The Last Frontier

Modern humans evolved in Africa, perhaps 130,000 years ago. Soon their curiosity led them to explore lands beyond Africa. By about 100,000 years ago some had settled in the Mediterranean region and others travelled eastwards through India to reach China and South East Asia. By about 60,000 years ago some had crossed the narrow waterway to New Guinea and Australia. Humans were also in Western Europe and Siberia by 40,000 years ago.

During this time the earth was gripped by the last great ice age and a huge ice sheet covered the northern half of Eurasia and North America. Because of the ice, sea levels were much lower than they are today. For example, New Guinea and Australia were joined together.

After the ice started to recede, about 18,000 years ago, humans could travel across what was then a land bridge from Eurasia to North America (today’s Bering Strait). By about 12,000 years ago humans had travelled through
North America and right to the southern tip of South America.

Humans discovered and settled all the earth’s major land masses mainly on foot. The exception was crossing the waterway to New Guinea/Australia.

**The Pacific Ocean as the last frontier**

The one potential area remaining for humans to explore and settle was the islands of the Pacific Ocean. Travelling to these places was impossible before two great developments in human history — advances in agriculture and technology.

- Pacific islands were poor in resources. For example there were originally no food plants such as coconuts, yams or taro. Humans needed to be able to bring and grow their own food to live there. Only in the last 10,000 years did humans change from being hunters and gatherers to planting crops and domesticating animals.

- This large-scale travel required ocean-going vessels and a system of navigation — what is called a blue-water technology — to reach the islands. This technology only appeared about 4–5,000 years ago.

So the Pacific islands were the very last places on earth to be settled by humans. The story of their migrations through the Ocean is not just a magnificent Pacific event, it is also the last chapter in the story of the human settlement of the entire earth. By the time humans settled the remotest islands in the Pacific — and that was only about 700 years ago! — they had reached the end of their habitable world.

**The Ocean as a Home**

**The view from outside**

The Pacific Ocean covers one-third of the earth’s surface. It is truly a watery hemisphere.

Western explorers started to explore the Pacific ocean about 400 years ago (in the sixteenth century). It took them several hundred more years of difficult exploration before they had much understanding of the Pacific. Thus a common Western view was, and sometimes still is, that the ocean is vast, featureless, dangerous, and its tiny islands are hazardous to navigation. Overall, the Pacific seemed to offer few resources or lands worth bothering about.

**The view from inside**

Thousands of years before Western explorers arrived, there were people who had discovered and settled almost every island across that great ocean. To them it was not a place of fear, it was home.
For Pacific peoples, the sea provided them with abundant marine life for food and was not viewed as an obstacle, but as a highway. It represented a way back in time to where their ancestors had come from, and it offered a way into the future with the quest to find new islands. The stars became navigational beacons, and often representations of ancestors. The clouds also told them of coming weather patterns. Island peoples did not consider themselves isolated. Their islands were the very safe centres of their physical and spiritual worlds.

Most natural objects, such as the sea itself, the features of the island landscape, and plants and animals had names and stories about them, giving them a social or spiritual significance. These names and stories were commonly applied on many islands over time, so leaving a kind of road map of ancestral history and culture.

Islanders developed a very rich range of stories about their past. They had traditions about how the world and everything in it was made, and about the deeds of various hero ancestor-gods. They believed their world was governed by supernatural forces. Much of their culture involved elaborate beliefs and rituals which were designed to appease the gods, gain their help, and protect them against evil spirits.

Migration stories
In particular they had stories of how their ancestors had arrived at an island and its subsequent human history. Across many parts of the Pacific there are very diverse and detailed stories of human migration. These cannot be treated strictly as “factual” stories since they evolved to meet both political and social purposes, but they still have historical significance.

Many island societies have traditions of their ancestors arriving in great canoes “from the west” which is actually the case. Throughout Polynesia there is a tale about an ancestral homeland called Hawaiki or “Hawaiki Nui”. This may not even be an actual place, but it indicates awareness of the immediate common origins of the societies now scattered widely around eastern Polynesia.

