' parakeet morphology MP1 is only loosely correlated with the underlying genetic makeup of the parakeets and that cryptic hybrids (hybrids that have Forbes' parakeet morphology) are common.

In contrast, all three morphological Chatham Island red-crowned parakeets caught on Mangere Island were assigned either as hybrids (or unassigned) or Chatham Island red-crowned parakeets. Two of these birds had *P*(Forbes')≤0.10, and the remainder had *P*(Forbes')=0.51 in microsatellite assignment tests. None of the MP4 birds caught qualified by genetic criteria for classification as a Forbes' parakeet, and only 2 out of 12 MP3 birds captured qualified as Forbes' parakeets under genetic criteria. This suggested that extra red feathers in the crown is a reasonably good indicator of hybridisation history.

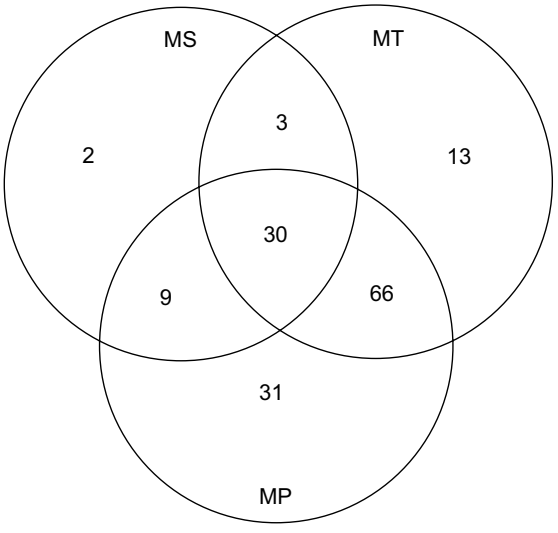

Figure 2. A breakdown of 154 Mangere Island parakeets sampled, showing Forbes' parakeet (*Cyanoramphus forbesi*) assignments at one or more of the variables. The MS circle includes birds that were assigned as Forbes' parakeet (MS1) by microsatellites, the MT circle includes birds that have the ancestral Forbes' parakeet mitochondrial control region haplotype (MT3), and the MP circle includes birds that show Forbes' parakeet crown plumage (MP1).

5. Discussion

5.1 COMPOSITION OF THE MANGERE ISLAND PARAKEET POPULATION

To supplement the previous identification scheme based on morphological features (Nixon 1982), a new system has been developed using nuclear and mitochondrial genetic markers and crown morphology to identify Forbes' parakeets, Chatham Island red-crowned parakeets and hybrids.

Under this system, a bird needs to satisfy three criteria to be considered a Forbes' parakeet:

- Assignment as a Forbes' parakeet using microsatellite markers in the NewHybrids assignment test (MS1) (Chan et al. 2006)
- Possession of a mitochondrial control region haplotype 3 (MT3) (Boon et al. 2001)
- Possession of a clear Forbes' parakeet crown morphology (MP1) (Nixon 1982)

Any bird that does not meet all these criteria is likely to have hybridisation in its ancestry.

The Forbes' parakeet crown morphology (MP1) and mitochondrial lineage (MT3) remained the dominant types in Mangere Island parakeets, but not all morphological Forbes' parakeets had an MT3 mitochondrial DNA lineage and vice versa (Fig. 2). By adding in the microsatellite assignment data, it was clearly shown that interspecific genetic introgression was widespread. Undoubtedly, this population is primarily made up of cryptic hybrids that look like Forbes' parakeets.

5.2 THE RANGATIRA ISLAND PARAKEET POPULATION

The Rangatira Island population, in contrast, has maintained much of its original Chatham Island red-crowned parakeet genetic integrity. The existence of MT2 parakeets with Chatham Island red-crowned parakeet morphology on Rangatira Island (Ballantyne et al. 2004) and a number of hybrid microsatellite assignments in this population (Appendix 1) raises minor concerns that genetic introgression from Forbes' parakeets to the Rangatira Island population is possible. Further investigation is required to identify the origin of MT2 parakeets in this population, so that it can be determined whether the MT2 parakeets have been historically part of this Chatham Island red-crowned parakeet population or have migrated from Mangere Island and are thus hybrids.

5.3 EFFECTS OF CULLING HYBRIDS

In the past, culling of hybrids and Chatham Island red-crowned parakeets was carried out to prevent hybridisation on Mangere Island by eliminating opportunities for Forbes' parakeets to form interspecific pairs (Greene 2000). In light of the current genetic data, we can now examine whether this practice achieved its purpose and whether this is a solution for the problem in the present population.

