Ancient DNA Analysis of Māori Feather Cloaks and Kete: Implications for Conservation and Culture

Katie Hartnup

A thesis presented in fulfilment of the requirements for the degree of Doctor of Philosophy in Molecular Biosciences at Massey University, Auckland, New Zealand 2012

Abstract

Feather cloaks (*kakahu*) and bags (*kete*), particularly those adorned with kiwi feathers, are treasured items or *taonga* to the Māori people of New Zealand. They are considered iconic expressions of Māori culture. Despite their status, much of our knowledge of the materials used to construct these artefacts, the provenance of these artefacts and the origins of these traditions, has been lost. We used ancient DNA methods to recover mitochondrial DNA sequences from 849 feather samples taken from 109 kiwi feathered cloaks (*kahu kiwi*) and 161 feather samples from 55 kiwi feathered *kete* (*kete kiwi*). We show that almost all (>99%) of the cloaks and all (100%) of the *kete* were constructed using feathers from North Island brown kiwi (*Apteryx mantelli*). Just one cloak was found to have been constructed using feathers from little spotted kiwi (*Apteryx owenii*). The remaining three species of kiwi (*Apteryx haasti, Apteryx rowi* and *Apteryx australis*) were not found in any of the cloaks and *kete* sampled. Molecular sexing of nuclear DNA from 92 feather cloak samples also revealed that the sex-ratio of birds deviated from a ratio of 1:1 observed in reference populations, with a male skew observed. Additionally, a reference database of 185 North Island brown kiwi mitochondrial control region DNA sequences was constructed, comprising samples collected from 26 North Island locations together with data available from the literature. For contemporary populations, we saw a phylogeographic structuring of haplotypes using both SAMOVA and Nested Clade Analysis into Eastern, Northern and West and Central populations. Utilising this structuring, it was possible to infer the provenance of 847 kiwi feathers from 108 cloaks and 153 kiwi feathers from 52 kete. A surprising proportion of cloaks (15%) and some kete (5.5%) were found to contain feathers from different geographic locations providing evidence of either kiwi trading among Māori tribes (iwi), tribal displacement, or organised hunting trips into other tribal areas. The data also suggests that the east of the North Island was the most prolific of all kiwi cloak and kete making areas, accounting for over 50% of all cloaks analysed and over 58% of all kete. This could indicate that the East of the North Island was the epicentre for this cultural tradition. Also, the structuring

observed in the reference database will prove to be useful to conservationists, such as the New Zealand Department of Conservation, when deciding strategies to maintain populations of New Zealand's most iconic bird. The genetic analysis of these treasured items has been invaluable in enriching our knowledge and rebuilding their lost histories. Additionally, genetic data from historical items can aid our understanding or how populations change overtime, thus aiding conservation of valuable species.

Acknowledgements

I feel lucky to have been part of a unique and special project. As a British citizen, the opportunity to be involved in a project so central to New Zealand and Māori culture has been a privilege for which I am extremely grateful. I have my supervisors Professor David Lambert, Dr Craig Millar and Dr Leon Huynen to thank for matching my skill set to a project that has continued to interest me, challenge me and, has allowed me to immerse myself into the culture of a country I have fallen in love with and now call home. The project was conceived by my supervisors, and funding obtained, thus making this study possible. Beyond that my supervisors have provided invaluable guidance, patience and advice. I truly appreciate their individual and collaborative roles in the production of this thesis. Thanks also to Dr Evelyn Sattelegger for taking me on as an extra student when circumstances changed during the course of my study.

I would like to extend a special thank you to Rangi Te Kanawa. Rangi's collaboration on the project was pivotal in its success. Her ability to liaise with museums coupled with her experience handling such valuable objects effectively made sampling of these *taonga* possible. I travelled to museums with Rangi during sampling and was always impressed with her kindness and graciousness, even when my choice of accommodation wasn't quite what either of us was expecting. During my travels with Rangi, a number of museums allowed us to sample from their collections. I would like to thank Awhina Tamarapa and staff at Te Papa Tongawera, Chanel Clarke and staff at Auckland War Memorial Museum, Hawkes Bay Museum and Regional Trust, Waikato Museum, Whanganui Regional Museum, Canterbury Museum, The British Museum and, The Horniman Museum. Without access to samples, this study would not have been possible.

Modern kiwi DNA samples were also vital to the project's success. For this I would like to extend thanks to the Department of Conservation (DOC) for provision of blood and feather samples from current kiwi populations. Rainbow Springs, Kiwi Encounter, Rotorua, provided us with the largest number of samples. I am grateful

to all of the team at kiwi encounter for their assistance, particularly Claire Travers, Emma Bean and Beverly Wilkinson.

Lara Shepherd has been a great help throughout the project. She conducted the preliminary work on the project and was always available to give me advice and comments on my work. I appreciate her continued support.

I would like to thank all of the sources of funding. First and foremost the Royal Society of New Zealand for the Marsden Fund which made the project financially viable; Massey University for tuition fees, provision of a computer and travel money; The University of Auckland and Craig Millar for additional financial support towards sequencing costs; and The Allan Wilson Centre for travel to the Evolution conference in 2007 and to their annual meetings in Palmerston North. Thanks go to Vivian Ward, Judith Robins and Kristine Boxen at the University of Auckland for assistance with figure preparation (Vivian), sequencing (Kristine) and independent verification of results (Judith).

I would like to thank members of the lab at Albany past and present for providing me with advice, support and light relief. Thanks to Gabby Beans, Jyothsna Visweswaraiah, Martina Dautel, Elmira Mohandesan, Reynald Castaneda, Monique van Rensburg, Jarod Young, Hayley Lawrence, Chris Rodley, Muharram Khoussainova, Monica Merriman, Saumya Agrawal, Tim Heupink and John Waugh.

I am lucky to have great family friends supporting me. I thank my partner Jonathan for his enduring patience and support.

Table of Contents

List of Figures

List of Tables

Chapter 1

General Introduction

Genetic analysis and molecular studies are no longer the reserve of any distinct discipline. DNA has become a multidisciplinary molecule. Analysis of the molecule itself has allowed for a greater understanding of its functions and mechanisms and, it is this understanding that has allowed the application of molecular analysis to a wide range of fields. Its nature as a variable, unique identifier has made it the 'go to' tool for ecologists and conservationists interested in pedigree reconstruction to explore heritable traits, population structure and diversity, migration, speciation and mating systems amongst others. The relatively predictable nature of DNA mutation provides a tangible companion to the fossil record for evolutionary biologists looking at divergence, convergence, rates of evolution, evolutionary trees and how particular genes evolve, e.g. genes for flight, vision, pigmentation. DNA is invaluable to anthropologists, especially given recent advances in ancient DNA (aDNA) techniques (Haak *et al* 2010, Destro-Bisol *et al* 2010). DNA allows anthropologists to reconstruct the history of human populations, characterisation of DNA in extinct humans and ancient populations and to explore the role of adaptive processes in shaping the diversity of our species (Destro-Bisol *et al* 2010). DNA is becoming of increasing importance to historians. Previously limited to written accounts and oral histories, DNA provides a measurable addition to complement or challenge these histories. Indeed, DNA has the ability to recreate histories lacking written or oral accounts.

This is not a typical biological thesis. It is multidisciplinary, with applications in both conservation and culture, backed by biological genetic theory and techniques. This project aims to aid reconstruction of the histories and whakapapa of culturally significant Māori feather cloaks (kakahu) and bags (kete) from the 19th century. Also given that the focus is on cloaks adorned with feathers from the endangered kiwi (*Apteryx* spp.), it allows a snapshot of how these species have changed genetically in response to their decline.

Genetic Analysis of Historical Artefacts and Museum Specimens

Museum specimens of plants and animals have recently proven to be of great use to taxonomy, population ecology, conservation biology, and evolutionary genetics, since well-preserved specimens can provide a source of ancient DNA (Wanderler et al. 2007). Such genetic information has been used to estimate past population sizes (Brown et al. 2007), changes in genetic diversity over time (Ciborowski et al. 2007), rates of DNA sequence evolution (Lambert et al. 2002, 2010), and to correctly identify specimens. For example, the latter approach has been employed to identify species of moths and parasitic wasps (Hajibabaei et al. 2006), an Indian lion (*Panthera leo persica*) skeleton previously thought to have been a Cape Lion (*Panthera leo melanchita*) on display at the Zoological museum in Amsterdam (Barnett et al. 2007), and to identify species of kiwi skeletons (*Apteryx* spp.) with indistinguishable bone morphologies (Shepherd & Lambert 2008). In addition, recent work has allowed species level identification of moa and other birds from eggshell surfaces alone (Chilton and Sorenson 2007; Huynen et al. 2010; Oskam et al. 2010).

The large number of artefacts of cultural and anthropological significance held in museums worldwide is staggering. For example, many of the 1.8 million objects comprising the British Museum collections alone are ethnographic artefacts. These artefacts are typically constructed from a combination of animal and / or plant materials such as skin, bone, feathers, and wood. Material comprising these artefacts derives from a wide variety of species used by many endemic cultures. Examples include 18th / 19th century buffalo hide containers from North America, Roman 3rd Century crocodile skin suits of armour from Egypt, and 18th / 19th century feather cloaks from Hawaii and New Zealand (Figure 1.1). Each of these artefacts is typically unique to particular cultures or geographic regions and can provide insights into the cultural and social evolution of the people who constructed them. Molecular analyses and ancient DNA methods have the potential to contribute significantly to the study of such artefacts, since DNA recovered from their composite materials can identify the species of plants and animals used to make them, and even their provenance. Such information might never have been

recorded or, alternatively might have been lost. The aim of this thesis is to investigate the composition and the traditions used to construct the large number of culturally significant cloaks adorned with feathers made by the Māori of *Aotearoa* / New Zealand (Pendergrast 1987).

The History of Māori Textiles

New Zealand Māori, by virtue of long residence in a temperate climate (since about AD1350, Howe 2003), diverged considerably from the other branches of the Polynesian race in their arts and crafts. This divergence is particularly marked in the manufacture of clothing (Te Rangi Hiroa, 1924). New Zealand was a different environment to the rest of Polynesia, with unfamiliar materials available. This environment stimulated entirely new inventions or led to the adaptation of a known technique to new materials and requirements.

Climate is the obvious stimulus to changes in both the style of clothing and the materials used to create them. However, the biological materials available in any one particular habitat also play a role (Te Rangi Hiroa, 1924). Polynesians historically used the finely interwoven inner bark of trees for clothing. Typically this inner bark was harvested from the paper mulberry ((*Broussonetia papyrifera*) Best 1952; Te Rangi Hiroa 1923), the bread-fruit ((*Artocarpus incisa*) Te Rangi Hiroa 1923), and the fig tree ((*Ficus prolixa*) Te Rangi Hiroa). Bark was stripped from young saplings, soaked in water, the outer bark was scraped off and the remainder was beaten in order to soften the fibres for clothing. It is thought that the great Hawaiiki migration of AD1350 of Polynesians to New Zealand occurred with the specific purpose of colonisation (Howe 2003; Te Rangi Hiroa 1924). With them they brought cultivated food such as kumara, taro and gourd, which still flourish in New Zealand to this day. Paper mulberry (*aute*) was amongst the plants and seeds Polynesians brought with them in their canoes.

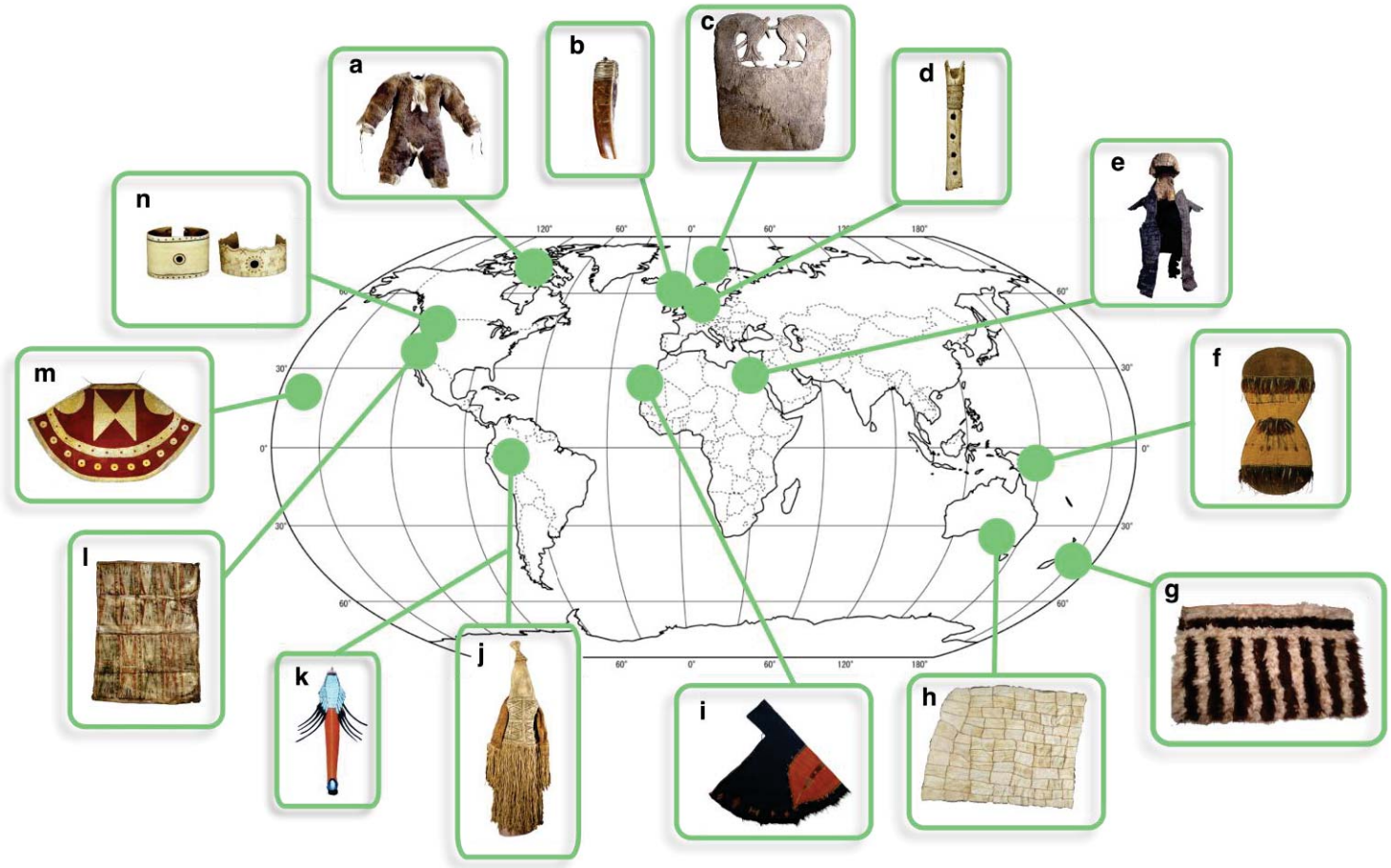


Figure 1.1 a) Boys caribou suit, 1976, Igloolik, Northern Canada; **b)** Beaver tooth pendant, C^{7th} AD, Wigber Low, Derbyshire, UK; **c)** Whalebone Plaque, C^{9th} AD Viking, Lilleberge, Namdalen, Norway; **d)** Bone flute, 32,000 years old, Dordogne, France; **e)** Roman crocodile suit of armor, C^{3rd} AD, Manafalut, Egypt; **f)** Feather shield, late C^{17th} AD, Papua New Guinea; **g)** Maori kiwi feather cloak, mid C^{19th} AD, New Zealand; **h)** Possum skin cloak, mid C^{19th} AD, Maidens Point, Tasmania; **i)** Wool and goat hair hooded cloak, C^{19th} AD, Morocco; **j)** Spirit mask, mid C^{19th} AD, Cuebo people, Uaupes River, Amazon; **k)** Feather lip ornament, Amazon; **l)** Buffalo hide container / Parfleche, pre C^{19th} AD, North America; **m)** Hawaiian feather cloak, C^{18th} AD, Hawaii, Polynesia; **n)** Antler wrist guards, pre C^{19th} AD, American prairies / plains.

Unfortunately New Zealand's temperate climate did not suit the growing requirements of the paper mulberry. Although it did survive until the period of European occupation, plants were rare and highly prized by Māori.

'*After this they showed us a great rarity, six plants of what they called aouto (aute), from which they made cloth like that of Otaheiti. The plant proved to be exactly the same, as the name is the same. The same plant is used by the Chinese to make paper. Whether the climate does not well agree with it I do not know, but they seem to value it very much; that it is scarce among them I am inclined to believe, as we have not yet seen among them pieces large enough for any use, but only bits sticking into holes in their ears*' – **Sir Joseph Banks whilst accompanying Cook on his first voyage in 1769 (Banks Journal. Edited by Hooker, 1896, page 206. Sourced from Te Rangi Hiroa, 1924)**

In the absence of paper mulberry, an alternative clothing material was needed. New Zealand flax provided a good substitute. Flax fibres run straight, parallel, are easily separated from each other and can be extracted to make a pliable thread. This thread could then be woven into a textile. There are two species of New Zealand flax, *Phormium tenax* and *Phormium cookanium*. *P.tenax*, is known as *harakeke*, swamp flax or common flax. It is deemed especially good for weaving due to its stiff, broad leaves that can grow up to three metres in height. Hence, longer fibres can be extracted for weaving than from its smaller relative, *P.cookanium.* When *harakeke* is harvested blades are taken from the outside of the plant, as harvesting the centre (*rito*) or the two surrounding blades (*awhi rito*) could cause the plant to die (Te Kanawa, 1992). Once harvested the blades were either cut into strips to be woven into baskets (*kete*) and skirts/kilts (*piu piu*). Alternatively, a fibre called *muka* can be extracted to construct finer garments. The *muka* is extracted from the inside of the flax blade by scraping it with a mussel shell (*makoi*). Once extracted this fibre is soaked and pounded until it has softened, after which it can be rolled into threads of the desired thickness on the knee. The collection of *harakeke* and the preparation process is a lengthy one, often taking three months to prepare enough material for one cloak (Te Kanawa, 1992). Cloak

construction uses a hand knotting process, using a wooden frame consisting of two wooden sticks in the ground (Best, 1952). The structure consists of thicker vertical strands of *muka* (the *whenu*) joined together by finer, single stranded horizontal strands of *muka* (the *aho*). Cloaks are constructed from the bottom up, with the top edge of the cloak being finished last.

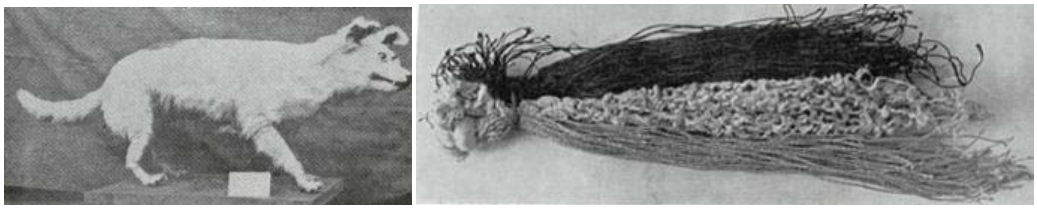


Figure 1.2 A Māori dog or kuri (left) and examples of dyed, woven muka strands (right). Photographs from Best 1952.

Although *harakeke* provided a good alternative to the paper mulberry tree, flax was not the only biological material used in the construction of textiles. Māori discovered that the bark from other trees could be used to dye the prepared *muka*. For example, *muka* steeped in a liquid preparation of hinau bark (*Elaeocarpus dentus*) and rubbed with a steely grey mud called *paru* dyed the fibres black or *mangu*. *Muka* was also steeped in a *tanekaha* or celery pine (*Phyllocladus trichomanoides)* bark solution and rubbed into ashes whilst still wet, producing a tan coloured fibre. A yellow or *kowhai* dye was achieved by boiling muka with the bark from the kanono (*Coprosma australis areolta*) or raurekau (*Grandifloia spp*.) trees (Te Kanawa, 1992). Some of the most prestigious older cloaks comprised of a finely woven *muka* backing with strips of dog skin attached. This dog skin belonged to that of the *kuri*, brought to New Zealand by Polynesians in their canoes. *Kuri* were highly prized amongst Māori as they were used for hunting and as a food source (Best 1898). Figure 1.2 shows an example. Dog skin cloaks or *kahu kuri* were reserved for individuals of high status.

The arrival of Europeans in the late 18th Century sparked a trade in dog-skinned cloaks, resulting in greatly reduced numbers of *kuri* (Best 1898). Cloaks completely covered in feathers became increasingly important and common. Feathers from a variety of bird species were used in cloak construction, both native and non-native.

Native species included the kaka (*Nestor meridionalis*), the crowned parakeet or kakariki (*Cyanoramphus* spp.), the tui (*Prosthemadera novaeseelandiae*), the New Zealand wood pigeon or kereru (*Hemiphaga novaeseelandiae*), the pukeko (*Porphyrio porphyrio*), the weka (*Gallirallus australis*), the ground dwelling parrot, the kakapo (*Strigops habroptila*) and the kiwi (*Apteryx* spp.). Non-native species included pheasant (*Phasianus* spp.), peacock (*Pavo* spp.) and chicken (*Gallus* spp.). However, it must be noted that identification of the species of birds used to adorn feathered cloaks has, up to this point, been determined by feather morphology alone.

The most prestigious of all feathered cloaks were those adorned completely in kiwi feathers (*kahu kiwi*). These cloaks were reserved for those of high status such as chiefs. Weaving was much more than a just means of adornment and carried significant cultural importance. Prestigious cloaks, such as *kahu kiwi* and *kahu kuri* were empowered by *mana* a Māori term signifying a combination of authority, integrity, power and prestige. Some cloaks were of particular significance, renowned throughout the land and even had personal names (Pendergrast 1997). They were, on occasions, gifted or traded. In 1836 one celebrated cloak named *karamaene* was exchanged for a *waka* (war canoe) called *Te Toki a Tapiri.* Cloaks also played a significant role in battle. There are records of cloaks being thrown over warriors to protect them on the battlefield. There are also records that before battle cloaks were soaked in water to cause the *muka* fibres to swell, thus eliminating gaps in the fabric and making them more impervious to spears (Best 1902). The weaving process itself was performed much like a ceremony. Māori ethnologist Elsdon Best spent time with the Tuhoe *iwi* in the Ureweras and was witness to such a ritual. Best was stationed with the Tuhoe in 1893 to act as a mediator after government survey teams met with hostile opposition from Tuhoe when attempting to survey a road through the Ureweras. Best was New Zealand's first professional ethnographer. Although it must be noted that Best's evolutionary and racial views at the time detracted from the value of much of his writing, he was known to write in great detail regarding many of the practises of the Tuhoe.

Figure 1.3 Examples of Māori Textiles a) *kahu kuri* or dog skin cloak, b) *kahu huruhuru* or feathered cloak, c) *kahu kiwi* or kiwi feathered cloak, d) *kaitaka* finely woven *muka* cloak, e) *kete kiwi* or kiwi feathered bag, f) *kete,* plaited basket. Artefacts a,b,d,e,f and photographs are sourced from Te Papa Tongawera museum, artefact c is from Canterbury Museum and the photograph was taken by K. Hartnup.

The *whare pora* was a house specially set aside for teaching the art of weaving, and was also used to perform ceremonies related to the teaching and initiation (Best

1898). When a young woman enters the *whare pora* in order to be taught the art of weaving, she must first perform a ritual with the aid of a *tohunga*, who is a priest or wise man. The pupil, *tauira,* and the *tohunga* enter the *whare pora* together. The pupil sits before the *turuturu,* which are two sticks roughly 1 inch in diameter and 4 ft in length, stuck into the ground at a garments width apart from each other. Attached to these sticks is the *tawhiu,* the first of the horizontal threads. To this the vertical *whenu* are attached and hang down to the floor of the *whare pora.* The second horizontal thread (or *aho*) to be woven is known as the *aho tapu* or the sacred thread. It represents the sacredness of the *whare*, the weaver and the related ceremonies. The pupil takes some prepared fibre in her hand whilst the priest recites a passage. Once the priest has finished the pupil stoops and bites the upper part of the right weaving stick. She then takes the prepared fibre she has been holding and weaves the *aho tapu* (sacred thread) across the frame. This signifies that the pupil has come under the influence of the priest's incantations and has been accepted into the *whare pora.* After the pupil has woven the sacred thread, she weaves a band a few inches in depth, copying the work of a fine garment placed before her. Those who have passed through the *whare pora* will, if shown a new pattern of weaving, faithfully reproduce that pattern on the first attempt as the gods are behind them (Best, 1898).

These rituals illustrate the cultural importance of the weaver and pieces that they create. The pieces are more than clothing; they are treasured items or *taonga*. They represent a living culture, their histories and *whakapapa* being as important as the garments themselves. There are hundreds of these beautiful cloaks in museums worldwide that we know very little about. It is all too common to have no details regarding provenance, or the species of the feathers used to adorn these garments. With advances in molecular techniques and the ability to work successfully with biological materials containing very little, damaged DNA, it is possible to perform genetic analyses that allow us to delve into the histories of these culturally valuable items, with the aim of re-establishing their living culture. Given the sheer number of these cloaks in storage in museums, this work will focus on the prestigious kiwi feather cloaks or *kahu kiwi*, with one exception (see chapter 3.).

The Kiwi – *Apteryx* spp.

Recent mitochondrial DNA (mtDNA) analysis of kiwi (*Apteryx spp.*) has prompted their reclassification into five distinct species (Baker *et al* 1995; Burbidge *et al* 2003). Kiwi were found to have extremely subdivided population structure due to their low dispersal power (Baker *et al* 1995). Long-term geographical isolation, lack of hybridisation in introduced populations and the accumulation of new biological characteristics within these lineages has resulted in distinct species (Burbidge et al 2003).

Current classification and species distribution

There are two species of spotted kiwi; the great spotted kiwi (*Apteryx australis haasti*) and the little spotted kiwi (*Apteryx australis owenii*). Great spotted kiwi are currently distributed in the north west of the South Island of New Zealand. The current distribution of great spotted kiwi is thought to reflect past distributions (Shepherd and Lambert 2008). Little spotted kiwi were once widespread across both the North and South Island, but the population has declined to such a degree that they are restricted to conservation refuge islands in the Hauraki Gulf and the Cook Strait (Shepherd and Lambert 2008). The three species of brown kiwi are morphologically similar to the point that they were once deemed to be one species, divided into two subspecies *Apteryx australis australis* (South Island) and *Apteryx australis mantelli* (North Island). However, mitochondrial DNA analysis (Burbidge *et al* 2003) revealed that there are actually three distinct species, the North Island brown kiwi (*Apteryx australis mantelli*), the South Island and Stewart Island tokoeka (*Apteryx autralis australis*) and the Okarito rowi (*Apteryx australis rowi*). The North Island brown kiwi is currently distributed in the far north, the Coromandel, the east of the North Island and the west of the North Island and are currently extinct from the lower portion of the North Island, although they are being reintroduced to this region (Holzapfel et al 2008). Tokoeka are currently distributed in the south west of the South Island and Stewart Island. However, ancient DNA analysis has revealed that their distribution was once much more widespread with subfossil bones from that species being found in the east of the South Island (Shepherd and Lambert 2008). Rowi are currently restricted to one population in Okarito on the west coast of the South Island, although ancient DNA

analysis suggests they were once found on both the South Island and lower North Island of New Zealand.

All kiwi species are endangered. The rowi and the Haast Tokoeka are deemed nationally critical, North Island brown kiwi are seriously declining, great spotted kiwi and Southern tokoeka are gradually declining and little spotted kiwi are range restricted (Sales 2005). For example, between 1996 and 2005 there has been a decline in the North Island brown kiwi from 35,000 to 20,000 individuals (Sales 2005). This decline is largely attributed to predation from introduced mammals such as cats, dogs, ferrets, pigs, possums, stoats and weasels (McLennan *et al* 1996) and loss of habitat.

Past distributions

Shepherd and Lambert (2008) used ancient mitochondrial DNA analysis to contrast past and present levels of genetic variation in kiwi. Looking to identify species boundaries and reveal former ranges among morphologically cryptic taxa. However, sample ages were either unknown or highly variable, dating back 4000 years in some cases. Also the sample sizes were limited to those available in museums (n=47). With Māori cloaks we have the advantage of kiwi feather samples all of a similar age (~150 years before present (BP)) for the majority of cloaks analysed and also at an age where arguably humans were contributing to the kiwis' largest period of decline either through direct action (food, clothing, habitat destruction) or through the action of mammalian predators brought to New Zealand by humans. Additionally, with over a hundred kiwi feather cloaks available and potentially 12 kiwi per cloak (Te Kanawa, 1992), this would result in a vastly increased sample size to look at changes in kiwi diversity in the recent past.

Summary

Utilising ancient DNA methods (Chapter 2), this thesis will use mtDNA analysis to identify the species of birds used in the construction of feather cloaks and kete (Chapters 3, 5, 6). It will also look at current populations of North Island brown

kiwi (*Apteryx mantelli*), the phylogeographic structure of these populations and temporal changes from a conservation angle (Chapter 4). Finally chapters 5 and 6 focus on the how DNA can be used to enrich the cultural knowledge of cloaks and kete, the provenance, origins and methods of construction of these valuable *taonga*.

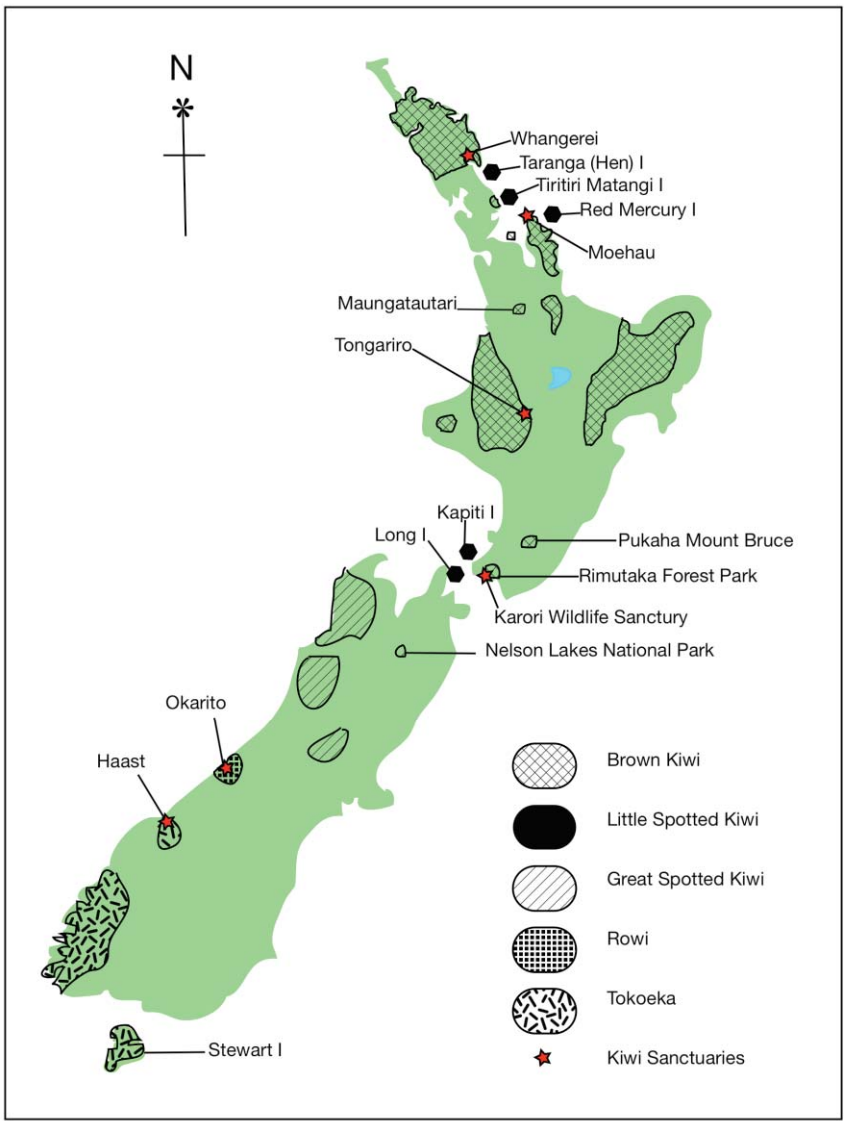


Figure 1.4. Current Distribution of Kiwi Species (Apteryx spp.) in New Zealand. Figure adapted from Holzapfel 2008.

References

Baker AJ, Daugherty CH, Colbourne R, McLennan JL. 1995. Flightless brown kiwi of New Zealand possess extremely subdivided population structure and cryptic species like small mammals. *Proceedings of the National Academy of Sciences U.S.A* 92: 8254–8258.

Barnett R, Yamaguchi N, Shapiro B, Nijman V. 2007. Using ancient DNA techniques to identify the origin of unprovenanced museum specimens as illustrated by the identification of a 19th century lion from Amsterdam. *Contributions to Zoology*. 76(2):87-94.

Best E. 1952. The Māori as he was. A brief account of Māori life as it was in pre European days. R.E. Owen, Govt. Printer.

Best E. 1902. Notes on the art of war as conducted by the Māori of New Zealand, with accounts of various customs, rites, superstitions and pertaining to war as practised and believed in by the ancient Māori. *Journal of the Polynesian Society*. 11(2):47-75.

Best E. 1898. The art of the Whare Pora: Notes on the clothing of the ancient Māori, their knowledge of preparing, dyeing, and weaving various fibres, together with some account of dress and ornaments, and the ancient ceremonies and superstitions of the Whare Pora. *Transactions and Proceedings of the Royal Society of New Zealand*. 31:625-628.

Brown JW, van Coeverden de Groot PJ, Birt TP, Suetin G, Boag PT, Friesen VL. 2007. Appraisal of the consequences of the DDT- induced bottleneck on the level of genetic variation in Canadian peregrine falcons, *Falco peregrinus. Molecular Ecology*. 16:237-343.

Burbidge L, Colbourne RM, Robertson HA, Baker AJ. 2003. Molecular and other biological evidence support the recognition of at least three species of brown kiwi. *Conservation Genetics*. 4:167-177.

Chilton G, Sorenson MD. 2007. Genetic identification of eggs purportedly from the extinct Labrador Duck (*Camptorhynchus labradorius*). *Auk*. 1224(3):962-968.

Ciborowski KL, Consuegra S, Garcia de Leaniz C, Wang J, Beaumont MA, Jordan WC. 2007. Stocking may increase mitochondrial DNA diversity but fails to halt the decline of endangered Atlantic salmon populations. *Conservation Genetics*. 8:1355-1365.

Destro-Bisol G, Jobling MA, Rocha J, Novembre J, Richards MB, Mulligan C, Batini C, Manni F. 2010. Molecular anthropology in the genomic era. *Journal of Anthropologoical Sciences*. 88:93-112.

Haak W, Balanovsky O, Sanchez JJ, Koshel S, Zaporozhchenko V, Alder CJ, Sarkissian CSID, Brandt G, Schwarz C, Nicklish N, Dresely V, Fritsch B, Balanovska E, Villems R, Meller H, Alt KU, Cooper A. 2010. Ancient DNA from European early Neolithic farmers reveals their near eastern affinities. *Plos Biology*. 8(11):1-16.

Hajibabaei M, Smith MA, Janzen DH, Rodriguez JJ, Whitfield JB, Hebert PDN. 2006. A minimalist barcode can identify a specimen whose DNA is degraded. *Molecular Ecology Notes*. 6:959-964.

Holzapfel S, Robertson HA, McLennan JA, Sporle W, Hackwell K, Impey M (2008): Kiwi (*Apteryx spp.)* recovery plan: 2008–2018. *Threatened Species recovery plan* 60. Dept. of Conservation, Wellington. 71 p.

Howe KR. 2003. The quest for origins: who first discovered and settled New Zealand and the Pacific Islands? Auckland (New Zealand): *Penguin Books*.

Huynen L, Gill B, Millar CD, Lambert DM. 2010. Ancient DNA reveals extreme nesting behaviour in New Zealand's extinct moa. *Proceedings of the National*

Academy of Sciences U.S.A. 107:16201-16206.

Lambert DM, Millar CD, Swaminathan S, Baroni C. 2010. Ancient DNA: the tempo and mode of evolution. *American Scientist*. 98:386-393.

Lambert DM, Ritchie PA, Millar CD, Holland B, Drummond AJ, Baroni C. 2002. Rates of evolution in ancient DNA from Adelie penguins. *Science*. 295:2270-2273.

McLennan JA, Potter MA, Robertson HA, Wake GC, Colbourne R, Dew L, Joyce L, McCann AJ, Miles J, Miller PJ, Reid J. 1996. Role of predation in the decline of the kiwi, Apteryx spp., in New Zealand. *New Zealand Journal of Ecology*. 20(1):27-35.

Oskam CL, Haile J, Mclay E, et al. 2010. Fossil avian eggshell preserves ancient DNA. *Proceedings of the royal society of London B Biological Sciences*. 277:1991-2000.

Pendergrast M. 1984. Feathers and fibre: a survey of traditional and contemporary Māori craft. Auckland (New Zealand): Penguin Books.

Pendergrast M. 1987. Te Aho Tapu, the sacred thread. Auckland (New Zealand) Reed Publishing Limited.

Pendergrast M. 1997. Kakahu, Māori cloaks. Auckland (New Zealand): Auckland Museum.

Sales J. 2005. The endangered kiwi: a review. *Folia Zoologica* 54: 1-20.

Shepherd LD, Lambert DM. 2008. Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Te Kanawa D. 1992. Weaving a kakahu. Wellington (New Zealand): Bridget Williams Books Limited.

Te Rangi Hiroa. 1924. The evolution of Māori clothing. *Journal of the Polynesian Society*. 33(29):25-47.

Wanderler P, Hoek PEA, Keller LF. 2007. Back to the future: museum specimens in population genetics. *Trends in Ecology and Evolution*. 22(12):634-642.

Chapter Two

Materials and Methods

Sampling

Reference database

Twenty-one North Island brown kiwi mitochondrial DNA control region Domain I sequences from modern kiwi populations were available on genbank (Burbidge et al 2003 (Accession numbers AY150609–AY150623) Shepherd 2006, Shepherd and Lambert 2008 (Accession numbers AY713315, AY713332, AY713335, AY713336, DQ295829, DQ2952830)). To further build upon the reference database, 174 North Island brown kiwi samples from known locations were kindly provided to us by the Department of Conservation and Rainbow Springs Kiwi Encounter, Rotorua, (see table 4.1, chapter 4). Samples consisted of either a blood sample stored in ethanol or plucked feathers stored in paper envelopes. Ten of the samples provided to us were either from reintroduced populations or from wildlife parks without robust population histories. As a result of this, these samples were omitted from the study leaving us with 164 samples, to give a total of 185 mtDNA CR sequences.

Cloaks

Museums Visited

Preliminary research on the numbers of cloaks held in museums in New Zealand and overseas revealed a wealth of kiwi feather cloaks. Hence, the sampling effort was redirected from feathered cloaks in general to concentrate on kiwi feather cloaks (Table 2.1) and kete (Table 2.2).

Table 2.1 Museums from which cloak samples were obtained

Museum	Number of Cloaks Sampled	Number of Samples Taken (total)
Hawkes Bay Museum and Cultural Trust, Napier (HB)	16	94
British Museum, London (BM)	9	90
Te Papa Tongawera, Wellington (TP)	27	383
Canterbury Museum, Christchurch (C)	17	170
Waikato Museum, Hamilton (WK)	4	37
Hornimann Museum, London (HM)	3	30
Auckland Museum (AK)	13	153
Wanganui Museum (WG)	24	253
Totals	113	1210

Sampling Technique

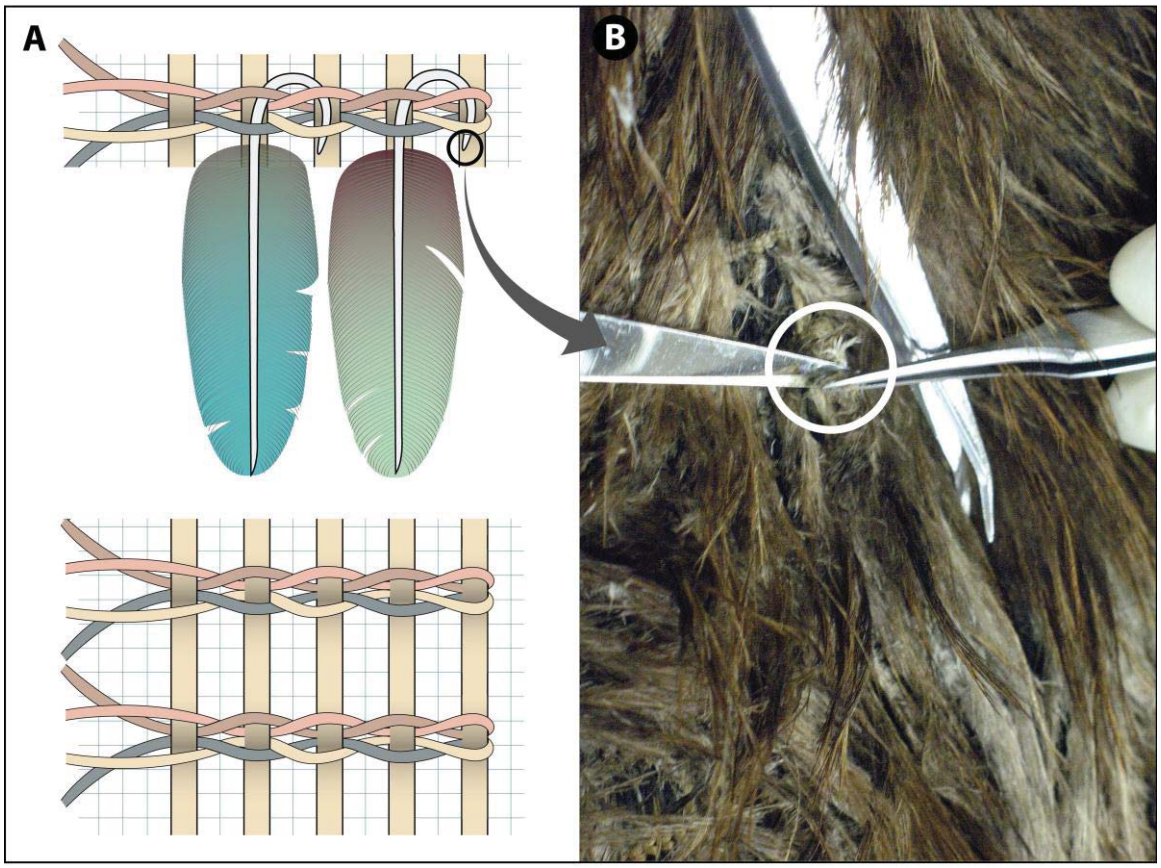


Figure 2.1. How feathers are woven into the flax fibres (*muka*) comprises the body of the cloak (A) and a photograph of a sample being taken from a kiwi feather cloak (B).

During cloak construction kiwi feathers are grouped into 3 or 4 feathers and woven into the cloak. Each group of feathers is woven into the cloak twice (see figure 2.1). This enabled us to remove approximately a 2mm section of tissue from the shaft of the feather using sterilised forceps and surgical scissors. Importantly, this minimises any damage to the integrity and the appearance of cloaks. We

sampled feathers from 113 cloaks, taking typically 10-15 randomly (figure 2.2) selected samples per cloak with a total of 1210 samples. Samples were stored in paper envelopes in a dedicated ancient DNA facility prior to DNA extraction.