Many migratory traditions in fact give support to modern scholarly findings about Pacific people’s distant homelands.

Pacific Peoples’ Origins
The Austronesians
The people who first discovered and settled the remote islands of the Pacific - all those to the east of the Solomon Islands - have a common origin. They were all members of the Austronesian societies that lived throughout southern China and Southeast Asia some 5,000-6,000 years ago. This predates modern Chinese civilisation.

In addition to curiosity and daring, the Austronesians had the two skills necessary to settle the Pacific islands:

- they were experts at planting and harvesting crops, and they domesticated animals such as dogs, pigs, and chickens.
- they developed the world’s first effective ocean-going craft using sails and outriggers.

Austronesian migrations
About 4,000 years ago some Austronesians had reached the New Guinea region, where there were already people settled. Later they headed out beyond the Solomon Islands and entered oceanic regions never before seen by humans.

They travelled along the Melanesian island chain, as well as into Micronesia to reach Fiji, Samoa and Tonga. They then crossed to the region of the Society Island in Polynesia and from there radiated out to the far distant islands of that group – Hawai’i, Easter Island, and New Zealand. They may have also reached South and even Central America.
Evidence Trails

The Austronesians have left behind evidence of their migrations enabling modern research to track their movement across the oceans.

• Artefact and activity trails

Archaeologists have uncovered a vast number of items of material culture — such as tools, cooking and domestic equipment, garden implements, weapons, fishing gear, decorative items, and stone work. The trails of these items can be dated by radiocarbon dating. The Austronesians also modified the landscape in many ways, such as digging fortification and irrigation ditches, creating gardens and clearing forests.

One of the best and most important examples of an artefact trail is Lapita pottery. The Austronesians started making this type of pottery near New Guinea 3,500 years ago, and continued to make it as they moved through the Melanesian island chain and reached Fiji, Samoa and Tonga at least 3,000 years ago. The Lapita trail shows that the first settlers of central Polynesia came via the Melanesian islands, and when this took place.

• Biological trails

Using modern DNA studies, scientists can show the ancient genetic trails across the Pacific ocean of people, plants and animals.

- People Modern peoples of Polynesia have an ancestral genetic trail which leads back into South East Asia, via Melanesia.

- Plants Most of the major food plants on the Pacific islands have genetic origins in the New Guinea/ South East Asian regions and were introduced by the Austronesians — these included coconuts, yams, taro and sugar cane. Well over 30 new species of plants were introduced from the west. The one notable exception is the sweet potato which originates in Peru. It is now believed the sweet potato was introduced to eastern Polynesia by Austronesians returning from South America.
Animals
Pigs, chickens and dogs found throughout the Pacific originated in South East Asia and were brought by the Austronesians. They also introduced the Polynesian rat (*Rattus exulans*), plus a New Guinea night lizard.

Language trails
All languages spoken in island South Asia and throughout the Pacific Ocean (excluding Australia and most of New Guinea) belong to a single language family called Austronesian. This language group consists of over 1000 different languages, but they are all related like a family tree. Languages spoken throughout the Pacific islands can all be traced back to founding ancestral Austronesian languages in South East Asia. For example, Maori spoken in New Zealand is most closely related to Cook Island Maori, then Tahitian, which in turn derives from ancient Samoan and so on back through island Melanesia and into South East Asia.

Cultural trails
Examination of patterns of cultural behaviour across the Pacific, including place naming, social, political and religious practices, and especially oral traditions, all provide trails back into the far west of Oceania.

Vaka
An evolving technology
The migrating Austronesians did not simply get onto ready-made voyaging canoes and sail across the Pacific from South East Asia. Instead over perhaps a 4-5,000 year period they experimented with many kinds of hull and sail designs, according to the resources available and particularly as they sailed increasingly longer distances across empty seas moving eastwards.

The major technical breakthrough initially came in South East Asia when the sail was either invented or introduced to the region, and outriggers were constructed to stabilise a canoe with a mast and a sail. This provided the basis for the world’s first blue water vessels.
Nowhere else on earth did people develop successful ocean-going vessels until thousands of years later.