It is unrealistic to genetically test every parakeet on Mangere Island. Therefore, culling must rely solely on morphological features to identify the hybrid status of the birds. Very few obvious morphological hybrids and Chatham Island red-crowned parakeets (MP3–MP5) were collected from Mangere Island for this genetic study, suggesting that past culling had effectively eliminated birds with more red feathers in the crown than an 'ideal' (MP1) Forbes' parakeet morphotype. Our genetic tests confirmed that extra red feathers is a good marker for hybridisation; therefore, past culling has been quite successful in reducing the number of hybrid individuals. However, this culling practice totally failed to eliminate cryptic hybrids (those that have a Forbes' parakeet morphology), which now form the majority of the present population.

By eliminating morphological hybrids, the Forbes' parakeet morphotype MP1 is favoured. So in a real sense, the practice of culling selects for the Forbes' parakeet appearance, regardless of the actual genetic makeup underlying this morphotype. Under this regime, any hybrid progeny that show Forbes' parakeet morphology will have a selective advantage over hybrids showing other morphotypes. Therefore, culling can be viewed as applying a selective pressure against any alleles in loci related to crown morphology determination in the population that do not code for Forbes' parakeet crown morphology, but having very little effect on other loci. In view of these factors, morphologically based culling encourages cryptic hybrids to prosper rather than stopping further hybridisation. Further, considering the current low proportion of MP2–MP5 parakeets in the samples, we doubt whether culling is still an economically effective practice to control hybridisation on Mangere Island.

5.4 MANAGEMENT OF FORBES' PARAKEETS

There are two main clear objectives in conserving the Forbes' parakeet: to stop further hybridisation and to restore the original Forbes' parakeet. Considering the already extensive hybridisation on Mangere Island and the lack of genetically well-defined 'pure' Forbes' parakeets, restoring the original Forbes' parakeet would be a very difficult task. Moreover, as hybridisation occurred naturally between the two species for many generations, it is likely that every parakeet on Mangere Island has some greater or lesser hybridisation history. Therefore, it is reasonable to accept that hybridisation is a fact of life and forms part of the natural history of Forbes' parakeet.

Efforts in saving the Forbes' parakeet will, therefore, be more effective if concentrated in preventing further hybridisation. Taylor (1975) suggested that the two parental parakeet species on Mangere Island had different habitat

preferences, with Forbes' parakeets favouring forest habitats. Therefore, the current reforestation of Mangere Island would benefit Forbes' parakeet in the long term and would encourage breeding between Forbes' parakeets in forested parts of the island.

Eliminating existing hybrids in the population (over 50% of the population) carries a significant risk to the survival of the population itself. The negative impact caused by the resultant population crash and subsequent inbreeding would most likely outweigh the benefits to be gained by the elimination of hybrids to preserve the genetic integrity of Forbes' parakeets. However, immigration of Chatham Island red-crowned parakeets from Pitt Island and Rangatira Island must be controlled to prevent further genetic introgression into the Mangere Island population.

Forbes' parakeet currently exists as a single population on Mangere Island. This population is vulnerable to environmental impacts on Mangere Island. Therefore, an 'insurance' population should be set up elsewhere to lower the risk of extinction of Forbes' parakeet in case any natural disasters strike Mangere Island. Any newly founded population should, however, only include genetically tested Forbes' parakeets as founders and should be sufficiently large to preserve genetic diversity.

Our genetic testing of the Mangere Island parakeet population suggested that Forbes' parakeet has already received substantial genetic introgression from Chatham Island red-crowned parakeet. Genetically, Forbes' parakeet is still highly vulnerable to extinction by genetic assimilation. The continued survival of Forbes' parakeet will rely heavily both on population management and genetic management of hybridisation in this species.

6. Recommendations

Considering genetic implications and practical limitations, we recommend consideration of the following strategies in order to conserve the genetic integrity of Forbes' parakeet:

- Prevent further genetic introgression from Chatham Island red-crowned parakeets by careful monitoring and the removal of new immigrants
- Found new Forbes' parakeet populations using genetically tested Forbes' parakeets as founders
- Monitor the dynamics of change in the genetic makeup of the Mangere Island population by periodic genetic testing of 50 random samples from the population every 5 years
- Redirect resources invested in culling of hybrids to population monitoring or reforestation of Mangere Island

7. Acknowledgements

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Appendix 1

ASSIGNMENT OF MANGERE ISLAND AND RANGATIRA ISLAND PARAKEETS USING MICROSATELLITES, mtDNA AND MORPHOLOGICAL MARKERS

Birds were assigned using microsatellite allele frequencies, mitochondrial control region haplotype and crown plumage variation. The NewHybrids Bayesian assignment test was used to determine the probabilities of being a Forbes' parakeet (*Cyanoramphus forbesi*) (*P*(FB)), Chatham Island red-crowned parakeet (*C. novaezelandiae chathamensis*) (*P*(RC)), F_1 hybrid ($P(F_1)$) and F_2 hybrid ($P(F_2)$). In the overall assignment, F, H, R, – and ? represent Forbes' parakeets, hybrids, Chatham Island red-crowned parakeets, data not available and assignment not made due to insufficient data, respectively.

TABLE A1.1. MANGERE ISLAND POPULATION OF PARAKEETS.