Figure 2.2 Samples were taken at random points across the surface of each cloak.

Given the precious nature of the cloaks and kete being sampled from, it was imperative that the number of samples taken from each item was minimal, whilst still allowing a significant amount of data to be recovered. A haplotype discovery graph was constructed in order to ascertain this number using sequence data from preliminary data produced for this thesis and from Shepherd 2006 (Figure 2.3). This graph showed that 12 sequences resulted in the greatest mean number of haplotypes. However, preliminary work (Shepherd 2006) coupled with a pilot study has shown that the sequence recovery rate from ~ 150-year-old cloak feather samples is below 70%. Therefore the number of samples taken from each individual cloak would ideally be around 17 to account for this success rate. Given the delicate nature of the artefacts and advice from textile conservator Rangi Te Kanawa, coupled with time and cost constraints, it was not feasible to take 17 samples from each cloak. However, when as many as 23 sequences were obtained from a single cloak, this resulted in only three haplotypes to be present. Hence, the decision to take 10 – 15 samples per cloak where appropriate does not impact on the significance of this work.

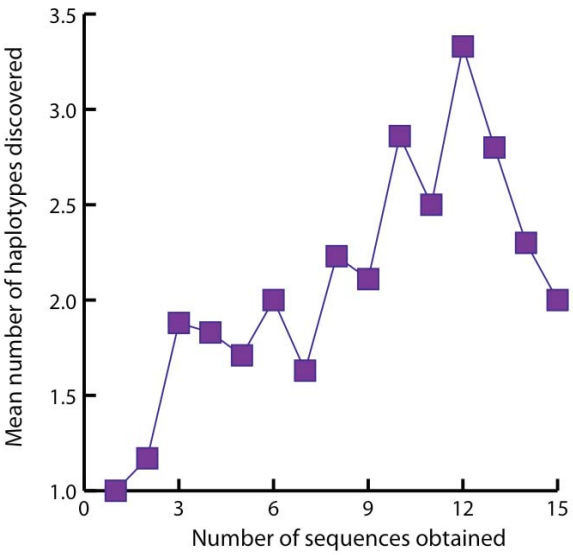


Figure 2.3 Haplotype discovery graph plotting the number of haplotypes discovered against the number of sequences obtained for each cloak.

Kete

In addition to sampling kiwi feather shafts from cloaks, samples were obtained from kete (woven bags) the sampling technique was the same, although, as these artefacts are much smaller than cloaks, fewer samples were taken. Typically 2-6 samples were taken per kete, with the samples taken divided equally between the two sides of the artefacts.

Table 2.2 Museums from which kete were sampled

Museum	**Number of Kete Sampled**	**Number of Samples Taken (total)**
British Museum, London (BM)	5	20
Te Papa Tongawera, Wellington (TP)	9	34
Canterbury Museum, Christchurch (C)	13	54
Waikato Museum, Hamilton (WK)	5	17
Hornimann Museum, London (HM)	1	4
Auckland Museum (AK)	18	62
Wanganui Museum (WG)	11	44
Totals	62	235

DNA Extraction

Preparation and extraction of samples took place in a dedicated ancient DNA facility at Massey University's Albany campus. This facility is physically separated from modern laboratories that handle amplified PCR products and modern sources of DNA. It also undergoes regular decontamination with bleach and is subjected to UV radiation. As previously mentioned, kiwi feathers are woven into cloaks in groups of 3-4. However, there is no guarantee that all of the feathers came from the same bird. Prior to extraction feather shafts from one sample were separated into single shafts to avoid contamination and to ensure DNA from two or more individuals were not present in any one extract. Following isolation of single feather shafts, each shaft was put into a 1.7ml micro centrifuge tube with 200µl of SET buffer (100mM Tris-HCL pH 8.0, 100mM NaCl, 1mM EDTA), 20µl of Proteinase K (20mg/ml), 10µl of 1M Dithiothreitol (DTT) and 20µl of 10% SDS. The micro centrifuge tubes were incubated at 55°C overnight. A negative extraction was completed for every 20 samples to account for contamination during the extraction process.

Following incubation, 750µl of Phenol: Chloroform: Isoamyl alcohol (25:24:1) was added to all samples, vortexed and centrifuged at 20, 000 x g for 1 minute. Following centrifugation, 200µl of the top layer of each sample was transferred to a fresh micro centrifuge tube and the remaining liquid was discarded. The remainder of the extraction process was conducted using a DNeasy Blood and Tissue Extraction kit (Qiagen). The only deviations from the protocol were that the elution buffer was heated to 50°C prior to addition to the columns in order to improve DNA yield, and DNA was eluted in 100µl of this buffer.

Modern samples for the reference database were extracted using the same method with the exception that the extraction process took place in a laboratory that handles modern sources of DNA and amplified PCR products.

For extraction of the emu feather in chapter 3 the extraction process deviated from above. DNA was extracted from each feather shaft by overnight incubation, with rotation, at 55°C in 300 µl of extraction buffer (10mM Tris-HCl pH 8.0, 50mM NaCl, and 1mM EDTA) supplemented with 30 µl of 10% SDS, 5µl of 1M DTT, and 5µl of 20mg/ml proteinase K. 200 µl of each mix was then purified using a QIAamp DNA Mini Kit (Qiagen) as outlined by the manufacturer.

Mitochondrial DNA Sequencing

Kiwi feathers

A 200bp fragment of the mtDNA control region domain I was amplified using kiwi specific primers kcf (5'CAGTATGGTCACCGAACAC) and kcr (5'ACAGGGGTTGCTGATTTCA) in a 20µl PCR mixture containing 2µl of DNA, 1xPCR buffer (50mM Tris pH8.8, 200mM ($(NH_4)_2SO_4$), 1.5mM $MgCl_2$, 2mg/µl BSA, 0.5 Units of Platinum Taq (Invitrogen), 0.5µM of each primer, 200µM of each DNTP and ddH_2O. The PCR Program consisted of 1 cycle of 94°C for 2 minutes, 10 cycles of 94°C for 20 seconds, 55°C for 20 seconds and 72°C for 1 minute, 32 cycles of 94°C for 20 seconds, 50°C for 20 seconds and 72°C for 1 minute with a final extension time of 72°C for 5 minutes. All PCRs contained PCR and extraction negatives to account for potential contamination. PCRs for the cloak samples were prepared in a dedicated ancient DNA facility.

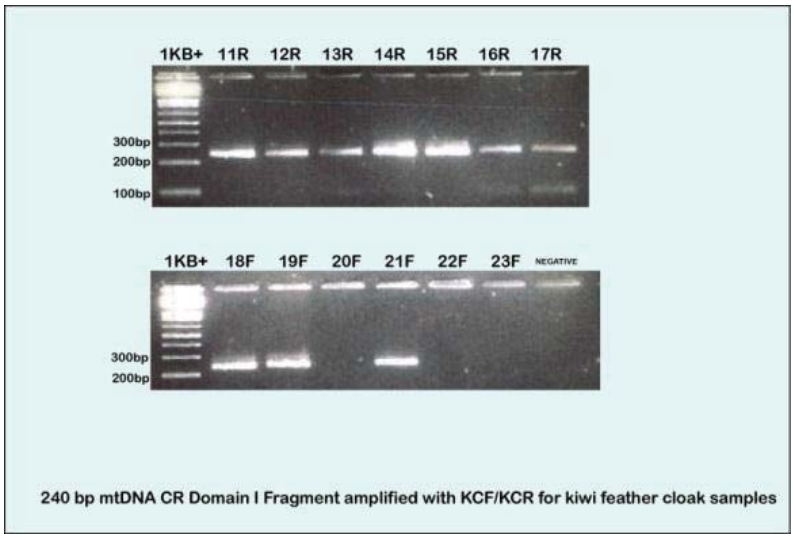


Figure 2.4 Amplification of ~240bp mtDNA HVRI fragment for cloak samples using primers Kcf and Kcr.

Samples were checked for amplification success by size fractionation of products on a 2% agarose gel with a 1KB+ ladder. Samples that produced a clean product ~240bp in size were selected for sequencing. Prior to sequencing samples were purified to remove excess salts and DNTP's using Agencourt AMPure magnetic bead-based PCR purification system (Agencourt Bioscience) according to the manufacturer's instructions with the following modifications. Only 10μl of the magnetic bead mixture was added to each sample with 50μl of 70% ETOH to reduce the number of wash steps. The purified product was then re-suspended in 25μl of ddH_2O.

Sequencing was then conducted in 15μl volumes using 1μl of Big Dye V3.1, 3.5μl of sequencing buffer, 3.2picomoles (1μl) of primer (kcf or kcr), 5ng/μl (1μl) of DNA, and 8.5μl of ddH_2O. Each sample was sequenced in both directions from independent PCR amplifications to account for potential contamination and miscoding lesions (Willerslev & Cooper 2005).

Emu feathers

Chapter 3 of this thesis aims to identify ratite feathers on an unusual cloak. This method relates directly to that chapter.

Ratite-specific mitochondrial 12S primers, ratite12S1 (5'CCTCAGAAGGCGGATTTAGCAGTAA) and ratite12S4 (5'-ATCTTTCAGGTGTAAGCTGAATGCTT), were designed using sequences retrieved from GenBank: rhea (*Rhea americana* – AJ002923), ostrich (*Struthio camelus* – AF069429), great spotted kiwi (*Apteryx haasti* – AF338708.2), cassowary (*Casuarius casuarius* – AF338713.2) and emu (*Dromaius novaehollandiae* – AF338711.1). DNAs extracted from cloak feathers and moa bone (*Emeus crassus*, Canterbury Museum CM_Av9132) were then amplified using the primers ratite12S1 and ratite12S4 as described in Huynen *et al.* (2003). Successfully amplified fragments of ~220 bp were sequenced in both directions using Applied Biosystems BigDye Terminator v3.1 chemistry and aligned to homologous sequences from other ratites using the Sequencher program.

Sexing

It is possible to recover the sex of individual birds from the feathers used to construct Māori cloaks. An observed skew in the sex ratio could give us insight into Māori hunting practices and selection of birds of different sexes. In addition, it could also have implications for the behavioural ecology of kiwi species. For example, it is known in the North Island brown kiwi (*Apteryx australis mantelli*) males, not the females that incubate the eggs (Colbourne 2002). This could make them more vulnerable to predation and therefore, more likely to be hunted by Māori.

The genetic basis of avian sex is now well established (Griffiths et al 1998, Huynen et al 2002). In kiwi (*Apteryx spp.)* it is difficult to distinguish between the sexes, as juveniles are morphologically and behaviourally similar. Older individuals (>1yr old) are distinguishable through differences in weight, calls and behaviour (Huynen *et al* 2003). In the case of feathers obtained from cloaks, distinguishing between the sexes is not possible without the aid of genetic diagnosis. Also, given that the feather samples obtained from cloaks are old (~150-yrs-old), DNA is fragmented and low in copy number, specifically the nuclear DNA required for sexing. To overcome this problem we used primers previously used to sex moa and that amplify very small fragment sizes. These were tested and proved effective (Huynen *et al* 2003). These comprised of female specific primers moa1 (5'CCATGTTCACTGTTTTCTTACTAAT) and moa2 (5'ATGTTAAGCAATGCTCTATGACAGA), which produced a 67bp product. The presence of nuclear DNA was determined by the amplification of 65bp of the nuclear CHD gene using primers pM0 (5'GATAGTGACTCCATCTCAGAA) and pM1 (5'GGGAATAGTTCGTTGGTCTTCC).

Reactions for both primer pairs were carried out in 20μl reactions containing 2μl of template DNA, 50Mm Tris-HCL (pH8.8), 20mM $(NH_4)_2SO_4$, 2.5mM $MgCl_2$, 1mg/μl

BSA, 100μM of each DNTP, 0.2 Units of Platinum Taq (Invitrogen) and 0.5μM of each primer (either moa1/moa2 or pM0/pM1). The reaction mixture was amplified using a PCR program of 94°C for 2 minutes, 10 cycles of 94°C for 20 seconds, 54°C for 20 seconds, and 72°C for 20 seconds followed by 40 cycles of 94°C for 20 seconds, 50°C for 20 seconds and 72°C for 20 seconds. A positive (female) and negative control was run with each PCR reaction. Also, to account for potential allelic dropout, a multiple tube approach was used (Taberlet *et al* 1996), with each feather cloak sample undergoing three independent amplifications for each of the two primer pairs to produce a consensus sex for each sample. To determine sex, PCR product was visualised in a 1% low melting point and 1% standard agarose gel under UV.

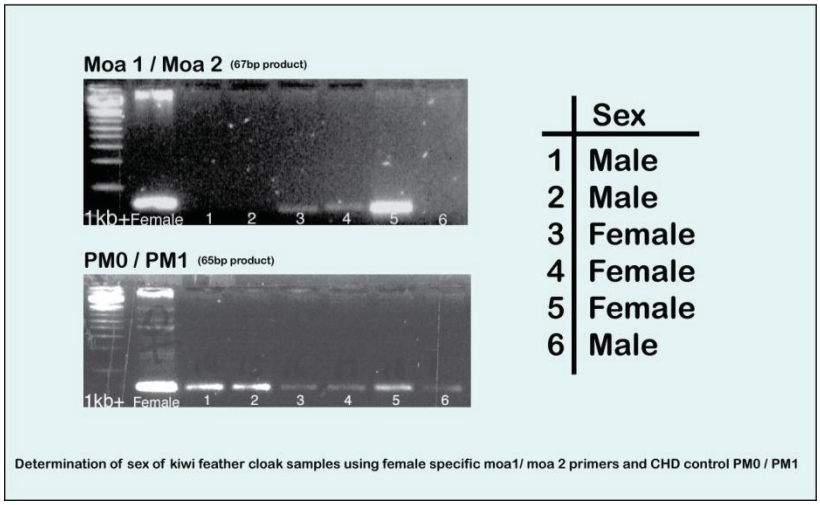


Figure 2.5 Determination of sex using W chromosome (female) specific Moa 1 / Moa 2 primers and CHD control primers PM0 / PM1. Absence of amplification for Moa 1 / Moa 2 coupled with a successful amplification for PM0 / PM1 would suggest the sex of the individual as male. Successful amplification for both primers would suggest the sex of the individual as female.

Rules of Sex Assignment

The accurate amplification of nuclear DNA fragments from ancient / damaged DNA is rife with problems and the potential for error is high. The most common problems encountered are allelic dropout and the generation of false alleles (Creel et al 2003). The most stringent method to lessen or avoid these errors is the adoption of a multiple tube approach (Taberlet et al 1996). Such an approach was employed in the sexing of kiwi cloak feathers. There is always a fine balance

between a conservative, accurate approach and the limitations impeded on the execution of such measures. Resources must be taken into account, such as the costs involved and the amount of precious DNA available. Taking such limitations on board, the following multiple tubes approach was applied in the case of sexing. All samples were amplified with both sets of primers (moa1/moa2, p0/p1) a minimum of three times. Sexing was assigned on the basis of the following rules.

- If a band was present for the control (p0/p1), but not for the female specific marker for at least 2/3 amplifications, the sex was assigned as male.
- If a band was present for the control (p0/p1) and for the female specific marker for at least 2/3 amplifications, the sex was assigned as female.
- If no bands were present for any of the 3 amplification attempts then samples were considered to have failed to amplify and were not included in further analysis.
- If 1/3 amplifications resulted in bands either for the control or the female specific marker a 4th amplification was conducted. If the 4th amplification matched the previous amplification, sex was assigned accordingly. In the event of a mismatch or a failed amplification, that sample was excluded from further analysis.
- If a band was present at least 2/3 times for the female specific marker (moa1/ moa2) but absent in 1, 2 or 3 of the control reactions (p0/p1), the sex was still assigned as female to lessen the chances of an overrepresentation of males.

Independent verification of results

Fifteen feathers from cloaks were selected for independent extraction, amplification and sequencing (see table 2.3). This was to ensure that sequences obtained were reliable and not subject to contamination or sequencing-based errors such as miscoding lesions and nuclear mitochondrial DNA (numts (Gilbert et al 2003, Sorenson and Quinn 1998)). As previously mentioned, it is unlikely that all the feathers from a cloak came from just one kiwi. Also, although feathers are woven into the cloak in groups of 3 or 4, there is no guarantee that all these

feathers came from the same individual. This makes replication of results difficult because results must be replicated from one single feather shaft.

The selected feather shafts were cut down the middle to allow one half to be extracted, amplified and sequenced at Massey University's aDNA laboratory (Albany campus). The other half was taken to a dedicated aDNA laboratory at the University of Auckland for extraction, amplification and sequencing. All samples were sequenced in both directions with kiwi specific mtDNA Control Region primers kcf and kcr.

Table 2.3. Independent verification of cloak sequences

Cloak	Sample Number	Haplotype Massey University		Haplotype University	Auckland	Match?
		KCF	KCR	KCF	KCR	
TP_ME14499	268A / 268B	5	5	Failed	Failed	N / A
TP_ME14499	269A / 269B	8	8	Failed	Failed	N / A
TP_ME14499	270A / 270B	8	8	8	8	YES
TP_ME14499	272A / 272B	13	13	13	13	YES
TP_ME14499	273A / 273B	8	8	8	8	YES
TP_ME15753	326A / 326B	9	9	9	9	YES
TP_ME15753	329A / 329B	9	9	9	9	YES
TP_ME15753	330A / 330B	10	10	10	10	YES
TP_ME15753	331A / 331B	10	10	10	10	YES
TP_ME15753	332A / 332B	Failed	Failed	Failed	Failed	N / A
TP_ME1378	344A / 344B	8	8	8	8	YES
TP_ME1378	345A / 345B	10	10	10	10	YES
TP_ME1378	346A / 346B	8	8	8	8	YES
TP_ME1378	347A / 347B	10	10	10	10	YES
TP_ME1378	348A / 348B	Failed	Failed	Failed	Failed	N / A

Sequence Analysis

All forward and reverse sequences were imported into Sequencher Version 2.6 for editing and alignment. A reference sequence obtained from genbank from NIBK was included in all alignments.

Miscoding Lesions

Upon the occurrence of a miscoding lesion when forward and reverse sequences were aligned, the samples were to be sequenced again in both directions from independent reactions to resolve the discrepancies. However, no miscoding lesions or other sequencing errors were encountered during the course of this work.

PAUP version 4.0 (Swofford 2000) was used to construct Statistical Parsimony and Neighbor Joining trees for sequences obtained from the reference database and cloak samples for North Island brown kiwi. Reference sequences for the other four kiwi species were obtained from Genbank and included in the analyses.

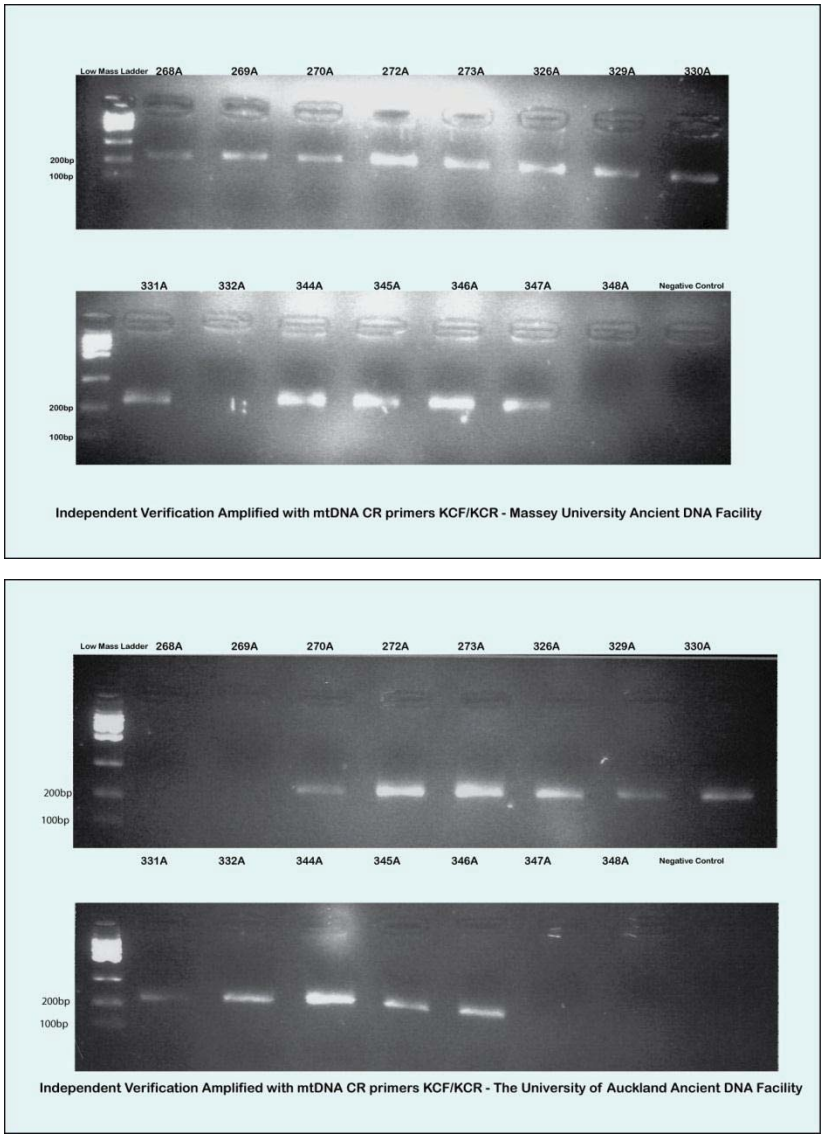


Figure 2.6. Independent verification of cloak samples using mtDNA HVRI primers Kcf / Kcr. Each sample was independently extracted and amplified at Massey University (top) and the University of Auckland (bottom).

Statistical Parsimony Network

The freely available software programme TCS (Clement et al 2000) was used to create Statistical Parsimony networks of NIBK haplotypes. A 95% parsimony limit was imposed.

Nested Clade Analysis Using GeoDis

Freely available software programme GeoDis (Posada et al 2000) was used to explore the geographic distribution of haplotypes in modern North Island Brown Kiwi using the control region sequences obtained for the reference database Firstly Google Earth software was used to assign a central grid reference to each of the populations sampled from. Then, using the statistical parsimony network constructed using TCS and the laws of NCA as a guide (Templeton et al 1995), haplotypes within the network were assigned to a particular clade (see chapters 4 and 5 for details). Once clades were assigned this information was used, together with the grid references obtained for each population in a data file. Analyses using NCA were then performed and the results interpreted in chapter 4.

References

Burbidge L, Coulbourne RM, Robertson HA, Baker AJ. 2003. Molecular and other biological evidence support the recognition of at least three species of brown kiwi. *Conservation Genetics*. 4:167-177.

Clement M, Posada D, Crandall KA. 2000. TCS: a computer program to estimate gene genealogies. *Molecular Ecology*. 9:1657-1659.

Colbourne R 2002. Incubation behaviour and egg physiology of kiwi (*Apteryx* spp.) in natural habitats. *New Zealand Journal of Ecology*. 26(2):129-138.

Creel S, Spong G, Sandy JL, Rotella J, Zeigle J, Joe L, Murphy KM, Smith D. 2003. Population size estimation in Yellowstone wolves with error-prone noninvasive microsatellite genotypes. *Molecular Ecology*. 12:2003-2009.

Gilbert MTP, Hansen AJ, Willerslev E, Rudbeck L, Barnes I, Lynnerup N, Cooper A. 2003. Characterization of genetic miscoding lesions caused by post mortem damage. *American Journal of Human Genetics*. 72:48-61.

Griffith R, Double MC, Orr K, Dawson RJG. A DNA test to sex most birds. *Molecular Ecology.* 7:1071-1075.

Huynen L, Millar CD, Lambert DM. 2002. A DNA test to sex ratite birds. *Molecular Ecology.* 11(4):851-856.

Huynen L, Millar CD, Scofield RP, Lambert DM. 2003. Nuclear DNA sequences detect species limits in moa. *Nature.* 425:175-178.

Posada D, Crandall KA, Templeton AR. 2000. GeoDis: a program for the cladistic nested analysis of the geographical distribution of genetic haplotypes. *Molecular Ecology*. 9:487-488.

Shepherd LD. 2006. Ancient DNA studies of the New Zealand kiwi and wattlebirds: evolution, conservation and culture. [PhD Thesis]. [Auckland (New Zealand)]: Massey University.

Shepherd LD, Lambert DM. 2008. Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Sorenson MD, Quinn TW. 1998. Numts: a challenge for avian systematics and population biology. *The Auk.* 115(1):214-221.

Swofford DL. 2000. PAUP*. Phylogenetic analysis using parsimony (*and other methods). Version 4. Sunderland (MA): SinauerAssociates.

Templeton AR, Routman E, Phillips CA. 1995. Separating population structure from population history: a cladistic analysis of the geographical distribution of

mitochondrial DNA haplotypes in the tiger salamander, *Ambystoma tigrinum. Genetics*. 140:767-782.

Willerslev E, Cooper A. 2005. Ancient DNA. *Proceedings of the Royal Society of London B biological sciences*. 272:3-16.

Chapter 3

A Molecular Study of a rare Māori Cloak[1]

Abstract

Kakahu or Māori cloaks are *taonga* (treasures) and are iconic expressions of Māori culture. Unfortunately much of the original information relating to the origins of these cloaks has been lost. We present mitochondrial 12S sequence data from feathers sampled from a rare cloak that had the potential to be adorned with feathers from New Zealand moa. These species belonged to the ratite group of birds and have been extinct soon after human arrival in New Zealand. Using microscopic amounts of feather tissues from this cloak, we have been able to show that this garment was actually constructed from Australian emu feathers. At the likely time of construction of the cloak, the then Governor of New Zealand, George Grey, kept emu on Kawau Island in the Hauraki Gulf. It seems probable that the remains of these individuals were the source of the feathers used, although we are not able to exclude the possibility that Māori obtained them as a result of early trading with Australia. To our knowledge, this study is the first to use genetic techniques to identify the species of bird used in feather adorned Māori cloaks and illustrates the potential for molecular techniques to provide important information pertaining to these *taonga.*

Introduction

During part of a larger study of Māori feathered textiles, this unusual cloak was

[1] This chapter has also been published in a peer reviewed journal and as a book chapter.
Hartnup K, Huynen L, Te Kanawa R, Shepherd L, Millar C and Lambert D. 2009. A molecular study of a rare Maori cloak. Archaeological Science Under a Microscope, Terra Australis 30, 15 (198-206). Terra Australis ANU Press.

KH researched and wrote the manuscript, assisted with figure preparation and collected samples.

identified in collections at the Hawkes Bay Museum and Cultural Trust. This was the first cloak of this type to have been observed (Figure 3.1A). The cloak's construction comprised a finely woven *muka* body or *kaupapa*, completely adorned with feathers that were extremely similar in morphology to moa feathers (Worthy and Holdaway 2002) (Figure 1B). Moa (Aves: Dinornithiformes) were foremost among the evolutionary novelties of New Zealand. Richard Owen first brought the presence of moa in New Zealand to the attention of European scientists in 1842, when he described a femur shaft. Since that time the number and age of fossil specimens has grown considerably and suggests that moa inhabited New Zealand from over two million years ago (Anderson 1989, Worthy and Holdaway 2002). Although small groups of moa likely survived in remote locations for slightly longer, the main populations were probably extinct by AD 1400 (Anderson 1989, Worthy and Holdaway 2002). Ancient DNA work has identified as many as 10 species of extinct moa in New Zealand, varying greatly in habitat and morphology (Bunce et al 2009, Huynen et al 2010). Very few moa specimens have been excavated with their feathers intact. The few feathers recovered possessed a range of colours including white, reddish brown grading distally to black with a white tip, and purplish brown with a yellow stripe. Feathers were typically no longer than 18 cm in length, although feathers up to 23 cm in length have been recorded (Worthy and Holdaway 2002). Recently genetic analysis has been carried out on a range of subfossil moa feathers, with an aim to determine species, successfully obtain DNA from previously overlooked areas of the feather, and look at pigmentation and to reconstruct how moa plumage would have appeared. Short fragments of mitochondrial DNA sequences were retrieved from these sub-fossil feathers, allowing the species of moa to be determined. Also, the study showed that feather pigmentation of these sub-fossil feathers faded at a measurable rate and thus, the phenotype of the moa could be inferred (Rawlence et al 2009). However, at the time our work was conducted, this paper had not yet been published. It is possible to estimate the age of Māori cloaks due to variations in weaving techniques over time. The potential 'moa' cloak has been estimated (Rangi Te Kanawa, Māori Textile Conservator, pers. comm.) to have been constructed in ~1850. Therefore, despite the similarity in feather morphology between the cloak and moa feathers, there is a large disparity between the time

that moa became extinct and the estimated time of cloak construction. Despite this disparity, it is possible that moa feathers were stored for some time prior to their use in the construction of the Hawkes Bay cloak. In order to test the possibility of a 'moa' cloak, ancient DNA techniques were employed to recover DNA sequences from cloak feathers and to compare these sequences with those obtained from moa bones and from a range of other ratite species.

Figure 3.1 (A) Cloak #45_264 from Hawkes Bay Museum and Cultural Trust. (B) Moa feathers found in Moncks Cave, near Christchurch, Canterbury.

Materials and Methods

A total of 7 feather samples were taken from the suspected moa cloak #45_264 from the Hawkes Bay Museum and Cultural Trust. DNA was extracted from these feathers as described in the methods chapter (2) and this DNA was amplified and sequenced using ratite-specific mitochondrial 12S primers, ratite12S1 (5'CCTCAGAAGGCGGATTTAGCAGTAA) and ratite12S4 (5'-ATCTTTCAGGTGTAAGCTGAATGCTT), also described in the methods chapter of this thesis (chapter 2). This process was repeated for a moa bone (*Emeus crassus*, Canterbury Museum CM_Av9132) for sequence comparison with the cloak feather samples.

Results

Two of the seven feather shafts sampled from cloak #45_264 amplified for a 220 bp sequence from the 12S region of the mitochondrial genome. These two sequences were aligned with homologous data from ratite species as shown in figure 3.2A. The two cloak sequences differed from each other at just two sites of the ~220 bp fragment (sites 5 and 16), suggesting the use of feathers from at least two different individuals in cloak construction. Cloak sample 2 was identical to the sequence of emu from Genbank. Both of the cloak sequences varied substantially from the moa sequence (11% average), and from other ratites for which sequences were available (rhea - 14.3%, kiwi - 8.6%, ostrich - 6.8% and cassowary - 5.9%). On average, the cloak sequences differed from the emu sequence by just 0.45%. Figure 3.2 presents an unrooted, Neighbor-Joining tree of 12S sequences implemented in PAUP* (Swofford 2002). The tree groups the sampled cloak feathers with emu. As the 12S mtDNA sequences targeted in this study are highly variable and difficult to align, they do not effectively resolve relationships amongst ratites. Haddrath and Baker (2001) used whole mitochondrial genomes to successfully investigate ratite phylogeny. It should be noted that more recently phylogenies have been reconstructed (Harshman et al 2008, Phillips et al 2010). Previously assigned flighted sister group of the tinamous (*Tinamidae*) has been found to be nested within ratites. Tinamous were found to align closely with moa. The tinamou / moa group aligned closely with kiwi, emu and cassowaries, with rhea and ostriches being more divergent. The newly constructed phylogenies also suggest multiple losses of flight in the ratites, supporting parallel or convergent evolution. Although the 12S region fails to elucidate this phylogeny, the variability within the 12S region is ideal for species identification, making it a suitable choice for identifying the cloak samples.

Discussion

We can conclude that this unique cloak from the Hawkes Bay Museum and Cultural Trust was not constructed using moa feathers. It was, however, adorned with

feathers from emu, a ratite that originated in Australia and is not found in wild populations in New Zealand. Taking these findings into account, how did Māori in

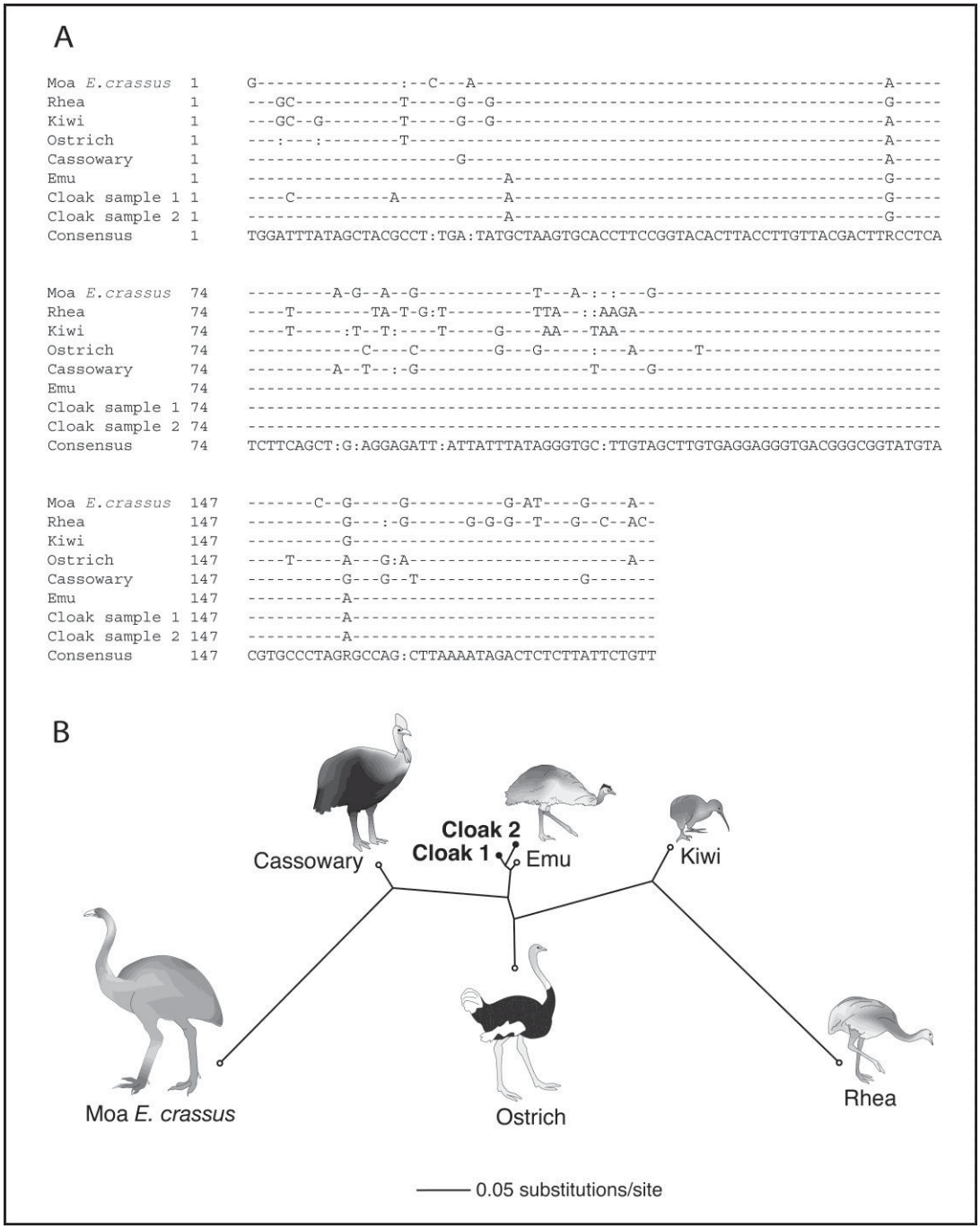


Figure 3.2. Aligned mitochondrial 12S DNA sequences of cloak feather samples, moa and other ratites (A). (-) indicates a base identical to the consensus sequences, (:) indicates a deletion in relation to the consensus sequence. An unrooted, Neighbor-Joining tree of 12S sequences from a range of ratite species (B), together with the two sequences recovered from the cloak samples.

the second half of the 19th century obtain feathers from a native Australian bird

species? There are two possible explanations for this. First, the emu feathers may have come from Sir George Grey's exotic flora and fauna collection on Kawau Island, north of Auckland. Second, the emu feathers may have been brought from Australia during a period of extensive timber and flax trading.

Sir George Grey

George Grey had a relationship with New Zealand spanning many years. He was appointed governor of New Zealand in 1845. Arguably his greatest success during this nine-year period was his management of Māori affairs. He scrupulously observed the terms of the Treaty of Waitangi and assured Māori that their rights to their land were fully recognised. He subsidised schools for Māori children, built several hospitals and encouraged Māori agriculture (Sinclair 2007). Grey enjoyed great *mana* (power, respect and prestige) among Māori, often travelling with chiefs. He was instrumental in efforts to record Māori traditions, legends and customs in written form. Te Rangikaheke, a Te Arawa tribal leader, taught Grey to speak Māori and lived with Grey and his wife in their house.

Although Grey's second term as Governor from 1860-1868 was less successful because of extensive battles between Māori and settlers, he remained respected by Māori. Grey purchased Kawau Island, located north of Auckland in the Hauraki Gulf, in 1862 (Figure 3.3). He poured a great deal of his energy, effort and fortune into the 2000 ha island. He turned the existing copper miner's cottage into the formidable Mansion House and turned the land around the house into a botanical and zoological park. Grey imported seeds and cuttings from all over the world including redwood (*Sequoia sempervirens*) from Western USA, the Chilean wine palm (*Jubaea spectabilis*), the giant bird of paradise (*Strelitza nicolai*) from South Africa and the Japanese cedar (*Cryptomeria japonica*). Grey also imported various exotic fauna. Four species of wallaby (*Macropus eugenii, Macropus parma, Petrogale penicillata* and *Wallabia bicolour*) (Eldridge *et al.* 2001) were introduced and remain on Kawau today. Other animals, such as the zebra imported to pull his carriage (Eldridge *et al*. 2001), failed to acclimatise to their new home. Grey also imported birds such as peacocks (*Pavo* spp.), kookaburra (*Dacelo* spp.), and notably for this study, emu (Graham 1919). It is highly likely that the feathers used to construct the emu feather cloak originated from Kawau, given the estimated

construction of the cloak in around 1850, Grey's purchase of Kawau in 1862, the presence of emu on Kawau, and Grey's favorable association with Māori. It should be noted that emu were also found in the Hauraki Gulf on Motutapu Island, which was purchased in 1869 by the Reid brothers from Victorian entrepreneur Richard Graham. They introduced exotic fauna such as emu, deer, ostriches and wallabies (McClure 2007). It is known, however, that the flock of emu on Motutapu Island was provided from Governor Grey's flock on Kawau Island (Graham 1919).

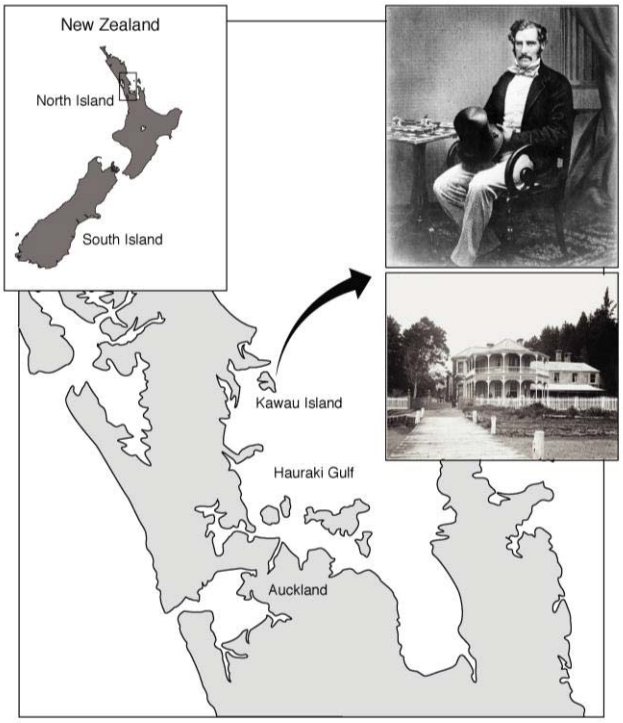


Figure 3.3 The location of Kawau Island off the coast of New Zealand north of Auckland, where Governor Grey kept his Zoological Park which included emu, together with a portrait of Governor Grey and an early photograph of Mansion House.

Trade with Australia

European explorers visiting New Zealand in the 1700s quickly sought to make use of and to export resources, including timber and flax. Māori fashioned flax into ropes for visiting ships and bartered flax and weaving for European goods. Merchants in Sydney showed an interest in flax fibre and by the 1820s a trade began with Australia, peaking in the 1830s (Wigglesworth 1981) (Figure 3.4).

Figure 3.4 North Island flax stations in the 1820's

Trading stations were set up around the coast of New Zealand. Stations were present on the coasts of Northland, Waikato, Taranaki, the Coromandel, the Bay of Plenty, the East Cape, Southland, both sides of the Cook Straight, and the Banks Peninsula. Taking into account the extent of the trade between these two countries, and the timing of that trade, at present it is not possible to rule out these trade routes as the source of the emu feathers used to adorn the cloak. It is known that Māori flax producers were not paid in cash but in goods, usually muskets, although other goods such as feathers cannot be discounted (Swarbrick 2007). Emu were known to be present on Kawau Island in about 1862. This coincides with the peak of the flax and timber trade with Australia (~1830). In addition, our estimate of the date of construction of the emu cloak is approximately 1850. This makes it difficult to confirm with certainty that the emu feathers adorning the cloak came from George Grey's emu on Kawau Island. However, the definite presence of emu on Kawau versus only the potential for emu to be brought from Australia during the timber and flax trade makes the Kawau Island option more compelling. Further investigation could be conducted to test this idea. For instance, it is possible to look at more variable regions of the mitochondrial DNA genome to distinguish between different emu populations. If there were emu remains on Kawau, it would be possible to see if the feathers adorning the cloak match

genetically to those remains and to compare these to Australian populations. Recently, two cloaks have been identified in the cloak collection at the Auckland War Memorial Museum. Both were constructed from feathers similar to those observed on the emu feather cloak from the Hawkes Bay.

Figure 3.5. Cloak #53492 from Auckland War Memorial Museum with similar feather morphology to the Hawkes Bay example.

One of these is a *kahu huruhuru* which is a cloak adorned with feathers from many different species of birds and the other is completely adorned with what appears to be emu feathers (Figure 3.5). It is estimated that both cloaks were manufactured more recently than the Hawkes Bay example. The bodies of both cloaks are constructed from candlewick as opposed to *muka*. Cloak making using this material was typically observed from 1890 onwards. Future work will be conducted to determine if the feathers of the two newly observed cloaks are indeed emu, and if they are, how genetically similar these feathers are to those from the Hawkes Bay cloak. Generally, this study highlights the effectiveness of genetic analyses in recovering lost history from important ethnological artifacts.

Update since publication

The two cloaks sampled from Auckland War Memorial Museum unfortunately failed to provide viable DNA for analysis. As it was only possible to sample 2 feathers from each of these two cloaks and given that 5/7 of the samples taken from the Hawkes Bay cloak failed to amplify, this result is not surprising, although disappointing.

References

Anderson A. 1989. Prodigious birds. Moas and moa hunting in prehistoric New Zealand. Cambridge (United Kingdom): Cambridge University Press.