**Hull types**

In the more sheltered waters of South East Asia, a vessel typically had a lateen sail and an outrigger on each side of the hull.

Heading into the more open seas of island Melanesia and Micronesia the single hull and single balancing outrigger became common. In the more open seas around Fiji, Samoa, and Tonga large double but unequal-size hulls were developed. In eastern Polynesia they developed double, equal-size hulls. These provided a large, effective and very stable platform for people and goods travelling over the vast empty seas. Early European explorers recorded some vessels at over 33 metres in length. A typical voyaging vessel in eastern Polynesia might have been about 20 metres long.

Where there were large trees, such as on Fiji, hulls could be made of hollowed logs. Many islands had no large trees so smaller pieces of timber were used to create ribs over which were lashed small planks of timber.

**Sail types**

Sail and mast designs also changed radically along with hull shapes. The basic lateen sail of South East Asia went through a remarkable set of modifications across the Pacific, including the self-standing “claw” sail.

**Capabilities**

Ocean-going vessels were generally safe and efficient. They could sail against the wind. Some were very fast, especially certain single-hull, single outrigger types. The double hulled vessels of eastern Polynesia were capable of sailing safely and quickly over many thousands of kilometres. To simply call them all “canoes” gives a misleading impression of the scale of the world’s first ocean-going technology.
Navigation

Navigators and knowledge
To discover islands in the Pacific Ocean, the Austronesian explorers needed to know where their vessels were at sea, and how to find their way back home. Over a long period of time, they developed a range of navigational skills that proved extremely effective and enabled them to discover almost every island in the Pacific, and to cross its entire width.

Navigational skills were taught only to specially selected young men who were then trained in navigators' schools. Such learning was a closely guarded secret and the navigators had great prestige within communities since it was they alone who could guide them safely at sea.

There has been some debate in the past amongst Western scholars as to how effective the Austronesian navigators were. Thanks very largely to the work of David Lewis, in his book *We, the Navigators* (1972), there is now an understanding of how navigation worked. It is now believed that the ancient navigators could purposefully and deliberately navigate over vast distances of ocean. There is evidence of a method of recording navigational information in stick “charts” made by the Marshall Islanders. They did not simply travel by chance and accident.

Basic navigating skills

The Austronesian navigators obviously did not have a modern compass, marine charts, or a Western concept of latitude or longitude. Instead they had developed their own systems based on careful observation of stars, sea conditions, and wind and weather patterns.

This knowledge gave them the ability to “triple voyage” — that is travel from island A to find island B (voyage 1). From B they could travel back to (voyage 2). Back on they now knew where B was for a return voyage (voyage 3).
Since many islands are located in groups called archipelagos, their combined expanded targets offered a vast "screen" of islands. The navigator headed for the centre of the screen, then navigated within the archipelago to find the specific target island.

Island targets could be expanded by noting such things as:
- distinctive cloud patterns above islands (figure A)
- island colours, especially lagoons which reflected on the underside of clouds (figure B)
- deep ocean swells bouncing back from, and curving around islands (figure C)
- birds that roost on islands flying out to sea in the morning and back in the evening (figure D)
- changing sea colours near islands
- drifting objects from nearby land - coconuts, sea weed, drift wood

A grand plan?
It is now thought that the Austronesians had an overall strategy for exploration and that essentially involved heading into the tropical Pacific’s prevailing south-easterly winds, or waiting for the brief annual reversal of these winds. That way the navigator could readily return home whether new land was found or not. This would explain the way the Pacific was settled from west to east.

Landfall
Like humans everywhere on earth, island peoples adapted their societies and economies to suit their cultural values and their available resources. They introduced new plants and animals. They often changed their new environments by clearing forest, and depleting or even causing extinction amongst native birds and animals. They made an island a home.

There came a time when the great Austronesian voyages of exploration came to an end, and that was long before Westerners sailed into the Pacific.