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
	BR-G	0.5752	0.1693	0.0141	0.2414	MS2	–	–	?
	BW-G	0.9841	0.0000	0.0001	0.0158	MS1	MT3	MP1	F
	G-BG	0.9705	0.0060	0.0008	0.0227	MS1	MT4	MP1	H
	G-BO	0.9663	0.0081	0.0013	0.0243	MS1	MT3	MP1	F
	G-BR	0.9588	0.0103	0.0013	0.0296	MS1	MT3	MP1	F
	G-BW	0.7247	0.1101	0.0171	0.1481	MS2	MT1	MP1	H
	G-BY	0.9018	0.0140	0.0029	0.0813	MS2	MT3	MP1	H
	G-GW	0.8286	0.0540	0.0113	0.1061	MS2	MT2	MP1	H
	G-OW	0.0235	0.8580	0.0054	0.1131	MS2	–	–	?
	GO-W	0.9649	0.0078	0.0010	0.0264	MS1	–	–	?
	G-RB	0.9018	0.0140	0.0029	0.0813	MS2	MT3	MP1	H
	G-RG	0.8590	0.0359	0.0046	0.1006	MS2	MT3	MP1	H
	G-RO	0.9018	0.0140	0.0029	0.0813	MS2	MT3	MP1	H
	G-RW	0.0058	0.9687	0.0004	0.0251	MS3	MT1	MP1	H
	G-RY	0.9647	0.0088	0.0014	0.0251	MS1	MT3	MP1	F
	G-WB	0.8129	0.0460	0.0087	0.1324	MS2	MT3	MP1	H
	G-WG	0.8129	0.0460	0.0087	0.1324	MS2	MT3	MP1	H
	GW-G	0.0192	0.8163	0.0064	0.1582	MS2	MT3	MP1	H
	G-WO	0.0316	0.7513	0.0112	0.2059	MS2	MT3	MP1	H
	G-WR	0.9649	0.0078	0.0010	0.0264	MS1	–	–	?
	GW-W	0.9588	0.0103	0.0013	0.0296	MS1	MT3	MP1	F
	G-WY	0.0235	0.8580	0.0054	0.1131	MS2	MT1	MP1	H
	G-YR	0.0319	0.8126	0.0098	0.1457	MS2	MT3	MP1	H
	OW-G	0.6494	0.1747	0.0154	0.1606	MS2	MT4	MP1	H
	OY-G	0.9773	0.0063	0.0007	0.0158	MS1	MT3	MP1	F
	RB-G	0.0319	0.8126	0.0098	0.1457	MS2	MT2	MP1	H
	RG-G	0.9790	0.0063	0.0006	0.0141	MS1	MT3	MP1	F