Barnett R, Yamaguchi N, Shapiro B, Nijman V. 2007. Using ancient DNA techniques to identify the origin of unprovenanced museum specimens as illustrated by the identification of a 19th century lion from Amsterdam. Contributions to Zoology 76(2):87-94.

Best E. 1952. The Māori As He Was. Wellington, New Zealand: A.R. Shearer, Government Printer.

Bunce M, Worthy TH, Phillips MJ, Holdaway RN, Willerslev E, Haile J, Shapiro B, Scofield RP, Drummond J, Kamp PJJ, Cooper A. 2009. The evolutionary history of the extinct ratite moa and New Zealand Neogene paleogeography. *Proceedings of the National Academy of Sciences, U.S.A*. doi_10.1073_pnas.0906660106.

Eldridge MDB, Browning TL, Close RL. 2001. Provenance of a New Zealand bushtailed rock-wallaby (Petrogale pencillata) population determined by mitochondrial DNA sequence analysis. *Molecular Ecology,* 10:2561-2567.

Graham G. 1919. Rangi-Hua-Moa, a legend of the moa in the Waitemata district, Auckland. *Journal of the Polynesian Society*. 28(110):107-110.

Haddrath O, and Baker AJ. 2001. Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogenetics and the vicariance biogeography hypothesis. *Proceedings of the Royal Society B: Biological Sciences* 268:939-945.

Harshman J, Braun EL, Braun MJ, Huddleston CJ, Bowie RCK, Chojnowski JL, Hackett SJ, Han KL, Kimball RT, Marks BD, Miglia KJ, Moore WS, Reddy S, Sheldon FH, Steadmen DW, Steppan SJ, Witt CC, Yuri T. 2008. Phylogenomic evidence for multiple losses of flight in ratite birds. *Proceedings of the National Academy of Sciences U.S.A*. 105(36):13462-13467.

Huynen L, Millar CD, Scofield RP, Lambert DM. 2003. Nuclear sequences detect species limits in ancient moa. *Nature* 425:175-178.

Huynen L, Gill B, Millar CD, Lambert DM. 2010. Ancient DNA reveals extreme egg morphology and nesting behavior in New Zealand's extinct moa. *Proceedings of the National Academy of Sciences U.S.A*. 107(37):16201-16202.

Ling Roth H. 1923. The Māori Mantle. Halifax: Bankfield Museum.

McClure M. 2007. Auckland places. Te Ara - The Encyclopedia of New Zealand [URL:http://www.TeAra.govt.nz/Places/Auckland/AucklandPlaces/en].

Pendergrast M. 1987. Te Aho Tapu, The Sacred Thread. Auckland: Reed Publisher Ltd,.

Pendergrast M. 1997. Kakahu, Māori Cloaks. Auckland: Auckland Museum.

Phillips MJ, Gibb GC, Crimp EA, Penny D. 2010. Tinamous and moa flock together: mitochondrial genome sequence analysis reveals independent losses of flight among ratites. *Systematic Biology*. 59(1):90-107.

Rawlence N, Wood J, Armstrong K, Cooper A. 2009. DNA content and distribution in ancient feathers and potential to reconstruct the plumage of extinct avian taxa.

Proceedings of the Royal Society of London B. 276:3395-3402.

Shepherd LD, Lambert DM. 2008. Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Sinclair K. 2007. Grey, George 1812-1898. Dictionary of New Zealand Biography [URL:http://www.dnzb.govt.nz].

Swarbrick N. 2007. Flax and flax working. *Te Ara - the Encyclopedia of New Zealand* [URL:http://www.TeAra.govt.nz/TheBush/NativePlantsAndFungi/FlaxAndFlaxWorking/en].

Swofford DL. 2002. *PAUP* Phylogenetic Analysis Using Parsimony (*and other methods*). Sinauer Associates, Sunderland.

Te Kanawa, DR. 1992. *Weaving a Kakahu*. Wellington, New Zealand: Bridget Williams Books Limited.

Wanderler P, Hoek PEA, Keller LF. 2007. Back to the future: museum specimens in population genetics. *Trends in Ecology and Evolution* 22(12):634-642.

Wigglesworth, RP 1981. The New Zealand timber and flax trade 1769-1840. Unpublished PhD thesis, Massey University.

Worthy, TH, Holdaway RN. 2002. *The Lost World of the Moa.* Christchurch, New Zealand: Canterbury University Press.

Chapter 4

Temporal and Spatial Mitochondrial DNA Structure of North Island Brown Kiwi (Apteryx mantelli) Populations: Implications for Conservation Management.

Abstract

Numbers of North Island brown kiwi (*Apteryx mantelli*) are in serious decline. Using mtDNA control region sequences obtained from contemporary kiwi populations we explored current levels of genetic diversity in the species. Additionally, using mtDNA sequence data from ~ 150-year-old kiwi feather cloaks and kete, we have been able to look at changes in genetic diversity in the North Island brown kiwi over the past 150 years. For contemporary populations, we saw clear east / west genetic structuring of haplotypes. There was also a phylogenetic component to this structuring, relating to New Zealand's complicated geological past. We found that the number of haplotypes discovered for both contemporary and past populations has remained constant, indicating no loss in genetic diversity. However, there was an observed change in the frequency of each haplotype over time. These findings have implications for how to effectively manage populations of North Island brown and should prove useful to conservationists.

Introduction

New Zealand's iconic kiwi (*Apteryx* spp.) are in various stages of overall population decline (Holzapfel et al, 2008, Sales 2005, McLennan 1996). Conservation and maintenance of these populations is the responsibility of the New Zealand

government funded agency, the Department of Conservation. To manage these species effectively a detailed knowledge of their behaviour, habitat use, an understanding of species boundaries, classification, and both current and historic population dynamics is required. Significant progress has been made to achieve this goal (see Holzapfel et al 2008 for the Department of Conservation's 2008-2018 kiwi recovery plan), yet there is potential for conservation management policies to be implemented ahead of complimentary scientific research. In the worst case, this could lead to the mismanagement of these iconic species. This chapter will examine gaps in our knowledge, provide new molecular data and provide valuable information for management strategies.

Taxonomists, geneticists and conservation ecologists have long debated over what determines a species, subspecies and how to determine intra-specific management units (Fraser & Bernatchez 2001, Hoglund et al 2011, Roberts et al 2011). Recent mitochondrial DNA analyses of kiwi (*Apteryx* spp.) have prompted their reclassification into five distinct species (Baker et al 1995, Burbidge et al 2003). Kiwi were found to have extremely subdivided population structure due to their low dispersal power (Baker et al 1995). Long-term geographical isolation, lack of hybridisation in introduced populations and the accumulation of new biological characteristics is evidence for the existence of biologically distinct species (Burbidge et al 2003). These five species are outlined in the introductory chapter of this thesis. In short there are the great and little spotted kiwi (*Apteryx haastii* and *Apteryx owenii* respectively) and three species of brown kiwi, North Island (*Apteryx mantelli*), tokoeka (*Apteryx australis*) and the rowi (*Apteryx rowi*). Chapter 1 contains details regarding past and present distributions of each of these five species.

The kiwi (*Apteryx* spp.) recovery plan 2008-2018 written by the Department of Conservation (Holzapfel et al 2008) has split the five currently recognised species of kiwi into eleven recognised taxa for separate conservation management. The term taxa has been stipulated in the recovery plan, although maybe management units would be more appropriate. Great spotted kiwi, little spotted kiwi and rowi, remain three units as was previously recognised. However, the North Island brown

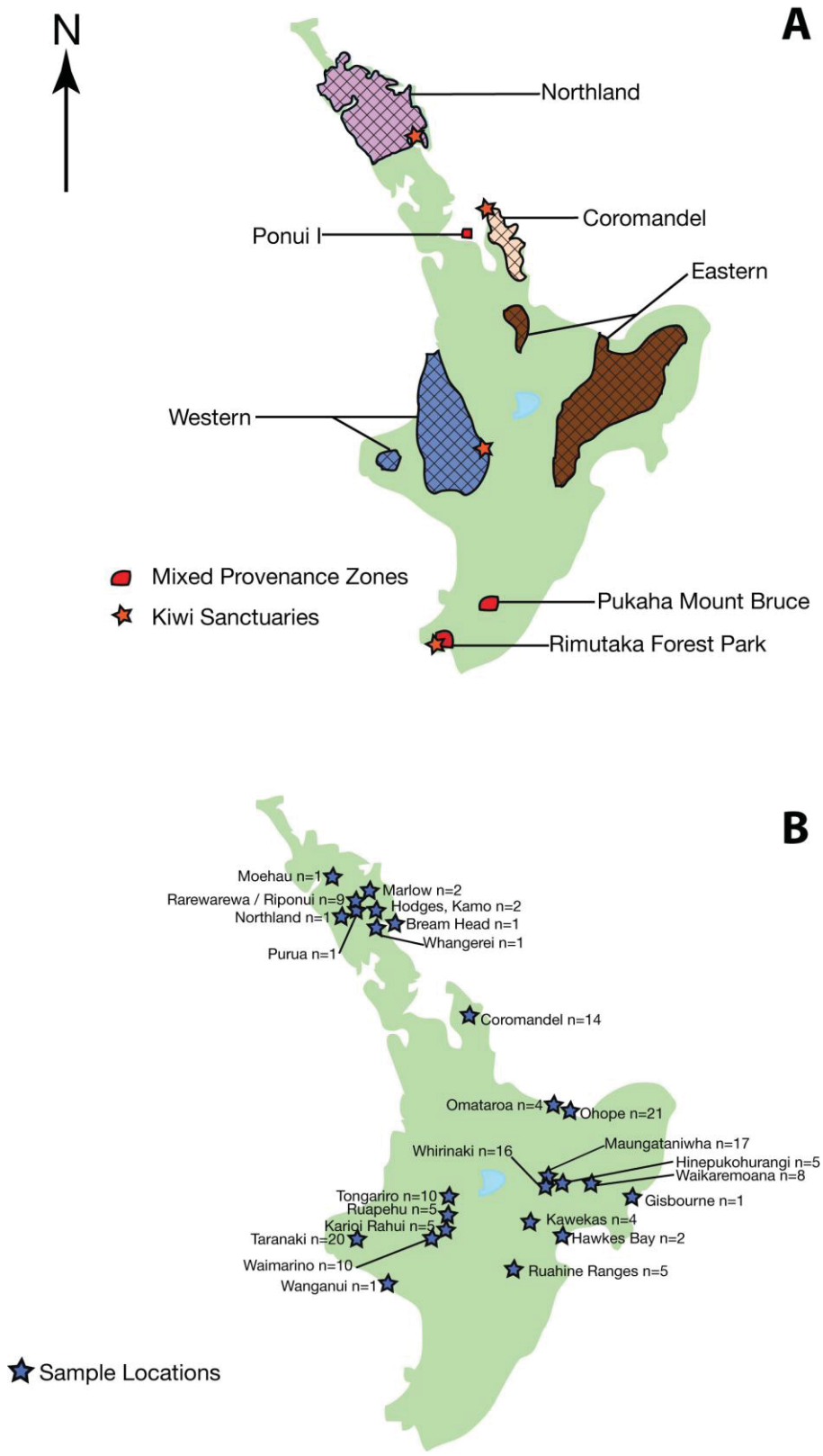


Figure 4.1. (A) Shows the four NIBK management units assigned by the Department of Conservation. Also shown are sanctuaries and mixed provenance zones. (B) Shows locations from which samples have be taken for mtDNA analyses. The number of samples taken from each location is included.

kiwi and the tokoeka are each split into four distinct management units. Tokoeka have been divided into four populations: Stewart Island (previously recognised as a subspecies), Haast, Northern Fiordland and Southern Fiordland. North Island brown kiwi have also been split into four populations: Northland, Coromandel, Eastern and Western (Fig 4.1). Aims of the Department of Conservation are to i) manage all eleven taxa as separate conservation management units and ii) to manage the fine scale diversity within the eleven assigned taxa. However, prior to this recovery plan, several mixed origin translocations of North Island brown kiwi have taken place on Little Barrier Island, Ponui Island, Pukaha Mount Bruce and the Rimutaka Forest Park. These translocations are now being re-labelled as mixed-provenance populations to investigate the consequences of isolation versus mixing. The mixed provenance populations may also be an integral part of recovery planning outside the core areas of distribution for each unit. This could especially useful if isolation of current units is a driver for speciation and could carry risks with it, such as inbreeding depression (Holzapfel et al 2008). The 2008-2009 Kiwi Recovery Group annual report (Kiwi Recovery Group 2010) gives 'essential' status to furthering research into taxonomy, with an emphasis on genetic research. Also it is important for conservationists to look not just to taxonomy, but also to phylogenetic analyses. Understanding phylogeography in terms of temporal natural geographic and geological events will allow separation of these events from those resulting from human disturbance (Wallis and Trewick 2009).

As previously mentioned, it was genetic research that prompted the reclassification of kiwi from three species to five (Baker et al 1995: Burbidge et al 2003). Coupled with some more recent work (Shepherd 2006, Shepherd & Lambert 2008) it were these same data that are credited in the 2008-2018 kiwi recovery plan to the establishment of the eleven taxa management units. However, the spatial mtDNA genetic structure of North Island Brown kiwi is currently limited to sequence data from 21 individuals (Burbidge et al 2003, Shepherd and Lambert 2008) present in table 4.2. Additionally ~40 sequences from ~ 150-year-old kiwi feather cloaks and bags has been available (Shepherd 2006). These sequence data are not only low in number, but also spans hundreds of years,

therefore using these combined sequences fails to recognise temporal changes in haplotype frequency and spatial structuring. Clearly more data are needed to a) provide mtDNA sequence data for a larger representation of current North Island brown kiwi populations and; b) separate the data temporally to allow changes to be elucidated over time.

This chapter provides substantial new mtDNA data for a 166 individuals from current North Island Brown kiwi populations. These data will be analysed to examine genetic and genetic spatial structure in kiwi and thus to provide greater insight for assignment of management units. Phylogenetic analyses of these data will give insights into the effect past geological processes have had on the genetic structure of existing populations. Additionally, 847 mtDNA sequences from ~ 150-year-old kiwi feathers have been generated that can be compared to contemporary data to look at recent temporal differences that may have been a result of human disturbance.

Materials and Methods

Current Kiwi Populations

Plucked feather samples (n=166) were kindly provided to us by Rainbow Springs Kiwi Encounter, Rotorua. Samples were from chicks being reared at the centre as part of Operation Nest Egg (Colbourne et al 2005). Eggs are removed from nests of wild kiwi populations, hatched in the centre and the chicks released when individuals were older. This was aimed at reducing the juvenile mortality rate and improving overall kiwi survivorship (Colbourne et al 2005). As the eggs were obtained directly from nests, the location of each sample could be recorded (Figure 4.1, Table 4.1). Samples provided to us from recently re-established kiwi populations such as Mount Bruce, were omitted as they do not represent the ancestral kiwi populations from those areas. These areas have recently been recognised as established mixed provenance populations by the Department of Conservation (Figure 4.1) as part of the 2008-2018 Kiwi Recovery Plan (Holzapfel et al 2008). Methods of DNA extraction are outlined in Chapter 2. The extracted

DNA was amplified and sequenced in both directions using mtDNA primers kcF and kcR (Shepherd and Lambert 2008), which target a 200bp fragment of the hypervariable region.

Table 4.1 mtDNA haplotypes assigned to individual kiwi from current populations

	Location	ID	Source	Haplotype
1	Bream Head	4e6Bh	Leon	1
2	Coromandel	Tango	Rainbow Springs	4
3	Coromandel	Marenui	Rainbow Springs	4
4	Coromandel	Taunis	Rainbow Springs	4
5	Coromandel	Bubbles	Rainbow Springs	4
6	Coromandel	Percy	Rainbow Springs	4
7	Coromandel	Homer	Rainbow Springs	4
8	Coromandel	Simo	Rainbow Springs	4
9	Coromandel	Rewarewa	Rainbow Springs	4
10	Coromandel	Guy	Rainbow Springs	4
11	Coromandel	alex	Rainbow Springs	4
12	Coromandel	palo	Rainbow Springs	4
13	Coromandel	Moneypenny	Rainbow Springs	4
14	Coromandel	Aru	Rainbow Springs	4
15	Coromandel	Minnie	Rainbow Springs	3
16	Gisbourne	Pinky	Rainbow Springs	12
17	Hawkes Bay	49	Leon	10
18	Hawkes Bay	Ari	Leon	10
19	Hinepukohurangi	Hinemoa	Rainbow Springs	10
20	Hinepukohurangi	Corona	Rainbow Springs	10
21	Hinepukohurangi	Magnum	Rainbow Springs	10
22	Hinepukohurangi	Maggy	Rainbow Springs	10
23	Hinepukohurangi	Tocha	Rainbow Springs	10
24	Hodges, kamo	198H	Leon	2
25	Hodges, kamo	FdaH	Leon	1
26	Karioi Rahui	Iguazu	Rainbow Springs	6
27	Karioi Rahui	Rio	Rainbow Springs	6
28	Karioi Rahui	Nugget	Rainbow Springs	6
29	Karioi Rahui	mayhem	Rainbow Springs	5
30	Karioi Rahui	kruze	Rainbow Springs	6
31	Kawekas	Waiwai	Rainbow Springs	9
32	Kawekas	Albert	Rainbow Springs	4
33	Kawekas	Pudding	Rainbow Springs	4
34	Kawekas	Hariana	Rainbow Springs	4
35	Marlow	3a2M	Leon	1
36	Marlow	22aM	Leon	1
37	Maungataniwha	Eco	Rainbow Springs	11
38	Maungataniwha	Hine	Rainbow Springs	8
39	Maungataniwha	Berry	Rainbow Springs	9
40	Maungataniwha	Blue Gum	Rainbow Springs	9

41	Maungataniwha	Taoka	Rainbow Springs	9
42	Maungataniwha	Bondi	Rainbow Springs	11
43	Maungataniwha	Darwin	Rainbow Springs	9
44	Maungataniwha	Trooper	Rainbow Springs	9
45	Maungataniwha	Shaggy	Rainbow Springs	9
46	Maungataniwha	Rowi	Rainbow Springs	11
47	Maungataniwha	Kora	Rainbow Springs	9
48	Maungataniwha	Splash	Rainbow Springs	9
49	Maungataniwha	Chute	Rainbow Springs	10
50	Maungataniwha	Fred	Rainbow Springs	10
51	Maungataniwha	Domino	Rainbow Springs	9
52	Maungataniwha	Cookie	Rainbow Springs	9
53	Maungataniwha	Pavlova	Rainbow Springs	9
54	Moehau	Kina	Rainbow Springs	3
55	Northland	Nib.75	Leon	3
56	Ohope	Wedgie	Rainbow Springs	12
57	Ohope	Quazi	Rainbow Springs	10
58	Ohope	Chitchat	Rainbow Springs	9
59	Ohope	Manuka	Rainbow Springs	9
60	Ohope	Wafer	Rainbow Springs	11
61	Ohope	Boxer	Rainbow Springs	11
62	Ohope	Ohiwa	Rainbow Springs	12
63	Ohope	Teva	Rainbow Springs	12
64	Ohope	Rangi	Rainbow Springs	9
65	Ohope	Mako	Rainbow Springs	9
66	Ohope	Koripo	Rainbow Springs	9
67	Ohope	Lag	Rainbow Springs	9
68	Ohope	Champers	Rainbow Springs	9
69	Ohope	Diamond	Rainbow Springs	12
70	Ohope	Breeze	Rainbow Springs	9
71	Ohope	Fig	Rainbow Springs	9
72	Ohope	Stinger	Rainbow Springs	9
73	Ohope	Bear	Rainbow Springs	11
74	Ohope	Epi	Rainbow Springs	9
75	Ohope	Whiturau	Rainbow Springs	9
76	Ohope	Twinkle	Rainbow Springs	9
77	Omataroa	Flipper	Rainbow Springs	11
78	Omataroa	Teer	Rainbow Springs	9
79	Omataroa	Vollie	Rainbow Springs	9
80	Omataroa	Hydee	Rainbow Springs	11
81	Purua	88bp	Leon	2
82	Rarewarewa	424Rr	Leon	1
83	Rarewarewa	157Mo	Leon	1
84	Rarewarewa	ob1Mo	Leon	2
85	Rarewarewa	099Bh	Leon	1
86	Rarewarewa	9e9D	Leon	1
87	Rarewarewa	5ffRr	Leon	2
88	Rarewarewa	891Rr	Leon	3
89	Riponui	2dbRp	Leon	2

90	Riponui	624Rp	Leon	2
91	Ruahine Ranges	Camo	Rainbow Springs	3
92	Ruahine Ranges	Rubiks	Rainbow Springs	8
93	Ruahine Ranges	Mokai	Rainbow Springs	3
94	Ruahine Ranges	Allbut	Rainbow Springs	8
95	Ruahine Ranges	Blue	Rainbow Springs	3
96	Ruapehu	Libby	Leon	13
97	Ruapehu	Kuraiti	Leon	5
98	Ruapehu	Putiputi	Leon	13
99	Ruapehu	Kaha	Leon	5
100	Ruapehu	Ross	Leon	5
101	Taranaki	Tk.Ure1/vogel	Rainbow Springs	5
102	Taranaki	Purangi	Rainbow Springs	5
103	Taranaki	Dawson	Rainbow Springs	5
104	Taranaki	Ringo	Rainbow Springs	5
105	Taranaki	Ingle	Rainbow Springs	5
106	Taranaki	Mautau	Rainbow Springs	5
107	Taranaki	Solstice	Rainbow Springs	5
108	Taranaki	Ford	Rainbow Springs	5
109	Taranaki	Bayfield	Rainbow Springs	5
110	Taranaki	Ra	Rainbow Springs	7
111	Taranaki	Jaime	Rainbow Springs	7
112	Taranaki	AWOL	Rainbow Springs	6
113	Taranaki	Rusty	Rainbow Springs	5
114	Taranaki	Tarata	Rainbow Springs	5
115	Taranaki	Kaimata	Rainbow Springs	5
116	Taranaki	Red	Rainbow Springs	5
117	Taranaki	Tahuna	Rainbow Springs	5
118	Taranaki	Harenge	Rainbow Springs	5
119	Taranaki	Runner	Rainbow Springs	5
120	Taranaki	Ironman	Rainbow Springs	5
121	Tongariro	Elmo	Leon	13
122	Tongariro	Robyn	Leon	5
123	Tongariro	Haki	Rainbow Springs	5
124	Tongariro	Possum	Rainbow Springs	13
125	Tongariro	Eddie	Rainbow Springs	5
126	Tongariro	Fleming	Rainbow Springs	5
127	Tongariro	Morton	Rainbow Springs	13
128	Tongariro	April	Rainbow Springs	13
129	Tongariro	Topo	Rainbow Springs	5
130	Tongariro	Pokano	Rainbow Springs	5
131	Waikaremoana	Dreads	John McLennan, Landcare Research, Havelock North	11
132	Waikaremoana	Moko	John McLennan, Landcare Research, Havelock North	9
133	Waikaremoana	Maggie	John McLennan, Landcare Research, Havelock North	9
134	Waikaremoana	Ry97.2	John McLennan, Landcare Research, Havelock North	9
135	Waikaremoana	Gonzo	John McLennan, Landcare Research, Havelock North	11
136	Waikaremoana	a96.1	Leon	12
137	Waikaremoana	M97.2	Leon	9
138	Waikaremoana	B97	Leon	9

139	Waimarino	Tanekaha	Rainbow Springs	5
140	Waimarino	Kowhai	Rainbow Springs	6
141	Waimarino	Mataritki	Rainbow Springs	5
142	Waimarino	Niglet	Rainbow Springs	5
143	Waimarino	Rudolph	Rainbow Springs	5
144	Waimarino	Moony	Rainbow Springs	5
145	Waimarino	Pea	Rainbow Springs	5
146	Waimarino	Gold	Rainbow Springs	5
147	Waimarino	Frankin	Rainbow Springs	5
148	Waimarino	Myrrh	Rainbow Springs	5
149	Wanganui	Sirius	Rainbow Springs	5
150	Whangarei	O9d11	Leon	1
151	Whirinaki	Timata	Rainbow Springs	12
152	Whirinaki	Awa	Rainbow Springs	10
153	Whirinaki	Te Wairoa	Rainbow Springs	10
154	Whirinaki	Karaponia	Rainbow Springs	10
155	Whirinaki	Maroke	Rainbow Springs	12
156	Whirinaki	Martini	Rainbow Springs	10
157	Whirinaki	Marmalade	Rainbow Springs	10
158	Whirinaki	Hone	Rainbow Springs	10
159	Whirinaki	Buster	Rainbow Springs	10
160	Whirinaki	Speights	Rainbow Springs	12
161	Whirinaki	Claus	Rainbow Springs	10
162	Whirinaki	Marley	Rainbow Springs	10
163	Whirinaki	Buttons	Rainbow Springs	8
164	Whirinaki	Roimata	Rainbow Springs	10
165	Whirinaki	Advent	Rainbow Springs	10
166	Whirinaki	Trig	Rainbow Springs	10

In addition to these present day kiwi samples, sequences available from the literature were also included in the analysis (Table 4.2).

Past Kiwi Populations

Using the same primer pair, North Island brown kiwi sequences were also obtained from 847 feather cloak samples. These samples have generally been estimated to be approximately 150 years old (Rangi Te Kanawa, personal communication). Additional details regarding these cloaks can be found in Chapters 1, 2 and 5.

Analyses

Sequences were aligned and edited using Sequencher V4.6. (Genes Codes Corporation, Ann Arbour, MI, USA. A phylogenetic tree was constructed in MEGA4

(Tamura et al 2007). Evolutionary distances were computed using the Tajima-Nei method (Tajima and Nei 1984). Rate variation between sites was modelled with a gamma distribution (shape parameter = 0.07). Phylogenetic networks were constructed using statistical parsimony in TCS version 1.21 (Clement et al 2000). For present day sequences, two measures of genetic differentiation were calculated using PERMUTCPSSR version 2.0 (Pons & Petit 1996): N_{ST}, which takes into account the relationships between haplotypes, and G_{ST}, which uses haplotype frequencies alone. A permutation test was performed to examine whether N_{ST} was significantly larger than G_{ST}. The geographic structuring within the present day dataset was analysed in two ways. First, spatial analysis of molecular variance, SAMOVA (Version 1; Dupanloup et al 2002) was used to determine the optimal number of differentiated groups (K) that best fit the data and the composition of each group was determined by maximising F_{CT}. K was varied from 2 to 12 and 1000 permutations were run from each of 100 random initial conditions. Second, a nested clade analysis (NCA, Templeton et al 1987, 1992) was performed using GEODIS version 2.5 (Posada et al 2000) to explore relationships between haplotype distribution and geography, building upon work by Shepherd and Lambert (2008). Construction of hierarchical nested clades was determined using networks constructed in TCS and the rules outlined in Templeton et al. (1987, 1993, 2004; figure 4.4). To look at temporal changes in haplotype frequencies between present day and cloak samples, a Chi square test was performed.

Results

For both modern and cloak feather DNA samples, eight variable sites comprising 13 haplotypes were observed for the 200 bp HVRI sequence (Figures 4.2, 4.3). Haplotype frequencies observed for each of the 13 haplotypes are represented in the modern and cloak samples as, respectively; 1, 4.69%/0.94%; 2, 4.17%/1.42%; 3, 6.77%/7.56%; 284 4; 9.38%/1.65%; 5, 20.31%/18.46%; 6, 4.17%/0.23%; 7, 2.08%/4.73%; 8, 2.1%/36.3% 9, 18.75%/11%: 10, 13.54%/13.23%; 11, 5.73%/2.95%; 12, 5.21%/0.23%; 13, 3.12%/1.3% (fig. 4.4). Overall there was a significant change in the frequencies of the haplotypes ($\chi 2=585.89$, df=12, $p=<0.0000001$). However, the degree of change is dependent on the haplotype. For

example, a single haplotype, haplotype 8, is massively overrepresented in cloaks, being present in over 36% of all cloak feather samples, but only in 2.1% of the modern reference samples. This has resulted in a 17.3 fold decrease in this haplotype over time. Notable also, is haplotype 12, being present in just 0.23% of cloak samples, but representing 5.21% of the modern samples indicating a 22.7 fold increase in frequency over time. There was also a 5.7 fold increase observed for haplotype 4, which has a distribution limited almost exclusively to the Coromandel. Haplotype 6 has increased in frequency over time, being present in 0.23% of cloak samples but 4.17% of modern samples. The frequencies of the remaining 10 haplotypes seem to have remained very similar for over 150 years.

Table 4.2 mtDNA haplotypes assigned for sequences from Genbank

Accession Number	Location	Source	Haplotype
AY150609	Northland	Burbidge *et al* 2003	1
AY150611	Northland	Burbidge *et al* 2003	2
DQ295829	Northland	Shepherd & Lambert 2008	2
DQ295830	Northland	Shepherd & Lambert 2008	2
AY150610	Northland	Burbidge *et al* 2003	3
AY713315	West North Island, Wanganui	Shepherd & Lambert 2008	3
AY150623	West North Island, Taranaki	Burbidge *et al* 2003	3
AY150618	West North Island, Taranaki	Burbidge *et al* 2003	5
AY150621	West North Island, Taranaki	Burbidge *et al* 2003	5
AY150622	West North Island, Taranaki	Burbidge *et al* 2003	5
AY713332	West North Island, Waverly	Shepherd & Lambert 2008	6
AY150619	West North Island	Burbidge *et al* 2003	6
AY150617	West North Island, Taranaki	Burbidge *et al* 2003	6
AY713335	West North Island, Ohakune	Shepherd & Lambert 2008	7
AY150620	West North Island, Taranaki	Burbidge *et al* 2003	7
AY150614	Bay of Plenty	Burbidge *et al* 2003	9
AY150612	Bay of Plenty	Burbidge *et al* 2003	10
AY150613	Bay of Plenty	Burbidge *et al* 2003	10
AY713315	Hawkes Bay, Waikaou	Shepherd & Lambert 2008	3
AY150616	Hawkes Bay	Burbidge *et al* 2003	9
AY150615	Hawkes Bay	Burbidge *et al* 2003	11

The genetic structure among modern kiwi populations from Northland, the Coromandel, the West and Central North Island, and the East North Island regions was shown using a statistical parsimony network constructed in TCS v1.21 with a 95% parsimony connection limit (figure 4.3) (Clement et al. 2000). Measures of genetic differentiation, GST and NST, indicate that subdivision exists amongst the

kiwi populations (G_{ST} = 0.45, standard error = 0.07; N_{ST} = 0.63, standard error = 0.05). N_{ST} was significantly higher than G_{ST} ($P<0.01$) indicating that there was a phylogeographic component to this structuring. The SAMOVA performed identified the following groups with K = 3 (a) Central and West North Island, (b) Northland,

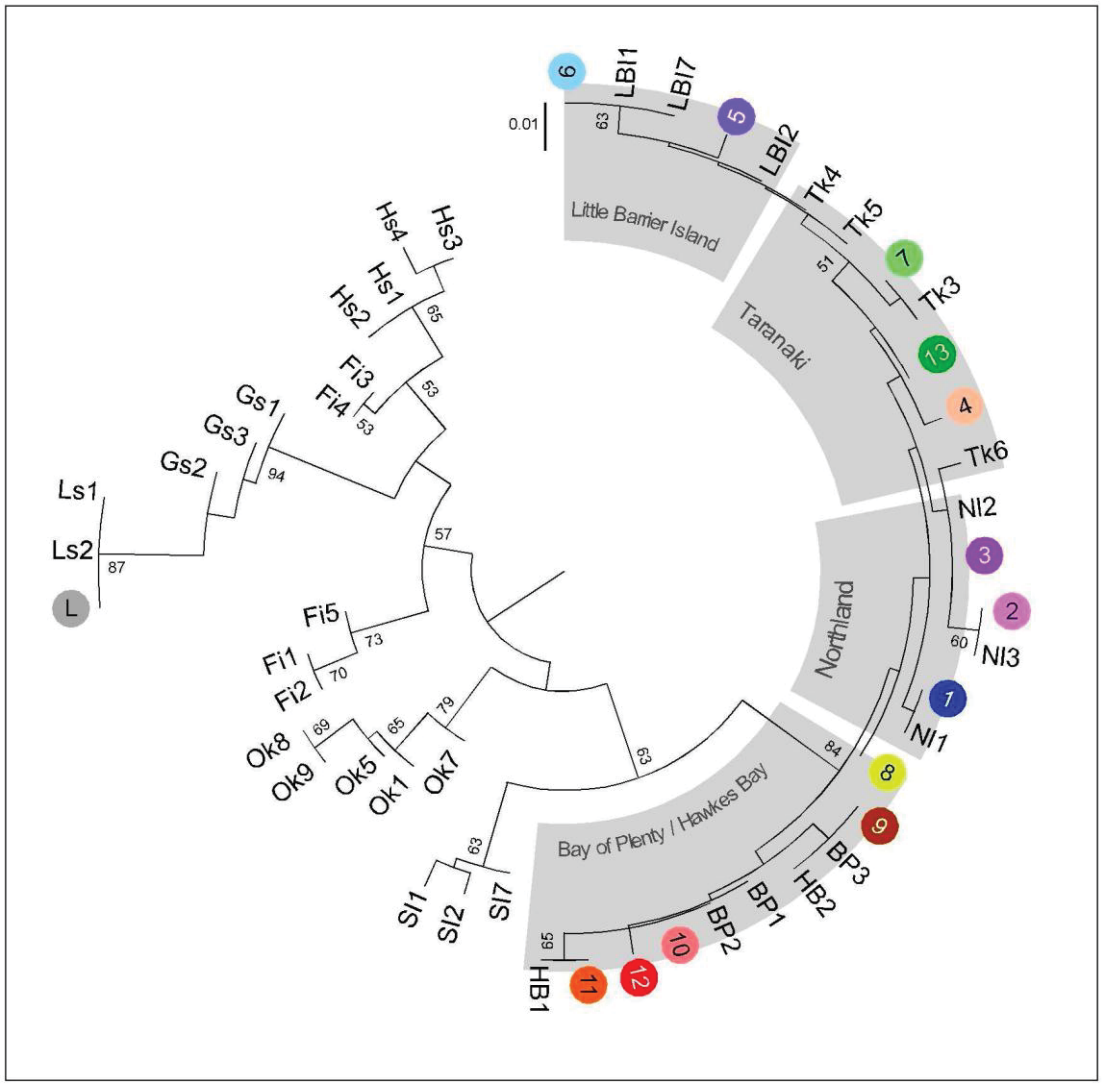


Figure 4.2 Radial distance Neighbour-Joining tree for 200bp of the mtDNA HVR1 region. The 13 North Island brown kiwi haplotypes are shown in colour. Little spotted and great spotted kiwi are Ls and Gs respectively. Rowi from Okarito are (Ok). Tokoeka kiwi are from Haast (Hs), Fiordland (Fi) and Stewart Island (Si). The Location of North Island brown kiwi are shown in grey boxes. North Island brown kiwi from Little Barrier Island (LBI) were originally translocated from taranaki.

the Coromandel, Ruahine Ranges and the Kaweka Forest Park, and (c) the East of the North Island (fig. 4.4). At higher values of K single populations were partitioned as individual groups although FCT only increased marginally to its maximum at K = 10 (from FCT = 0.67 at K = 3 to FCT = 0.73 at K = 10).

Using the suggested rules of Templeton et al (1987) four lower order and two higher order clades were assigned to the TCS statistical parsimony network (Figure 4.5). Each clade was defined as a 'tip' or 'interior' clade (Templeton 2004). The haplotypes assigned to each clade and the geographic location (grid reference) of every modern sample and associated haplotype was input into a matrix. Observed data were compared with data simulated using a hypothesis of spatial panmixia. NCA was implemented in GeoDis ver 2.6 (Posada et al 2000) and a revised inference key (Templeton, 2008) was used to interpret results. Three out of the four lower level clades and one out of the two higher level clades showed significant values for either within clade analysis (D_c), nested clade analysis (D_n) or interior Vs tip clade analysis (I-T). This meant that for these clades (Table 4.3), the null hypothesis of no geographical association between haplotypes could be rejected. Utilising the most recent inference key (http://darwin.uvigo.es/software/geodis.html), each of the significant clades were examined to explore phylogeographic patterns. At the higher level (clade 2-1) allopatric fragmentation was the inferred scenario, whereas phylogeography at lower level clades was a result of either continuous range expansion (clade 1-1) or long distance colonisation and/or fragmentation. Although lower order clade 1-4 contained significant values in Geodis, there were only interior haplotypes present within the clade, leading to an inconclusive outcome when analysed with the inference key.

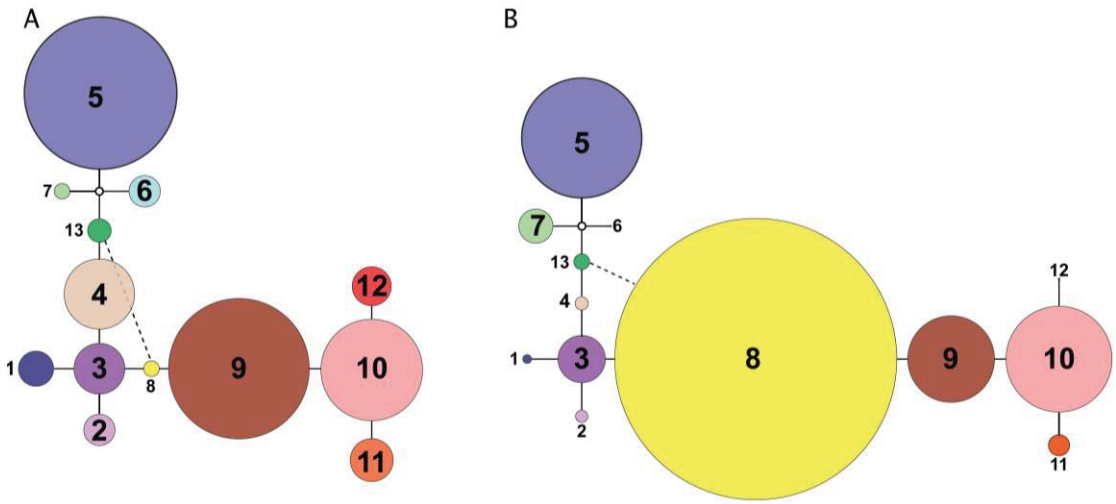


Figure 4.3. Statistical parsimony networks for kiwi HVR1 DNA sequences from present day and ~ 150-year-old samples. Each connector denotes a 1bp change. The sizes of the haplotype frequencies observed (calculated as a percentage) are shown, and the frequencies for the present day (a) and ~ 150-year-old samples (b) are directly comparable.

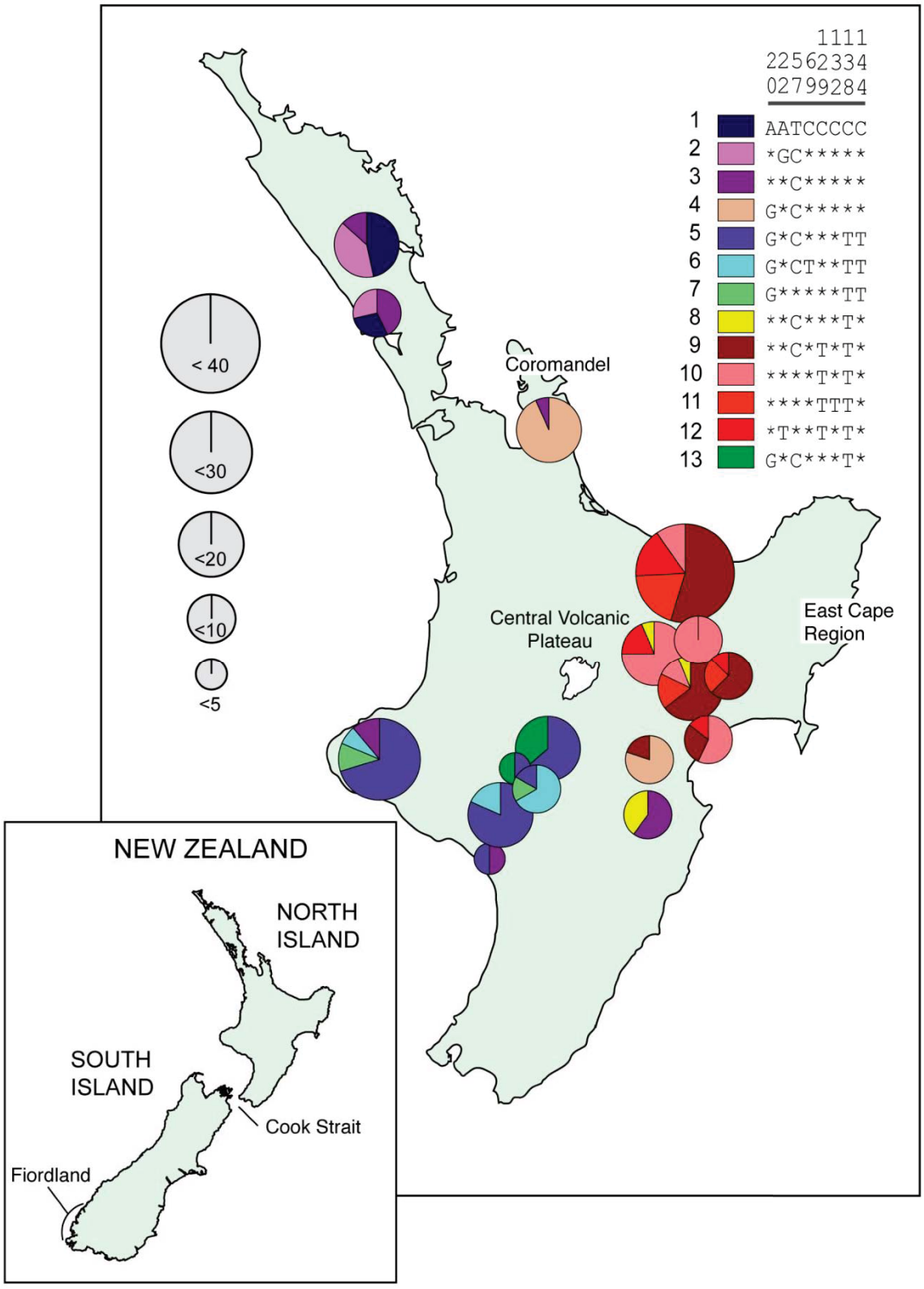


Figure 4.4. Geographic distribution of mitochondrial HVR1 sequences obtained from the reference database. Eight variable sites among 13 haplotypes were observed. Pie charts depict sample sizes together haplotypes frequencies at each location.