The major Austronesian explorations came to an end probably because they were no longer necessary:
- they had eventually discovered most islands in the Ocean.
- they had crossed the entire Ocean from South East Asia to the Americas.
- they had been as far north as Hawai‘i and as far south as the tiny islands well south of New Zealand.

Also as island societies became established over hundreds and even thousands of years, the Islanders developed strong emotional, spiritual, political, social and economic bonds to their lands. Life centred around the island home, and no longer on the endless quest to sail away looking for
new ones. The developing requirements of politics, warfare and trade meant that different types of sailing vessels were developed.

By the time of the first Western contact, some of the islanders’ long distance ocean-going technology, and navigational knowledge, had diminished.

Two Worlds

Encounter overview

Pacific island societies had been developing and changing for as long as they had existed in the Pacific. The most sudden and extensive changes came with the arrival of Westerners, particularly after the voyages of Captain Cook in the eighteenth century. Numerous other explorers followed Cook, then came missionaries and traders and eventually European settlers and government officials. By the end of the nineteenth century almost all Pacific islands were controlled by European powers - Spain, France, Britain, Germany and the United States.

Even if their extreme long distance sailing had largely ceased, many islanders still voyaged extensively on cultural, military and trading routes within their island groups. They remained a highly skilled maritime people but their sailing skills were now more commonly applied to regional travels rather than trans-oceanic exploration.

Over time many island values and institutions were dramatically changed, and often to the Islanders’ disadvantage. Diseases also came with Western contact and these caused suffering and depopulation.

Early maritime encounters

Western explorers were often amazed to learn that island peoples had explored and settled the Pacific islands long beforehand. They were very interested to try to find out where the Islanders came from and how they travelled. They recorded many details of the Islanders’ sailing vessels and were often very impressed by their size and speed. They also tried to learn something of their navigational techniques. But particularly by acting as guides, sailors and beyond realising that island navigators used stars, sun and moon, they gained little knowledge of how they navigated.

Captain Cook took a Ra’iatean high priest - Tupaia - on his voyage south to New Zealand. He was astounded that Tupaia was aware of distant islands and could always point accurately in the direction of his home.

Many island societies responded enthusiastically to foreign presence. They were often very keen to trade in order to get new Western goods and they were very interested in new ideas such as Christianity and literacy.
Islanders were also extremely interested in European ships and were very keen to travel on board, particularly by acting as guides, sailors and labourers with Western traders. For example, the vast Pacific whaling fleets of the 1830s and ‘40s contained very large numbers of Islanders amongst their crews. Island leaders in many places, including Tahiti and Hawai‘i, saw the military and trading potential of Western vessels, and ended up owning considerable fleets.

One direct result of extensive contact with Westerners was that the Islanders’ own sailing craft and sailing routes were sometimes abandoned as were traditional navigational skills. Only in some more remote parts of the Pacific, especially in parts of Micronesia, did these skills survive.

Renaissance

Saving the vanishing art

By the mid-twentieth century it was widely assumed that ancient Pacific navigational skills had died out, as had so much traditional island knowledge and customs.

Then Andrew Sharp launched an attack on the idea that these skills had ever existed. In his book Ancient Voyagers in the Pacific (1956), he argued that the early navigators had made their way more by wind-blown chance and accident than deliberate navigation. This idea created much debate.

David Lewis challenged Sharp by noting that some old navigators in Micronesia - such as Hipour and Tevake - still practised the old navigational skills. Lewis sailed with some of them and then started to use their techniques sailing about the islands himself. He described their ways of navigation in his book We, the Navigators (1972), [see Navigation, above]. Today Lewis is widely credited with “saving the vanishing art” of navigation.

Replica voyaging

In the 1970s the modern Renaissance of traditional navigation and sailing began in earnest in Hawai‘i, notably with Ben Finney and the Polynesian Voyaging Society’s double hulled vessel Hokule‘a. In 1975 it made a ground-breaking voyage from Hawai‘i to Tahiti. Hokule‘a has since sailed to most parts of Polynesia including New Zealand and Easter Island.