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Table A1.1—continued

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
	RO-G	0.8590	0.0359	0.0046	0.1006	MS2	MT3	MP1	H
	RW-G	0.9588	0.0103	0.0013	0.0296	MS1	–	–	?
	RW-W	0.9588	0.0103	0.0013	0.0296	MS1	MT2	MP1	H
	RY-G	0.0199	0.7732	0.0218	0.1851	MS2	MT2	MP1	H
	WB-G	0.3381	0.4470	0.0072	0.2077	MS2	MT1	MP1	H
	WG-G	0.6858	0.1518	0.0145	0.1479	MS2	MT4	MP1	H
	WO-G	0.9841	0.0000	0.0001	0.0158	MS1	MT3	MP1	F
	WR-G	0.9563	0.0116	0.0014	0.0306	MS1	MT3	MP1	F
	W-RW	0.0302	0.8162	0.0052	0.1484	MS2	MT3	MP1	H
	W-WB	0.9590	0.0099	0.0016	0.0295	MS1	MT3	MP1	F
	W-WR	0.0077	0.9179	0.0023	0.0721	MS2	–	–	?
	WY-G	0.3381	0.4470	0.0072	0.2077	MS2	MT1	–	?
	YW-G	0.1174	0.6166	0.0251	0.2409	MS2	MT1	–	?
	Y-YG	0.0055	0.9892	0.0001	0.0052	MS3	MT4	–	?
D171508	GG-M	0.9588	0.0103	0.0013	0.0296	MS1	MT2	MP2	H
D171511	BW-M	0.2206	0.5455	0.0151	0.2187	MS2	MT1	MP1	H
D171514	M-RW	0.9702	0.0001	0.0001	0.0296	MS1	MT3	MP1	F
D171515	M-RB	0.4117	0.1852	0.0570	0.3461	MS2	MT2	MP2	H
D171516	M-RY	0.9781	0.0061	0.0006	0.0152	MS1	MT2	MP1	H
D171517	M-RG	0.8062	0.0409	0.0032	0.1497	MS2	MT3	MP1	H
D171518	M-RO	0.8463	0.0285	0.0069	0.1183	MS2	MT4	MP1	H
D171519	M-WR	0.8591	0.0376	0.0055	0.0978	MS2	MT1	MP1	H
D171520	M-WB	0.4090	0.3450	0.0097	0.2363	MS2	MT3	MP1	H
D172001	M-WY	0.2668	0.4303	0.0313	0.2717	MS2	MT3	MP1	H
D172002	M-WG	0.9744	0.0000	0.0001	0.0255	MS1	–	–	?
D172003	M-WO	0.2738	0.4898	0.0102	0.2262	MS2	–	–	?
D172005	M-BW	0.8871	0.0267	0.0074	0.0788	MS2	MT1	MP1	H
D172006	M-BY	0.4294	0.3379	0.0209	0.2118	MS2	–	–	?
D172007	M-YR	0.0049	0.9517	0.0001	0.0432	MS3	MT3	MP3	H
D172008	M-YG	0.3955	0.2768	0.0114	0.3163	MS2	MT3	MP1	H
D172010	M-YB	0.8053	0.0544	0.0075	0.1327	MS2	MT3	MP1	H
D172011	M-GR	0.9647	0.0088	0.0014	0.0251	MS1	MT3	MP1	F
D172012	M-GW	0.4620	0.0567	0.0524	0.4289	MS2	–	–	?
D172013	M-GB	0.8871	0.0267	0.0074	0.0788	MS2	MT1	MP1	H
D172015	M-GO	0.1515	0.5966	0.0067	0.2452	MS2	MT3	MP1	H
D172016	RW-M	0.7565	0.0822	0.0158	0.1456	MS2	MT4	MP3	H
D172017	RB-M	0.9666	0.0070	0.0011	0.0253	MS1	–	–	?
D172018	RY-M	0.9801	0.0059	0.0004	0.0136	MS1	–	–	?
D172019	RG-M	0.9633	0.0084	0.0011	0.0273	MS1	–	–	?
D172020	RO-M	0.5941	0.1348	0.0163	0.2548	MS2	MT3	MP2	H
D172021	WR-M	0.9695	0.0071	0.0010	0.0224	MS1	MT4	MP1	H
D172022	WB-M	0.3264	0.4178	0.0247	0.2312	MS2	MT3	MP1	H
D172023	WY-M	0.9379	0.0123	0.0022	0.0475	MS2	–	–	?
D172024	WG-M	0.8920	0.0147	0.0016	0.0918	MS2	MT3	MP1	H
D172025	BR-M	0.9773	0.0063	0.0007	0.0158	MS1	–	–	?
D172026	WO-M	0.9195	0.0141	0.0031	0.0633	MS2	MT3	MP1	H
D172027	BW-M	0.4706	0.2265	0.0160	0.2870	MS2	MT3	MP1	H
D172028	BY-M	0.9695	0.0071	0.0010	0.0224	MS1	MT1	MP1	H
D172029	BG-M	0.9315	0.0142	0.0035	0.0508	MS2	MT3	MP1	H