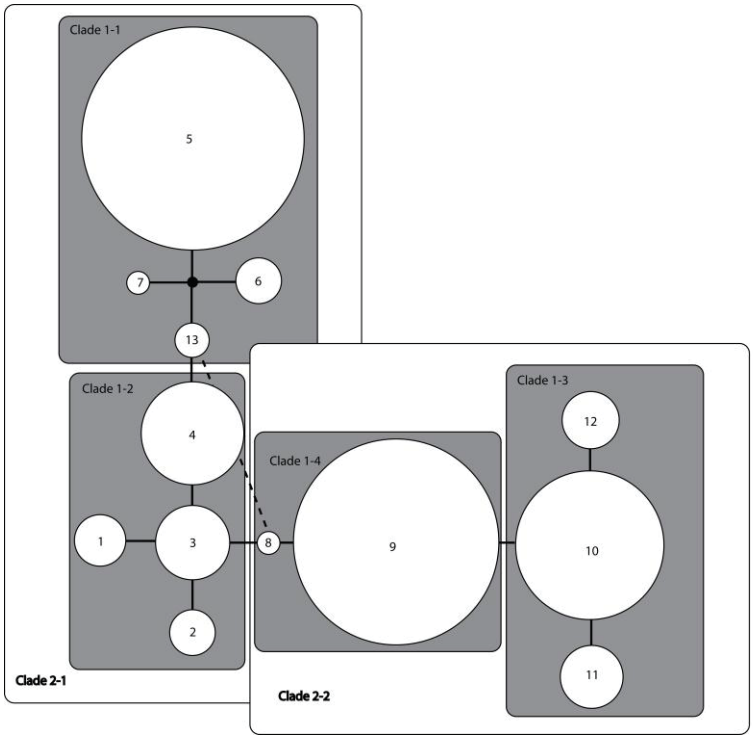


Figure 4.5. Statistical parsimony network created using TCS V1.21 with a 95% parsimony connection limit and hierarchical nested clades.

Table 4.3. Significant clades and inferred scenarios using Templeton's (2008) Inference guide

Significant Clade	Chain of Inference	Inferred Scenario
Clade 1-1	1-2-11-12-NO	Continuous range expansion
Clade 1-2	1-2-3-5-6-13-14-NO	Long distance colonization and/or fragmentation
Clade 1-4	1-2-Interior Vs Tip status not determined.	Inconclusive outcome
Clade 2-1	1-2-3-4-9-NO	Allopatric fragmentation

Discussion

Spatial distribution of mtDNA haplotypes

The present day database of the assembled mtDNA HVRI shows a generally high level of geographic structure with many of the 13 haplotypes having limited geographic ranges (Figure 4.4). Phylogenetic analyses corroborate this structuring. Both Gst and Nst values were high, however, with Gst being significantly higher than Nst, suggesting a phylogenetic component to the structuring. The SAMOVA analysis assigned populations into three groups, the West and Central North Island, the East of the North Island, and Northland and the Coromandel. Two eastern populations (Kaweka Forest Park and the Ruahine Ranges) were grouped

with Northland and the Coromandel. The Kaweka Forest Park contains individuals with haplotype 4 which is only present elsewhere in the Coromandel, and haplotype 9 which is only found in the East of the North Island. The Ruahine Ranges population contains haplotypes 3, which is found in greatest frequencies in Northland, and haplotype 8 that is found exclusively in the East. However, the sample sizes for these populations are small (Ruahine Ranges n=5, Kaweka Forest park n=4) which may explain why, despite containing exclusively eastern haplotypes, they were grouped with Northland and the Coromandel populations. Nested Clade Analysis also detected a significant geographical association between haplotypes. However, phylogenetic inferences differ between clade orders and within lower level clades. This seems counter-intuitive. New Zealand has a very complicated geological and climatic history, which has to be taken into consideration when interpreting phylogenetic analyses. New Zealand forms part of the now largely submerged land mass Zealandia, which is estimated to have split from the super continent Gondwana approximately 80mya (Goldberg et al 2008) during the Cretaceous period of the Mesozoic era. Ancestors of kiwi are now thought to have potentially arrived in New Zealand after this separation 72-55.6mya with colonization occurring from Australia via New Caledonia (Tennyson 2010) and were potentially flighted at this time (Harshman et al 2008, Phillips et al 2010). Since the estimated arrival of kiwi ancestors in New Zealand, the country has undergone countless geographic processes throughout the millennia including sinking, uplift, tilting, sea level changes, erosion, volcanism and glaciation (Stevens 1975, Wallis and Trewick 2009). During the Oligocene (~30mya) the continent of Zealandia was largely submerged and remains approximately 93% submerged to this day. It is suggested that much of New Zealand was submerged during this time with possibly islands composing Otago / Southland, the Nelson region and Northland (Wallis & Trewick 2009). The final major marine transgression took place during the late Miocene, early Pliocene period, approximately 10Mya. During this time there were numerous sea straits in the North Island. This period must have had a marked effect on New Zealand flora and fauna. Significant environmental changes continued through the Quaternary period. The Pleistocene saw repeated cycles of glaciation. Despite this glaciation, large areas of New Zealand remained unscathed, including the majority of the North Island. It is

possible that the North Island Volcanic Plateau is an exception to this. However, for the most part, it would appear that glaciation is unlikely to be a determining factor in the phylogeography of North Island brown kiwi, unlike its counterparts in the South Island (Shepherd & Lambert 2008). Volcanism has played a significant role in shaping the North Island of New Zealand. All volcanoes on the North Island are relatively young (~2mya, Newnhan et al 1999). The Taupo Volcanic Zone (TVZ), active since 2mya, is the largest and most frequently erupting rhyolitic magmatic system on Earth. The Ultraplinian Eruption in the TVZ, the last major event, occurred 1.5kya and is thought to be the most violent volcanic event in the past 5000 years (Newnhan et al 1999). The event would have had global climatic implications and destroyed much of the central North Island, although pre-eruption ecosystems are thought to have recovered within 200 years. Volcanism is potentially a huge factor in explaining the phylogeography of North Island brown kiwi. However, this more recent volcanism may partially mask previous phylogenetic structure cased by processes such as the Oligocene transgression and Pliocene sea straits (Wallis and Trewick 2009). New Zealand's complicated geological history makes interpretation of phylogenetic analyses difficult. Also knowledge of kiwi dispersal capabilities is another factor that must be taken into account. At least since kiwi have lost the ability to fly, if indeed, the ability was ever present, kiwi dispersal power is low. In fragmented populations, North Island brown kiwi were found to migrate a maximum of 1.2km (Potter 1990). This poor dispersal power makes kiwi especially vulnerable to significant geographical changes.

SAMOVA analyses revealed that kiwi from the east and west of the North Island were genetically distinct, assigning samples from those regions to two distinct groups. Given the severity of volcanism in the Central North Island, especially in the TVZ, it is entirely reasonable to suggest volcanism and volcanic events as a barrier to gene flow. This east/west genetic split has been observed in other New Zealand flora and fauna (Wallis and Trewick 2009; Lloyd 2003; Holzapfel et al. 2002). It is possible, given the severity of some past eruptions, that the third group comprising Northland and the Coromandel was isolated geographically from the east and west at some point due to volcanism. However, volcanism could be masking the effects of past processes and the conflicting results of the Nested

Clade Analysis would suggest a more complicated phylogenetic history.

Shepherd and Lambert (2008), reported a significant Fu's F_S value for North Island brown kiwi, suggesting expansion out of refugia following volcanic eruptions. Their Nested Clade Analysis did not provide any significant values, possibly due to a smaller sample size. Nested Clade Analysis in this current study inferred continuous range expansion for clade 1-1. This clade consists of exclusively west and central North Island haplotypes (5,6,7,13) that are located geographically either in or close to the TVZ. The geographic distribution of these haplotypes is consistent with expansion out of refugia following volcanic eruptions as suggested by Shepherd and Lambert. The other significant lower order clade from which a scenario could be inferred was clade 1-2. This clade contained haplotypes that are located almost exclusively in Northland (1,2,3) or the Coromandel (4). The inferred scenario for this clade was long distance colonization and/or past fragmentation. Of the two scenarios past fragmentation is most likely as two of the haplotypes are found in low frequencies in other geographic areas (haplotype 3, west and eastern North Island; haplotype 4, Eastern North Island) and kiwi dispersal power is low, making long distance colonization unlikely. The causes of this fragmentation could be volcanism, but it is difficult to separate this from past geological processes and potentially more recent ones caused by human disturbance. The significant higher-level clade 2-1 contains the two lower level significant clades (1-1,1-2) with an inferred scenario of allopatric fragmentation. Allopatric fragmentation suggests long standing barriers to gene flow between the two lower order clades. This could possibly be due to North Island sea straits during the early Pliocene, possibly separating Northland and the Coromandel from the rest of the North Island although it is difficult to elucidate these past barriers from more recent ones such as volcanism. No significant values were found within eastern clades, most likely because all haplotypes overlap geographically in this region.

Temporal Changes in Haplotype Frequencies – Human Disturbance

All haplotypes present ~150 years ago in North Island brown kiwi are still remaining today. There has been no loss of large-scale genetic diversity. However, the frequencies of these haplotypes have changed significantly over this time period. Over the past 150 years there has been a 17.3 fold decrease in haplotype 8

and a 22.7 fold increase in Haplotype 12. The decrease in haplotype eight could be directly attributed to human activity (see Chapter 5). Both of these haplotypes have a distribution in the east of the North Island. As the prevalence of Haplotype 8 decreased, this could have allowed expansion of individuals with haplotype 12. Haplotype 6 has increased significantly over time. This may have been a relatively new haplotype ~150 years itself that has become more established over time. Haplotype 4 may be overrepresented in the present day samples, due to high accessibility to samples from the Project Kiwi conservation effort in the Coromandel. Therefore the huge increase in the frequency of that haplotype over time is most likely a sampling effect.

Implications for conservation

Given the results of the phylogenetic analyses, separating North Island brown kiwi into the four proposed 'taxa' seems appropriate, although the term taxa does not. Management units may be a better term. Given that the genetic differentiation between these populations can be attributed to New Zealand's geographic past, and not the effect of human disturbance, maintaining the current genetic differentiation between these populations is justified. The presence of the Coromandel specific haplotype in the Kaweka Forest Park should be further investigated with an increased sample size, as this would have implications for the proposed four-taxon plan. Additionally, finer scale genetic analyses are needed using a combination of mitochondrial and nuclear markers to examine population dynamics at a more localized level. Also, the edges of these populations should be studied in more detail, to look for potential admixture and hybridization. The mixed provenance zones established by the Department of Conservation in light of past translocations, such as Rimutaka and Mt Bruce, will allow investigation into the hybridization of east and west taxon. The mixed provenance zones may provide insurance if the decision to maintain current genetic differentiation has negative consequences associated with inbreeding. To further elucidate past phylogenetic patterns, more ancient samples need to be analysed. In short the management of North Island brown kiwi populations appears to be concordant with genetic data although caution should be applied to ensure that the primary research progresses at the same speed as policy making.

References

Baker AJ, Daugherty CH, Colbourne R, McLennan JL. 1995. Flightless brown kiwi of New Zealand possess extremely subdivided population structure and cryptic species like small mammals. *Proceedings of the National Academy of Sciences U.S.A* 92: 8254–8258.

Burbidge L, Colbourne RM, Robertson HA, Baker AJ. 2003. Molecular and other biological evidence support the recognition of at least three species of brown kiwi. *Conservation Genetics*. 4:167-177.

Clement M, Posada D, Crandall KA. 2000. TCS: a computer program to estimate gene genealogies. *Molecular Ecology*. 9:1657-1659.

Colbourne R, Bassett S, Billing T, McCormick H, McLennan J, Nelson A, Robertson H. 2005. The development of operation nest egg as a tool in the conservation management of kiwi. Science & Technical Publishing, Department of Conservation, Wellington, New Zealand.

Dupanloup I, Schneider S, Excoffier L. 2002. A simulated annealing approach to define the genetic structure of populations. *Molecular Ecology*. 11:2571-2581.

Fraser DJ, Bernatchez L. 2001. Adaptive evolutionary conservation: towards a unified concept for defining conservation units. *Molecular Ecology*. 10(12):2741-2752.

Goldberg J, Trewick SA, Paterson AM. 2008 Evolution of New Zealand's terrestrial fauna: a review of molecular evidence. *Philosophical Transactions of the Royal Society, London.* 363: 3319–3334.

Harshman J, Braun EL, Braun MJ, Huddleston CJ, Bowie RCK, Chojnowski JL, Hackett SJ, Han KL, Kimball RT, Marks BD, Miglia KJ, Moore WS, Reddy S, Sheldon

FH, Steadmen DW, Steppan SJ, Witt CC, Yuri T. 2008. Phylogenomic evidence for multiple losses of flight in ratite birds. *Proceedings of the National Academy of Sciences U.S.A*. 105(36):13462-13467.

Hoglund J, Larsson JK, Corrales C, Santafe G, Baines D, Segelbacher G. 2011. Genetic structure among black grouse in Britain: implications for designing conservation units. *Animal Conservation*. 14:400-408.

Holzapfel S, Faville MZ, Gemmill CEC. 2002. Genetic variation of the endangered holoparasite *Dactylanthus taylorii* (*Balanaphoraceae*) in New Zealand. *Journal of Biogeography*. 29:663-676.

Holzapfel S, Robertson HA, McLennan JA, Sporle W, Hackwell K, Impey M. 2008. Kiwi (*Apteryx spp.)* recovery plan: 2008–2018. *Threatened Species recovery plan* 60. Dept. of Conservation, Wellington. 71 p.

Kiwi Recovery Group. 2010. Annual Report 2008-2009. Internal report for the Department of Conservation. DOCDM-647527 (.pdf)

Lloyd B. 2003. Intraspecific phylogeny of the New Zealand short tailed bat Mystacina tuberculata inferred from multiple mitochondrial gene sequences. *Systematic Biology*. 52:460-467.

McLennan JA, Potter MA, Robertson HA, Wake GC, Colbourne R, Dew L, Joyce L, McCann AJ, Miles J, Miller PJ, Reid J. 1996. Role of predation in the decline of the kiwi, Apteryx spp., in New Zealand. *New Zealand Journal of Ecology*. 20(1):27-35

Newnham RM, Lowe DJ, Williams PW. 1999. Quaternary environmental change in New Zealand: a review. *Progress in Physical Geography*. 23(4):567-616.

Phillips MJ, Gibb GC, Crimp EA, Penny D. 2010. Tinamous and moa flock together: mitochondrial genome sequence analysis reveals independent losses of flight among ratites. *Systematic Biology*. 59(1):90-107.

Pons O, Petit RJ. 1996. Measuring and testing genetic differentiation with ordered versus unordered alleles. *Genetics.* 144:1237-1245.

Posada D, Crandall KA and Templeton AR. 2000. GeoDis: A program for the Cladistic Nested Analysis of the Geographical Distribution of Genetic Haplotypes. *Molecular Ecology.* 9(4):487-488.

Potter MA. 1990. Movement of North Island brown kiwi (*Apteryx australis mantelli*) between forest remnants. *New Zealand Journal of Ecology*. 14:17-24.

Roberts DG, Baker J, Perrin C. 2011. Population genetic structure of the endangered Eastern Birstlebird, *Dasyornis brachypterus*; implications for conservation. *Conservation Genetics.* 12:1075-1085.

Sales J. 2005. The endangered kiwi: a review. *Folia Zoologica* 54: 1-20.

Shepherd LD. 2006. Ancient DNA studies of the New Zealand kiwi and wattlebirds: evolution, conservation and culture [PhD Thesis]. [Auckland (New Zealand)]: Massey University.

Shepherd LD, Lambert DM. 2008. Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Stevens GR. 1975. Rugged landscape. The geology of central New Zealand. Wellington (New Zealand). Reed Publishing Limited.

Tajima F, Nei M. 1984. Estimation of evolutionary distance between nucleotide sequences. *Molecular Biology and Evolution*. 1:269-285.

Tamura K, Dudley J, Nei M, Kumar S. 2007. MEGA4: molecular evolutionary genetic analysis (MEGA) software version 4.0. *Molecular Biology and Evolution*. 24:1596-1599.

Templeton AR, Boerwinkle E, Sing CF. 1987. A cladistic-analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping .1. basic theory and an analysis of alcohol-dehydrogenase activity in drosophila. *Genetics*. 117(2):343-351.

Templeton AR, Crandall KA, Sing CF. 1992. A cladistic-analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping and dna-sequence data .3. cladogram estimation. *Genetics*. 132(2):619-633.

Templeton AR, Sing CF. 1993. A cladistic-analysis of phenotypic associations with haplotypes inferred from restriction endonuclease mapping .4. nested analyses with cladogram uncertainty and recombination. *Genetics*. 134(2):659-669.

Templeton AR. 2004. Statistical phylogeography: methods of evaluating and minimizing inference errors. *Molecular Ecology*. 13(4):789-809.

Templeton AR. 2008. Nested clade analysis: an extensively validated method for strong phylogeographic inference. *Molecular Ecology*. 17(8):1877-1880.

Tennyson AJD. 2010. The origin and history of New Zealand's terrestrial vertebrates. *New Zealand Journal of Ecology*. 34(1):6-27.

Wallis GP, Trewick SA. 2009. New Zealand Phylogeography: Evolution on a small continent. *Molecular Ecology*. 18:3548-3580.

Chapter 5

Ancient DNA recovers the origins of Māori feather cloaks[2]

Abstract

Feather cloaks (*kakahu*), particularly those adorned with kiwi feathers, are treasured items or *taonga* to the Māori people of New Zealand. They are considered iconic expressions of Māori culture. Despite their status, much of our knowledge of the materials used to construct the cloaks, the provenance of the cloaks and the origins of cloak making itself, has been lost. In this thesis, I used ancient DNA methods to recover mitochondrial DNA sequences from 849 feather samples taken from 109 cloaks. I showed that almost all (>99%) of the cloaks were constructed using feathers from North Island brown kiwi (*Apteryx mantelli*). Molecular sexing of nuclear DNA recovered from 92 feather cloak samples also revealed that the sex ratio of birds deviated from a ratio of 1:1 observed in reference populations. Additionally, I constructed a reference database of 185 mitochondrial control region DNA sequences of kiwi feathers comprising samples collected from 26 North Island locations together with data available from the literature. Utilising these data, I was able to determine the geographic provenance of 847 cloak feathers from 108 cloaks. A surprising proportion (15%) of cloaks

[2] Elements of this chapter have been published; therefore, there will be overlap between the two documents in both content and figures. KH is 1st author on the published manuscript, performed sample collection, laboratory work, data analysis and aided figure preparation. LH performed lab work and data analysis. RTK and KH performed sample collections. LDS performed preliminary laboratory work and data analysis. CDM designed the project and aided figure preparation. DML designed the project and helped to write the manuscript. All authors provided comments on the manuscript.

K. Hartnup, L. Huynen, R. Te Kanawa, L.D. Shepherd, C. D. Millar and D.M. Lambert. 2011. Ancient DNA recovers the origins of Maori feather cloaks. Molecular Biology and Evolution, in press.

were found to contain feathers from different geographic locations, providing evidence of kiwi trading among Māori tribes (*iwi*), or organised hunting trips into other tribal areas. Our data also suggest that the east of the North Island was the most prolific of all kiwi cloak making areas, accounting for over 50% of all cloaks analysed. Similar molecular approaches have the potential to discover a wealth of lost information from artefacts of endemic cultures worldwide.

Introduction

New Zealand was colonised by Europeans in recent history, with substantial numbers of colonisers arriving in the mid 1800's (McLintock 1966). The arrival of Europeans had a dramatic impact on the country and its inhabitants, the Māori. The 1800's marked a disruptive period amongst Māori. Warfare between tribes resulted in migration, expansion, retreat and displacement of tribes and tribal boundaries (Crosby 2001). However, amongst this disruption, the cultural traditions of Māori were largely maintained (Best 1908). This included the weaving of fine, feathered cloaks (*kakahu*). Large numbers of these cloaks survive in museums to this day including hundreds of kiwi feather cloaks (*kahu kiwi*). *Kahu kiwi* were particularly revered amongst Māori, and were reserved for chiefs of high social status (Ling Roth 1923). Given that the peak of kiwi cloak making was in the 1800's, each of these *taonga* is intricately linked to New Zealand's volatile history of that time. Despite this rich history, the majority of the cloaks held in museums have little accompanying information. Essentially their unique histories have been lost over the years. Here, a molecular approach has been taken, with the aim of elucidating some of these lost histories.

An ancient DNA approach (Bunce et al 2003; Huynen et al 2003; Shepherd and Lambert 2008) was used to recover both nuclear and mitochondrial DNA (mtDNA) sequences from the feathers comprising kahu kiwi. Utilising the reference database of current kiwi populations built in Chapter 4, it was possible to determine the provenance of these cloaks. Also, given the similarity in feather morphology between the five recognised species of kiwi, this molecular approach allowed the species of kiwi used in each cloak to be determined. Using nuclear sex markers it was possible to determine sex ratios of kiwi used in cloak construction

and compare these to current kiwi sex ratios. Finally, the data were used to shed light on cloak construction in the 1800's. The null hypotheses is that cloaks were constructed from avian species randomly selected from those commonly found in local areas and that cloak samples will be equally represented by both sexes. An alternative hypothesis is that feathers were either exchanged between Māori tribes (iwi) or that warfare forced tribes to search further afield for feathers. The latter, alternative hypothesis would predict that individual cloaks would comprise feathers from diverse geographical regions. In addition, the sex ratio of birds used in cloak construction was used to clarify the nature of kiwi capture methods by Māori. Direct testing of the predications of the above hypotheses could result in a new understanding of methods used by Māori to collect materials from cloak construction, understanding the traditions of cloak making itself and, how New Zealand's history has influenced the construction of these *taonga*.

Methods

Samples

A total of 1212 feather samples were obtained from 113 cloaks from museums across New Zealand, the United Kingdom (British Museum *n*=9, Horniman Museum *n*=3, Hawkes Bay Museum and Cultural Trust *n*=16, Canterbury Museum *n*=17, Auckland Museum *n*=13, Whanganui Regional Museum *n*=24, Waikato Museum *n*=4, and Te Papa Tongarewa *n*=27). The location on the cloak from which each sample was taken was recorded to help to determine the methods of cloak construction. Further information is available in chapter 2. A reference database using samples from current kiwi populations and sequences available in the literature was also built. See chapters 2 and 4 for further details.

Molecular Methods

Procedures outlined for the extraction and analysis of ancient DNA were followed (Huynen et al. 2003; Gilbert et al 2005; Willerslev and Cooper 2005). Ancient DNA sequences were verified by independent replication of 15 randomly selected samples. DNA was extracted, amplified and sequenced for a 200 bp fragment of the

mitochondrial hypervariable region I (HVRI) using kiwi specific primers kcF and kcR (Shepherd and Lambert 2008). These methods are explained in detail in chapter 2 of this thesis.

Molecular Sexing

A subset of 200 cloak samples was chosen at random for molecular sexing. Molecular sexing was conducted using ratite specific primers moa1 and moa2 (Huynen et al 2003) to amplify a ~67bp product from the female specific W chromosome. The presence of nuclear DNA was determined by the amplification of 65bp of the Chromo-Helicase-DNA-binding gene (CHD) using primers pM0 and pM1 (Huynen et al 2003). See chapter 2 of this thesis for more details. A total of 183 North Island brown kiwi feather samples (separate from the reference database) from a range of locations were obtained from Rainbow Springs Kiwi Encounter, Rotorua, New Zealand. The sex of these samples was determined through amplification of a 170bp female W-chromosome specific product using primers k9 and w13, and a fragment of the CHD gene using primers p2 and p3 (Griffiths and Tiwari 1995; Huynen et al. 2003). Again, further details are provided in chapter 2 of this thesis.

Results

Species Determination of Cloak Feathers

A 200 base pair fragment of the mitochondrial DNA control region was successfully amplified and sequenced for 849 of the 1212 feather samples obtained from cloaks. This resulted in an overall success rate of 70%. However, the success rate varied between museums (figure 5.1). Sequence data were recovered from 109/113 cloaks, with 4 cloaks failing to amplify for any of the feather samples taken. Phylogenetic analyses identified 847 of the sequences as North Island brown kiwi (*Apteryx mantelli*). The remaining two sequences, sampled from the same cloak, were identified as little spotted kiwi. The phylogenetic tree shown in the previous chapter (figure 4.2) shows the relationships between the kiwi feather samples and the five kiwi species.

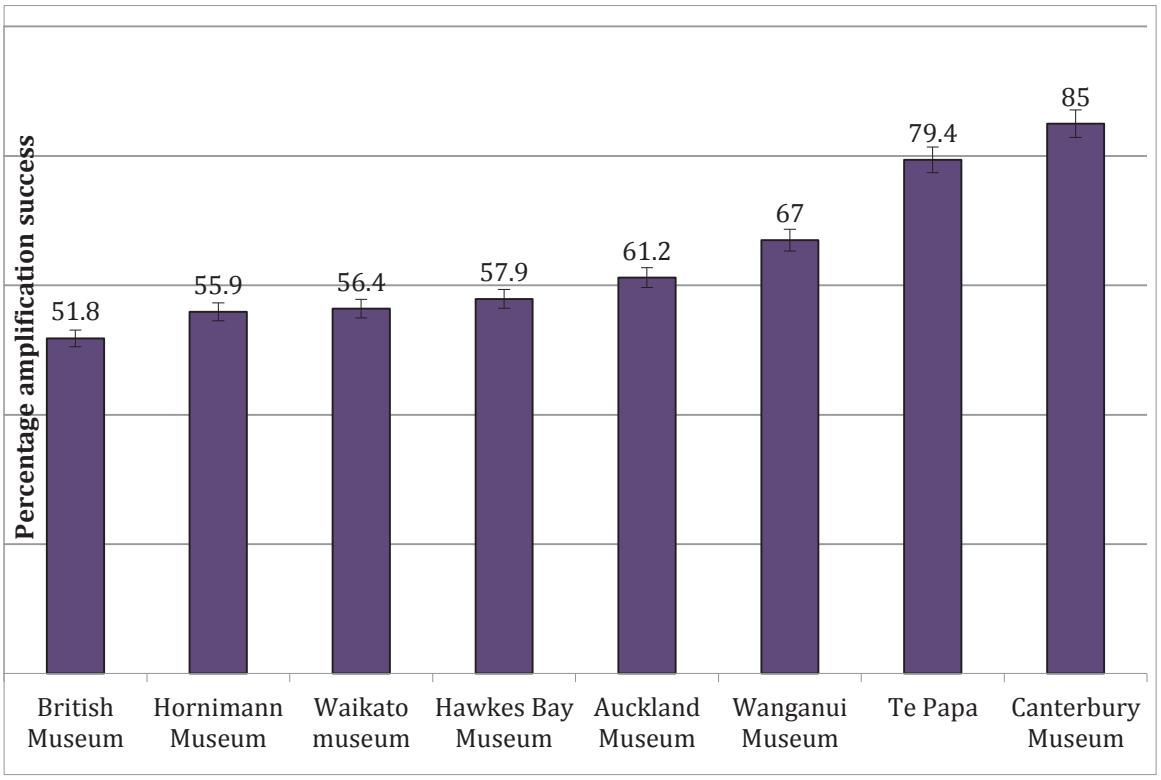


Figure 5.1. Amplification success rates (expressed as a percentage) of kiwi feather samples using primers kcF and kcR for cloaks from each of the museums visited.

Haplotype Structure and Frequency

For both modern and cloak feather DNA samples, eight variable sites comprising 13 haplotypes were observed for the 200bp HVRI sequence (figures 4.2, 4.3, 4.4). Haplotype frequencies are reported in Chapter 4 where there was a significant change in haplotype frequencies over time, with a notable reduction in the observed frequency of haplotype 8 between cloak and reference samples.

Determining the Provenance of Kiwi Feather Cloaks

The geographic structuring of modern North Island brown kiwi sequences observed in Chapter 4 (figures 4.4, 5.2) allows inferences to be made with regard to the provenance of samples from cloaks. Of the cloaks sampled, 50.5% contained feathers that came exclusively from the east of the North Island (57/113), 26.6% came from the west and central North Island (30/113), 3.5% came from Northland and the Coromandel (4/113), 15% were of mixed origin (17/113), 3.5% failed to amplify any samples (4/113) and, 0.9% was adorned with little spotted kiwi

feathers (1/113). The number of haplotypes in any one cloak was variable. Of the 108 cloaks shown to be adorned with North Island brown kiwi feathers, 29.6% had just one haplotype (32/108), 40.7% had 2 haplotypes (44/108), 25% had 3 haplotypes (27/108) and 4.7% had the maximum observed 4 haplotypes (5/108). Figure 5.2 shows examples of cloaks showing either 1,2,3 or 4 haplotypes. Cloak A, from Canterbury Museum, Christchurch (accession number E173.149), had nine samples of one haplotype only, haplotypes 5. In modern samples this haplotype was observed geographically in the west and Central of the North Island of New Zealand suggesting that this cloak was produced in this area. Additionally, this was one of the few cloaks that contained provenance information in the museum records. The records suggest that the cloak was made in Hawera, which is located south of New Plymouth, in Taranaki (Figure 5.2). Haplotype 5 has been observed in this region. Therefore, in this instance, the genetic and historical data are complementary to one another. Cloak B, from Te Papa Tongawera Museum, Wellington (accession number ME15753), contained feather sequences of haplotype 9 and haplotype 10. Both of these haplotypes are found exclusively in the east of the North Island of New Zealand in the modern samples, suggesting that the origin of the cloak was this region. Unfortunately there are no complementary museum records to corroborate the DNA data. Cloak C, from Canterbury Museum, Christchurch (accession number 2001.196.6), harboured feather sequences representing haplotypes 5, 9 and 10. In comparison to the distribution of modern haplotypes, this cloak contains a mixture of west and central (haplotype 5) and eastern (haplotypes 9 & 10) haplotypes. Cloak D, from Te Papa Tongawera Museum, Wellington (accession number ME14499), contained the maximum number of haplotypes observed for any cloak, four (haplotypes 5, 7, 8 and 13). Haplotypes 5 and 7 were observed exclusively in the west and central North Island in modern samples; haplotype 13 was only found in the central North Island, and haplotype 8 was detected in the east of the North Island only. Therefore this cloak is somewhat unusual as it contains a mixture of west and central (haplotypes 5 and 7), central (haplotype 13), and eastern haplotypes (haplotype 8).

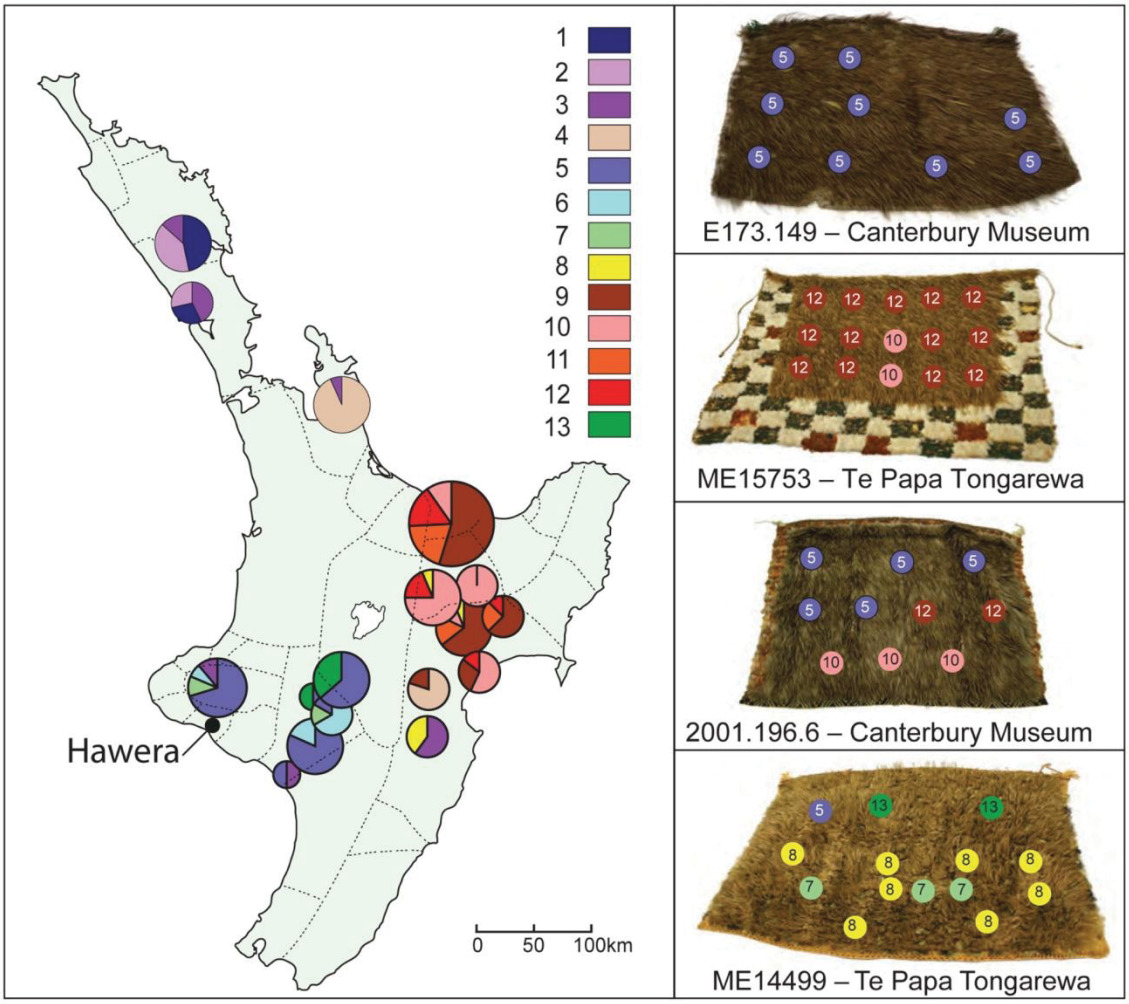


Figure 5.2. Provenance of kiwi feathers from four representative cloaks. Mitochondrial HVRI haplotypes recovered from cloaks are shown, together with the geographic distribution of these haplotypes. Also shown are the approximate tribal boundaries in the 1800's. Figure taken from Hartnup et al 2011.

Cloak Samples Exhibit a Skewed Sex Ratio

Of the 200 feather samples selected at random for sex determination, 39.5% (n=79) failed to amplify and one sample provided an ambiguous result and was therefore removed from the study. Of the remaining 120 samples (overall amplification success rate of 60%), 40.8% (n=49) were assigned as female and 59.2% (n=71) were assigned as male. For a small number of samples, sexing was successful in the absence of mitochondrial DNA amplification. Previous work with ancient moa DNA showed that short nuclear genome fragments (~70bp) were

retained at approximately the same frequency as the larger mitochondrial DNA fragments (~220bp) (Huynen et al 2003), and hence in ancient DNAs of low concentration there is a chance of amplifying one locus at the expense of another. Although feasible, we considered it prudent to remove from further analysis samples that amplified for nuclear DNA, yet failed to amplify mitochondrial DNA. This occurred in 20 of the 120 samples, reducing the sample size to 92 of which 40.2% were female (n=37) and 59.8% were male (n=55).

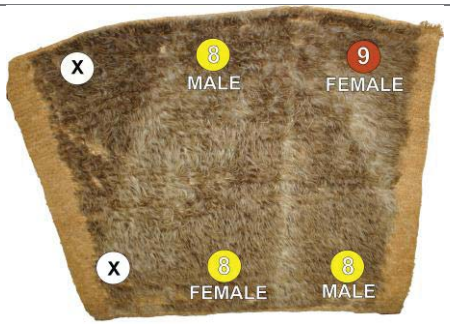
In parallel, molecular methods were used to sex a total of 183 kiwi feathers from modern populations. These individuals came from locations across the North Island of New Zealand. A total of 90 males and 93 females were identified using these methods. To test the significance of this result a likelihood ratio G-test was performed (Hardy 2002) using the freely available statistical software, R, and a script based on one available at http://www.psych.ualberta.ca/~phurd/cruft/. The modern sex assignment data show no statistical excess of either sex (G-test, p=0.486). Assuming the ratio of 1:1 directly observed in modern populations, the values obtained for cloak feather samples deviated significantly from expected values (G-test, p=0.0488), with an observed excess of males.

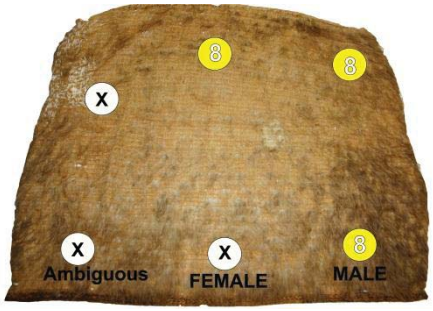
Individual Cloak Results

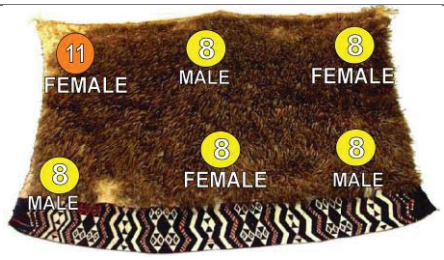
Although it is important to look at the results of these cloaks as a whole, each cloak is a significant ethnographic artefact and treasure (taonga) in its own right. Due to the cultural significance of each individual cloak, it is imperative that each cloak be examined separately. The following table (Table 5.1) contains information on museum records, sexing (where applicable), haplotype information and inferred provenance details.

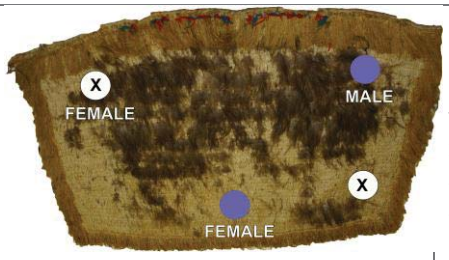
Table 5.1 Individual Cloak Results

Cloaks housed at the Hawkes Bay Museum and Cultural Trust

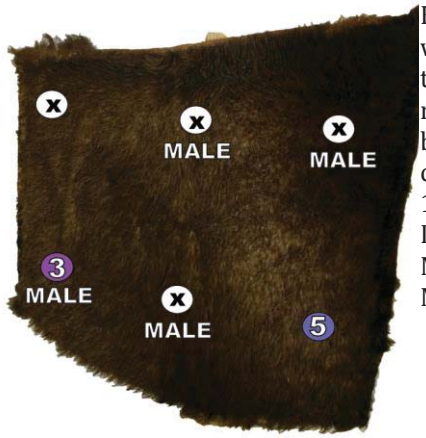
Cloak 2554	Description	Haplotype Information	Sexing Information	Origins
	Muka cloak covered with NIBK feathers. Size 140x121cm. McLean collection. Donated by Lady Florence McLean.	4/6 samples amplified. Two haplotypes found: Haplotype 8 (n=3) Haplotype 9 (n=1)	2 males and 2 female samples identified. Minimum of 3 individuals.	Haplotypes 8 and 9 restricted to the East of the North Island, making this region the likely origin.

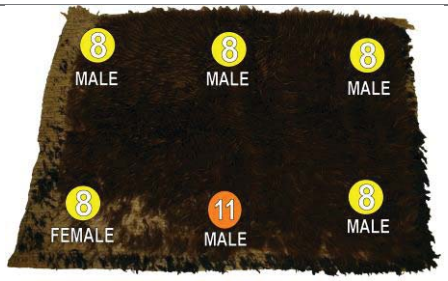
Cloak 25657	Description	Haplotype Information	Sexing Information	Origins
	Muka cloak covered with NIBK feathers. Many now missing. Poor condition. Size 130x90cm. Hawkes Bay collection. Donated by Mrs G Chapman of Havelock North.	3/6 samples amplified. Haplotype 8 identified (n=3).	1 male, 1 female and, 1 ambiguous amplification identified. This is a case where the nuclear sexing primer amplified when mitochondrial amplification failed.	Haplotype 8 is restricted to the East of the North Island, making this region the likely origin.

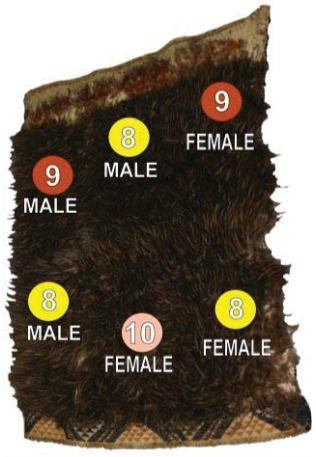
Cloak 2624	Description	Haplotype Information	Sexing Information	Origins
	Muka cloak covered with NIBK feathers. Taniko border along the bottom edge. Size 140x106cm. Donated by Mrs ML Smith of Napier.	6/6 samples amplified. Two haplotypes identified. Haplotype 8 (n=5) Haplotype 11 (n=1).	3 males and 3 females identified. Minimum number of 3 individual kiwi used in construction.	Haplotypes 8 and 11 are restricted to the East of the North Island, making this region the likely origin.

Cloak 2633	Description	Haplotype Information	Sexing Information	Origins
	Small muka NIBK feather covered cloak with dyed flax fringe and red and blue wool along top edge. Size 90x57cm maybe made for a child. Donated by The Misses Grant of Napier.	2/4 samples amplified. Both samples were Haplotype 5.	1 male and 2 females identified. Nuclear DNA amplified in the absence of mitochondrial DNA amplification in one instance.	Haplotype 5 is restricted to the west and central parts of the North Island and these regions are the likely origins of this cloak.

Cloak 2637	Description	Haplotype Information	Sexing Information	Origins
- 	Kahu kiwi with evidence of repair, patch of feathers added post construction. Size 170x109cm. Donated by Lady Florence Maclean	1/7 samples amplified. Haplotype 7 identified.	1 female identified. Nuclear DNA amplified in the absence of mitochondrial DNA amplification in one instance.	Haplotype 7 is restricted to the west and central parts of the North Island and these regions are the likely origins of this cloak.

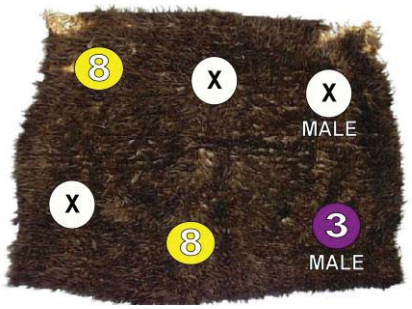
Cloak 2641	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with braided top edge, old repair on bottom right corner. Size 133x81cm. Donated by Mrs PS McLean.	2/6 samples amplified. Haplotypes 3 and 5 identified.	4 males identified. Nuclear DNA amplified in the absence of mitochondrial DNA amplification.	Haplotypes 3 and 5 are restricted to the west and central parts of the North Island and these regions are the likely origins of this cloak.

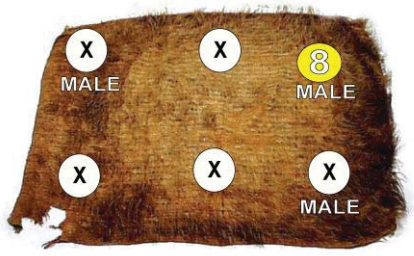
Cloak 2642	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with braided top edge. Blue tui feathers along the sides and bottom edge. Size 124x85cm. Donated by Mrs EW Navin	6/6 samples amplified. Haplotypes 8 and 11 identified.	5 males and 1 female identified.	Both of these haplotypes are restricted to the East of the North Island, making this area the cloaks likely origin.

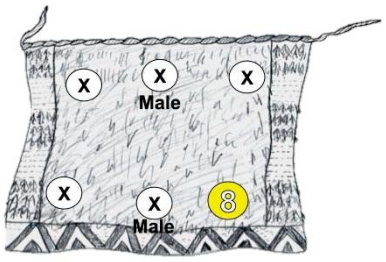
Cloak 2643	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with kaka feathers along the top edge and a taniko border along the bottom edge. Size 89x83cm. Donated by Mr J Kelly	6/6 samples amplified. Haplotypes 8,9,10 identified.	3 males and 3 females identified.	All of these haplotypes are restricted to the East of the North Island, making this area the cloaks likely origin.