Numerous replica voyaging vessels have since been built and they have been sailed using the traditional navigational skills, including: Taratai from Kiribati — James Siers, Hawaikinui from Tahiti — Matahi Gregory Whakataka Brightwell/ Francis Puara Cowan, Takitumu from the Cook Islands — Sir Tom Davis, Te Aurere from New Zealand — Hekenukumai Busby.

Cultural revival

Replica voyaging was in part about proving the effectiveness of traditional navigation. A new generation of island navigators has emerged — men like
Nainoa Thompson in Hawai‘i and Hek Busby in New Zealand.

But replica voyaging is also about a revival of cultural pride throughout many parts of the Pacific. Voyaging canoes have become centre pieces of a pan-Polynesian nationalism. They gather in force at Polynesian cultural festivals and have been on cultural and ceremonial tours. Seven vessels once raced 3,000 kilometres from the Marquesas Islands to Hawai‘i.

The deeds of ancestral island navigators and their skills are now being celebrated and relived.

Illustrations
KH – Prof. Kerry Howe
AWMM – Auckland War Memorial Museum

Reference

DNA Barcoding Life
Will a new type of science revolutionise our understanding of nature?

What do supermarket check-outs and endangered species have in common? Nothing...yet; however, in five years’ time that could change thanks to a scientific revolution involving biologists, biomolecules, and barcodes. And this revolution is being powered by New Zealand researchers.

Borrowing a concept from scannable barcodes on supermarket products, this international project will develop an electronic inventory to identify every organism in the world, but will use a molecular barcode instead of a black-and-white striped pattern. If all goes to plan, nature enthusiasts and amateur biologists may soon be able to buy portable DNA barcode ‘scanners’ to identify–within minutes–the species, habitat, and life-cycle of individual organisms encountered in their backyards. Such a device may also help to identify previously undiscovered species, and provide an overall estimate of the Earth’s biodiversity and extinction rates.

At the forefront of the international DNA barcoding project is a group of New Zealand scientists led by Professor David Lambert from the Allan Wilson Centre for Molecular Evolution and Ecology, one of New Zealand’s Centres of Research Excellence. His role is to co-ordinate a DNA-based identification system for the country’s flora and fauna, beginning with native birds, and later including other animals, plants, insects, and fungi. The project will help to preserve New Zealand’s ecosystems by monitoring the number of endangered species, and helping to detect the introduction of exotic pests.

But how can all this information be extracted from just a fragment of DNA—the genetic ‘blueprint’ for life?

Deoxyribonucleic acid (DNA), the molecule that contains the ‘instructions’ responsible for inheritance, is the basic component of genes. DNA molecules consist of two long chains wound around each other to form a characteristic double helix—similar to a twisted ladder.

Making up the rungs of the ladder are chemical building blocks or nucleotides, which can be one of four types
(adenine, cytosine, guanine, or thymine, shortened to A, C, G, and T). Nucleotides are arranged in sequences, similar to the way in which letters are arranged into words, and words into sentences, to create meaning and convey instructions. Copies of DNA molecules are passed from parent to offspring, and an organism’s entire set of genetic information is called its genome.

All living entities use this model of genetic code. Differences between organisms (the basis of biodiversity) are simply a different way of expressing information in a common language.

DNA barcoding makes use of the gradual accumulation of molecular changes that occur within DNA over millions of years. All organisms contain DNA sequences that remain almost identical between individuals of the same group, but differ between species. The amount of time since different species shared a common ancestor influences this genetic variation, with recently diverged ‘sister’ species sharing more DNA sequences. Thus, these DNA sequences can be used as barcodes to sort, for example, the large number of bird species and to detect species new to science. This genetic barcoding information can also be used to assess the evolutionary relationship between different species.