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Table A1.1—continued

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
D172030	BO-M	0.9797	0.0000	0.0001	0.0202	MS1	–	–	?
D172031	YR-M	0.2990	0.3306	0.0197	0.3508	MS2	–	–	?
D172032	YW-M	0.5370	0.2435	0.0081	0.2113	MS2	MT3	MP1	H
D172033	YB-M	0.8792	0.0318	0.0079	0.0811	MS2	–	–	?
D172034	YG-M	0.0891	0.7246	0.0067	0.1797	MS2	MT1	MP1	H
D172035	YO-M	0.6494	0.1747	0.0154	0.1606	MS2	MT3	MP1	H
D172036	GR-M	0.9704	0.0000	0.0002	0.0294	MS1	–	–	?
D172037	GW-M	0.6723	0.1526	0.0151	0.1600	MS2	MT3	MP1	H
D172038	GB-M	0.0395	0.8307	0.0062	0.1235	MS2	MT3	MP3	H
D172040	M-BO	0.8935	0.0005	0.0003	0.1058	MS2	–	–	?
D172042	M-YO	0.9588	0.0103	0.0013	0.0296	MS1	MT3	MP1	F
D172043	GO-M	0.7942	0.0764	0.0103	0.1191	MS2	MT2	MP1	H
D172044	M-OO	0.8602	0.0299	0.0115	0.0984	MS2	–	–	?
D172046	M-BB	0.9790	0.0063	0.0006	0.0141	MS1	–	–	?
D172047	M-	0.9246	0.0002	0.0004	0.0748	MS2	–	–	?
D172048	OW-M	0.0131	0.9095	0.0028	0.0745	MS2	–	–	?
D172049	OR-M	0.8062	0.0409	0.0032	0.1497	MS2	MT3	–	?
D172050	OY-M	0.9588	0.0103	0.0013	0.0296	MS1	–	–	?
D172051	OG-M	0.0068	0.9486	0.0008	0.0438	MS2	–	–	?
D172052	OB-M	0.7883	0.0433	0.0076	0.1608	MS2	MT1	–	?
D172053	M-OW	0.0088	0.8198	0.0110	0.1604	MS2	–	–	?
D172054	M-OR	0.9110	0.0001	0.0006	0.0884	MS2	–	–	?
D172055	M-OY	0.9695	0.0071	0.0010	0.0224	MS1	–	–	?
D172056	M-OG	0.7883	0.0433	0.0076	0.1608	MS2	MT2	–	?
D172057	M-OB	0.7429	0.0795	0.0094	0.1682	MS2	–	–	?
D172058	M-YY	0.0112	0.9180	0.0026	0.0681	MS2	–	–	?
D172059	M-GG	0.4389	0.1830	0.0227	0.3554	MS2	MT3	MP3	H
D172061	M-WW	0.5283	0.2723	0.0189	0.1804	MS2	MT3	MP1	H
D174701	R-GO	0.0630	0.7814	0.0039	0.1517	MS2	MT3	–	?
D174702	R-RW	0.3381	0.4470	0.0072	0.2077	MS2	–	–	?
D174703	R-BY	0.8871	0.0267	0.0074	0.0788	MS2	–	–	?
D174704	R-RB	0.5546	0.2268	0.0178	0.2009	MS2	–	–	?
D174705	R-OR	0.2005	0.5023	0.0277	0.2695	MS2	–	–	?
D174706	R-OY	0.0333	0.7325	0.0058	0.2284	MS2	–	–	?
D174707	R-GW	0.0694	0.8102	0.0044	0.1160	MS2	–	–	?
D174708	R-RY	0.0915	0.6325	0.0324	0.2436	MS2	–	–	?
D174709	R-BO	0.9685	0.0072	0.0006	0.0236	MS1	–	–	?
D174710	R-OG	0.6140	0.1090	0.0184	0.2586	MS2	–	–	?
D174711	R-GY	0.8871	0.0267	0.0074	0.0788	MS2	MT3	MP1	H
D174712	R-RG	0.3959	0.3347	0.0285	0.2409	MS2	MT3	MP1	H
D174713	R-WO	0.0851	0.6911	0.0180	0.2058	MS2	MT1	MP1	H
D174714	R-RO	0.9633	0.0084	0.0011	0.0273	MS1	MT3	MP1	F
D174715	R-YB	0.3959	0.3347	0.0285	0.2409	MS2	MT2	MP1	H
D174716	R-WY	0.9562	0.0093	0.0010	0.0334	MS1	–	–	?
D174717	R-YR	0.9649	0.0078	0.0010	0.0264	MS1	MT3	MP1	F
D174718	R-GB	0.9753	0.0068	0.0008	0.0171	MS1	MT3	MP1	F
D174719	R-OB	0.9649	0.0078	0.0010	0.0264	MS1	MT1	MP1	H
D174774	R-YG	0.1731	0.5534	0.0293	0.2442	MS2	MT3	MP1	H
D175001	BY-G	0.9505	0.0098	0.0011	0.0386	MS1	MT3	–	?