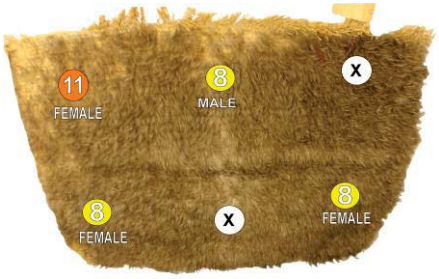
Cloak 2644	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with braided top edge. Size 102.7x101cm . Donated by Mr AR Wilkie.	6/6 samples amplified. Haplotypes 8,10,11 identified.	4 males identified.	All of these haplotypes are restricted to the East of the North Island, making this area the cloaks likely origin.

Cloak 2646	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with a diagonal pattern of kiwi feathers across the surface of the cloak. Kiwi feather edging is also present. Size 153x115cm. Donated by Lady Florence Maclean.	2/6 samples amplified. Both samples were haplotype 8.	2 males identified.	Haplotype 8 is restricted to the East of the North Island, making this area the cloaks likely origin.

Cloak 2647	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi, damaged along the top edge. There are also holes in the body of the cloak. Size 123x105cm. Unknown source.	3/6 samples amplified. Haplotypes 3,8 identified.	2 males identified. Nuclear DNA has amplified where mtDNA amplification has failed in one instance.	Haplotype 8 and haplotype 3 are only found together in the Ruahine Ranges towards the South East of the North Island. This may be the cloaks origin, however, haplotype 3 is also found in the North and West of the North Island, possibly resulting in a mixed origin.

Cloak 2649	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in poor condition. Feathers on the cloak in poor condition, with bald patches in places. Size 108x91cm. Donated by Mrs G Chapman.	1/6 samples amplified. Haplotype 8 identified.	3 males identified. Nuclear DNA has amplified where mtDNA amplification has failed in two instances.	Haplotype 8 is only present in the east of the North Island, making this region the likely origin of the cloak.

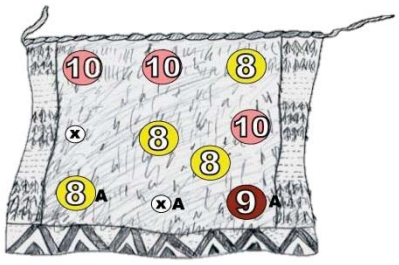
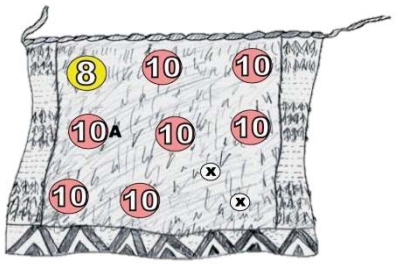
Cloak 2653	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with taniko border along the sides and bottom edge of the cloak. Size 166x128.5cm Donated by Lady Florence Maclean. No photograph available.	1/6 samples amplified. Haplotype 8 identified.	2 males identified. Nuclear DNA has amplified where mtDNA amplification has failed in both instances.	Haplotype 8 is only present in the east of the North Island, making this region the likely origin of the cloak.

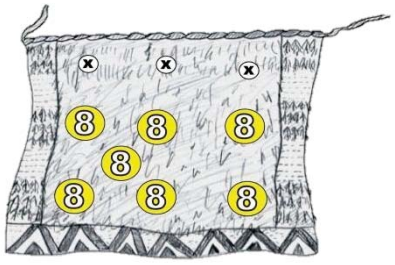
Cloak 2654	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with pale feathers. Top edge of cloak in poor condition. Size 139x106cm. Donated by Lady Florence Maclean.	4/6 samples amplified. Haplotypes 8 and 11 identified.	1 male and 2 females identified.	Haplotypes 8 and 11 are only present in the east of the North Island, making this region the likely origin of the cloak.

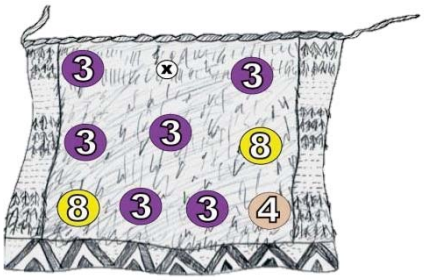
Cloak 4009	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi covered in dark feathers. Size 160x99cm. Donor unknown.	5/6 samples amplified. Haplotypes 8 and 9 identified.	3 females identified.	Haplotypes 8 and 9 are only present in the east of the North Island, making this region the likely origin of the cloak.

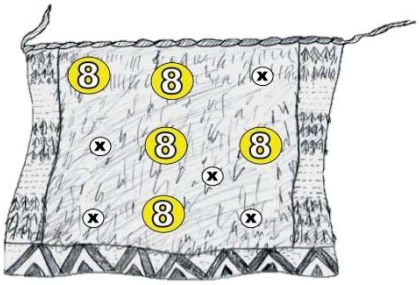
Cloak 26077	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with fringing at top corners. Muka is dyed black along the bottom edge and yellow along the top edge. Size 111x80cm. Donated by Lady Florence Maclean.	3/6 samples amplified. Haplotypes 8 and 9 and 13 identified.	3 females identified. Amplification of nuclear DNA has occurred in the absence of mtDNA amplification in 2 cases.	Haplotypes 8 and 9 are only present in the east of the North Island. However, haplotype 13 is only found in the central North Island. Therefore, this cloak has feathers from mixed origins.

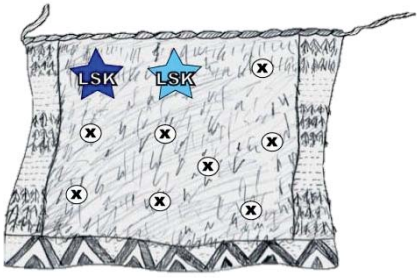
Cloaks housed at the British Museum, London, United Kingdom

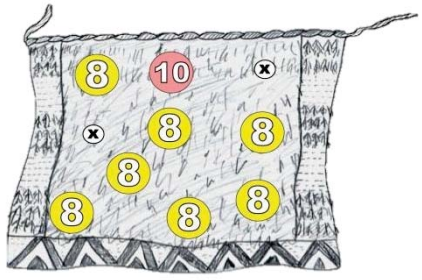
Cloak Q82OC737	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. Brown and albino kiwi feathers are present. Origin unknown. No Photograph available. 3 albino (**A**) samples.	8/10 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing information available.	Haplotypes 8, 9 and 10 are only present in the east of the North Island. Making this region the cloaks likely origin.
Cloak Q82OC736	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi with a mixture of brown and albino kiwi feathers. Taniko borders and coloured wool decorations. Unknown donor. 1 albino sample indicated with (**A**). No photograph available.	8/10 samples amplified. Haplotypes 8 and 10 identified.	No sexing information available.	Haplotypes 8 and 10 are only present in the east of the North Island. This region is the likely origin for the cloak.

Cloak OC1914/1215.1	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi with coloured wool borders. Donated to the museum in 1914 by Mrs HJ Tozer. No photograph available.	7/10 samples amplified. Haplotype 8 identified.	No sexing information available.	Haplotype 8 is only present in the east of the North Island. This region is the likely origin for the cloak.

Cloak OC1913/612.2	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with wool along bottom edge. Donated in 1913 by CH Waterlow. No photograph available.	9/10 samples amplified. Haplotypes 3, 4 and 8 identified.	No sexing information available.	This cloak is of mixed origin with all three haplotypes predominatel y represented in different geographic areas.

Cloak OC82Q704	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. No other information available. No photograph available.	5/10 samples amplified. All samples haplotype 8.	No sexing information available.	Haplotype 8 is only present in the east of the North Island, making the eastern region the cloaks most likely origin.

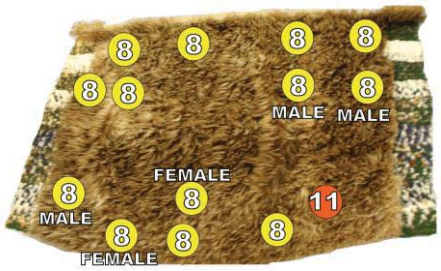
Cloak OC82726	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. With a taniko border of wool. Note by Mick Pendergrast indicates the cloak may be adorned with spotted kiwi feathers. Does not differentiate between great and little spotted.	2/10 samples amplified. Both samples belong to little spotted kiwi (*Apteryx owenii*). The two samples were different haplotypes and therefore come from 2 individuals.	No sexing information available.	Little spotted kiwi were once widespread throughout New Zealand, making the origin of this cloak difficult to infer.

Cloak OC1995Q4	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. Lower edge trimmed with tui feathers. Circumstantial evidence suggests that the cloak may have entered the museum as part of Royal Loan 1902, Loan 1. No Photograph available.	8/10 samples amplified. Haplotypes 8 and 10 identified.	No sexing information available.	Both of these haplotypes are restricted to the east of the North Island, making this region the cloaks likely origin.

Cloaks housed at Te Papa Tongawera Museum, Wellington, New Zealand

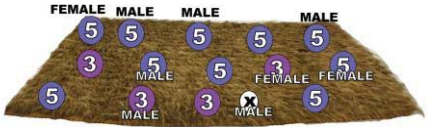
Cloak ME4274	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in poor condition with tui feathers down each side.	7/15 samples amplified. Haplotypes 5 and 13 identified.	2 males and 6 females identified. Nuclear DNA amplified in the absence of mtDNA amplification in 5 instances.	Haplotype 5 is found in the west and central North Island whereas haplotype 13 is only found in the central North Island, making the central North Island the most likely origin of this cloak.

Cloak ME144404	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in good condition. Kaka and kereru feathers form a border down both sides.	15/15 samples amplified. Haplotypes 8 and 10 identified.	8 males and 3 females identified.	Haplotypes 8 and 10 are both restricted to the east of the North Island. The east is therefore, the likely origin of this cloak.

Cloak ME2700	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in good condition. Kereru and pukeko feathers form a border down both sides.	14/15 samples amplified. Haplotypes 8 and 11 identified.	3 males and 2 females identified.	Haplotypes 8 and 11 are both restricted to the east of the North Island. The east is therefore, the likely origin of this cloak.

Cloak ME3714	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with suspected huia feathers dotted across the body of the cloak.	11/15 samples amplified. Haplotypes 8 and 11 identified.	10 males and 3 females identified. Nuclear amplification has occurred in the absence of mtDNA amplification in 4 instances.	Haplotypes 8 and 11 are both restricted to the east of the North Island. The east is therefore, the likely origin of this cloak.

Cloak ME14499	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with kakapo feathers dotted across the body of the cloak.	14/15 samples amplified. Haplotypes 5, 7, 8 and 13 identified.	7 males and 4 females identified. Nuclear amplification has occurred in the absence of mtDNA amplification in 1 instance.	This cloak is of mixed origin with a mixture of western and central (5, 7), central (13) and eastern (8) North Island haplotypes.

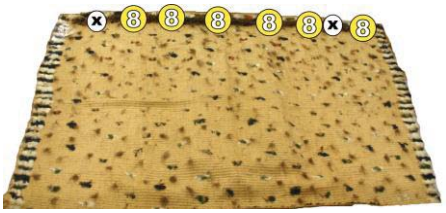
Cloak ME15755	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in good condition, no additional information available.	14/15 samples amplified. Haplotypes 3 and 5 identified.	6 males and 3 females identified. Nuclear amplification has occurred in the absence of mtDNA amplification in 1 instance.	Haplotypes 3 and 5 are both present in the West of the North Island, making this the likely location of the origin of this cloak.

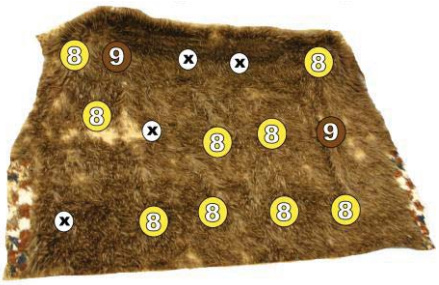
Cloak ME16934	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in reasonable condition, no additional information available.	9/15 samples amplified. Haplotypes 5 and 8 identified.	3 males and 5 females identified. Nuclear amplification has occurred in the absence of mtDNA amplification in 3 instances.	This cloak is of mixed origin as haplotype 5 is only found in west and central areas of the North Island whereas haplotype 8 is only found in the east.

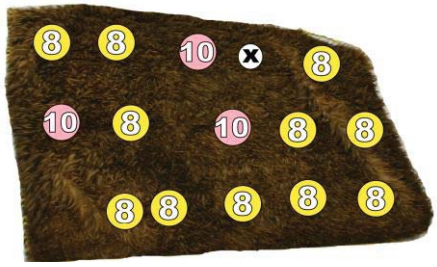
Cloak ME38885	Description	Haplotype Information	Sexing Information	Origins
	Very pale kahu kiwi with kaka feathers along the bottom edge.	14/15 samples amplified. Haplotype 9 identified.	No sexing data.	Haplotype 9 is found exclusively in the east of the North Island and is the likely origin of this cloak.

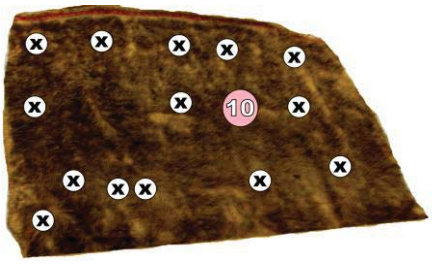
Cloak ME15753	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with a chequered border of kaka and kereru feathers along the sides and bottom of the cloak.	15/15 samples amplified. Haplotypes 9 and 10 identified.	No sexing data.	Haplotypes 9 and 10 are found exclusively in the east of the North Island and is the likely origin of this cloak.

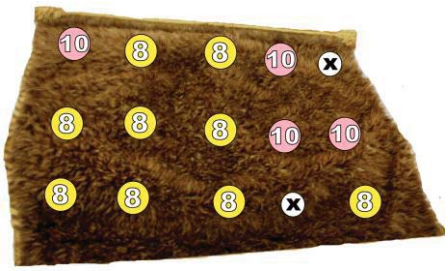
Cloak ME1378	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with brown kiwi feathers and 5 vertical strips of albino kiwi feathers.	13/15 samples amplified. Haplotypes 8, 10 and 11 identified.	No sexing data.	These three haplotypes are all found exclusively in the east of the North Island. It is likely this cloak was made in this region.

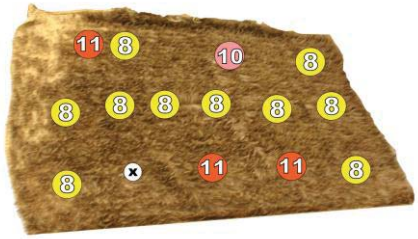
Cloak ME2691	Description	Haplotype Information	Sexing Information	Origins
	Kahu huruhuru (mixed feather) with kiwi feathers along the top edge.	6/8 samples amplified. Haplotype 8 identified.	No sexing data.	Haplotype 8 is found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced.

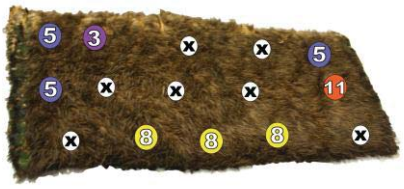
Cloak ME10760	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi threadbare in places. No additional information available.	11/15 samples amplified. Haplotypes 8 and 9 identified	No sexing data.	Haplotypes 8 and 9 are found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced.

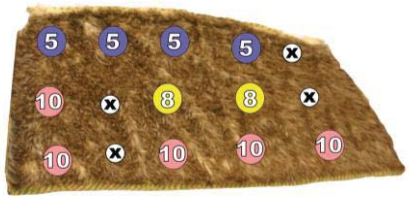
Cloak OL98.F	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with very dark brown kiwi feathers. No additional information available.	14/15 samples amplified. Haplotypes 8 and 10 identified	No sexing data.	Haplotypes 8 and 10 are found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced.

Cloak ME14915	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in very poor and threadbare condition.	1/15 sample amplified. Haplotype 10 identified.	No sexing data.	Haplotype 10 is found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced. However, this is based on only one sample.

Cloak ME2701	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in average condition. No additional information available.	13/15 samples amplified. Haplotypes 8 and 10 identified.	No sexing data.	Haplotypes 8 and 10 are found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced.

Cloak ME8697	Description	Haplotype Information	Sexing Information	Origins
	Light coloured kahu kiwi with a bare patch in the top left hand corner.	14/15 samples amplified. Haplotypes 8, 10 and 11 identified.	No sexing data.	Haplotypes 8, 10 and 11 are found exclusively in the east of the North Island. It is likely that the East of the North Island is where this cloak was produced.

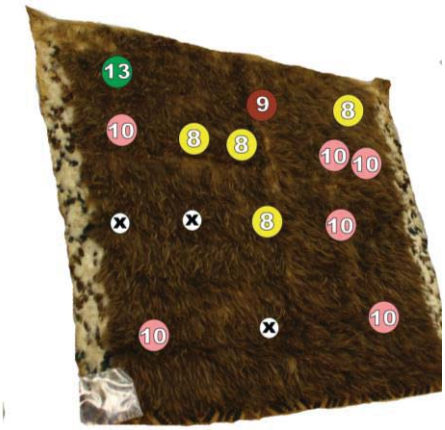
Cloak ME3716	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with tui and kererus border along the sides and bottom edge. Some bare patches at the top of the cloak.	8/15 samples amplified. Haplotypes 3, 5, 8 and 11 identified.	No sexing data.	The feathers on this cloak come from different geographical areas, making it of mixed origin.

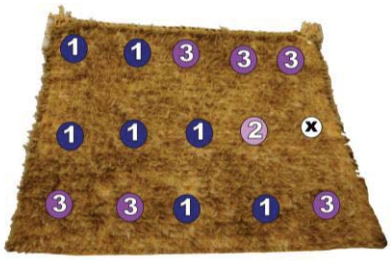
Cloak ME2055	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with a taniko border up both sides and a woollen border along the top and bottom edges.	11/15 samples amplified. Haplotypes5, 8 and 10 identified.	No sexing data.	The feathers on this cloak come from different geographical areas, making it of mixed origin.

Cloak ME7612	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in reasonable condition. No additional information available.	14/15 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing data.	All these haplotypes are exclusive to the east of the North Island, making this area the likely origin of this cloak.

Cloak ME6598	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi good condition with a taniko border along the bottom edge.	11/15 samples amplified. Haplotypes 8, 9 and 11 identified.	No sexing data.	All these haplotypes are exclusive to the east of the North Island, making this area the likely origin of this cloak.

Cloak ME15605	Description	Haplotype Information	Sexing Information	Origins
	Kahu huruhuru (mixed feather) with triangles of kaka and kereru feathers over the body of the cloak and kiwi feathers up both sides.	10/10 samples amplified. Haplotypes 9, 10 and 11 identified.	No sexing data.	All these haplotypes are exclusive to the east of the North Island, making this area the likely origin of this cloak.

Cloak ME15102	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with green and white feathers as borders along both sides and a taniko border along the bottom of the cloak	12/15 samples amplified. Haplotypes 8,9,10 and 13 identified.	No sexing data.	Haplotypes 8, 9 and 10 are exclusively from the east of the North Island. However, haplotype 13 is exclusively from the central North Island. This cloak has feathers of mixed origin.

Cloak ME15350	Description	Haplotype Information	Sexing Information	Origins
	Pale coloured kahu kiwi. No additional information available.	14/15 samples amplified. Haplotypes 1, 2 and 3 identified.	No sexing data.	These three haplotypes are found in Northland, which is the likely origin of this cloak.

Cloak ME14381	Description	Haplotype Information	Sexing Information	Origins
	Dark coloured kahu kiwi, no additional information available.	14/15 samples amplified. Haplotypes 4 and 7 identified.	No sexing data.	Haplotype 4 is found in the Coromandel, with a few reference samples in the east of the North Island. Haplotype 7 is only found in the west and central North Island. This suggests a mixed origin.

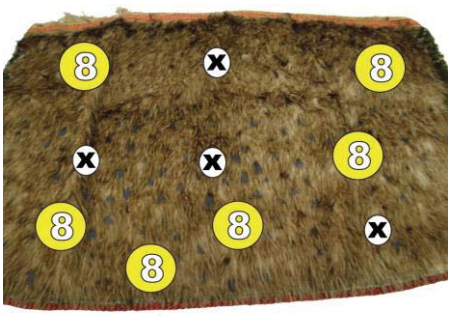
Cloak ME15351	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi with a black and white taniko border along the bottom edge. No additional information.	13/15 samples amplified. Haplotypes 1, 2 and 3 identified.	No sexing data.	All three haplotypes are found in Northland, making this location the most likely origin of this cloak.

Cloak ME13120	Description	Haplotype Information	Sexing Information	Origins
	Unusual kahu kiwi dotted with feathers from another bird (could be emu?). Very thickly braided ties at the top edge.	10/10 samples amplified. Haplotypes 5 and 7 identified.	No sexing data.	Both these haplotypes are found in the central and western North Island and the cloak is likely to have originated from this region.

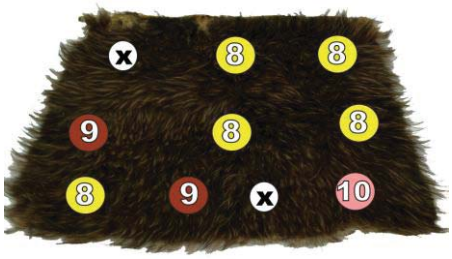
Cloak ME737	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in poor condition, balding in places.	6/10 samples amplified. Haplotypes 5 and 13 identified.	No sexing data.	Both these haplotypes are found in the central North Island and the cloak is likely to have originated from this region.

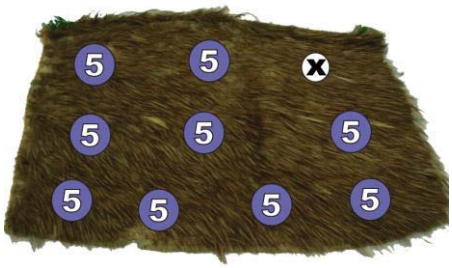
Canterbury Museum, Christchurch, New Zealand.

Cloak E192.130	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka with kaka feathers dotted across the body of the cloak. No donor information. Size 111x102cm.	4/10 samples amplified. Haplotype 5 identified.	No sexing data.	Haplotype 5 is found in the west and central North Island, the likely origin of this cloak.

Cloak E70.47	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka with pukeko feathers dotted across the body of the cloak. Green kereru feathers along the sides. Black and red wool along the bottom. Size 152x107cm	6/10 samples amplified. Haplotype 8 identified.	No sexing data.	Haplotype 8 is found in the east of the North Island, the likely origin of this cloak.

Cloak E161.51	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka. No additional details available. Size 153x100cm	8/10 samples amplified. Haplotypes 8 and 9 identified.	No sexing data.	Both of these haplotypes are found exclusively in the east of the North Island. It is likely that this cloak originated from this region.

Cloak E152.210	Description	Haplotype Information	Sexing Information	Origins
	Small kahu kiwi on muka. No additional details available. Size 62x49cm	8/10 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing data.	All three of these haplotypes are found exclusively in the east of the North Island. It is likely that this cloak originated from this region.

Cloak E173.149	Description	Haplotype Information	Sexing Information	Origins
	Small kahu kiwi on a Berlin wool backing. Yellow feathers dotted through cloak (possibly stitchbird?) Records suggest provenance as Hawera (west North Island).	9/10 samples amplified. Haplotype 5 identified.	No sexing data.	This haplotype is exclusive to the west and central North Island. This coupled with provenance details in the museum records would strongly suggest that this cloak is from the Hawera region on the west coast.

Cloak E173.482	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka. Bottom border decorated with kaka, tui and kakriki feathers. Kaka feathers also border the top and sides. 114x89cm	8/10 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing data.	All three of these haplotypes are found exclusively in the east of the North Island. It is likely that this cloak originated from this region.

Cloak E146.285	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka. Borders of kaka, kereru and tui feathers. 'Purchased, Mrs Bean' is written on the label. Size 103x75cm	8/10 samples amplified. Haplotypes 9 and 10 identified.	No sexing data.	Both of these haplotypes are found exclusively in the east of the North Island. It is likely that this cloak originated from this region.

Cloak E158.977	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka, incomplete. Used as a weaving demonstration. Records suggest the cloak is from Rotorua (east North Island).	10/10 samples amplified. Haplotype 9 identified.	No sexing data.	Records suggest this cloak is from Rotorua in the east of the North Island. As haplotype 9 is exclusive to the east, this would corroborate this provenance.

Cloak E147.760	Description	Haplotype Information	Sexing Information	Origins
	Striking cloak with alternate vertical strips of kiwi feathers and seabird feathers (albatross?). 8 kiwi samples, 2 albatross. Size 93x64cm	7/8 kiwi samples amplified. Haplotypes 8 and 11 identified. Both seabird feather samples failed to amplify with a range of primers.	No sexing data.	Haplotypes 8 and 11 are exclusive to the east of the North Island. This region is the likely provenance of the cloak.

Cloak E146.286	Description	Haplotype Information	Sexing Information	Origins
	Chequered pattern on cloak with squares of kiwi and tui feathers. Label states 'Purchased by Mrs Bean'. Size 114x89cm.	10/10 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing data.	Haplotypes 8, 9 and 10 are exclusive to the east of the North Island. This region is the likely provenance of the cloak.

Cloak 2001.196.6	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka. Kaka feather border along top and sides of cloak. Taniko border along the bottom edge. Size 104x80cm	10/10 samples amplified. Haplotypes 5, 9 and 10 identified.	No sexing data.	This cloak is made from feathers of mixed origin with haplotypes 9 and 10 being from the east and 5 from the west and central North Island.

Cloak E149.689	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka in poor condition. Has red wool decoration on borders. 161x116cm	6/10 samples amplified. Haplotypes 8 and 10 amplified.	No sexing data.	Haplotypes 8 and 10 are found exclusively in the east of the North Island. This region is the likely origin of this cloak.

Cloak IR1296	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on candlewick backing. Wool along the top edge, tui and pheasant feathers along the sides and bottom. Name on the label says Wendy Haase.	9/10 samples amplified. Haplotypes 3 and 4 identified.	No sexing data.	Haplotypes 3 and 4 are both found in the Coromandel. This may be the origin of the cloak. However, haplotype 3 is also found in the north and west of the North Island, which could indicate a mixed provenance.

Cloak E147.759	Description	Haplotype Information	Sexing Information	Origins
	Dark brown kahu kiwi on muka. Size 149x88cm. No additional details available.	9/10 samples amplified. Haplotypes 5 and 13 identified.	No sexing data.	Haplotype 13 is restricted to the central North Island and haplotype 5 is found in the west and central North Island. It is most likely this cloak originated from the central North Island.

Cloak E158.639	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on cotton backing. Tui and kaka feather border. Name on label is Forbes. Size 128x94cm	8/10 samples amplified. Haplotype 5 identified.	No sexing data.	Haplotype 5 is found in the West and central North Island. This is the cloaks likely provenance.

Cloak E158.638	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on cotton backing. The body of the cloak is dotted with kaka feathers. Green and white kereru feathers decorate the sides and bottom of the cloak. Forbes is written on the label. Size 100x98cm.	9/10 samples amplified. Haplotypes 3 and 7 identified.	No sexing data.	Both of these haplotypes are found in the west of the North Island, making this region the likely provenance of the cloak.

Cloak E158.640	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi on muka. Taniko borders along the sides and the bottom of the cloak. These may have been stitched on at a later date. Forbes is written on the label. Size 137x98cm.	10/10 samples amplified. Haplotypes 5, 7, 8 and 10 identified.	No sexing data.	This cloak is of mixed provenance. Haplotypes 5 and 7 are from the west and central North Island whereas haplotypes 8 and 10 are from the east.

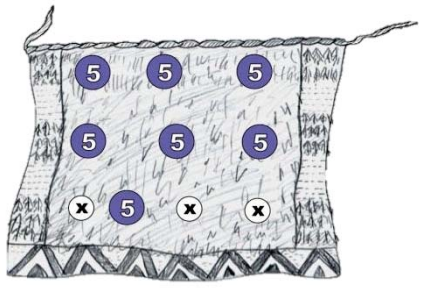
Waikato Museum, Hamilton, New Zealand

Cloak L2004/17/7	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi with taniko border running along the bottom edge. Quite a modern cloak made ~1981 by Rangimarie Hetet. Size 117x102cm	11/16 samples amplified. Haplotypes 3 and 5 identified.	No sexing data.	These haplotypes occur in the west North Island. The weaver, Rangimarie Hetet is from Te Kuiti in this region. The haplotypes compliment the museum records.

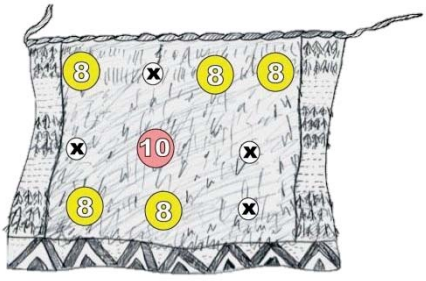
Cloak L2004/10/1	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Muka cloak decorated with kereru feathers and kiwi feathers. Taniko border running along the bottom edge. Modern cloak ~1990's. Made by Dame Diggeress Te Kanawa.	4/7 samples amplified. Haplotype 3 identified.	No sexing data.	Haplotype 3 occurs in the west and central North Island as well as Northland. However, as Dame Te Kanawa is from Te Kuiti, in the West, this is the most likely origin of the kiwi feathers.

Cloak L2004/6/1	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu huruhuru with kiwi, pukeko and kaka feathers. Taniko border. Named *Nga Rau O Nga Manu E Rima.* Made by Dame Diggeress Te Kanawa ~1990's.	7/10 samples amplified. Haplotype 3 identified.	No sexing data.	Haplotype 3 occurs in the west and central North Island as well as Northland. However, as Dame Te Kanawa is from Te Kuiti, in the West, this is the most likely origin of the kiwi feathers.

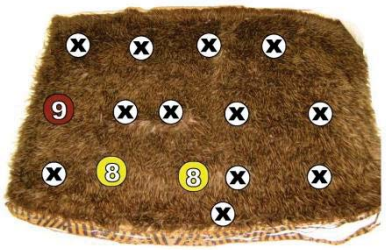
Horiman Museum, London, United Kingdom

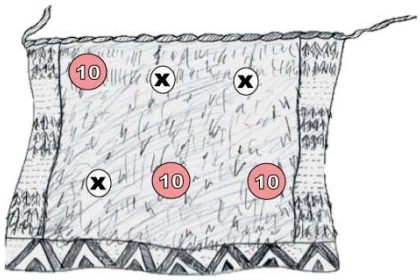
Cloak 1974.1	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. No additional information or photograph available.	7/10 samples amplified. Haplotype 5 identified.	No sexing data.	Haplotype 5 occurs in the west and central North Island, making this the likely provenance of this cloak.

Cloak 37.82	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. No additional information or photograph available.	2/10 samples amplified. Haplotypes 3 and 5 identified.	No sexing data.	Both haplotypes occur in the west and central North Island, making this the likely provenance of this cloak.

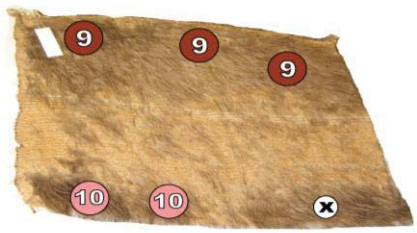
Cloak NN907	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. No additional information or photograph available.	6/10 samples amplified. Haplotypes 8 and 10 identified.	No sexing data.	Both haplotypes occur exclusively in the east of the North Island, making this the likely provenance of this cloak.

Auckland Museum, Auckland, New Zealand

Cloak 2666	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. In poor condition with frayed taniko border along the bottom edge.	3/15 samples amplified. Haplotypes 9 and 10 identified.	No sexing data.	Both haplotypes occur exclusively in the east of the North Island, making this the likely provenance of this cloak.

Cloak 45775	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. In poor condition. No other information available. No photograph available.	3/6 samples amplified. Haplotype 10 identified.	No sexing data.	Haplotype 10 occurs exclusively in the east of the North Island, making this the likely provenance of this cloak.

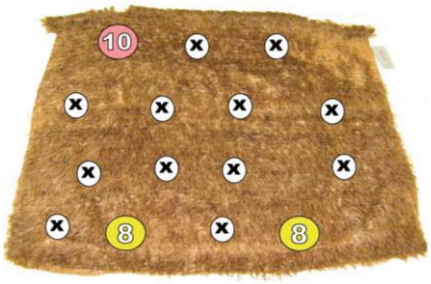
Cloak 18213	**Description**	**Haplotype Information**	**Sexing Information**	**Origins**
	Kahu kiwi. In poor condition.	2/10 samples amplified. Haplotype 5 identified.	No sexing data.	Haplotype 5 occurs exclusively in the west and central North Island, making this the likely provenance of this cloak.

Cloak 46164	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. In poor condition. A number of bald patches are present where the feathers have fallen out or worn away.	5/6 samples amplified. Haplotypes 9 and 10 identified.	No sexing data.	Both of these haplotypes occur exclusively in the east of the North Island. This cloak most likely originated from this region.

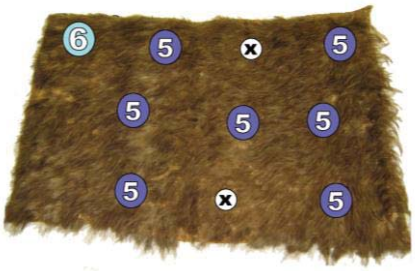
Cloak 19263	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. With bald patches in places across the body of the cloak.	11/15 samples amplified. Haplotypes 3, 5 and 7 identified.	No sexing data.	These three haplotypes all occur together in the west of the North Island. This region is the likely provenance of the cloak.

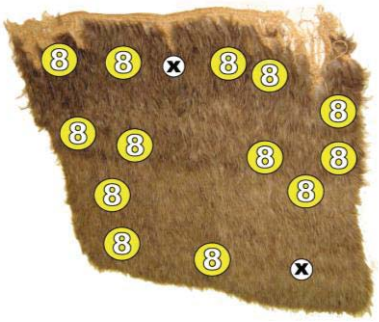
Cloak 38886	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. With bald patches in places across the body of the cloak. Taniko border along the bottom edge of the cloak.	13/15 samples amplified. Haplotypes 8, 9 and 10 identified.	No sexing data.	These three haplotypes all occur together in the east of the North Island. This region is the likely provenance of the cloak.

Cloak 6464	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. With bald patches in places across the body of the cloak. Taniko border along the bottom edge of the cloak.	13/15 samples amplified. Haplotypes 3, 5, 7 and 8 identified.	No sexing data.	This cloak is made using feathers from mixed origins. Haplotype 8 is exclusive to the east of the North Island whereas, the remaining three occur in the west and central North Island.

Cloak 35031	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi. Pale in colour. Bald patches in places.	3/15 samples amplified. Haplotypes 8, and 10 identified.	No sexing data.	These two haplotypes all occur together in the east of the North Island. This region is the likely provenance of the cloak.

Cloak 55668	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in very poor condition. Threadbare and balding in places.	5/10 samples amplified. Haplotypes 5 and 7 identified.	No sexing data.	These two haplotypes all occur together in the west and central North Island. This region is the likely provenance of the cloak.

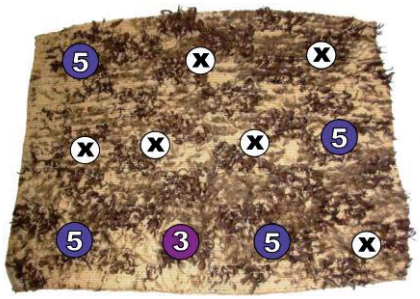
Cloak with no accession number	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in patchy condition.	8/10 samples amplified. Haplotypes 5 and 6 identified.	No sexing data.	These two haplotypes all occur together in the west and central North Island. This region is the likely provenance of the cloak.

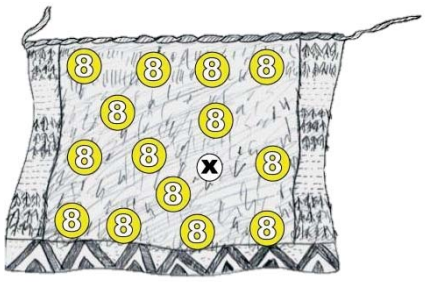
Cloak 35448	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in poor condition, the weave has become to unravel in places.	13/15 samples amplified. Haplotype 8 identified.	No sexing data.	This haplotype has a distribution restricted to the east of the North Island. It is likely that this cloak originated from this region.

Cloak 35448	Description	Haplotype Information	Sexing Information	Origins
	Kahu kiwi in reasonable condition.	10/15 samples amplified. Haplotypes 9, 10 , 11 and 12 identified.	No sexing data.	All these four haplotypes have distributions exclusive to the east of the North Island. This is the likely provenance of this cloak.

Whanganui Regional Museum, New Zealand

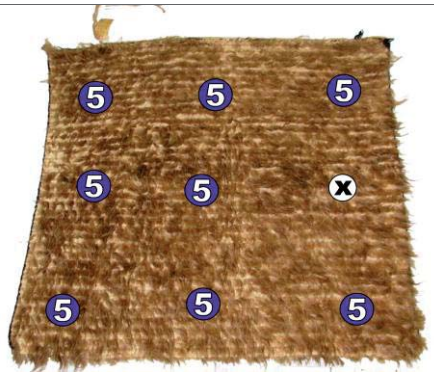
Cloak 1977.1.1	**Description**	**Haplotype Information**	**Origins**
	Child's kahu kiwi on candlewick. Taniko border along the bottom edge. 'Rena – Te Aroha Te Huna 18 Wikitoria Road Putiki' is written on the back of the cloak. Size 86x53cm	9/9 samples amplified. Haplotypes 5 and 7 identified.	Putiki is in the Whanganui District in the west of the North Island. Haplotypes 5 and 7 are also from this region. This is the likely origin of this cloak.

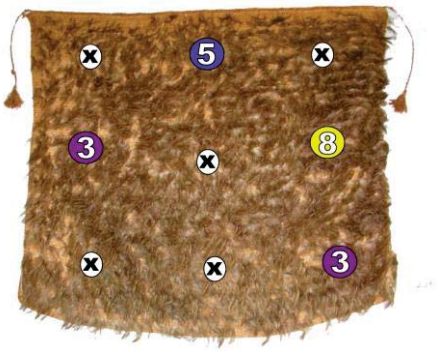
Cloak 1970.4	**Description**	**Haplotype Information**	**Origins**
	Kahu huruhuru (mixed feather) with kiwi and weka feathers. Feathers woven into a candlewick base. 132x107cm.	5/11 samples amplified. Haplotypes 3 and 5 identified.	These two haplotypes are found in the west of the North Island. It is likely that this cloak came from this region.

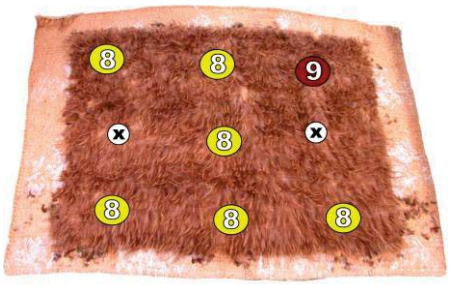
Cloak 1953.26	**Description**	**Haplotype Information**	**Origins**
	Kahu kiwi decorated with tui, kaka, kereru and kakariki feathers on muka. Kaitiaki (guardianship) Ngati Tuwharetoa iwi (Central North Island).	14/15 samples amplified. Haplotype 8 identified.	Haplotype 8 is found in the east of the North Island. However, records would suggest that the cloak originates from the central North Island. See discussion for further information.

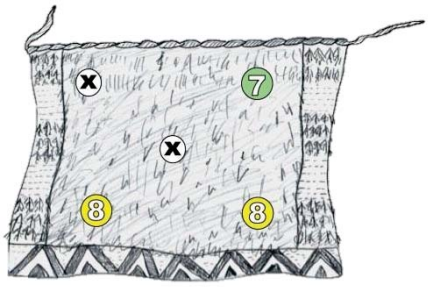
Cloak W. Shenton Collection	Description	Haplotype Information	Origins
	Kahu kiwi, no other information available. No photograph.	23/24 samples amplified. Haplotypes 8, 9 and 10 identified.	These three haplotypes are found in the east of the North Island. It is likely that this cloak came from this region.

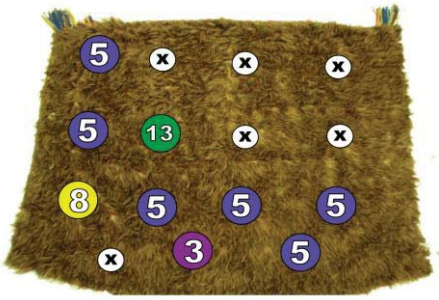
Cloak 1980.70	Description	Haplotype Information	Origins
	Kahu kiwi on cotton backing. Donor's grandmother, Mrs Lilian May Day (1883-1949) was given the cloak by Guide Rangi (Rotorua) after the Duke and Duchess of Windsor visited in the 1920s. Worn in Rotorua by Guide Rangi.	3/9 samples amplified. Haplotype 2 identified.	Haplotype 2 has a distribution limited to Northland. The cloak has strong ties to Rotorua (east North Island) yet it looks as though the feathers were sourced many hundreds of kilometres north of this location.

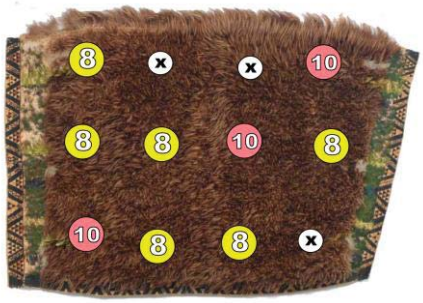
Cloak 1957.146	Description	Haplotype Information	Origins
	Kahu kiwi on a woven cotton backing. Edges are bound with black wool. May have been made in 1900. Locality, Parikino, Whanganui, New Zealand.	8/9 samples amplified. Haplotype 5 identified.	Haplotype 5 has a distribution limited to the west and central North Island. This haplotype distribution matches the locality in the museum records.

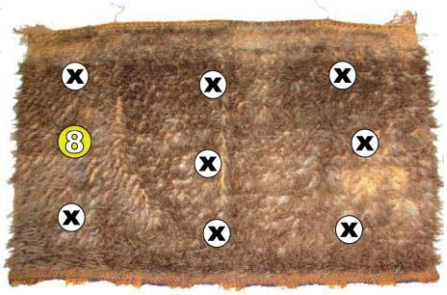
Cloak 1992.29.1	Description	Haplotype Information	Origins
	Commissioned by Charles Handley (Jerusalem, Pipiriki) to be made by weaver Mrs Williams, from Jerusalem, in the 1930s. Kahu kiwi on muka.	4/9 samples amplified. Haplotypes 3, 5 and 8 identified.	Haplotypes 3 and 5 are both found near the location where this cloak was commissioned. However, haplotype 8 has a distribution limited to the east of the North Island.