The potential of DNA barcodes was recognised by Canadian evolutionary biologist Paul Hebert, who examined a portion of the genome of North American birds. Hebert used a short sequence at the beginning of a gene coding for cytochrome c oxidase (or CO1 for short), an enzyme involved in the cell’s energy conversion system. The CO1 gene has the characteristics of an ideal barcode: it is common to all animals, each cell contains many identical copies, and, in many cases, its sequence is species-specific.

Hebert and colleagues analysed a section at the beginning of the CO1 gene using a technique called the polymerase chain reaction (PCR). This reaction is analogous to a molecular photocopier: it uses an existing piece of DNA as a template and amplifies it (makes billions of copies) within a few hours, providing a workable amount of DNA that can be sequenced and analysed.

Using these methods, Hebert’s team discovered that the CO1 genetic barcode varies by more than two per cent between bird species, but by less than one per cent between members of the same species, demonstrating DNA barcoding’s potential to identify individuals as well as group membership.

And that is precisely what David Lambert plans to do for New Zealand’s birds, as part of an international pilot study to DNA barcode the birds of the world. Using the same portion of the CO1 gene, Allan Wilson Centre researchers will sample approximately 10 individuals from every native bird species and use these barcodes to calibrate species-level differences. The barcodes will assist the conservation of New Zealand’s endangered birds, including kiwi, North Island Saddleback, and Black Robins—species all threatened because of introduced predators and habitat changes. The New Zealand team will also barcode backwards in time using ancient bones, skin, and feathers, to identify ancient

birds, such as moa, and their genetic similarity to living species.

Despite the Jurassic Park overtones, this project has the potential to offer far more than a script for a blockbuster film. DNA barcoding is a rapid, high-throughput method that does not require specialist knowledge of biological classification. Sequences can be stored electronically, creating a readily accessible, standardised scientific database, by working with traditional taxonomists. This, in turn, will make it easier to determine the species of individual organisms where visual identification fails, such as morphologically identical species, sub-adult life-cycle stages, and body parts. Identifying new species, both living and extinct, will be more accurate and provide a more fine-scale estimate of global biodiversity. Such information is important because only a fraction of the millions of species on Earth has yet been identified, and species are becoming extinct faster than they can be described using traditional taxonomic methods. This trend will undoubtedly worsen as environmental pressures increase, reducing biodiversity to a critical level. A new species identification method that can keep up with extinction rates—and help to reduce them—is clearly needed.

The practical outcomes of DNA barcoding are far-reaching. Benefits extend from the protection of agriculture crops by preventing weed spread, to strengthening conservation management, improving health by identifying pathogens, and foiling bioterrorism attacks. With a cost of US$2.5 billion and a time-frame of 20 years, DNA barcoding rivals the Human Genome Project, not only in size and complexity, but also in significance. In the current era when Earth’s species are disappearing at unprecedented rates, a global system to measure present—and past—levels of biodiversity is timely.

Further reading:


Emu Feathers and Moa Cloaks

Moa ‘seemed to have been metaphors for a wilderness in which, many thought, they might still exist’ (Anderson, 1989; p8)

In late 2004, molecular ecologists Professor David Lambert and Dr Leon Huynen of Massey University’s Allan Wilson Centre were contacted with an unusual request. In the Hawke’s Bay Museum, Napier, a collection of feather cloaks—traditional Maori garments and cultural treasures—was being examined and re-housed to preserve it for future generations. Many of these cloaks were of unknown age and origin, and were in varying states of preservation. Textiles conservator Rangi Te Kanawa, an expert in the preservation of traditional fibres and materials, was in charge of assessing each cloak and recommending appropriate storage conditions.

Within the collection was one particular cloak that caught her attention. It was dark in colour and made of long, pliable feathers, quite unlike any of the other cloaks. Altogether, the feathers appeared suspiciously similar to those of the moa—a giant, extinct New Zealand bird. Ms Te Kanawa compared them with a photograph of eight moa feathers found in a sealed cave near Christchurch in 1865. These feathers were donated to the Southland Museum and Art Gallery in 1992, and were a mixture of light- and medium-brown colours. The feathers from the Hawke’s Bay cloak were identical.