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Table A1.1—continued

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
D175002	G-YW	0.8457	0.0296	0.0044	0.1204	MS2	MT2	MP1	H
D175003	G-YB	0.9732	0.0005	0.0008	0.0255	MS1	MT3	MP1	F
D175004	YB-G	0.9647	0.0088	0.0014	0.0251	MS1	MT3	MP3	H
D175005	G-YO	0.3139	0.3872	0.0323	0.2666	MS2	MT3	MP1	H
D175006	BG-G	0.7942	0.0764	0.0103	0.1191	MS2	MT3	MP1	H
D175007	G-YG	0.0916	0.6470	0.0153	0.2461	MS2	MT3	MP1	H
D175009	YG-G	0.9633	0.0084	0.0011	0.0273	MS1	MT3	MP2	H
D175010	BO-G	0.0656	0.7731	0.0070	0.1543	MS2	MT3	MP1	H
D175013	GR-G	0.9704	0.0000	0.0002	0.0294	MS1	MT3	MP1	F
D175014	G-GY	0.0055	0.9821	0.0002	0.0122	MS3	MT4	MP5	R
D175015	G-GO	0.2399	0.5949	0.0049	0.1603	MS2	MT3	MP2	H
D175016	G-OR	0.6191	0.1534	0.0135	0.2140	MS2	MT1	MP1	H
D175017	G-OB	0.0081	0.9271	0.0037	0.0611	MS2	MT4	MP4	H
D175018	GO-G	0.9685	0.0072	0.0006	0.0236	MS1	–	–	?
D175019	GB-G	0.5137	0.1787	0.0119	0.2956	MS2	MT2	MP5	H
D175020	GY-G	0.7181	0.0034	0.0005	0.2780	MS2	MT4	MP1	H
D175021	G-OG	0.7942	0.0764	0.0103	0.1191	MS2	MT3	MP1	H
D175022	G-OY	0.0060	0.9581	0.0006	0.0353	MS3	MT4	MP5	R
D175023	OR-G	0.0981	0.7065	0.0072	0.1882	MS2	MT1	MP1	H
D175101	RW-B	0.0262	0.8550	0.0055	0.1133	MS2	MT3	MP2	H
D175102	RB-B	0.0109	0.9118	0.0038	0.0735	MS2	MT2	MP1	H
D175103	RY-B	0.9845	0.0000	0.0000	0.0154	MS1	MT3	MP1	F
D175104	RG-B	0.9797	0.0001	0.0000	0.0202	MS1	MT3	MP1	F
D175105	B-RW	0.0549	0.6652	0.0213	0.2585	MS2	MT3	MP1	H
D175106	B-RB	0.0612	0.7482	0.0072	0.1833	MS2	MT3	MP1	H
D175107	B-RY	0.0342	0.8477	0.0031	0.1150	MS2	MT3	MP3	H
D175108	B-RG	0.1053	0.6002	0.0138	0.2807	MS2	MT3	MP1	H
D175109	B-RO	0.0165	0.7146	0.0044	0.2645	MS2	MT3	MP1	H
D175110	B-WR	0.7634	0.0774	0.0040	0.1552	MS2	–	–	?
D175111	B-WB	0.9563	0.0116	0.0014	0.0306	MS1	MT3	MP1	F
D175112	RO-B	0.9647	0.0088	0.0014	0.0251	MS1	–	–	?
D175113	B-WY	0.7783	0.0898	0.0108	0.1212	MS2	MT3	MP1	H
D175114	WR-B	0.9883	0.0000	0.0000	0.0116	MS1	MT3	MP1	F
D175115	WB-B	0.0161	0.8979	0.0034	0.0825	MS2	MT3	MP1	H
D175116	B-WG	0.0182	0.9058	0.0023	0.0738	MS2	MT3	MP1	H
D175117	WY-B	0.8792	0.0318	0.0079	0.0811	MS2	MT3	MP1	H
D175118	BW-B	0.8733	0.0026	0.0042	0.1199	MS2	MT3	MP1	H
D175119	B-WO	0.0096	0.9212	0.0024	0.0668	MS2	MT3	MP1	H
D175120	B-BR	0.2063	0.5930	0.0071	0.1936	MS2	MT3	MP1	H
D175121	B-BW	0.5908	0.1732	0.0142	0.2218	MS2	MT3	MP1	H
D175122	B-BY	0.0517	0.8150	0.0087	0.1246	MS2	MT3	MP1	H
D175123	WG-B	0.5610	0.2184	0.0081	0.2126	MS2	MT3	MP1	H
D175124	B-BG	0.9010	0.0301	0.0035	0.0654	MS2	MT3	MP2	H
D175125	B-BO	0.9745	0.0062	0.0005	0.0187	MS1	MT3	MP3	H
D175126	WO-B	0.0131	0.8850	0.0053	0.0965	MS2	MT3	MP1	H
D175127	BR-B	0.0252	0.8475	0.0024	0.1249	MS2	MT3	MP2	H
D175128	B-YR	0.9741	0.0072	0.0009	0.0178	MS1	MT3	MP1	F
D175129	BY-B	0.9130	0.0189	0.0033	0.0648	MS2	MT3	MP1	H
D175130	B-YW	0.9321	0.0178	0.0023	0.0478	MS2	MT1	MP1	H