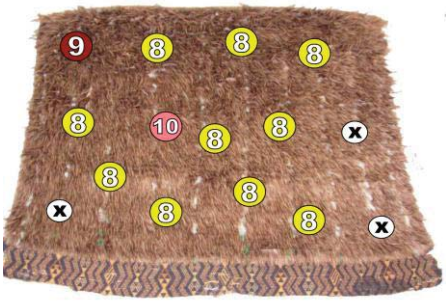
Cloak 2001.46.1	Description	Haplotype Information	Origins
	The original owner was Mrs Brook's mother-in-law, Ruihi Pakahiwi. Ruihi was murdered at Wahi Pa at the southern end of lake Taupo for having an affair after her husband had died and she deserted her children. Kahu kiwi on muka with kereru feathers. In poor condition.	7/9 samples amplified. Haplotypes 8 and 9 identified.	Haplotypes 8 and 9 have a distribution limited to the east of the North Island. Wahi Pa, where Ruihi Pakahiwi was murdered is in the central North Island. This indicates that the cloaks feathers and even the cloak itself has origins in the east.

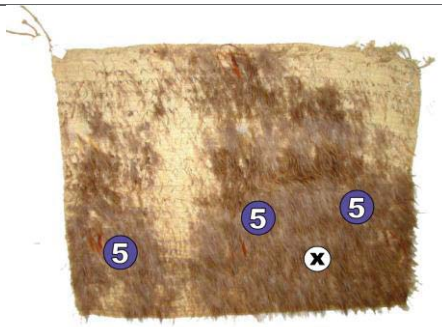
Cloak 1802.700	Description	Haplotype Information	Origins
	Kahu kiwi, no additional information available. No photograph available.	3/5 samples amplified. Haplotypes 7 and 8 identified.	This cloak contains a mixture of an eastern (8) and a western / central (7) haplotype.

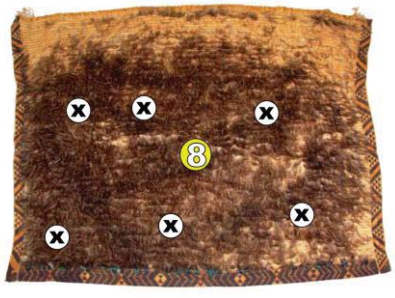
Cloak 2002.110	Description	Haplotype Information	Origins
	Purchased in Wanganui between 1889-1914 by Robert MacKenzie Gatenby from a Māori chief who was sitting outside his chemist business. The cloak has since been to England (1914) and Australia (1952) before returning to New Zealand in 2002. Kahu kiwi on muka with wool on the top edge.	9/15 samples amplified. Haplotypes 3, 5, 8 and 13 identified.	This cloak contains a mixture of eastern (8) haplotypes, central (13) and western and central (3,5) haplotypes. This cloak was therefore made using feathers from mixed geographic origins.

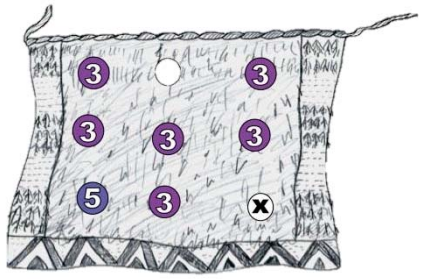
Cloak 1948.64.3	Description	Haplotype Information	Origins
	Kahu kiwi decorated with kereru, kakapo and tui feathers down each side of the cloak. Taniko border present down both sides and along the bottom of the cloak.	9/12 samples amplified. Haplotypes 8 and 10 identified.	Both haplotypes 8 and 10 have a distribution limited to the east of the North Island. It is likely that this cloak also originated from this region.

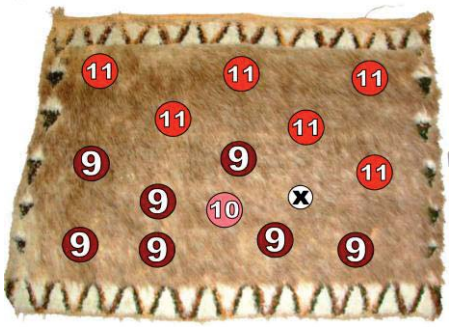
Cloak 1802.29	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Upper border of interlaced black and yellow fibre. Lower border of black and yellow taniko. I A M written in ink on the body of the cloak.	1/9 samples amplified. Haplotype 8 identified.	Haplotype 8 has a distribution limited to the east of the North Island. It is likely that this cloak also originated from this region.

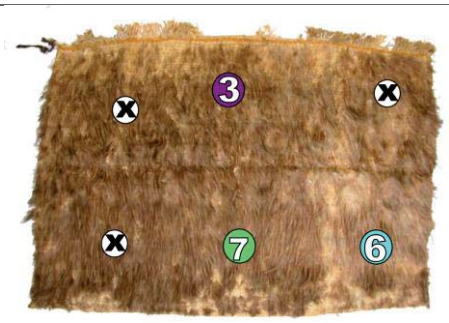
Cloak 1968.100.2	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Brown kiwi feathers interspersed with albino kiwi and domestic fowl feathers. Lower taniko border. Cloak worn by Mrs Stephens at the opening of Māori Court on 7th July 1968. Weaver is Tarahira Kereti (born 1825, died ~1878).	12/15 samples amplified. Haplotypes 8, 9 and 10 identified.	Haplotypes 8, 9 and 10 have geographic distribution limited to the east of the North Island. This is the likely origin of the kiwi feathers used to adorn this cloak.

Cloak 1802.24	Description	Haplotype Information	Origins
	Kahu kiwi on muka in poor, threadbare condition. Main body of the cloak decorated with kiwi feathers. Isolated patches of brown pheasant feathers. No borders or fringes.	3/4 samples amplified. Haplotype 5 identified.	Haplotype 5 has a geographic distribution limited to the west and central regions of the North Island. It is likely that the kiwi feathers used to adorn this cloak also came from this region.

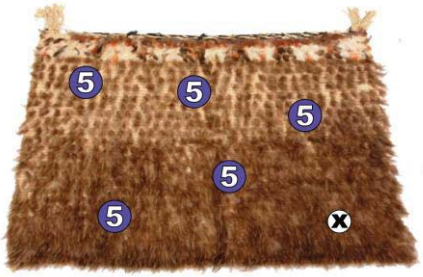
Cloak 1802.21	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Lower taniko border and side borders are present. Taniko is niho taniwha design. The brown dye is tanekaha, which is not in ready supply in Wanganui. Tui and kaka feathers along the lower edge.	1/7 samples amplified. Haplotype 8 identified.	The records suggest that this cloak is not from Wanganui in the west of the North Island due to the tree from which the brown dye is obtained is not in supply in that region. The haplotype results compliment this as haplotype 8 has a distribution limited to the east of the North Island.

Cloak W R Steadman Collection	Description	Haplotype Information	Origins
	Kahu kiwi. No additional information available. No photograph available.	7/9 samples amplified. Haplotype 3 and 5 identified.	Both of these haplotypes are found in the west of the North Island. It is likely that the kiwi feathers used to adorn this cloak originated form this region.

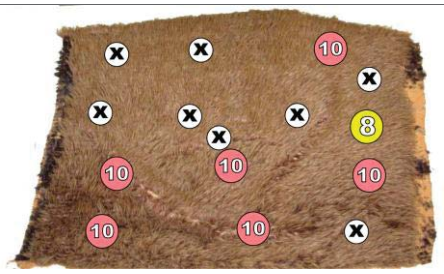
Cloak 1936.33.1	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Feather borders in a taniko design consisting of kaka and kereru feathers. Edges bound with red and grey wool. Kaitaki (guardianship) is Ngati Apa iwi (south western North Island).	14/15 samples amplified. Haplotypes 9, 10 and 11 identified.	These three haplotypes have a distribution limited to the east of the North Island. This suggests that the kiwi feathers on this cloak come from that region.

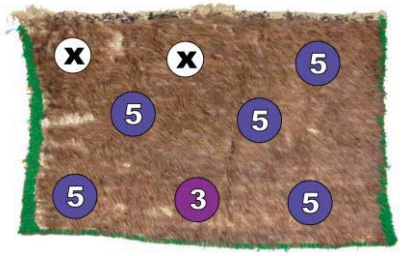
Cloak 1802.25	Description	Haplotype Information	Origins
	Kahu kiwi on muka. In poor condition. Balding in places.	3/6 samples amplified. Haplotypes 3, 6 and 7 identified.	These three haplotypes have a distribution limited to the west and central North Island. This suggests that the kiwi feathers on this cloak come from that region.

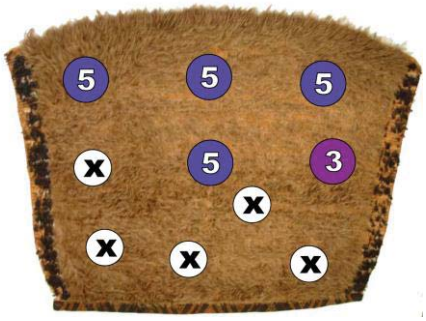
Cloak 1977.4	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Edges bound in green, orange or yellow wool. Tui feathers down both sides. Blocks of kaka, tui and kereru feathers decorate the kiwi feather body of the cloak. Presented to W. J. Birch of Erewhon Station, Inland Patea by a Māori chief between 1867-1900.	11/15 samples amplified. Haplotypes 5, 8 and 10 identified.	The Inland Patea is an old Māori track linking the Hawkes Bay in the east to Taihape in the west of the North Island, along which Erewhon Station was located. This location may explain the presence of eastern (8 and 10) and western (5) haplotypes on this cloak.

Cloak 1802.26	Description	Haplotype Information	Origins
	Kahu kiwi on candlewick backing. Body of the cloak is kiwi feathers with kaka and kereru feathers along the top edge. No provenance details.	5/6 samples amplified. Haplotype 5 identified.	Haplotype 5 has a distribution limited to the west and central North Island. It is likely that the kiwi feathers decorating this cloak came from this region.

Cloak 1909.107	Description	Haplotype Information	Origins
	Kahu huruhuru (mixed feather) consisting of kiwi, kaka, kereru and tui feathers. Made by Māori at Huiakama, Taranaki ~1900.	6/6 samples amplified. Haplotypes 5 and 7 identified.	Haplotypes 5 and 7 have a distribution limited to the west and central North Island. It is likely that the kiwi feathers decorating this cloak came from this region, especially when museum records are taken into account.

Cloak 1953.22	Description	Haplotype Information	Origins
	Kahi kiwi on muka. Bordered with weka feathers. Lower taniko border present. No provenance details.	7/15 samples amplified. Haplotypes 8 and 10 identified.	Haplotypes 8 and 10 have a distribution limited to the east of the North Island. It is likely that the kiwi feathers decorating this cloak came from this region.

Cloak 1959.125.1	Description	Haplotype Information	Origins
	Kahu kiwi on candlewick. Tui feathers on top edge. Green wool loops on sides and bottom of cloak. Edge bound with pink wool on the right side.	6/8 samples amplified. Haplotypes 3 and 5 identified.	Haplotypes 3 and 5 have a distribution together in the west of the North Island. It is likely that the kiwi feathers decorating this cloak came from this region.

Cloak 1957.14	Description	Haplotype Information	Origins
	Kahu kiwi on muka. Tui and kereru feather side borders and there is a narrow taniko border along the bottom edge. 'H. A.' stitched on the lower left hand side of the cloak.	5/10 samples amplified. Haplotypes 3 and 5 identified.	Haplotypes 3 and 5 have a distribution together in the west of the North Island. It is likely that the kiwi feathers decorating this cloak came from this region.

Discussion

Variation in Amplification Success

Although the overall mtDNA amplification success of cloak samples was 70%, this varied greatly between the museums where the cloak samples came from. The highest success rates came from Canterbury Museum (85%) and Te Papa Tongawera (79.4%). The lowest success rates were observed for cloaks from the British (51.8%) and Hornimann (55.9%) museums, both located in London in the United Kingdom. DNA begins to degrade the moment it is no longer part of a living organism. It is susceptible to the environment, especially heat, moisture and excess light (Willerslev & Cooper 2005). This makes appropriate storage of cloaks and ethnographic artefacts in general essential. The cloaks in the UK museums had a long journey to reach their current destination. The conditions on these journeys are of course unknown and could have contributed to DNA degradation. Also, during our sampling effort, the feather samples were couriered from the UK to New Zealand and, although every precaution was taken, they may have been subjected to adverse environmental conditions, thus contributing to DNA degradation further. This variation in amplification successes also highlights the care needed when transporting ethnographic objects between museums and when either displaying or storing these items.

In general, 70% is a high amplification success rate for artefacts of this nature. The cloak construction process may go some way to explain this. The ends of each group of feathers to be woven into a cloak were secured together using flax (Harakeke) sap. In more recent times, soap is used to achieve a similar result (Te Kanawa 1992). The flax sap may have acted to protect the feather bases from environmental factors, thus slowing down the degradation of DNA.

Species Determination of Cloak Feathers

Given the potential for extensive trade between iwi, it is surprising that almost all of the feathers sequenced were from North Island brown kiwi. It is known that North Island Māori made trips to the South Island of New Zealand to hunt for moa (Anderson 1989), and there was a greenstone trade established well before the production of the first kahu kiwi (Coutts 1971; Skinner 1912). Despite these historical trade and travel routes, no South Island kiwi species appear on any of the cloaks sampled. This would suggest a lack of trade in feathers between the two islands. Alternatively, the lack of cloaks harbouring feathers from South Island kiwi

species (*Apteryx australis, Apteryx rowi, Apteryx haasti*) could be explained simply by numbers. In pre-European times, population estimates of Māori vary greatly. Captain Cook estimated the Māori population to be around 100, 000 individuals at the turn of the 19th century. However, the interior of the North Island had no contact with Europeans until 1840, where a large number of Māori lived. In 1800 the Māori population estimates fluctuate between 100,000 to as many as 500, 000 individuals. It has also been estimated that only 8, 000 to 10,000 lived on the South Island (Lewthwaite 1999, 1950; McLintock 1966). With at least ten-fold more Māori inhabiting the North Island than the South, it would be expected that vastly more North Island kiwi feather cloaks would survive to this day. Taking this into account, perhaps it is not so surprising that 108/109 cloaks were made from North Island brown kiwi. It is likely that South Island kiwi cloaks do exist but are extremely rare. Additionally, it should be noted that Māori did not just make cloaks from kiwi feathers. Perhaps South Island iwi favoured the feathers from other bird species. A worthy future study would be to use molecular methods to examine the provenance of feather cloaks (kakahu) made using a variety of feathers. This work would be valuable in giving a more complete picture of national cloak making trends.

One of the 109 cloaks (British Museum, accession number OC82726), was found to have been made using little spotted kiwi (*Apteryx owenii*) feathers. We know that at least two individuals were used to make the cloak as the two sequences recovered were from two separate haplotypes. The present day distribution of little spotted kiwi is restricted to a scattering of offshore islands in the north of the North Island, Kapiti Island off the coast of Wellington, Cook Strait in the South Island, and possibly very small populations around Dusky Sound in Fiordland (Colbourne 2005). In the past little spotted kiwi were distributed across both islands (Shepherd and Lambert 2008). The smaller number of Māori on the South Island would explain the lack of feathers from the three kiwi species represented in the cloaks analysed (*Apteryx australis, Apteryx rowi, Apteryx haasti*). However, given that little spotted kiwi were present on both islands, including the more populated North, the presence of just one cloak is surprising. Perhaps it indicates that little spotted kiwi numbers were lower than North Island brown kiwi

numbers in the 1800's. Alternatively, brown kiwi could have been favoured culturally over little spotted kiwi. Also, given that little spotted kiwi are smaller than all other species of kiwi, it would have taken many more birds to complete one cloak, making North Island brown kiwi a more practical choice.

Haplotype Frequency and Structure

The 17.3 fold decrease in haplotype 8 coupled with the 22.7 fold increase in haplotype 12 observed in chapter 4 could be linked. Both of these haplotypes overlap geographically. Haplotype 8 was represented in over 30% of cloak samples and it is possible that use of kiwi by Māori for food and cloaks could have contributed to the reduction observed in this haplotype. As haplotype 8 decreased, this could have resulted in an increase in haplotype 12.

There was also a 5.7 fold difference in the observed frequency of haplotype 4, being more common in modern populations. This haplotype has a distribution limited almost exclusively to the Coromandel. However, as mentioned in chapter 4 of this thesis, the proportion of modern kiwi samples available from the Coromandel is likely to be greater than observed naturally and may have skewed the results. Also, the frequency of haplotype 6 varies ~18 fold, being more common in modern samples than in samples taken from cloaks (Hartnup et al 2011). The increase in the frequency of haplotype 6 observed, and its position on the tip of the haplotype network (figure 4.3) suggests that it may be a relatively new haplotype that has become more established in the west and central North Island over the past ~150 years.

Cloaks of mixed provenance

In the absence of substantial kiwi population shifts over the past 200 years (see chapter 4), in 15% of cases, feathers used in the construction of a single cloak were found to have derived from different geographic areas, potentially hundreds of kilometres apart (Figure 5.2). The mountainous, volcanic, interior of the North Island may have provided a barrier for North Island brown kiwi, evidenced through the phylo-geographic structure observed in chapter 4. However, this terrain caused no such barrier for Māori, who were capable of travelling hundreds of kilometres. Māori oral traditions record great feats of exploration (Taonui 2009)

such as Rãhiri who travelled from the far North of the North Island to Auckland, the Kaimai mountains (including their highest peak, Te Aroha), Tauranga, around the East Cape to Gisborne, Wairoa, Napier, Wellington, Taranaki and Kawhia on the west coast, essentially circumnavigating the entire of the North Island. Another example is of Te Arawa iwi, Kahumatamomoe and his nephew Ihenga who travelled from Maketu (the original landing place for many Māori waka) to Rotorua, south to the Waikato river, west to Raglan on the coast, north to Manukau harbour and on to the Wairoa river in the north. The oral traditions of Māori are likely to be based upon a mixture myth real accounts. Therefore, it is highly likely that journeys similar to these did take place. It is likely that Māori travelled either around the coast, or across the centre of the North Island. Methods of transport used by Māori included sea and river specific canoes (waka), or travel by foot. This tendency of Māori to travel large distances is further evidenced by activities during the inter-iwi musket wars (1810-1830). It has been estimated that as many as 60,000 Māori died during this volatile period. Muskets (ngutu parera, supplied to Māori by Europeans) changed the face of intertribal warfare, decimating some iwi and drastically shifting tribal boundaries. The Nga Puhi are renowned for their part in the musket wars, sending out raiding parties from their northern stronghold to an astonishingly large area, from the Waikato to Napier and as far south as Wellington (Crosby 2001). Given this propensity for travel and displacement during the same period as the construction of kahu kiwi, it is logical that cloaks would exist with feathers from several different geographic areas. Māori may have been forced to move to different areas to hunt for kiwi. Also as European influence became more prevalent, there may have been an increase in the trade of valuable items such as kiwi feathers. The numbers of Europeans in New Zealand increased dramatically in the 19th century, from only ~50 individuals in 1800, to ~200 Europeans by 1815 and, ~2000 by 1830. Most notably between the period of 1840-1850, the European population increased ten-fold from 2050 to 22,108 (McLintock 1966). European exploration, establishment of tracks, deforestation and displacement of Māori for land would have further precipitated forced movement by Māori.

Given that this dynamic period in New Zealand history coincides with cloak construction, this makes the task of revealing the individual story of each cloak more difficult. This is especially so because much happened during a relatively short historical timeframe, yet we cannot pinpoint the exact age of each cloak. For example if a cloak was estimated to have been woven between 1820 – 1850, it would not be possible to distinguish which historical event was influencing that particular cloak's story. However, using clues from a mixture of museum records, the genetic data and our knowledge of New Zealand history it is possible to make some inferences, particularly given cloaks of mixed provenance. One cloak from Wanganui Museum (accession number 1977.4) has a mixture of haplotypes with distributions limited to the east of the North Island (haplotypes 8 & 10), and the west and central North Island (haplotype 5). The museum holds detailed records on the cloak's history, noting that the cloak was presented to W. J. Birch at Erewhon station by a Māori chief between 1867 and 1900. This does not indicate the age of the cloak but does reveal that the cloak is at least 111 years old. Erewhon station was a sheep station leased by the Birch brothers in 1867. The station was located on the Inland Patea, 34km north-east of Taihape. The Inland Patea is a track (now a road) linking Hastings in the east, with Taihape in the west of the North Island, negotiating mountainous high country (Beaglehole 2010. Figure 5.3). The track was originally a Māori track, named after Patea who, according to Māori legend went on a long hunting trip, returning with very little, only to find his woman had filled the storehouse by herself. Angered by her insults he took her for a walk, where she fell from a cliff. To avoid the backlash from his iwi, Patea fled to the high country inland, now called the Inland Patea. The first European to use this route was William Colenso in 1851 (Elder 1959, Colenso 1878) and crossed several times in his time spent in the region recording botany. At the time Erewhon station was established in 1867, Napier was the nearest primary port, leading to large trains of packhorses carrying wool navigating a dangerous track over the Inland Patea (See the photograph in Figure 5.3). This track was likely one of the busiest and longest in New Zealand at the time. This track also provides a direct trade route between the east and west and may go some way into explaining the mixed provenance seen in this cloak, as well as some of the others.

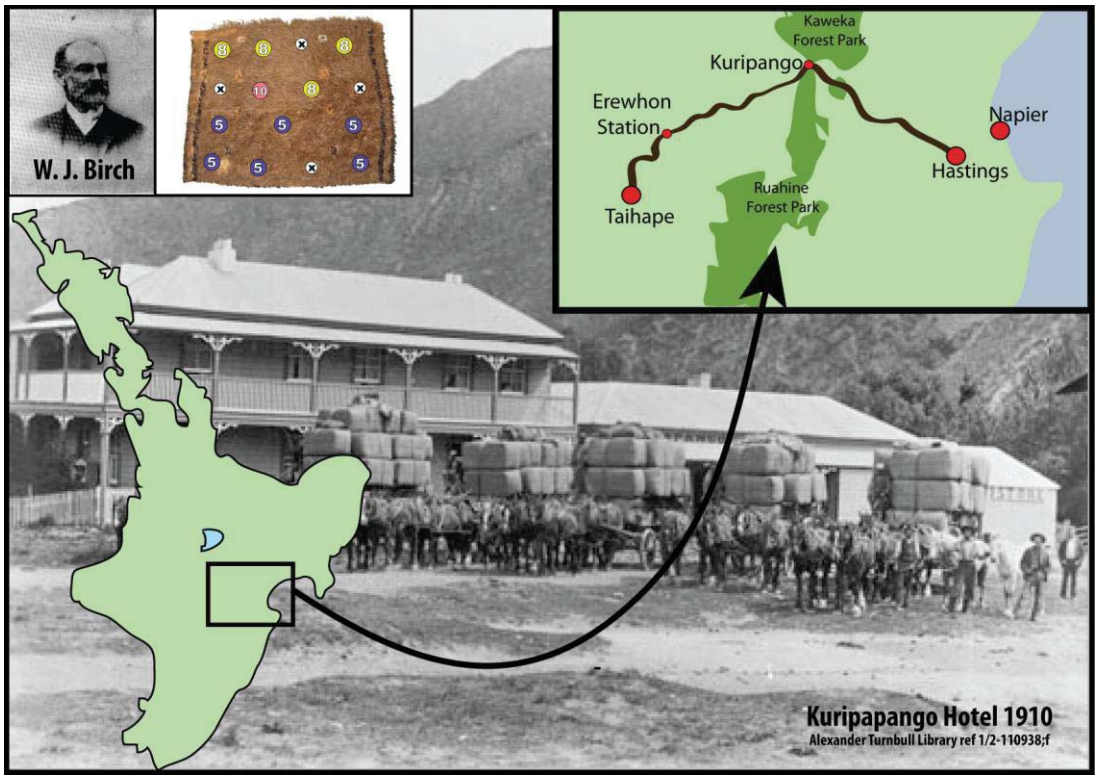


Figure 5.3. The Inland Patea trail traverses mountainous terrain linking the east of the North Island near Hastings with Taihape in the west and central North Island. This trail, where the mixed provenance cloak pictured was found (Wanganui Museum accession number 1977.4) at Erewhon Station under the care of William Birch, could explain the mixture of east and west haplotypes.

Insights into Cloak Making Practices

The location of each sample taken was plotted to its approximate position on the body of each cloak. The patterns of haplotypes can then provide insights into the methods of cloak construction employed. Historical information suggests that cloaks were woven on sticks stuck directly into the ground and that cloaks were woven from left to right, top to bottom, starting from what would eventually be the bottom right hand corner (Best 1908). The pattern of haplotypes in figure 5.2 (cloak 2001.196.6) provides evidence that this was indeed the case. Similar patterns have also been seen on many of the other cloaks analysed in the study (e.g

Te Papa cloaks ME16934, ME2055, ME14381, ME15351; Canterbury Museum cloaks 2001.196.6, IR1296, E158.638; Auckland Museum cloaks 19263, 38886, 6464, 35448; Wanganui Museum cloak 1977.4).

Of the haplotype frequencies observed, one mitochondrial haplotype is dramatically overrepresented in kiwi feather cloaks, despite the fact that in present day populations, it has a very limited distribution in a small region of the east of the North Island. All of the other haplotype frequencies either stayed at similar frequencies or increased over time (haplotypes 4, 6 and 12). Haplotype 8 is present in over 30% of cloak samples compared with only 2.1% of reference samples (fig4.3). It is unlikely that this haplotype was more widespread in the early 19th century (when feather cloak making likely originated) or even in the early 20th century. This is because previous ancient DNA studies of North Island brown kiwi skins and sub-fossil remains failed to record haplotype 8 at any other locations (Shepherd & Lambert 2008), although caution should be applied as only 3 North Island brown kiwi were represented. The current distribution of haplotype 8 corresponds with the tribal homelands (in the 19th century) of the Tuhoe iwi from the Ureweras, the Ngati Kahungunu Ki Wairoa, the Ngati Kahungunu Ki Heretaunga, and the Ngati Ruapani iwi. It is known that feather cloaks were made by the Tuhoe people in the 19th century since Best (1908) observed this practice during his stay in the Ureweras. The approximate ages of these cloaks, combined with their detailed construction, suggest that cloak making was well advanced in the east of the North Island of New Zealand by the mid 1800's and possibly even earlier. In combination with the genetic data, which show over 50% of the 108 cloaks harboured only feathers originating from the North Islands east coast, suggest that this area was likely to have been the centre of kiwi cloak making in early New Zealand.

Cloak Samples Exhibit a Skewed Sex Ratio

The molecular sexing data revealed a significant male skew in the sexes of kiwi feathers used to adorn cloaks. In contrast molecular sexing results from the modern reference material show a very slight excess of females, but this is not statistically different from a 1:1 ratio. This male skew in the observed sex ratio for feather in cloaks may be a result of paternal egg incubation in North Island brown

kiwi (Colbourne 2002), thus making the males more vulnerable to Māori hunting methods. However, during the day both males and females roost in burrows. Certainly in early European times, dogs were used to catch kiwi nesting in burrows (Best 1908; Trotter & McCulloch 1977). Elsdon Best, New Zealand's first European ethnographer, spent time with the Tuhoe iwi in the Ureweras in 1893 and observed their hunting methods first hand. During hunting, which occurred at night, Māori would make a lure-call (whistling), which kiwi would reply to. Dogs would then follow the sound to locate kiwi.

Conclusions

Genetic information from modern and ancient populations of kiwi has been successfully utilised to infer cloak-making practices of a once widespread cultural tradition of the indigenous people of New Zealand. Rediscovering aspects of the lost histories of these artefacts will no doubt enhance their cultural value. This approach has the potential to recover a wealth of lost information from a wider range of ethnographic artefacts held in museums worldwide. Genetic analyses such as those conducted here may also play a significant role in the repatriation of priceless items to their original countries, regions, or tribal homelands. This illustrates the benefits of a molecular approach to biological anthropology and highlights the potential for enriching our knowledge of culturally valuable items.

References

Anderson A. (1989). Prodigious birds: moas and moa hunting in prehistoric New Zealand. Cambridge University Press.

Beaglehole D. (2010). Whanganui places inland patea: Te Ara- The Encyclopaedia of New Zealand. Updated 18/1/2010. URL:http://www.TeAra.govt.nz/en/whanganui-places/8

Best E. (1908). Māori forest lore: being some account of native forest lore and woodcraft, as also of many myths, rites, customs, and superstitions connected with

the flora and fauna of the Tuhoe of Urewera district – Part 2. *Transactions and Proceedings of the Royal Society of New Zealand*. 41:231-285.

Bunce M, Worthy T H, Ford T, Hoppit W, Willerslev E, Cooper A. (2003). Extreme reversed sexual size dimorphism in the extinct New Zealand moa *Diornis*. *Nature* 425:172-175.

Colbourne R. (2002). Incubation behaviour and egg physiology of kiwi (*Apteryx* spp.) in natural habitats. *New Zealand Journal of Ecology*. 26(2):129-138.

Colbourne R. (2005). Kiwi (*Apteryx* spp.) on offshore New Zealand islands: populations, translocations and identification of potential release sites. Wellington (New Zealand): DOC Research and Development Series 208. Department of Conservation. P.24

Colenso W. (1878). Memorandum of my first journey to the Ruahine Mountain region and the flora of that region. Read before the Hawkes Bay Philosophical Institute.

Coutts P J F. (1971). Greenstone: The Prehistoric exploitation of bowenite from Anita Bay, Milford Sound. *Journal of the Polynesian Society*. 80 (1): 42-75.

Crosby R D. (2001). The musket wars: a history of inter-iwi conflict 1806-1845. Auckland (New Zealand): Reed Publishing Limited.

Elder N L (1959). Vegetation of the Kaweka Range. *Transactions of the Royal Society of New Zealand.* 87(1,2): 9-26.

Gilbert M T, Bandelt H J, Hofreiter M, Barnes I. (2005). Assessing ancient DNA studies. *Trends in Ecology and Evolution*. 20(10):541-544.

Griffiths R & Tiwari B. (1995). Sex of the last wild Spix's macaw. *Nature* 375:454.

Lewthwaite G R. (1999). Rethinking Aotearoa's human geography. *The Social Science Journal*. 36 (4): 641-658.

Hardy I C W. (2002). Sex ratios: concepts and research methods. Chapter 3: statistical analysis of sex ratios: 56. Cambridge University Press.

Huynen L. Millar C D, Scofield R P, Lambert D M. (2003). Nuclear DNA sequences detect species limits in moa. *Nature* 425:175-178.

Lewthwaite G R (1950). The Population of Aotearoa: Its number and distribution. *The New Zealand Geographer*. 6 (1): 35-52.

Ling Roth H. (1923). The Māori Mantle. Halifax (UK): Bankfield Museum.

McLintock A H. (1966). Population, population trends and the census. An Encyclopaedia of New Zealand. Te Ara – The Encyclopaedia New Zealand, Updated 22/04/2009. URL:http://www.TeAra.govt.nz/en/1966/population/1

Shepherd L D & Lambert D M. (2008). Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Skinner H D. (1912). Māori life on the Poutini Coast, together with some traditions of the natives. *Journal of the Polynesian Society*. 21 (4): 141-151.

Toanui R. (2009). Nga waewae tapu- Māori exploration- exploration traditions. Te Ara- The Encyclopaedia of New Zealand. Updated 1/3/2009. URL:http://www.TeAra.govt.nz/en/nga-waewae-tapu-Māori-exploration/1

Te Kanawa D. (1992). Weaving a kakahu. Wellington (New Zealand): Bridget William Books Limited.

Trotter M & Muculloch B. (1997). Digging up the past. New Zealand archaeological history. Auckland (New Zealand): Penguin Books.

Willerslev E. & Cooper A. (2005). Ancient DNA. *Proceedings of the Royal Society of London B Biological Sciences*. 272:3-16.

Photograph and Figure References

Figure 5.2. From Hartnup K, Huynen L, Te Kanawa R, Shepherd LD, Millar CD, Lambert DM. (2011). Ancient DNA recovers the origins of Māori feather cloaks. *Molecular Biology and Evolution*. First published online May 10, 2011 doi:10.1093/molbev/msr107

Picture of W.J. Birch used in Figure 5.3. The Cylopedia of New Zealand (Wellington Provincial District) Cyclopedia Company Limited 1897.

Photograph of the Kuripapango Hotel 1910 used in Figure 5.3. Alexander Turnbull Library. John Moore Collection ref 1/2-110938;f.

Chapter 6

Ancient DNA Analysis of Kiwi Feather bags (*kete* kiwi)

Abstract

In addition to cloaks, kiwi feathers were also used by Māori to decorate small bags or *kete*. Similarly to the cloaks, information relating to the history of each *kete* had been lost. Using ancient DNA methods, mitochondrial DNA sequences were recovered from 161/241 samples from 55/63 *kete*. Every single feather sample amplified was identified to belong to North Island brown kiwi (*Apteryx mantelli*), complementing the cloak chapter, as the most common kiwi species used in the construction of these artefacts. Haplotype frequencies for *kete* found not to be significantly different from those observed in cloaks, showing a similar excess of haplotypes 8 (29.8% in *kete*, 36.3% in cloaks, 2.1% in reference samples). However, haplotype frequencies for *kete* were found to be significantly different from those obtained from the reference database. Additionally, utilising the reference database constructed in Chapter 4, the provenance was determined for the majority of the *kete* (52/55), from which sequences were obtained. The instance of mixed provenance items was less than that of cloaks (2/55, 3.63%, compared to 15% of cloaks). This is likely to relate to the comparative sizes of cloaks versus *kete*. In likeness with cloaks, eastern haplotypes were dominant, being represented in 60.2% of all samples and 58.9% of *kete*.

Introduction

In addition to the construction of kiwi feather cloaks, Māori also used kiwi feathers to decorate small bags woven from flax fibre (*muka*), and later woven from candlewick. These kiwi feather bags are known as *kete kiwi.* Traditionally non-feathered *kete* were used for practical reasons such as carrying produce. It is thought that *kete kiwi* had a more ornamental purpose and may have been popular

with Victorian colonists as souvenirs and keepsakes. This is evidenced through the appearance of kiwi feather muffs, a European item used to keep hands warm (Figure 6.7). Although still culturally important, *kete kiwi* probably held less social status amongst Māori than kiwi feather cloaks (*kahu kiwi)*. Also, on average, these *kete kiwi* most likely originated at a later date than *kahu kiwi*, dating from the late 1800's onwards. *Kete kiwi* are much smaller than cloaks. A typical cloak is around 100cm x 100cm with feathers adorning one side (feathered area of 10000cm^2 (see cloak information In Chapter 5 for variation)), whereas *kete kiwi*, are typically 20cm x 20cm, with feathers adorning the front and back (feathered area of 800cm^2). Given that a typical *kete* is around 12 times smaller than a cloak and, that a suggested 12 kiwi are needed to make one kiwi feather cloak (Te Kanawa 1992), then it is reasonable to assume that one kiwi would provide sufficient feathers to adorn one *kete*. If this is the case then predictions would be that one, or at the most two haplotypes are present in feather samples in any one *kete* and that there would be fewer *kete* of mixed provenance recovered than in cloaks for this reason. Utilising the same ancient DNA approach applied in chapter 4, this chapter addresses the above predictions. Additionally it will look to see if *kete*, like cloaks, are predominantly constructed using North Island brown kiwi feathers. Also, given that cloaks showed a majority of eastern haplotypes, it would be interesting to see if this pattern translates to *kete*. Finally, given the significant change in haplotype frequencies between cloak and reference samples, it would be valuable to see if *kete* share the same 13 haplotypes observed and, whether *kete* haplotype frequencies reflect those of cloak or reference samples.

Materials and Methods

Samples

A total of 241 feather samples were obtained from 63 *kete* from museums across New Zealand and the United Kingdom (British Museum n=4, Horniman Museum n=1, Te Papa Tongawera n=9, Canterbury Museum n=13, Auckland Museum n=19, Waikato Museum n=6, Whanganui Museum n=11). Typically four samples were taken from each *kete*, two from each side. However, if the *kete* was larger than normal six samples were taken, three from each side and, if the *kete* was smaller

than normal or in poor condition, only two samples were taken, one from each side.

Molecular Methods

Procedures outlined for the extraction and analysis of ancient DNA were followed (Huynen et al. 2003; Gilbert et al 2005; Willerslev and Cooper 2005). Ancient DNA sequences were verified by independent replication of 15 randomly selected samples. DNA was extracted, amplified and sequenced for a 200bp fragment of the mitochondrial hypervariable region I (HVRI) using kiwi specific primers kcF and kcR (Shepherd and Lambert 2008). Details of these molecular methods can be found in chapter 2 of this thesis.

Statistical Analyses

Haplotype frequency data between cloak samples, reference samples and *kete* samples was analysed by performing a Chi Squared test using statistical analysis software 'R' as this test best fit the data. However, because frequencies (expressed as a percentage) in some cases were less than 1 and because in some cases over 20% of the data had values less than 5, p-values obtained could have been misleading. To overcome this, a Fisher's test was performed for cloak versus *kete* samples and p-values were compared. However, the data for reference versus *kete* samples could not be analysed in R due to restrictions of the program. To overcome this, Chi Squared tests were performed again, but this time Monte Carlo re-sampling was employed (999 repetitions) to overcome inaccuracies in p=values associated with low haplotype frequencies.

Results

Species Determination of Kete Feathers

A 200 base pair fragment of the mitochondrial control region was successfully amplified and sequenced for 161 of the 241 feather samples obtained from *kete*. This gave an overall success rate of 66.8%, slightly lower than that of cloaks (70%). Of the 63 *kete* sampled, 8 failed to provide any viable sequence data and are therefore excluded from the remainder of this chapter, a list of these 8 *kete* are

shown in table 6.1 below. Phylogenetic analyses identified all 161 sequences as North Island brown kiwi (*Apteryx mantelli*). The phylogenetic tree in chapter 4.2 shows the relationships between the kiwi feather samples and the five kiwi species.

Haplotype Structure and Frequency

For the *kete* feather DNA sequences, eight variable sites comprising 12 haplotypes were observed for the 200bp HVRI sequence (figure 6.1). This differs from cloaks and modern samples where 13 haplotypes were observed. There was no significant change in haplotype frequencies observed between cloaks and *kete* samples ($\chi 2=5.8097$, df=12, p=0.9254, (Fisher's Test p=0.9037), ($\chi 2$ with monte carlo resampling (n=999) $\chi 2=5.8097$, df=N/A, P=1)). There were significant changes detected in haplotype frequencies when comparing *kete* with modern samples ($\chi 2=47.2143$, df=12, p=0.00000486, (Fisher's test not possible in R for this data), ($\chi 2$ with monte carlo resampling (n=999) $\chi 2=47.2143$, df=N/A, p=0.002). The changes observed between modern and *kete* haplotype frequencies were most evident in haplotype 4 which has increased in frequency 15fold over time (0.62% to 9.38%), haplotype 8 which has decreased in frequency 14fold over time (29.8% to 2.08%) and haplotype 12 which has increased more than 5fold over time (0% to 5.21%). A comparison between haplotype frequencies for modern samples, cloaks and *kete* is shown in figure 6.1.

Table 6.1. *Kete* from which no sequences were obtained.

Museum	Accession Number	Failed Amplifications
British Museum	Oc81Q1401	4/4
Horniman Museum	NZ.133	4/4
Te Papa Tongawera	ME11528	2/2
Waikato Museum	24.43	4/4
Waikato Museum	1961/131/2	2/2
Auckland Museum	387.81	2/2
Whanganui Museum	1802.165	4/4
Whanganui Museum	1935.46	4/4

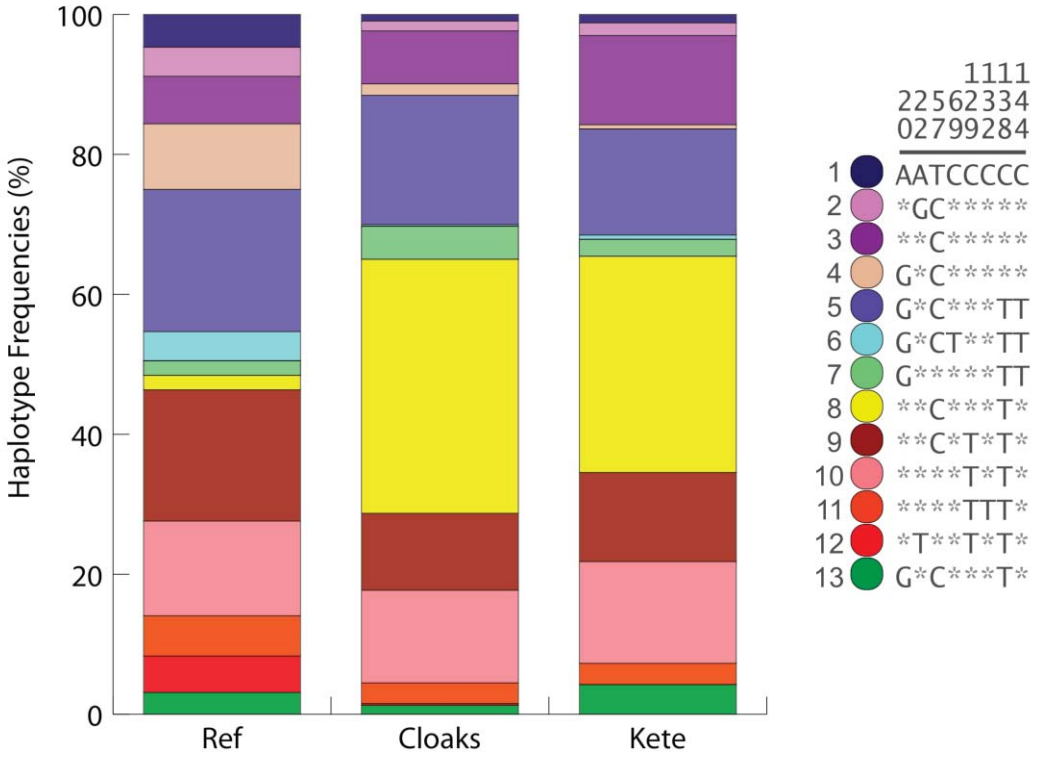


Figure 6.1. Observed haplotype frequencies for reference samples, cloak samples and, *kete* samples. Significant changes were observed between reference samples versus cloak samples and reference samples versus *kete* samples.

Determining the Provenance of Kete Kiwi

The maximum number of haplotypes present on any one *kete* was three. However, only 5.45% (3/55) of *kete* had three haplotypes. More commonly either two (45.45%, 25/55) or one (50.9%, 28/55) haplotype was observed per *kete*. As with cloak samples, the geographic structuring of modern kiwi populations discussed in chapter 4 has allowed inferences to be made with regard to the provenances of the *kete*. Of the *kete* analysed obtained an overwhelming 58.9% contained feather sequences hailing exclusively from the east of the north island (n=32/55), 21.8% contained feather sequences from the west and central North Island (n=12/55), 10.9% (n=6/55) contained feather sequences from Northland and the Coromandel, 3.6% (n=2/55) contained feather sequences from separate geographic regions and, 5.5% (n=3/55) contained feather sequences representing just haplotype 3 which, due to its widespread distribution, cannot be used alone to infer provenance.