Unfortunately, there was a problem: moa had become extinct by the seventeenth century. Rangi Te Kanawa estimated the Hawke’s Bay Museum cloak to be approximately 150 years old, based on its weaving style. This left a 350-year hiatus before the cloak was woven. It seemed unlikely that feathers of a dead bird would be stored for almost half a millennium before being used; however, moa research has been obscured by anecdotal evidence and controversy since their remains were first discovered by Europeans approximately 150 years ago. Well-preserved moa remains, mostly bones but also some soft tissues, have been found, so perhaps a 150-year-old cloak of moa feathers taken from preserved remains was not completely beyond the realms of possibility.

But there was an alternative explanation. Moa belong to a group of birds called ratites. This group contains a mixture of extinct and extant birds, including the kiwi, emu, cassowary, ostrich, rhea, and elephant bird. All are flightless, most are large, and the majority are restricted to the Southern Hemisphere, having diverged from a common ancestor between 80 and 130 million years ago. Although there is still debate about the amount of their genetic relatedness, moa are morphologically similar to the emu and...
their feathers have similar structural characteristics. The individual fibres (vanes) lack barbules—microscopic structures that interlink vanes and maintain feather shape. As a result, they have loose, open-webbed feathers that form a ‘shaggy’ coat, similar to mammalian fur. The feathers of both birds also vary greatly in size and colour, depending on the individual bird and location on the body; however, most are between 10 and 20 centimetres long, and range from fawn to a deep reddish-brown. Thus, distinguishing between feathers of the two species is difficult, particularly because relatively few moa feathers have been found, and even fewer have been described in detail.

If the Hawke’s Bay Museum cloak was made of moa feathers, the implications were extraordinary. If they turned out to be emu, however, there still remained the question of why. What was Australia’s avian emblem doing in New Zealand 150 years ago? The identity of the feathers was ambiguous enough to warrant further investigation, and Roger Mulvay, CEO of the Hawke’s Bay Museum came up with a novel solution. He contacted Dr Trevor Worthy, New Zealand’s moa expert. Dr Worthy, in turn, suggested that they also enlist the help of Professor Lambert, an expert in ancient DNA analysis of New Zealand’s native species. The project that eventuated—using DNA to identify the feather species—was an example of how molecular science can be used to rediscover history.

In October 2004, Professor Lambert travelled from Auckland to Hawke’s Bay to sample the cloak. Sensitive DNA analysis techniques meant that only a fragment of tissue was needed, so the feathers could be sampled without visible damage. Wearing sterile gloves and a facemask, Professor Lambert removed a two-millimetre fragment from the base of several exposed feather quills across the cloak. This section of the feather could be removed easily, and was chosen because it contained cells with abundant DNA.

Back in the Allan Wilson Centre’s Auckland laboratory, Dr Huynen prepared the quills for genetic analysis. Sample preparation was done in a laboratory specifically designed for ancient DNA research. Separation of amplified DNA and ancient samples is crucial to the success of ancient DNA analysis, because ancient DNA is characterised by poor preservation and relatively few numbers of surviving molecules. In contrast, modern DNA is intact, in great abundance, and can contaminate reactions at any time from the original sampling process to the final analysis. Consequently, strict anti-contamination procedures and highly sensitive extraction and amplification
techniques are needed to detect ancient DNA.

From such minute feather fragments, Dr Huynen was able to obtain large amounts of genetic information. His target was a short stretch of extra-nuclear DNA contained within mitochondria—tiny organelles that generate energy for the cell. Dr Huynen selected a region of mitochondrial DNA that is common to most animals, but which has enough variation to identify separate ratite taxa. After amplification and sequencing, Dr Huynen entered the results into an electronic database and compared them with known sequences from many other animals, including each member of the ratite group.

The results were interesting.

All six samples that yielded DNA aligned perfectly with emu DNA sequences. The cloak was not moa, after all. Dr Huynen was not surprised, because of the discrepancy between the age of the feathers and the cloak. But the origins of the emu feathers remained unsolved. There was still a final twist in the story.