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Table A1.1—continued

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
D175131	B-YB	0.2387	0.2483	0.0622	0.4508	MS2	MT4	MP1	H
D175132	BG-B	0.9674	0.0001	0.0001	0.0325	MS1	MT1	MP1	H
D175133	B-YG	0.0992	0.7027	0.0105	0.1876	MS2	MT2	MP1	H
D175134	BO-B	0.0189	0.8378	0.0132	0.1301	MS2	MT4	MP4	H
D175135	YR-B	0.9647	0.0088	0.0014	0.0251	MS1	MT3	MP1	F
D175136	YW-B	0.9753	0.0068	0.0008	0.0171	MS1	–	–	?
D175139	B-GR	0.8792	0.0318	0.0079	0.0811	MS2	MT3	MP1	H
D175140	B-GW	0.0060	0.9579	0.0006	0.0355	MS3	–	–	?
D175141	YG-B	0.3631	0.2892	0.0113	0.3364	MS2	MT3	MP1	H
D175142	B-GB	0.8939	0.0352	0.0037	0.0672	MS2	MT1	MP1	H
D175143	B-GY	0.0086	0.9223	0.0010	0.0680	MS2	MT4	MP4	H
D175144	YO-B	0.1287	0.3877	0.0830	0.4005	MS2	MT4	MP4	H
D175145	B-GO	0.0054	0.9641	0.0003	0.0302	MS3	MT2	MP4	H
D175146	B-BkW	0.3222	0.4241	0.0146	0.2391	MS2	MT3	MP1	H
D175173	GR-B	0.0055	0.9629	0.0013	0.0303	MS3	MT3	MP4	H
D175174	GG-B	0.0162	0.8840	0.0047	0.0950	MS2	MT3	MP1	H
D175175	GW-B	0.9705	0.0060	0.0008	0.0227	MS1	MT4	MP1	H
D175176	GY-B	0.0173	0.8742	0.0050	0.1034	MS2	MT3	MP1	H
D175177	OO-B	0.4073	0.2585	0.0187	0.3155	MS2	MT1	MP1	H
D175178	YY-B	0.7783	0.0898	0.0108	0.1212	MS2	MT3	MP1	H
D175179	RR-B	0.9649	0.0078	0.0010	0.0264	MS1	MT4	MP1	H
D175180	B-OR	0.3381	0.4470	0.0072	0.2077	MS2	MT3	MP1	H
D175181	B-	0.9802	0.0001	0.0000	0.0197	MS1	MT3	MP1	F
D175182	B-OW	0.0099	0.9367	0.0011	0.0522	MS2	MT3	MP1	H
D175183	B-OB	0.8162	0.0288	0.0101	0.1449	MS2	MT2	MP1	H
D175184	B-OG	0.1982	0.5586	0.0071	0.2360	MS2	MT3	MP1	H
D175186	OR-B	0.9026	0.0220	0.0028	0.0726	MS2	MT3	MP1	H
D175187	GO-B	0.9563	0.0116	0.0014	0.0306	MS1	MT3	MP1	F
D175190	OY-B	0.9588	0.0103	0.0013	0.0296	MS1	MT3	MP1	F
D175191	OY-B	0.2697	0.4204	0.0171	0.2928	MS2	MT2	MP3	H
D175192	OG-B	0.7942	0.0764	0.0103	0.1191	MS2	MT1	MP1	H
D175193	WW-B	0.9413	0.0108	0.0020	0.0459	MS2	MT1	MP1	H
D175194	BkR-B	0.1127	0.6411	0.0127	0.2335	MS2	MT3	MP1	H
D175197	B-BkR	0.8590	0.0359	0.0046	0.1006	MS2	MT3	MP1	H
D175198	B-BkO	0.0086	0.9302	0.0024	0.0588	MS2	MT4	MP4	H
D175199	B-BkG	0.0096	0.8590	0.0116	0.1199	MS2	MT2	MP4	H
D175200	B-BkY	0.6858	0.1518	0.0145	0.1479	MS2	MT3	MP1	H
D175201		0.0290	0.8622	0.0034	0.1054	MS2	MT3	–	?
D175202		0.5610	0.2184	0.0081	0.2126	MS2	MT3	–	?
D175203		0.8496	0.0425	0.0049	0.1030	MS2	MT3	–	?
D175204		0.1223	0.7090	0.0050	0.1637	MS2	MT3	–	?
D175205		0.9839	0.0059	0.0004	0.0099	MS1	MT3	–	?
D175206		0.3381	0.4470	0.0072	0.2077	MS2	MT1	–	?
D175207		0.9563	0.0116	0.0014	0.0306	MS1	MT3	MP1	F
D175208		0.0981	0.7065	0.0072	0.1882	MS2	MT3	MP2	H
D175209		0.3786	0.3669	0.0095	0.2450	MS2	MT3	MP1	H
D175210		0.7783	0.0898	0.0108	0.1212	MS2	MT3	MP1	H
D175211		0.9753	0.0068	0.0008	0.0171	MS1	MT2	MP3	H
D175212		0.6494	0.1747	0.0154	0.1606	MS2	MT3	–	?

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Table A1.1—continued

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	$P(F_1)$	$P(F_2)$	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
D175213		0.9695	0.0071	0.0010	0.0224	MS1	MT3	–	?
D175214		0.9563	0.0116	0.0014	0.0306	MS1	MT3	MP1	F
D175215		0.3381	0.4470	0.0072	0.2077	MS2	MT4	MP3	H
D175216		0.8479	0.0011	0.0005	0.1505	MS2	MT3	MP3	H
D175218		0.6494	0.1747	0.0154	0.1606	MS2	MT3	–	?
D175219		0.1496	0.6475	0.0071	0.1959	MS2	MT3	–	?
D175223		0.8652	0.0322	0.0043	0.0983	MS2	MT3	MP1	H
D175225		0.0981	0.7065	0.0072	0.1882	MS2	MT3	–	?
D175226		0.9376	0.0176	0.0021	0.0427	MS2	MT3	MP2	H
D175227		0.1127	0.6411	0.0127	0.2335	MS2	MT3	–	?
D175228		0.9590	0.0099	0.0016	0.0295	MS1	MT3	–	?
D175230		0.0116	0.9059	0.0043	0.0781	MS2	MT3	–	?
D175231		0.0068	0.9459	0.0007	0.0466	MS2	MT1	–	?
D175232		0.0162	0.8840	0.0047	0.0950	MS2	MT3	–	?
D175234		0.0696	0.6907	0.0119	0.2278	MS2	MT3	MP1	H
D175237		0.0260	0.8479	0.0062	0.1198	MS2	MT3	–	?
D175243		0.2571	0.4761	0.0296	0.2372	MS2	MT3	–	?
D175248		0.0099	0.9367	0.0011	0.0522	MS2	MT3	–	?
D175250		0.2918	0.3923	0.0275	0.2884	MS2	MT3	–	?
D175255		0.9802	0.0001	0.0000	0.0197	MS1	MT4	–	?
D175267		0.3101	0.3664	0.0283	0.2952	MS2	MT4	–	?
D175271		0.9633	0.0084	0.0011	0.0273	MS1	MT3	–	?
D175272	Y-GR	0.0053	0.9535	0.0009	0.0404	MS3	MT1	MP4	H
D175273	Y-OR	0.0056	0.9503	0.0021	0.0420	MS3	MT3	–	?
D175275	YB-Y	0.0055	0.9687	0.0006	0.0252	MS3	MT3	–	?
D175276	YO-Y	0.0059	0.9231	0.0044	0.0666	MS2	MT4	–	?
D175278	YW-Y	0.0055	0.9853	0.0001	0.0091	MS3	–	–	?