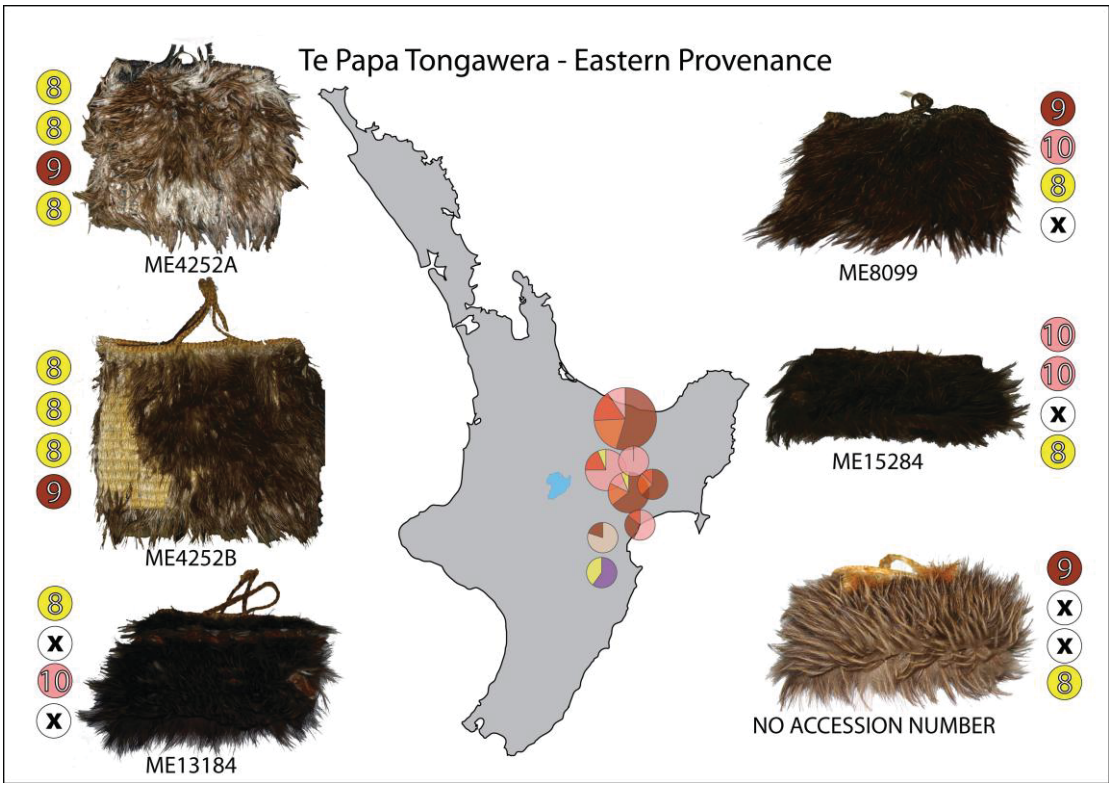


Figure 6.2. *Kete* from Te Papa Tongawera Museum. All of these *kete* have haplotypes with distributions limited to the east of the North Island of New Zealand. Due to their appearance, it is likely that ME4252A and ME4252B were made by the same weaver. The identical haplotype frequencies of these to *kete* complement this theory.

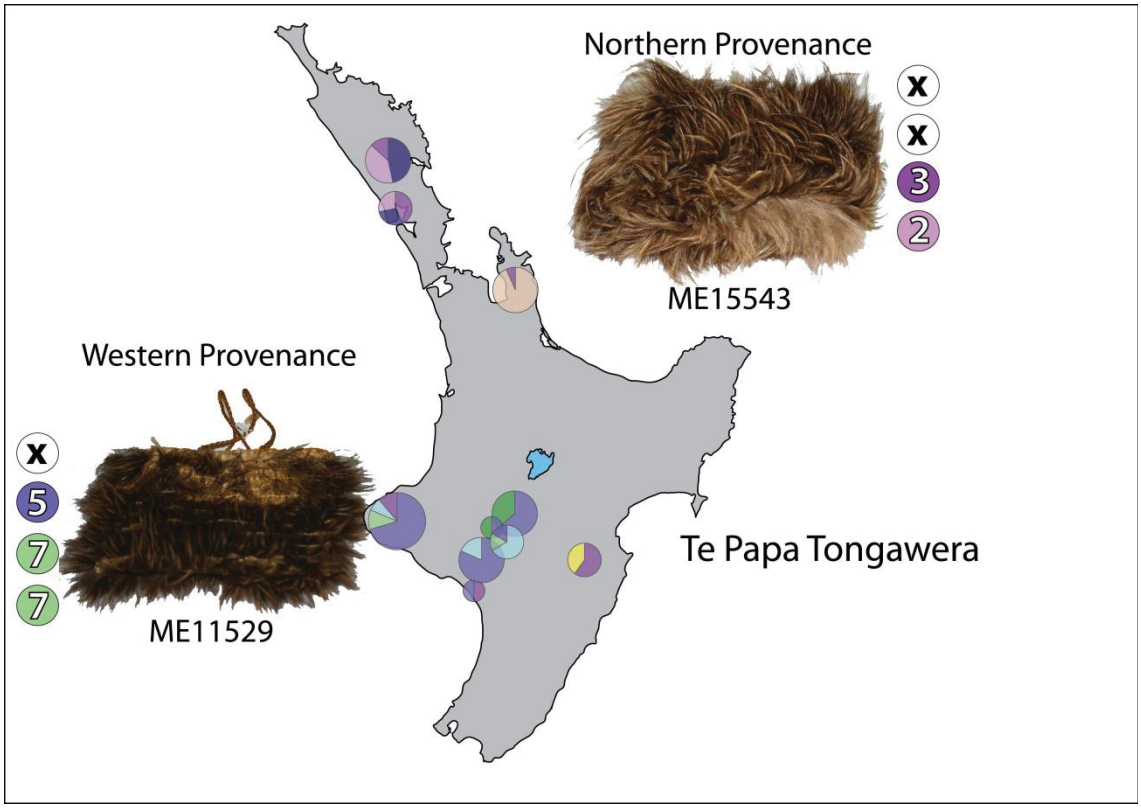


Figure 6.3. *Kete* sampled from Te Papa Tongawera with haplotypes inferring northern provenance (*kete* ME15543) and, west and central provenance (*kete* ME11529). X indicates a failed amplification.

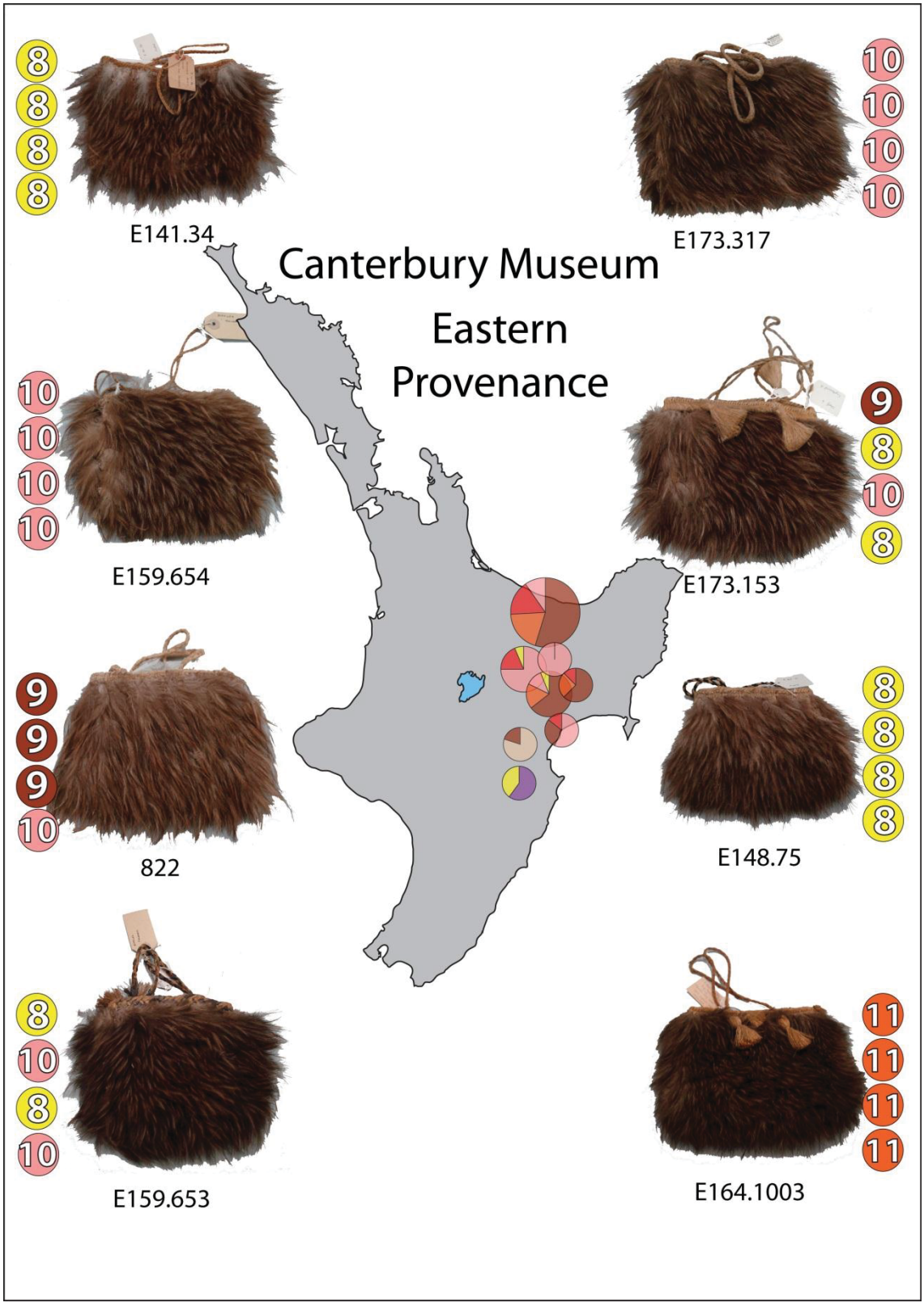


Figure 6.4. *Kete* sampled from Canterbury Museum, Christchurch. All eight of these *kete* harboured sequences that matched haplotypes found only in the east of the North Island of New Zealand, making this region the most likely origin of these *kete*.

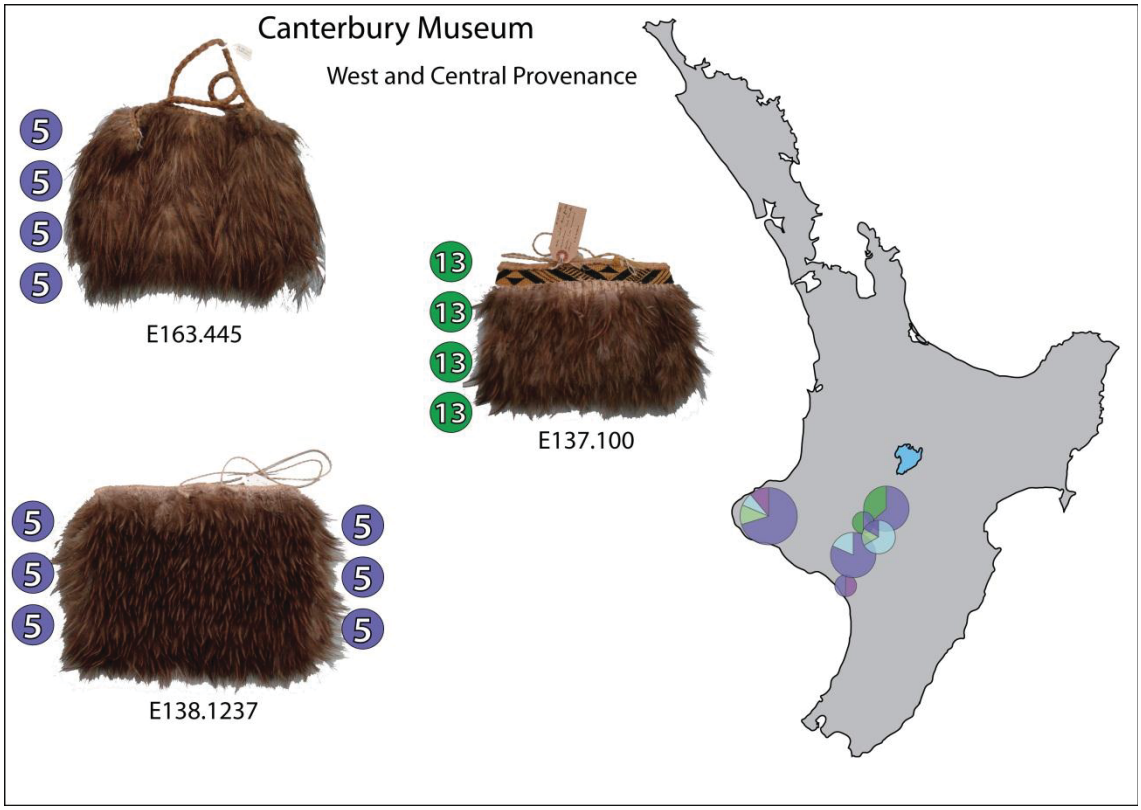


Figure 6.5. *Kete* sampled from Canterbury Museum that have haplotypes found exclusively in the west and central North Island. *Kete* E137.100 only exhibits haplotype 13, which is found only in the central North Island, the likely origin of this *kete*.

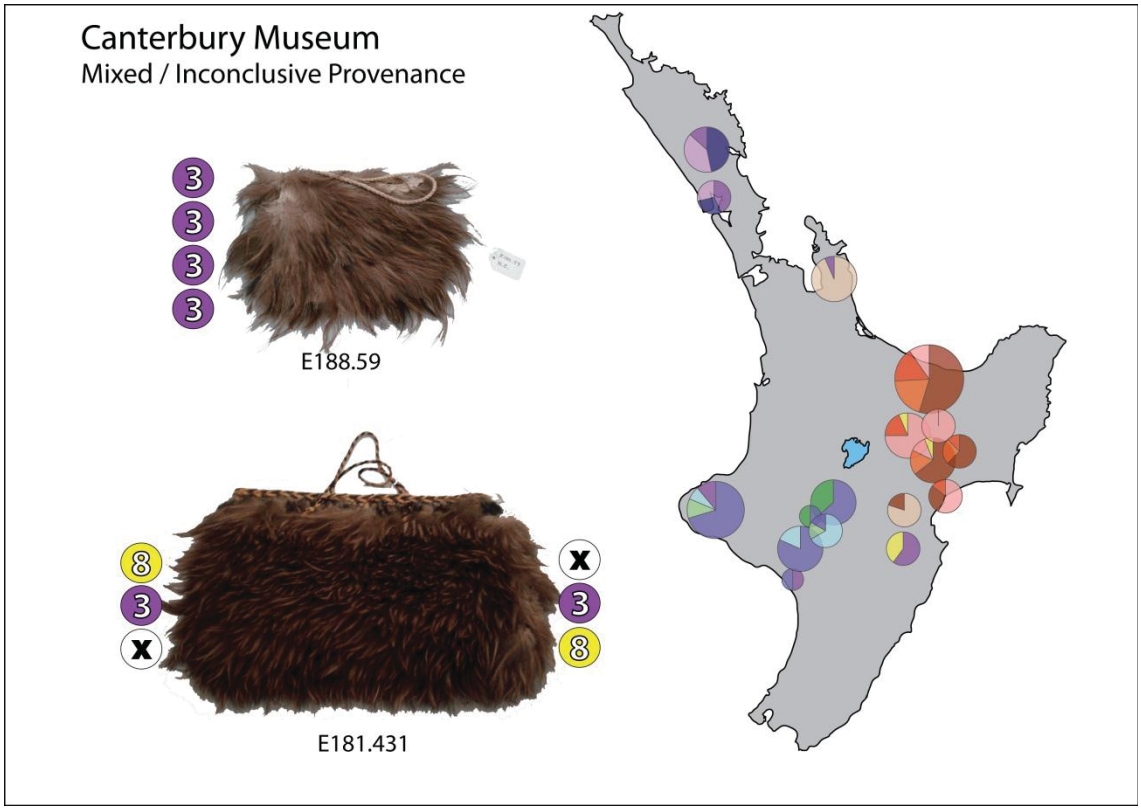


Figure 6.6. *Kete* sampled from Canterbury Museum. *Kete* E188.59 has haplotype 3. Because this haplotype is widespread, the provenance of the *kete* could not be determined. E181.431 contains eastern haplotype 8 and widely distributed haplotype 3. This *kete* could be of mixed provenance.

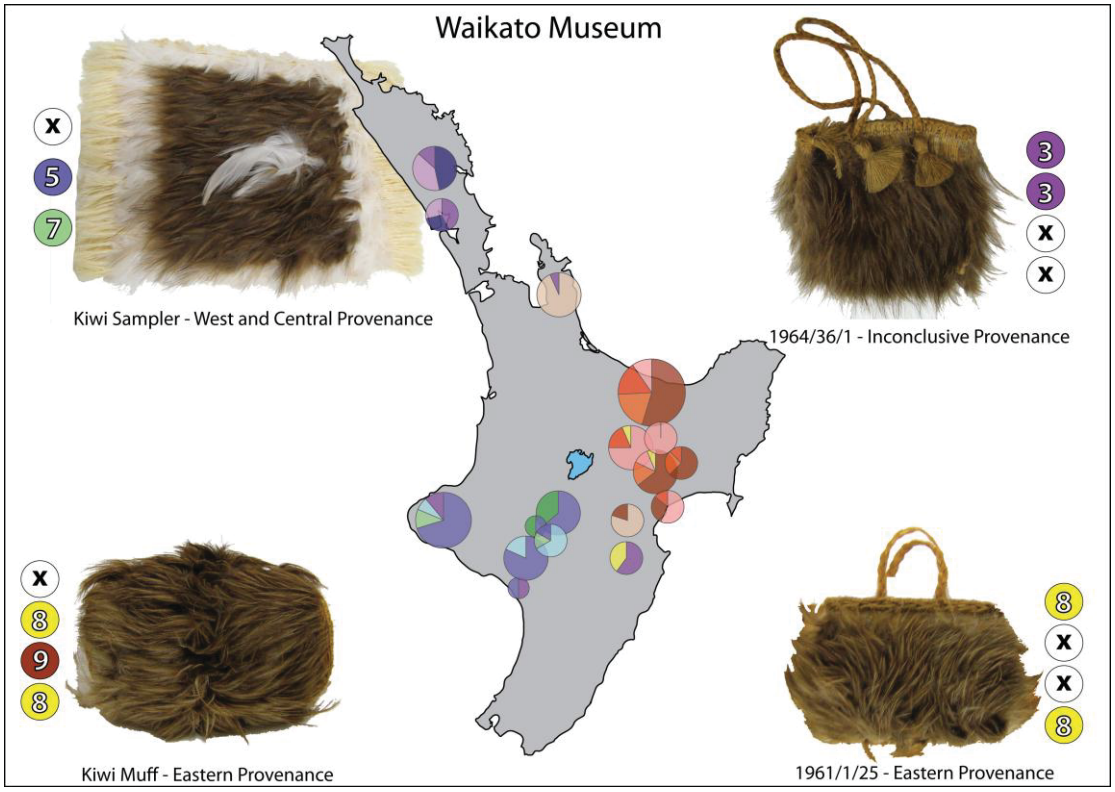


Figure 6.7. *Kete* and other kiwi feather artefacts sampled from Waikato Museum. The kiwi feather sampler had west and central haplotypes. The kiwi feather muff and *kete* 1961/1/25 had exclusively eastern haplotypes and due to the wide distribution of haplotype 3, the provenance of *kete* 1964/36/1 could not be inferred.

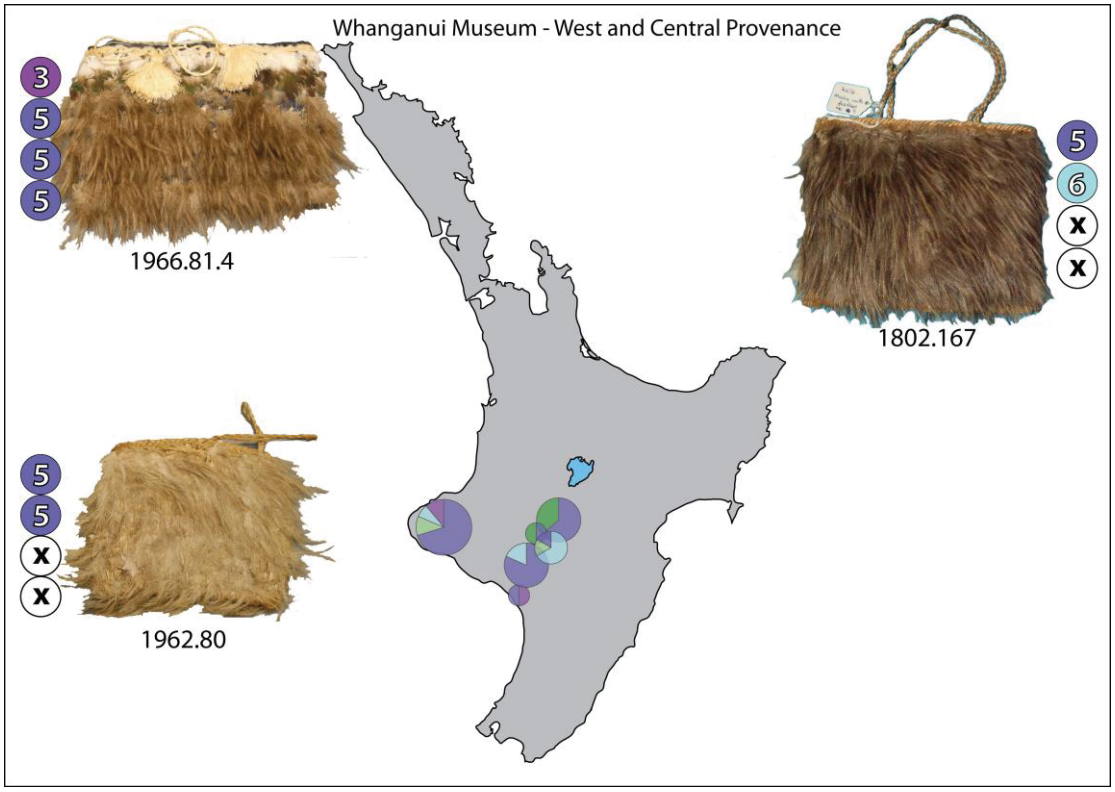


Figure 6.8. *Kete* sampled from Whanganui Museum containing west and central North Island haplotypes, making this region the most likely provenance of these *kete*. X denotes a failed amplification.

Figure 6.9. *Kete* sampled from Whanganui Museum containing eastern North Island haplotypes, making this region the most likely provenance of these *kete*. X denotes a failed amplification.

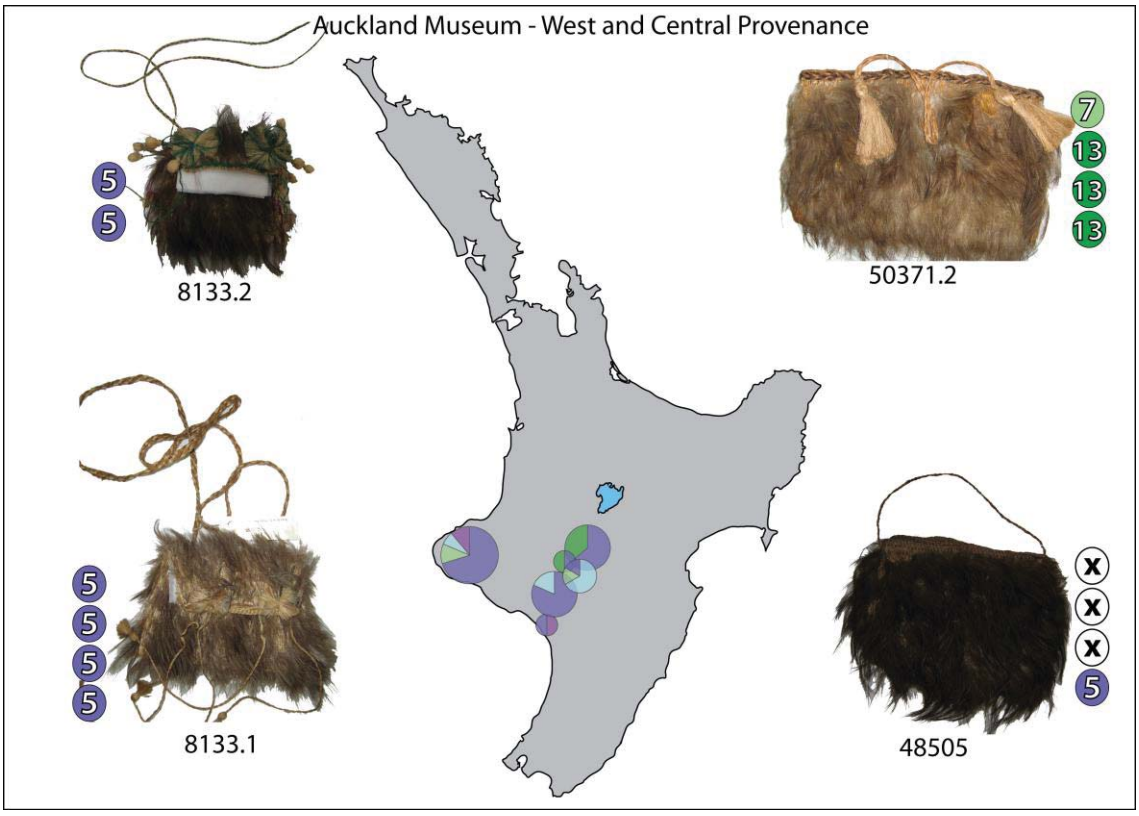


Figure 6.10. *Kete* sampled from Auckland Museum containing west and central North Island haplotypes, making this region the most likely provenance of these *kete*. 8133.1 and 8133.2 are particularly unusual as they have small woven balls or *poi* attached to the *kete* on woven flax strings. Due to their unique appearance and matching haplotypes, it is likely that they were made by the same weaver. X denotes a failed amplification.

Figure 6.11. *Kete* sampled from Auckland Museum containing eastern North Island haplotypes, making this region the most likely provenance of these *kete*. X denotes a failed amplification.

Figure 6.12. *Kete* sampled from Auckland Museum with Northland and Coromandel haplotypes. X denotes a failed amplification.

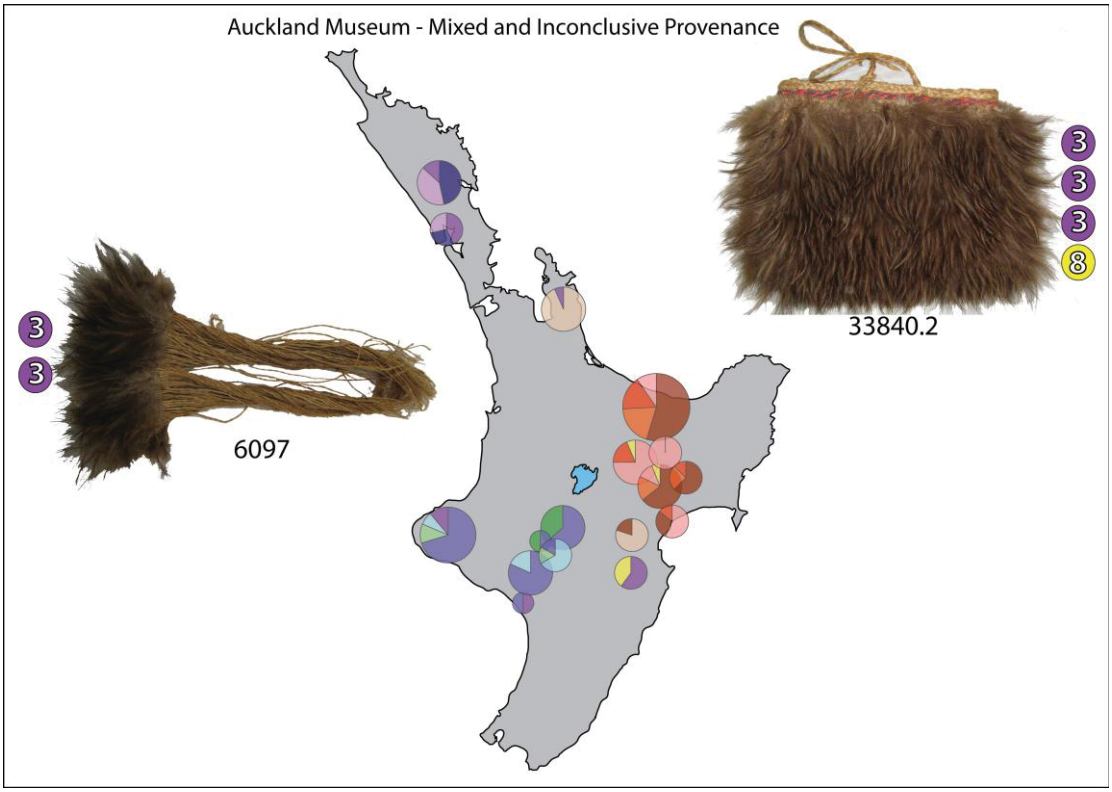


Figure 6.13. *Kete* sampled from Auckland Museum. *Kete* 33840.2 contains eastern haplotype 8 and widely distributed haplotype 3, therefore being likely to be of mixed origin. Unfinished *kete* 6097 only contains widely distributed haplotype 3, making it difficult to infer provenance.

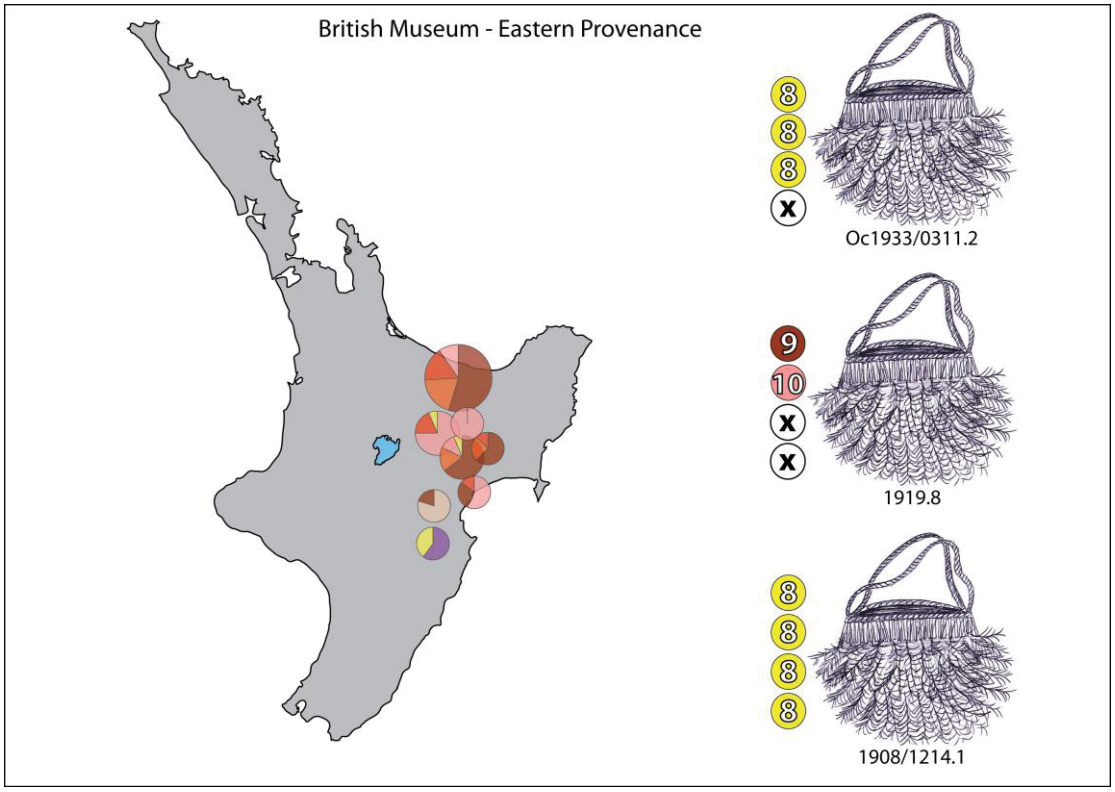


Figure 6.14. *Kete* sampled from the British Museum all contained exclusively eastern haplotypes, thus are likely to have originated from the east of the North Island of New Zealand. X denotes a failed amplification. No photographs were available for these *kete*, sketches are a representation only, not a true likeness.

Discussion

Species Determination of Kete Feathers

Out of the 161 samples successfully amplified and sequenced for *kete*, 100% came from North Island brown kiwi (*Apteryx mantelli*). This is similar to the species used in cloaks, where only 1 of the 108 cloaks which yielded sequence data was from little spotted kiwi (*Apteryx owenii*), with the remaining cloaks being made using North Island brown kiwi. As suggested in chapter 5, this could be because there were many more Māori inhabiting the North Island of New Zealand than the South. Logic would suggest that the vast majority of artefacts would be made on the North Island, where the population of Māori was greatest, and where North Island brown kiwi are distributed. However, with the *kete* and cloak data combined, the absence of any of the South Island brown kiwi species being represented in any of the artefacts, maybe the picture is more complicated than just population numbers. It is possible the South Island Māori didn't favour kiwi feathers for the construction of cloaks and *kete* as much as North Island Māori. A further stretch could suggest

that North Island brown kiwi feathers were traded between the islands, although this seems illogical given the abundance of similar looking kiwi species available on the South Island. As suggested in chapter 5 it would be useful to extend this cloak study in the future to encompass feather cloaks made using other species of birds, to see if any South Island populations or species are used.

Haplotype Structure and Frequency

Only 12 of the 13 haplotypes found in cloaks and reference samples were observed in *kete*. Haplotype 12, found in the east of the North Island is absent from the *kete* data. However, this haplotype has a very low frequency in cloaks, present in only 0.23% of samples. Haplotype 12 would have been present when *kete* were produced, as cloaks were being produced at the same time, however, frequencies of the haplotype were so low at that time it is not surprising that it was not detected in the 161 *kete* sequences.

There was no significant difference in haplotype frequencies between cloaks and *kete*. This would confirm that cloaks and *kete* were made during overlapping periods of time. As with cloaks, a significant difference was detected when *kete* haplotype frequencies were compared with haplotype frequencies from the reference database. The haplotypes with the most notable changes in frequency were 4, 8 and 12. Haplotype 4 increased 15 fold between the time when *kete* were produced and present day. As with cloaks, this could be a sampling effect. Haplotype 4 is found almost exclusively in the Coromandel. The number of samples available from the Coromandel for the reference database was probably disproportionately larger than the frequencies we would see normally. The elevated number of samples from the Coromandel is the most likely explanation for the increase in haplotype 4. As with cloaks a decrease in haplotype 8 was coupled with an increase in haplotype 12. As haplotype 8 decreased, this could have allowed the increase of haplotype 12 as these haplotypes overlap geographically. The decline of haplotype 8 could be attributed to its elevated use in cloaks and *kete* compared to other haplotypes.

As with cloaks, the geographic structuring in the reference database, allowed inferences to be made regarding the geographic provenance of each *kete*. Unlike cloaks, there were instances where provenance could not be inferred. This occurred in 5.5% of cases (n=3/55, accession numbers; Canterbury Museum E188.59; Waikato Museum 1964/36/1; Auckland Museum 6097) where only haplotype 3 was detected. Haplotype 3 is the most geographically widespread haplotype and possibly the ancestral haplotype. It is distributed in Northland, the Coromandel, the West of the North Island, and is represented by a small number of individuals in the Ruahine Ranges in the South East of the North Island.

When comparing results from the genetic data to museum records, there were a number of instances where the two complemented each other. For example *kete* 8133.2 (Auckland Museum, Figure 6.10) was noted to have come from Mataroa, near Taihape in the west of the North Island. This *kete* was found to be made using feathers with haplotype 5, which is distributed in the West of the North Island. This *kete* is also unusual in that it has small poi attached. Poi are small balls woven from flax and are a rare occurrence in *kete*. *Kete* 8133.1 (Auckland Museum, Figure 6.10) is also decorated with poi. This *kete* was probably made by the same weaver as *kete* 8133.2. This theory is strengthened by both of the *kete* sharing haplotype 5. However, there are cases where museum records are in conflict with the genetic data. For example *kete* 50371.1 and 50371.2 (Auckland Museum, Figures 6.11 and 6.10 respectively) are shown as coming from Kare Kare on Auckland's west Coast, in the north of New Zealand. However, *kete* 50371.1 harbours eastern haplotypes whereas *kete* 50371.2 harbours west and central haplotypes. This would suggest that the feathers used for making these two *kete* were sourced from different geographic regions. Additionally, both of these regions are hundreds of kilometres from Kare Kare in the north. However, the appearance of the two *kete* is very similar, suggesting the same weaver. This would also suggest that feather trade or travel for kiwi feathers did occur. Utilising the museum records alone, without the use of the genetic data to provenance *kete* would be unwise as provenance could relate to the most recent owner, as opposed to the weaver. Also, given the small size of *kete*, they are easily transportable and likely to end up some distance from

where they were made. Only with the complementing genetic data is it possible to begin to confirm the provenances suggested in the museum records.

Insights Into Kete Making Practises

The instance of *kete* containing haplotypes from different geographic areas was less than that observed in cloaks. In cloaks, 15% were found to be of mixed provenance, whereas this was only seen in 3.6% of *kete*. This result is as predicted because cloaks are much larger than *kete*, thus reducing the chance of detecting a *kete* of mixed geographic provenance. However, what is surprising is that up to three haplotypes were found on each *kete*. In theory, the feathers from one kiwi should be sufficient to make one *kete*. Instead in 49.1% of cases, two or three haplotypes were detected, meaning at least two or three individual kiwi were used to produce each of these *kete*. The reason for why this would occur is unclear. It could point to feather trade and exchange. Alternatively it could provide insights into how feathers were collected and stored. Possibly feathers from several kiwi were stockpiled (essentially mixed) and used in some cases. This would provide an explanation to the mix of haplotypes observed.

Additionally, as with cloaks, the majority of *kete* harboured feathers originating only from the North Island's Eastern region (58.9%). Haplotype 8 was also massively represented, being present in 29.8% of all *kete* samples taken. This would corroborate with the cloak data in suggesting that the East of the North Island was the most prolific kiwi feather cloak and *kete* making region of New Zealand and, may even be the epicentre from where this tradition spread.

Conclusions

The presence of mixed provenance *kete*, albeit fewer than observed in cloaks complements the theory that travel and trade during the 19th and 20th centuries has influenced the production of these *taonga*. Additionally the similarity in haplotype frequencies observed between cloaks and *kete* puts the epicentre of the use of kiwi feathers in weaving, firmly in the East of the North Island of New Zealand. Once again, given the lack of South Island kiwi species represented, it would appear that kiwi feathers were either less culturally relevant to tribes in the

South Island of New Zealand, or that due to a smaller population, fewer *kete* were made in the South. Finally, given the oral histories of these *taonga*, it is clear that museum records alone are insufficient to infer provenance of these items and that genetic data is invaluable for enabling the histories of these treasured artefacts to be rediscovered.

References

Gilbert M T, Bandelt H J, Hofreiter M, Barnes I. (2005). Assessing ancient DNA studies. *Trends in Ecology and Evolution.* 20(10):541-544.

Huynen L. Millar C D, Scofield R P, Lambert D M. (2003). Nuclear DNA sequences detect species limits in moa. *Nature,* 425:175-178.

Shepherd L D & Lambert D M. (2008). Ancient DNA and conservation: lessons from the endangered kiwi of New Zealand. *Molecular Ecology*. 17:2174-2184.

Te Kanawa D. (1992). Weaving a kakahu. Wellington (New Zealand): Bridget William Books Limited.

Willerslev E. & Cooper A. (2005). Ancient DNA. *Proceedings of the Royal Society of London B Biological Sciences.* 272:3-16.

Chapter 7

General Discussion

The potential for the use of molecular biology as a tool for recovering information from ethnographic artefacts is vast. The molecular methods applied in this thesis to treasured cloaks and *kete* have recovered a wealth of information that was either previously unknown, or lost, with the passing of time. Conversely, the use of ethnographic artefacts such cloaks and *kete* as a tool to aid conservation management has proven to be extremely useful. It has been possible to recover information relating to the histories of the artefacts themselves and, information relating to past populations of the species used in the construction of these artefacts.

Research Findings and Application to Conservation

This study illustrates that, for the mitochondrial sequence data obtained, genetic diversity has not decreased for the North Island brown kiwi (*Apteryx mantelli*) over the past ~150 years. The same 13 haplotypes observed at the time that kiwi feather cloaks were made still exist to this day in contemporary populations. Additionally, there is a phylogeographic structuring of haplotypes into Northland, the Coromandel, the east of the North Island and the west and central North Island. Nested clade analysis suggested that the structuring observed was most likely a result of New Zealand's complicated geological history. It is highly likely that the volcanism in the central North Island has acted as a barrier to gene flow between the east and west. It is also possible that expansion out of refugia following volcanic eruptions occurred in western North Island brown kiwi populations. However, although volcanism will have played an important role in the phylogeographic structure observed, it may be masking the effects that earlier geological processes may have had on the phylogeography of the North Island brown kiwi, such as the North Island sea straits during the early Pliocene. It is extremely encouraging that current conservation management protocols for North

Island brown kiwi take the observed genetic structuring into account. The Department of Conservation's decision to manage North Island brown kiwi in four units (Northland, Coromandel, east, west) is in line with the genetic data. The establishment of mixed provenance zones may prove useful to counteract possible inbreeding depression within the four units. The data presented in this thesis from contemporary and historical samples has provided additional support for current conservation management strategies. However, it also raised some issues, to be discussed below.

Future Suggestions for Conservation

There are some instances where haplotype structure on a finer scale is questionable. Two areas managed by the Department of Conservation that are exceptions to the phylogeographic patterns observed are the Kaweka Forest Park and the Ruahine Ranges. The haplotypes found in these regions do not reflect the east / west / north / Coromandel split observed in other populations. These regions need to be investigated in greater detail, at a finer genetic resolution. Due to their location to the south of the central volcanic region, it is possible that the barriers to gene flow observed further north did not apply to these regions. Therefore, a mixture of east and west haplotypes may be plausible. More molecular work is needed at the boundaries of populations. Also, this thesis uses only mitochondrial DNA analyses. Nuclear work either using microsatellites or making use of next generation sequencing technologies would give a clearer picture of the phylogenetic at a finer resolution. Also temporal genetic information would be beneficial. As more kiwi fossils are found, genetic analyses should be performed on them, where possible, to elucidate the drivers for the phylogeography observed today.

Historical genetic information was recovered for North Island brown kiwi from Māori cloaks and *kete*. It should be noted that Māori constructed cloaks using many more species of native, endangered, birds. Each feather cloak and *kete* could hold genetic information about past populations of endangered bird species that could have important implications for conservation management.

Research Findings and Application to Culture

Genetic analysis of Māori feather cloaks and *kete* has been an important step in retelling the stories of these *taonga*. With the exception of the emu feather cloak in chapter 3, all artefacts studied were made using kiwi feathers. Mitochondrial DNA analysis of these feathers revealed which species of kiwi were used. It remains surprising that all but one of the artefacts (a cloak made from little spotted kiwi, *Apteryx owenii*) were found to be made using feathers exclusively from the North Island brown kiwi (*Apteryx mantelli*). This would suggest that the majority of kiwi feather cloaks were made in the North Island of New Zealand. Also it would suggest that the North Island brown kiwi was favoured over the little spotted kiwi (Apteryx owenii), which also lived on the North Island, for either cultural or practical reasons.

The mitochondrial phylogeographic structuring observed in contemporary populations of North Island brown kiwi, coupled with their low dispersal power, allowed the provenances of the cloaks and *kete* to be inferred. Cases of mixed provenance could have been due to, feather trade, tribal displacement, or tribal migration. There were known trade routes, such as the Inland Patea, facilitating travel and trade of goods, tribal displacement will have occurred as more Europeans made New Zealand their home and, the Māori wars of the 19th century caused tribal boundaries and homelands to shift dramatically. All of these histories are reflected in the mixed provenances detected in the cloaks and *kete*. The majority of cloaks and kete had exclusively eastern haplotypes. This would suggest the east of the North Island as the origin of kiwi cloak and making, it was certainly the most prolific region. Haplotype 8, restricted to a small area in the east of the North Island, was massively overrepresented in cloak and *kete* samples. The region, in the east, where this haplotype is found could be the epicentre of kiwi cloak and kete making in New Zealand.

Through genetic analyses it was possible to make inferences into cloak and *kete* making practises. The pattern of haplotypes observed on some cloaks would suggest that feathers from one kiwi would be woven into the cloak, followed by

feathers from another kiwi, resulting in haplotype lines or blocks. However, for *kete* there often seemed to be more birds used than required. For example, three haplotypes on one kete would suggest three individuals. However, kete are small and would probably not require the feathers from three kiwi. This would suggest that, for *kete* construction, feathers from several kiwi were stockpiled and used at random. It is possible that *kete* were constructed using feathers left over from cloak construction as they did not hold the same status as cloaks.

Through nuclear DNA analyses it was possible to determine the sex of some cloak samples. The observed male skew in the sex ratio of cloak samples could relate to Māori hunting practices. Māori hunted with dogs and therefore egg incubating males may have been more at risk in their burrows than females.

In addition to the general cultural trends observed for cloaks and *kete*, the individual stories of each of these toanga are exceptionally valuable. The provenance information for each artefact suggested from the genetic data are extremely useful in beginning to rediscover their histories. A combination of the molecular information and historical records should reveal previously lost information. However, I believe that there is future molecular work that can be conducted to aid this, which shall be discussed below.

Future Suggestions for Culture

The mitochondrial sequences recovered from cloaks have revealed whether their provenance is from the east, west and central or north of the North Island of New Zealand. However, it would be beneficial to be able to provenance cloaks at a finer resolution. To do this either additional mitochondrial DNA sequences would need to be obtained or, ideally, a mixture of mitochondrial DNA and nuclear DNA data should be generated. During this thesis, it was not possible to consistently amplify microsatellites from the cloaks and *kete*. However, with advances in genomic sequencing, it may be possible to generate viable nuclear DNA data from these artefacts. Additionally some of the kiwi feather cloaks were decorated using feathers from other species of birds. Genetic information from other bird species on the same cloak could compliment the kiwi genetic data and reveal more

pertaining to the cloaks' individual histories. Likewise with the flax used to construct the body of the cloaks and *kete*. If it was possible to genetically determine the cultivar of flax used, it could aid in determining their provenance.

It would be beneficial if we could ascertain the date each cloak was made more accurately. Although most of the cloaks were estimated to be approximately 150 years old, there were certainly more recent cloaks included in the analyses and, possibly even some older examples. If cloaks could be aged to a finer scale, temporal trends in cloak making and style could be combined with the geographic provenance data. This would have great cultural value. Hopefully this thesis will be used as a resource to further explore this area of research.

Another approach to pinpointing the provenance of these artefacts could be to use a combination of genetic data and stable isotope analysis. However, stable isotope analysis uses relatively large volumes of starting matter and, given the precious nature of the artefacts, may prove to be too destructive to be a viable option.

I hope that this thesis is used as resource material by museums and historians to further delve into the unique histories of each of these remarkable *taogna*. There is a wealth of information we have yet to discover.

Appendix

Table A.1 Cloak haplotypes for mtDNA CR HVR1 using Kcf / Kcr and sexing data

						Amplification 1		Amplification 2		Amplification 3		Amplification 4		Sex
Museum	cloak	Forward (KCF)	Reverse (KCR)	Haplotype	SEXING	moa1/moa2	p0/p1	moa1/moa2	p0/p1	moa1/moa2	p0/p1	moa1/moa2	p0/p1	
Hawkes Bay	2554	y	y	8		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2554	y	y	9		y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2554	y	y	8		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2554					n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2554	y	y	8		y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2554					y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2657					y	n	y	n	y	n	n/a	n/a	Ambiguous
Hawkes Bay	2657					y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2657	y	y	8		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2657					n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2657	y	y	8		n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2657	y	y	8		n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2624	y	y	8		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2624	y	y	11		y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2624	y	y	8		y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2624	y	y	8		n	n	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2624	y	y	8		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2624	y	y	8		y	n	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2633	y	y	5		n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2633					n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2633	y	y	5		y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2633					y	y	y	y	y	y	n/a	n/a	Female

Hawkes Bay	2637				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2637				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2637				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2637				y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2637				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2637	y	y	7	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2637				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2641				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2641	y	y	3	n	n	n	n	n	y	n	y	Male
Hawkes Bay	2641				n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2641				n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2641	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2641				n	n	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2642	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2642	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2642	y	y	11	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2642	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2642	y	y	8	n	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2642	y	y	8	n	y	n	y	n	n	n/a	n/a	Male
Hawkes Bay	2643	y	y	8	y	y	n	n	y	y	n/a	n/a	Female
Hawkes Bay	2643	y	y	9	y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2643	y	y	10	y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2643	y	y	8	n	n	n	y	n	n	n	y	Male
Hawkes Bay	2643	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2643	y	y	9	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2644	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2644	y	y	10	n	y	n	n	n	n	n	y	Male
Hawkes Bay	2644	y	y	8	n	y	n	y	n	y	n/a	n/a	Male

Hawkes Bay	2644	y	y	10	n	n	n	n	n	n	n	n	FAIL
Hawkes Bay	2644	y	y	11	n	y	n	y	n	n	n/a	n/a	Male
Hawkes Bay	2644	y	y	11	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2646				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2646				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2646	y	y	8	n	n	n	n	n	y	n	y	Male
Hawkes Bay	2646				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2646				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2646	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2647	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2647				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2647	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2647				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2647				n	n	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2647	y	y	3	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2649	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2649				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2649				n	y	n	n	n	y	n/a	n/a	Male
Hawkes Bay	2649				n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2649				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2649				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2653				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2653				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2653				n	y	n	n	n	y	n/a	n/a	Male
Hawkes Bay	2653				n	y	n	y	n	y	n/a	n/a	Male
Hawkes Bay	2653				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2653	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2654				n	n	n	n	n	n	n/a	n/a	FAIL

Hawkes Bay	2654	y	y	8	n	n	n	n	n	y	n	y	Male
Hawkes Bay	2654	y	y	11	n	n	n	y	y	y	y	y	Female
Hawkes Bay	2654	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	2654				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	2654	y	y	8	n	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	4009	y	y	9	y	y	y	y	y	y	n/a	n/a	Female
Hawkes Bay	4009				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	4009	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	4009	y	y	9	n	n	y	y	y	y	n/a	n/a	Female
Hawkes Bay	4009	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	4009	y	y	8	y	y	y	y	y	n	n/a	n/a	Female
Hawkes Bay	26077				y	n	y	n	y	y	n/a	n/a	Female
Hawkes Bay	26077				y	n	y	y	y	y	n/a	n/a	Female
Hawkes Bay	26077	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	26077	y	y	9	n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	26077				n	n	n	n	n	n	n/a	n/a	FAIL
Hawkes Bay	26077	y	y	13	y	n	y	y	y	y	n/a	n/a	Female
British Museum	q82Oc737	y	y	10									
British Museum	q82Oc737	y	y	10									
British Museum	q82Oc737	y	y	8									
British Museum	q82Oc737												
British Museum	q82Oc737	y	y	8									
British Museum	q82Oc737	y	y	10									
British Museum	q82Oc737	y	y	8									
British Museum	q82Oc737												
British Museum	q82Oc737	y	y	9									
British Museum	q82Oc737	y	y	8									
British Museum	q82Oc736	y	y	8									

British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736	y	y	10
British Museum	q82Oc736			
British Museum	q82Oc736			
British Museum	Oc1914/1215.1			
British Museum	Oc1914/1215.1			
British Museum	Oc1914/1215.1			
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1914/1215.1	y	y	8
British Museum	Oc1913/612.2	y	y	3
British Museum	Oc1913/612.2			
British Museum	Oc1913/612.2	y	y	3
British Museum	Oc1913/612.2	y	y	3
British Museum	Oc1913/612.2	y	y	3
British Museum	Oc1913/612.2	y	y	8
British Museum	Oc1913/612.2	y	y	8
British Museum	Oc1913/612.2	y	y	3
British Museum	Oc1913/612.2	y	y	3

British Museum	Oc1913/612.2	y	y	4
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1933/1017.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc1938/1114.1			
British Museum	Oc82Q704	y	y	8
British Museum	Oc82Q704	y	y	8
British Museum	Oc82Q704			
British Museum	Oc82Q704			
British Museum	Oc82Q704	y	y	8
British Museum	Oc82Q704	y	y	8
British Museum	Oc82Q704			

British Museum	Oc82Q704	y	y	8										
British Museum	Oc82Q704													
British Museum	Oc82Q704													
British Museum	Oc82726	y	y	Little spotted kiwi										
British Museum	Oc82726	y	y	Little spotted kiwi										
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc82726													
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	10										
British Museum	Oc1995Q4													
British Museum	Oc1995Q4													
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	8										
British Museum	Oc1995Q4	y	y	8										
Te Papa	ME4274	y	y	5	n	y	n	y	n	n	n/a	n/a	Male	
Te Papa	ME4274				n	y	n	y	n	n	n/a	n/a	Male	
Te Papa	ME4274				y	y	y	y	y	n	n/a	n/a	Female	
Te Papa	ME4274	y	y	5	y	n	y	n	y	y	n/a	n/a	Female	
Te Papa	ME4274				n	n	n	n	n	n	n/a	n/a	FAIL	

Te Papa	ME4274	y	y	13	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME4274	y	y	13	y	y	y	y	y	n	n/a	n/a	Female
Te Papa	ME4274				y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME4274				y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME4274	y	y	5	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME144404	y	y	10	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME144404	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME144404	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME144404	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME144404	y	y	8	n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME144404	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME144404	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME144404	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME144404	y	y	10	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME144404	y	y	10	n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME144404	y	y	8	y	n	y	n	y	y	n/a	n/a	Female
Te Papa	ME144404	y	y	10	y	y	y	y	y	n	n/a	n/a	Female
Te Papa	ME144404	y	y	8	y	y	y	y	y	n	n/a	n/a	Female
Te Papa	ME144404	y	y	10	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME144404	y	y	10	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL

Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME2700	y	y	8	n	y	n	n	n	y	n/a	n/a	Male
Te Papa	ME2700	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME2700				y	y	y	y	y	n	n/a	n/a	Female
Te Papa	ME2700	y	y	11	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME2700	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME3714				n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714	y	y	11	n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME3714				n	n	n	n	n	y	n	y	Male
Te Papa	ME3714	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME3714	y	y	8	n	y	n	n	n	y	n/a	n/a	Male
Te Papa	ME3714				n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714				y	n	y	y	y	y	n/a	n/a	Female
Te Papa	ME3714	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME3714	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME3714	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME3714	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME3714	y	y	8	n	y	n	n	n	y	n/a	n/a	Male
Te Papa	ME14499	y	y	5	n	y	n	y	n	y	n/a	n/a	Male

Te Papa	ME14499				n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME14499	y	y	13	n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME14499	y	y	13	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME14499	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME14499	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME14499	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME14499	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME14499	y	y	7	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME14499	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME14499	y	y	7	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME14499	y	y	7	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME14499	y	y	8	n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME14499	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME14499	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME15755	y	y	5	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME15755	y	y	5	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME15755	y	y	5	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME15755	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME15755	y	y	5	n	n	n	n	n	y	n	y	Male
Te Papa	ME15755	y	y	3	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME15755	y	y	5	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME15755	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME15755	y	y	3	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME15755	y	y	5	n	n	n	y	y	y	y	y	Female
Te Papa	ME15755	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME15755	y	y	3	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME15755	y	y	3	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME15755				n	y	n	n	n	y	n/a	n/a	Male

Te Papa	ME15755	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	5	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME16934	y	y	5	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME16934	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	5	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME16934				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	8	n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME16934				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934				n	y	n	y	n	n	n/a	n/a	Male
Te Papa	ME16934				n	y	n	y	n	y	n/a	n/a	Male
Te Papa	ME16934				n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934	y	y	8	n	n	n	n	n	n	n/a	n/a	FAIL
Te Papa	ME16934				y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME16934	y	y	8	y	y	y	y	y	y	n/a	n/a	Female
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885												
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									
Te Papa	ME38885	y	y	9									

Te Papa	ME38885	y	y	9
Te Papa	ME38885	y	y	9
Te Papa	ME38885	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	10
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	10
Te Papa	ME15753	y	y	9
Te Papa	ME15753	y	y	9
Te Papa	ME1378	y	y	10
Te Papa	ME1378	y	y	8
Te Papa	ME1378	y	y	8
Te Papa	ME1378	y	y	10
Te Papa	ME1378	y	y	10
Te Papa	ME1378	y	y	11
Te Papa	ME1378	y	y	8
Te Papa	ME1378	y	y	10
Te Papa	ME1378	y	y	8
Te Papa	ME1378	[redacted]		

Te Papa	ME1378	y	y	10
Te Papa	ME1378	y	y	8
Te Papa	ME1378	[redacted]		
Te Papa	ME1378	y	y	8
Te Papa	ME1378	y	y	8
Te Papa	ME2691	y	y	8
Te Papa	ME2691	[redacted]		
Te Papa	ME2691	y	y	8
Te Papa	ME2691	y	y	8
Te Papa	ME2691	y	y	8
Te Papa	ME2691	y	y	8
Te Papa	ME2691	y	y	8
Te Papa	ME2691	[redacted]		
Te Papa	ME10760	y	y	8
Te Papa	ME10760	[redacted]		
Te Papa	ME10760	y	y	9
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	8
Te Papa	ME10760	[redacted]		
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	9
Te Papa	ME10760	[redacted]		
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	8
Te Papa	ME10760	y	y	8

Te Papa	OL689.F	y	y	8
Te Papa	OL689.F			
Te Papa	OL689.F	y	y	10
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	10
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	10
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	OL689.F	y	y	8
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915	y	y	10
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			
Te Papa	ME14915			

Te Papa	ME14915	[redacted]		
Te Papa	ME14915			
Te Papa	ME2701			
Te Papa	ME2701	y	y	10
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	10
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	10
Te Papa	ME2701	y	y	10
Te Papa	ME2701	y	y	8
Te Papa	ME2701	[redacted]		
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	8
Te Papa	ME2701	y	y	8
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	10
Te Papa	ME8697	[redacted]		
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	11
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	8

Te Papa	ME8697	y	y	8
Te Papa	ME8697	y	y	11
Te Papa	ME8697	y	y	11
Te Papa	ME8697	y	y	8
Te Papa	ME3716	y	y	5
Te Papa	ME3716			
Te Papa	ME3716			
Te Papa	ME3716	y	y	3
Te Papa	ME3716	y	y	5
Te Papa	ME3716	y	y	5
Te Papa	ME3716			
Te Papa	ME3716			
Te Papa	ME3716			
Te Papa	ME3716	y	y	11
Te Papa	ME3716			
Te Papa	ME3716	y	y	8
Te Papa	ME3716	y	y	8
Te Papa	ME3716	y	y	8
Te Papa	ME3716			
Te Papa	ME2055			
Te Papa	ME2055	y	y	5
Te Papa	ME2055	y	y	5
Te Papa	ME2055	y	y	5
Te Papa	ME2055	y	y	5
Te Papa	ME2055	y	y	10
Te Papa	ME2055			
Te Papa	ME2055	y	y	8
Te Papa	ME2055	y	y	8

Te Papa	ME2055	[redacted]		
Te Papa	ME2055	y	y	10
Te Papa	ME2055	y	y	10
Te Papa	ME2055	y	y	10
Te Papa	ME2055	[redacted]		
Te Papa	ME2055	y	y	10
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	8
Te Papa	ME7612	y	y	10
Te Papa	ME7612	y	y	8
Te Papa	ME7612	y	y	9
Te Papa	ME7612	[redacted]		
Te Papa	ME7612	y	y	8
Te Papa	ME7612	y	y	9
Te Papa	ME7612	y	y	8
Te Papa	ME7612	y	y	8
Te Papa	ME7612	y	y	8
Te Papa	ME6598	y	y	9
Te Papa	ME6598	y	y	11
Te Papa	ME6598	y	y	9
Te Papa	ME6598	[redacted]		
Te Papa	ME6598			
Te Papa	ME6598	y	y	9
Te Papa	ME6598	y	y	8

Te Papa	ME6598	y	y	8
Te Papa	ME6598	[redacted]		
Te Papa	ME6598	y	y	8
Te Papa	ME6598	[redacted]		
Te Papa	ME6598	y	y	9
Te Papa	ME6598	y	y	9
Te Papa	ME6598	y	y	9
Te Papa	ME6598	y	y	9
Te Papa	ME15605	y	y	11
Te Papa	ME15605	y	y	9
Te Papa	ME15605	y	y	9
Te Papa	ME15605	y	y	9
Te Papa	ME15605	y	y	10
Te Papa	ME15605	y	y	10
Te Papa	ME15605	y	y	10
Te Papa	ME15605	y	y	9
Te Papa	ME15605	y	y	10
Te Papa	ME15605	y	y	10
Te Papa	ME15102	y	y	8
Te Papa	ME15102	y	y	9
Te Papa	ME15102	y	y	13
Te Papa	ME15102	y	y	10
Te Papa	ME15102	y	y	8
Te Papa	ME15102	y	y	8
Te Papa	ME15102	y	y	10
Te Papa	ME15102	y	y	10
Te Papa	ME15102	[redacted]		
Te Papa	ME15102			

Te Papa	ME15102	y	y	8
Te Papa	ME15102	y	y	10
Te Papa	ME15102	y	y	10
Te Papa	ME15102	[redacted]		
Te Papa	ME15102	y	y	10
Te Papa	ME15350	y	y	3
Te Papa	ME15350	y	y	3
Te Papa	ME15350	y	y	3
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	2
Te Papa	ME15350	[redacted]		
Te Papa	ME15350	y	y	3
Te Papa	ME15350	y	y	3
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	1
Te Papa	ME15350	y	y	3
Te Papa	ME14381	y	y	7
Te Papa	ME14381	y	y	7
Te Papa	ME14381	y	y	7
Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	4
Te Papa	ME14381	[redacted]		

Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	7
Te Papa	ME14381	y	y	7
Te Papa	ME14381			7
Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	4
Te Papa	ME14381	y	y	4
Te Papa	ME15351	y	y	3
Te Papa	ME15351	y	y	3
Te Papa	ME15351	y	y	3
Te Papa	ME15351	y	y	3
Te Papa	ME15351			
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	2
Te Papa	ME15351			
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	1
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	2
Te Papa	ME15351	y	y	2
Te Papa	ME13120	y	y	7
Te Papa	ME13120	y	y	5
Te Papa	ME13120	y	y	7
Te Papa	ME13120	y	y	5
Te Papa	ME13120	y	y	5
Te Papa	ME13120	y	y	5

Te Papa	ME13120	y	y	5
Te Papa	ME13120	y	y	5
Te Papa	ME13120	y	y	7
Te Papa	ME13120	y	y	5
Te Papa	ME737			
Te Papa	ME737	y	y	13
Te Papa	ME737	y	y	13
Te Papa	ME737			
Te Papa	ME737			
Te Papa	ME737	y	y	13
Te Papa	ME737	y	y	5
Te Papa	ME737	y	y	5
Te Papa	ME737			
Te Papa	ME737	y	y	5
Canterbury Museum	E192.130	y	y	5
Canterbury Museum	E192.130			
Canterbury Museum	E192.130	y	y	5
Canterbury Museum	E192.130	y	y	5
Canterbury Museum	E192.130			
Canterbury Museum	E192.130			
Canterbury Museum	E192.130			
Canterbury Museum	E192.130	y	y	5
Canterbury Museum	E192.130			
Canterbury Museum	E192.130			
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E70.47			
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E70.47			

Canterbury Museum	E70.47			
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E70.47			
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E70.47	y	y	8
Canterbury Museum	E161.51	y	y	8
Canterbury Museum	E161.51	y	y	9
Canterbury Museum	E161.51	y	y	9
Canterbury Museum	E161.51	y	y	8
Canterbury Museum	E161.51	y	y	8
Canterbury Museum	E161.51	y	y	9
Canterbury Museum	E161.51			
Canterbury Museum	E161.51	y	y	8
Canterbury Museum	E161.51			
Canterbury Museum	E161.51	y	y	9
Canterbury Museum	E152.210	y	y	8
Canterbury Museum	E152.210	y	y	8
Canterbury Museum	E152.210			
Canterbury Museum	E152.210	y	y	9
Canterbury Museum	E152.210	y	y	8
Canterbury Museum	E152.210	y	y	8
Canterbury Museum	E152.210	y	y	10
Canterbury Museum	E152.210			
Canterbury Museum	E152.210	y	y	9
Canterbury Museum	E152.210	y	y	8
Canterbury Museum	E173.149			
Canterbury Museum	E173.149	y	y	5

Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.149	y	y	5
Canterbury Museum	E173.482	y	y	9
Canterbury Museum	E173.482	y	y	10
Canterbury Museum	E173.482	y	y	9
Canterbury Museum	E173.482	y	y	10
Canterbury Museum	E173.482	y	y	8
Canterbury Museum	E173.482	y	y	10
Canterbury Museum	E173.482	y	y	9
Canterbury Museum	E173.482			
Canterbury Museum	E173.482			
Canterbury Museum	E173.482	y	y	8
Canterbury Museum	E146.285	y	y	9
Canterbury Museum	E146.285	y	y	10
Canterbury Museum	E146.285	y	y	9
Canterbury Museum	E146.285			
Canterbury Museum	E146.285	y	y	10
Canterbury Museum	E146.285	y	y	9
Canterbury Museum	E146.285	y	y	9
Canterbury Museum	E146.285			
Canterbury Museum	E146.285	y	y	10
Canterbury Museum	E146.285	y	y	9

Canterbury Museum	E158.977			
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E158.977	y	y	9
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760	y	y	11
Canterbury Museum	E147.760			
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760	y	y	8
Canterbury Museum	E147.760			
Canterbury Museum	E147.760			
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	8
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	9
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	10

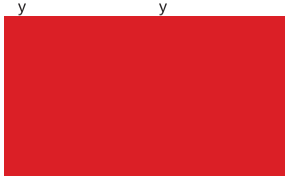
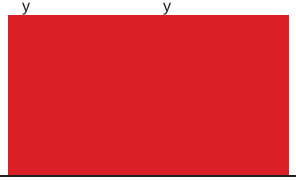
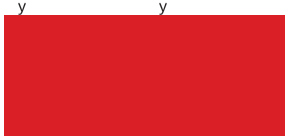
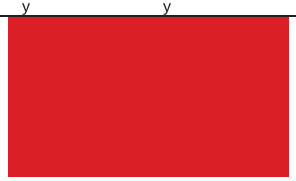
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	E146.286	y	y	10
Canterbury Museum	2001.196.6	y	y	5
Canterbury Museum	2001.196.6	y	y	5
Canterbury Museum	2001.196.6	y	y	5
Canterbury Museum	2001.196.6	y	y	9
Canterbury Museum	2001.196.6	y	y	9
Canterbury Museum	2001.196.6	y	y	5
Canterbury Museum	2001.196.6	y	y	5
Canterbury Museum	2001.196.6	y	y	10
Canterbury Museum	2001.196.6	y	y	10
Canterbury Museum	2001.196.6	y	y	10
Canterbury Museum	E146.689	y	y	8
Canterbury Museum	E146.689			
Canterbury Museum	E146.689	y	y	10
Canterbury Museum	E146.689	y	y	8
Canterbury Museum	E146.689	y	y	8
Canterbury Museum	E146.689			
Canterbury Museum	E146.689	y	y	10
Canterbury Museum	E146.689			
Canterbury Museum	E146.689			
Canterbury Museum	E146.689	y	y	10
Canterbury Museum	IR1296	y	y	4
Canterbury Museum	IR1296	y	y	4
Canterbury Museum	IR1296	y	y	4
Canterbury Museum	IR1296	y	y	4
Canterbury Museum	IR1296	y	y	4
Canterbury Museum	IR1296	y	y	3

Canterbury Museum	IR1296			
Canterbury Museum	IR1296	y	y	3
Canterbury Museum	IR1296	y	y	3
Canterbury Museum	IR1296	y	y	3
Canterbury Museum	E147.759			
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	13
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E147.759	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639			
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639	y	y	5
Canterbury Museum	E158.639			
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.638			
Canterbury Museum	E158.638	y	y	3

Canterbury Museum	E158.638	y	y	3
Canterbury Museum	E158.638	y	y	3
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.638	y	y	7
Canterbury Museum	E158.640	y	y	7
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	10
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	5
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	8
Canterbury Museum	E158.640	y	y	8
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7			
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7	y	y	5
Waikato Museum	L2004/17/7	y	y	5
Waikato Museum	L2004/17/7	y	y	5
Waikato Museum	L2004/17/7	y	y	5
Waikato Museum	L2004/17/7			
Waikato Museum	L2004/17/7			
Waikato Museum	L2004/17/7			
Waikato Museum	L2004/17/7			

Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/17/7	y	y	3
Waikato Museum	L2004/10/1	y	y	3
Waikato Museum	L2004/10/1			
Waikato Museum	L2004/10/1	y	y	3
Waikato Museum	L2004/10/1			
Waikato Museum	L2004/10/1			
Waikato Museum	L2004/10/1	y	y	3
Waikato Museum	L2004/10/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1			
Waikato Museum	L2004/6/1			
Waikato Museum	L2004/6/1			
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/6/1	y	y	3
Waikato Museum	L2004/17/30			
Waikato Museum	L2004/17/30			
Waikato Museum	L2004/17/30			
Waikato Museum	L2004/17/30			
Waikato Museum	L2004/17/30			
Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1	y	y	5

Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1			
Horniman Museum	1974.1	y	y	5
Horniman Museum	1974.1			
Horniman Museum	1974.1			
Horniman Museum	37.82	y	y	5
Horniman Museum	37.82	y	y	3
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	37.82			
Horniman Museum	NN907	y	y	8
Horniman Museum	NN907			
Horniman Museum	NN907	y	y	8
Horniman Museum	NN907	y	y	8
Horniman Museum	NN907			
Horniman Museum	NN907	y	y	10
Horniman Museum	NN907			
Horniman Museum	NN907	y	y	8
Horniman Museum	NN907	y	y	8
Horniman Museum	NN907			

Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666	y	y	9
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666	y	y	8
Auckland Museum	A2666	y	y	8
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A2666			
Auckland Museum	A45775	y	y	10
Auckland Museum	A45775			
Auckland Museum	A45775			
Auckland Museum	A45775			
Auckland Museum	A45775	y	y	10
Auckland Museum	A45775	y	y	10
Auckland Museum	A18213			
Auckland Museum	A18213			
Auckland Museum	A18213			
Auckland Museum	A18213			
Auckland Museum	A18213	y	y	5
Auckland Museum	A18213			
Auckland Museum	A18213			

Auckland Museum	A18213			
Auckland Museum	A18213			
Auckland Museum	A18213	y	y	5
Auckland Museum	A46164	y	y	9
Auckland Museum	A46164	y	y	9
Auckland Museum	A46164	y	y	9
Auckland Museum	A46164	y	y	10
Auckland Museum	A46164	y	y	10
Auckland Museum	A46164			
Auckland Museum	A19263			
Auckland Museum	A19263			
Auckland Museum	A19263	y	y	5
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263			
Auckland Museum	A19263	y	y	7
Auckland Museum	A19263			
Auckland Museum	A19263	y	y	3
Auckland Museum	A19263	y	y	7
Auckland Museum	A38886	y	y	10
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	10

Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	y	y	8
Auckland Museum	A38886	[redacted]		
Auckland Museum	A38886			
Auckland Museum	A38886	y	y	9
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	5
Auckland Museum	A6464	[redacted]		
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	8
Auckland Museum	A6464	y	y	5
Auckland Museum	A6464	[redacted]		
Auckland Museum	A6464	y	y	5
Auckland Museum	A6464	y	y	3
Auckland Museum	A6464	y	y	7
Auckland Museum	A6464	y	y	7
Auckland Museum	A35031	[redacted]		
Auckland Museum	A35031			

Auckland Museum	A35031	y	y	10
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A35031	y	y	8
Auckland Museum	A35031	y	y	8
Auckland Museum	A35031			
Auckland Museum	A35031			
Auckland Museum	A55668			
Auckland Museum	A55668	y	y	5
Auckland Museum	A55668			
Auckland Museum	A55668			
Auckland Museum	A55668	y	y	7
Auckland Museum	A55668	y	y	7
Auckland Museum	A55668	y	y	8
Auckland Museum	A55668	y	y	7
Auckland Museum	A55668			
Auckland Museum	A55668			
Auckland Museum	A48137			
Auckland Museum	A48137			
Auckland Museum	A48137			
Auckland Museum	A48137			
Auckland Museum	A48137			

Auckland Museum	A48137	[redacted]		
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	[redacted]		
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	y	y	6
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	Cloak no accession number	[redacted]		
Auckland Museum	Cloak no accession number	y	y	5
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	[redacted]		
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	[redacted]		
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A35448	y	y	8
Auckland Museum	A56357	y	y	11
Auckland Museum	A56357	y	y	11

Auckland Museum	A56357	y	y	11
Auckland Museum	A56357	y	y	11
Auckland Museum	A56357			
Auckland Museum	A56357			
Auckland Museum	A56357	y	y	10
Auckland Museum	A56357	y	y	10
Auckland Museum	A56357	y	y	9
Auckland Museum	A56357	y	y	12
Auckland Museum	A56357	y	y	10
Auckland Museum	A56357	y	y	12
Auckland Museum	A56357			
Auckland Museum	A56357			
Auckland Museum	A56357			
Wanganui Museum	W1977.1.1	y	y	7
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1977.1.1	y	y	7
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1977.1.1	y	y	7
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1977.1.1	y	y	5
Wanganui Museum	W1970.4	y	y	5
Wanganui Museum	W1970.4			
Wanganui Museum	W1970.4			
Wanganui Museum	W1970.4			
Wanganui Museum	W1970.4			
Wanganui Museum	W1970.4			

Wanganui Museum	W1970.4	y	y	5
Wanganui Museum	W1970.4	y	y	5
Wanganui Museum	W1970.4	y	y	3
Wanganui Museum	W1970.4	y	y	5
Wanganui Museum	W1970.4	[redacted]		
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	[redacted]		
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W1953.26	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8

Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	9
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W_SHENTON_COLL			
Wanganui Museum	W_SHENTON_COLL	y	y	10
Wanganui Museum	W_SHENTON_COLL	y	y	8
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70	y	y	2
Wanganui Museum	W1980.70	y	y	2
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70			
Wanganui Museum	W1980.70	y	y	2
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146	y	y	5

Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146			
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1957.146	y	y	5
Wanganui Museum	W1992.29.1			
Wanganui Museum	W1992.29.1	y	y	5
Wanganui Museum	W1992.29.1			
Wanganui Museum	W1992.29.1	y	y	3
Wanganui Museum	W1992.29.1			
Wanganui Museum	W1992.29.1	y	y	8
Wanganui Museum	W1992.29.1			
Wanganui Museum	W1992.29.1			
Wanganui Museum	W1992.29.1	y	y	3
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W2001.46.1	y	y	9
Wanganui Museum	W2001.46.1			
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W2001.46.1			
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W2001.46.1	y	y	8
Wanganui Museum	W1802.700			
Wanganui Museum	W1802.700	y	y	7
Wanganui Museum	W1802.700			
Wanganui Museum	W1802.700	y	y	8

Wanganui Museum	W1802.700	y	y	8
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W2002.110	y	y	13
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110	y	y	8
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W2002.110			
Wanganui Museum	W2002.110	y	y	3
Wanganui Museum	W2002.110	y	y	5
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3			
Wanganui Museum	W1948.64.3			
Wanganui Museum	W1948.64.3	y	y	10
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3	y	y	10
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3	y	y	10
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3	y	y	8
Wanganui Museum	W1948.64.3			

Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29	y	y	8
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1802.29			
Wanganui Museum	W1968.100.2	y	y	9
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	10
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2			
Wanganui Museum	W1968.100.2			
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2	y	y	8
Wanganui Museum	W1968.100.2			
Wanganui Museum	W1802.24	y	y	5
Wanganui Museum	W1802.24	y	y	5
Wanganui Museum	W1802.24	y	y	5
Wanganui Museum	W1802.24			

Wanganui Museum	W1802.21			
Wanganui Museum	W1802.21			
Wanganui Museum	W1802.21			
Wanganui Museum	W1802.21	y	y	8
Wanganui Museum	W1802.21			
Wanganui Museum	W1802.21			
Wanganui Museum	W1802.21			
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN			
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN	y	y	5
Wanganui Museum	W_R_STEADMAN	y	y	3
Wanganui Museum	W_R_STEADMAN			
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1	y	y	11
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1			
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1	y	y	9

Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1	y	y	10
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1936.33.1	y	y	9
Wanganui Museum	W1802.25			
Wanganui Museum	W1802.25	y	y	3
Wanganui Museum	W1802.25			
Wanganui Museum	W1802.25	y	y	7
Wanganui Museum	W1802.25	y	y	6
Wanganui Museum	W1802.25			
Wanganui Museum	W1977.4	y	y	8
Wanganui Museum	W1977.4	y	y	
Wanganui Museum	W1977.4			8
Wanganui Museum	W1977.4	y	y	8
Wanganui Museum	W1977.4			
Wanganui Museum	W1977.4	y	y	10
Wanganui Museum	W1977.4	y	y	8
Wanganui Museum	W1977.4			
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1977.4			
Wanganui Museum	W1977.4	y	y	5
Wanganui Museum	W1802.26	y	y	5
Wanganui Museum	W1802.26	y	y	5
Wanganui Museum	W1802.26	y	y	5

Wanganui Museum	W1802.26	y	y	5
Wanganui Museum	W1802.26	y	y	5
Wanganui Museum	W1802.26			
Wanganui Museum	W1909.107	y	y	5
Wanganui Museum	W1909.107	y	y	7
Wanganui Museum	W1909.107	y	y	5
Wanganui Museum	W1909.107	y	y	5
Wanganui Museum	W1909.107	y	y	5
Wanganui Museum	W1909.107	y	y	5
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22			
Wanganui Museum	W1953.22	y	y	8
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22	y	y	10
Wanganui Museum	W1953.22			
Wanganui Museum	W1959.125.1			
Wanganui Museum	W1959.125.1			
Wanganui Museum	W1959.125.1	y	y	5
Wanganui Museum	W1959.125.1	y	y	5

Wanganui Museum	W1959.125.1	y	y	5
Wanganui Museum	W1959.125.1	y	y	5
Wanganui Museum	W1959.125.1	y	y	3
Wanganui Museum	W1959.125.1	y	y	5
Wanganui Museum	W1957.14	y	y	5
Wanganui Museum	W1957.14	y	y	5
Wanganui Museum	W1957.14	y	y	5
Wanganui Museum	W1957.14			
Wanganui Museum	W1957.14	y	y	5
Wanganui Museum	W1957.14	y	y	3
Wanganui Museum	W1957.14			
Wanganui Museum	W1957.14			
Wanganui Museum	W1957.14			
Wanganui Museum	W1957.14			

Table A.2 Kete sequences for mtDNA CR HVR1 using Kcf / Kcr

Sample Number	Accession Number	Haplo type	Sequence
186	KeteOc81Q1401		
187	KeteOc81Q1401		
188	KeteOc81Q1401		
189	KeteOc81Q1401		
190	KeteOc1933/0311.2	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
191	KeteOc1933/0311.2	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
192	KeteOc1933/0311.2	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
193	KeteOc1933/0311.2		
194	Kete1919.8	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
195	Kete1919.8	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
196	Kete1919.8		
197	Kete1919.8		
198	Kete1908/1214.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
199	Kete1908/1214.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
200	Kete1908/1214.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
201	Kete1908/1214.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
202	NZ.133		
203	NZ.133		
204	NZ.133		
205	NZ.133		
589	KETEME4252B	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
590	KETEME4252B	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
591	KETEME4252B	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
592	KETEME4252B	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
593	KETEME4252A	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
594	KETEME4252A	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
595	KETEME4252A	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
596	KETEME4252A	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

597	KETEME13184	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
598	KETEME13184		
599	KETEME13184	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
600	KETEME13184		
601	KETEME11529		
602	KETEME11529	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
603	KETEME11529	7	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
604	KETEME11529	7	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
605	KETEME8099	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
606	KETEME8099	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
607	KETEME8099		
608	KETEME8099	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
609	KETEME11528		
610	KETEME11528		
611	KETEME15543		
612	KETEME15543		
613	KETEME15543	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
614	KETEME15543	2	ATTTCTTGGAGCCGGGGTTAAGTTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
615	KETEME15284	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
616	KETEME15284	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
617	KETEME15284		
618	KETEME15284	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
619	MYSTERYKETE	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
620	MYSTERYKETE		
621	MYSTERYKETE		
622	MYSTERYKETE	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
793	KETEE141.34	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
794	KETEE141.34	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
795	KETEE141.34	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
796	KETEE141.34	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

797	KETEE173.317	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
798	KETEE173.317	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
799	KETEE173.317	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
800	KETEE173.317	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
801	KETEE159.654	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
802	KETEE159.654	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
803	KETEE159.654	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
804	KETEE159.654	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
805	KETEE163.445	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
806	KETEE163.445	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
807	KETEE163.445	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
808	KETEE163.445	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
809	KETEE188.59	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
810	KETEE188.59	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
811	KETEE188.59	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
812	KETEE188.59	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
813	KETEE173.153	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
814	KETEE173.153	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
815	KETEE173.153	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
816	KETEE173.153	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
817	KETE822	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
818	KETE822	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
819	KETE822	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
820	KETE822	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
821	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
822	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
823	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
824	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
825	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
826	KETEE138.1237	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

827	KETEE137.100	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
828	KETEE137.100	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
829	KETEE137.100	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
830	KETEE137.100	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
831	KETEE181.431	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
832	KETEE181.431	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
833	KETEE181.431		
834	KETEE181.431		
835	KETEE181.431	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
836	KETEE181.431	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
837	KETEE148.75	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
838	KETEE148.75	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
839	KETEE148.75	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
840	KETEE148.75	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
841	KETEE159.653	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
842	KETEE159.653	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
843	KETEE159.653	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
844	KETEE159.653	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
845	KETEE164.1003	11	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGTCTACCTATGC TCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
846	KETEE164.1003	11	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGTCTACCTATGC TCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
847	KETEE164.1003	11	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGTCTACCTATGC TCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
848	KETEE164.1003	11	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGTCTACCTATGC TCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
887	KIWI/SAMPLER		
888	KIWI/SAMPLER	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
889	KIWI/SAMPLER	7	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
890	KETE1961/131/2		
891	KETE1961/131/2		
892	KETE1961/1/25	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
893	KETE1961/1/25		
894	KETE1961/1/25		

895	KETE1961/1/25	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
896	KETE1964/36/1	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
897	KETE1964/36/1	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
898	KETE1964/36/1		
899	KETE1964/36/1		
900	MUFF		
901	MUFF	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
902	MUFF	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
903	MUFF	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
934	KETE24.43		
935	KETE24.43		
936	KETE24.43		
937	KETE24.43		
1099	AK53500	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1100	AK53500	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1101	AK53500	11	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGTCTACCTATGC TCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1102	AK53500	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1103	AK5426.1		
1104	AK5426.1		
1105	AK5426.1		
1106	AK5426.1	2	ATTTCTTGGAGCCGGGGTTAAGTTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1107	AK5426.2	1	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1108	AK5426.2		
1109	AK5426.2		
1110	AK5426.2		
1111	AK45158	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1112	AK45158	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1113	AK45158	2	ATTTCTTGGAGCCGGGGTTAAGTTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1114	AK45158	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1115	AK45160	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1116	AK45160	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

1117	AK45160	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1118	AK45160	1	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1119	AK48505		
1120	AK48505		
1121	AK48505		
1122	AK48505	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1123	AK6097	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1124	AK6097	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1125	AK48141	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1126	AK48141	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1127	AK48141	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1128	AK48141	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1129	AK8133.2	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1130	AK8133.2	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1131	AK50371.2	7	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1132	AK50371.2	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1133	AK50371.2	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1134	AK50371.2	13	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1135	AK8133.1	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1136	AK8133.1	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1137	AK8133.1	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1138	AK8133.1	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1139	AK55391	4	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1140	AK55391		
1141	AK55391		
1142	AK55391		
1143	AK50371.1		
1144	AK50371.1	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1145	AK50371.1		
1146	AK50371.1		
1147	AK33840.2	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

1148	AK33840.2	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1149	AK33840.2	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1150	AK33840.2	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1151	AK55348		
1152	AK55348	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1153	AK46158	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1154	AK46158		
1155	AK46158		
1156	AK46158		
1157	AK52618		
1158	AK52618	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1159	AK52618	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1160	AK52618		
1161	AK48240	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1162	AK58240	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1163	AK38781		
1164	AK38781		
1265	WK1802.170	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1266	WK1802.170	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1267	WK1802.170		
1268	WK1802.170	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1269	WK1962.50		
1270	WK1962.50		
1271	WK1962.50		
1272	WK1962.50	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1324	WK1975.44.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1325	WK1975.44.1	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1326	WK1975.44.1		
1327	WK1975.44.1	9	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1328	WK1966.81.4	3	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCCATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1329	WK1966.81.4	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG

1330	WK1966.81.4	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1331	WK1966.81.4	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1332	WK1802.167	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1333	WK1802.167	6	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGTAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1334	WK1802.167		
1335	WK1802.167		
1336	WK1802.165		
1337	WK1802.165		
1338	WK1802.165		
1339	WK1802.165		
1340	WK1962.80	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1341	WK1962.80	5	ATTTCTTGGAGCCGGGGTTGAATTCAATAGACTAGGCTAAACGCATTAATAGCTACCTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCCCGCCTACCTATG CTTGTCAATCTGACTGCGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1342	WK1962.80		
1343	WK1962.80		
1446	WK1973.57.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1447	WK1973.57.1	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1448	WK1973.57.1	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1449	WK1973.57.1	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1450	WK1802.166		
1451	WK1802.166	10	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1452	WK1802.166		
1453	WK1802.166		
1454	WK1802.164		
1455	WK1802.164	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1456	WK1802.164	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1457	WK1802.164	8	ATTTCTTGGAGCCGGGGTTAAATTCAATAGACTAGGCTAAACGCATTAATAGCTACTTTATACATACGCAATGCTCTACCCCAACAGATTACCCGTAAGATCCTCGTTCAATGGTTAATGGACAAGTCTCGCCTACCTATG CTCGTCAATCTGACTGTGATTCCTAGCGCCAGATGGATTTCCTGATTCAACACCTCACG
1458	WK1935.46		
1459	WK1935.46		
1460	WK1935.46		
1461	WK1935.46		