TABLE A1.2. RANGATIRA ISLAND POPULATION OF PARAKEETS.

BAND		MICROSATELLITES					ASSIGNMENT		
METAL	COLOUR	*P*(FB)	*P*(RC)	*P*(F_1)	*P*(F_2)	ASSIGNMENT	mtDNA	MORPHOLOGY	OVERALL
	YY-M	0.0405	0.6491	0.0312	0.2793	MS2	–	–	?
D171523		0.0054	0.9766	0.0002	0.0178	MS3	MT2	MP5	H
D171524		0.3825	0.2422	0.0445	0.3308	MS2	MT4	MP5	H
D171525		0.0247	0.8649	0.0038	0.1066	MS2	MT4	MP5	H
D171526		0.0050	0.9728	0.0001	0.0222	MS3	MT4	MP5	R
D171527		0.0054	0.9606	0.0004	0.0336	MS3	MT4	MP5	R
D171528		0.0061	0.9360	0.0031	0.0548	MS2	MT4	MP5	H
D171531		0.0055	0.9629	0.0013	0.0303	MS3	MT4	MP5	R
D171532		0.0062	0.8967	0.0022	0.0949	MS2	MT2	MP5	H
D171533		0.0054	0.9622	0.0004	0.0320	MS3	MT4	MP5	R
D171534		0.7507	0.0590	0.0048	0.1855	MS2	MT2	MP5	H
D171535		0.0051	0.9667	0.0008	0.0274	MS3	MT4	MP5	R
D171536		0.0054	0.9626	0.0003	0.0317	MS3	MT4	MP5	R
D171537		0.0272	0.6694	0.0140	0.2894	MS2	MT4	MP5	H
D171538		0.0051	0.8658	0.0066	0.1225	MS2	MT4	MP5	H
D171539		0.0062	0.8967	0.0022	0.0949	MS2	MT4	MP5	H
D171540		0.0057	0.8647	0.0131	0.1164	MS2	MT4	MP5	H
D171541		0.0051	0.9174	0.0004	0.0771	MS2	MT4	MP5	H
D171542		0.1240	0.7257	0.0054	0.1448	MS2	MT4	MP5	H
D171583		0.0169	0.6735	0.0135	0.2960	MS2	MT4	MP5	H
D171584		0.0062	0.8967	0.0022	0.0949	MS2	MT4	MP5	H
D171585		0.0134	0.7810	0.0170	0.1886	MS2	MT4	MP5	H
D171586		0.0070	0.9523	0.0009	0.0398	MS3	MT4	MP5	R
D171587		0.0058	0.9571	0.0021	0.0350	MS3	MT4	MP5	R
D171588		0.0054	0.9766	0.0003	0.0177	MS3	MT4	MP5	R
D171589		0.0182	0.8922	0.0023	0.0873	MS2	MT4	MP5	H
D171590		0.4878	0.1703	0.0102	0.3317	MS2	MT4	MP5	H
D171591		0.0288	0.7626	0.0171	0.1915	MS2	MT2	MP5	H
D171592		0.0066	0.9323	0.0032	0.0579	MS2	MT4	MP5	H
D171593		0.0053	0.9794	0.0000	0.0152	MS3	MT4	MP5	R
D171594		0.0069	0.8911	0.0023	0.0996	MS2	MT4	MP5	H
D171595		0.3706	0.3132	0.0294	0.2867	MS2	MT4	MP5	H
D171596		0.0055	0.9890	0.0000	0.0055	MS3	MT4	MP5	R
D171597		0.0049	0.9645	0.0001	0.0305	MS3	MT4	MP5	R
D171598		0.2228	0.5827	0.0075	0.1871	MS2	MT4	MP5	H