Fifty-five kilometres North-East of Auckland is Kawau Island, a 2000-hectare site of historic and ecological importance. In 1862, Kawau Island was bought by George Grey, New Zealand’s governor. Grey, an Australian soldier, explorer, and politician, had also worked in South Africa before moving to New Zealand. From 1862-1888, he developed his Kawau Island house and gardens on the island into a botanical and zoological legacy of his time in Australia and South Africa. Emu, wallabies, zebra, antelope, monkeys, and various types of exotic plants were introduced to the island in an effort to trial new species of potential economic value. The remains of this menagerie are still evident today. Peacocks and kookaburras still inhabit the island, and wallabies have adapted so successfully that they have been declared a pest. Ironically, the original populations of this wallaby species, the Tammar wallaby, are now extinct on mainland Australia, and the Kawau Island stock represents a valuable store of genetic diversity that can be exported back to Australia.

As for the emu, there are none left on Kawau Island now. In the past, perhaps they were recognised as an ideal substitute for moa feathers. Cloak designs and materials have evolved to reflect New Zealand’s changing natural and social environments and incorporated the feathers of both native and introduced bird species. The cultural significance of the cloaks remained unaltered, however, and emu feathers may have symbolised a link with the past when moa were an important resource.

Moa are still shrouded in mystery. Anecdotal evidence of recent sightings aside, it seems certain that none remained when Europeans first arrived; however, what caused their extinction remains contentious. Both climate change and human intervention have been suggested, with the latter being more likely according to the archaeological record. Over the last 150 years, moa have been the subject of exhaustive research in an attempt to elucidate their natural history. Ancient DNA extracted from subfossil remains has provided an insight into their genetic origins and species organisation. Some mummified remains, including a preserved head and limbs, have been found with feathers still attached, but the similarity of the feathers from the Southland Museum and those from the Hawke’s Bay cloak seems to warrant a closer examination. So far, no one has successfully, and conclusively, extracted DNA from moa feathers.

The results of the feather cloak project have raised more questions than answers. According to Professor Lambert, this is the nature of good science. Emu, as well as being living relatives of the moa, have a certain amount of historical significance for New Zealand, and the project’s novel application of scientific techniques to an historical puzzle revealed an interesting fragment of New Zealand’s near and distant past.
Immune System Variation and Conservation of Tuatara

Why are some individuals more susceptible to disease than others? The answer often lies in the genes, particularly those in the Major Histocompatibility Complex, or MHC. The MHC forms a central part of the immune system in vertebrates. These are the genes that recognise when the body is invaded by a foreign organism and stimulate an immune response.

MHC genes are the most polymorphic genes known in vertebrates. In any given population, few individuals will share exactly the same MHC type, leading to differences in disease resistance between individuals. When populations decline, this genetic variation may be lost, and the population may be more susceptible to new diseases and disease epidemics.

MHC genes are also thought to play a role in how individuals choose mates. Experiments on mice, humans and fish have found that individuals prefer the scent of mates with a differing MHC genotype to their own, a phenomenon arising from a link between MHC molecules and the olfactory system.

Most of what we know about MHC genes comes from studies on fish, birds and mammals, but few studies have investigated MHC genes in reptiles. At Victoria University we are addressing this by examining the MHC region in tuatara. We are aiming to find out how MHC genes are organised in tuatara, how variable they are in wild populations, and whether tuatara choose mates on the basis of their MHC genotype.

**MHC variation in tuatara populations**

We have compared MHC variation in the largest tuatara population on Stephens Island with that of the small population on North Brother Island. North Brother Island tuatara are genetically distinct from all other tuatara populations and are regarded as a different species. North Brother Island is a tiny, 4ha rock stack in Cook Strait and is home to around 450 adult tuatara. The population was almost exterminated in the 19th century due to over-collection by naturalists and curiosity hunters, and construction of a lighthouse on the island.

Our research has shown that this population has extremely low levels of variation at MHC genes. Similarly low levels of variation are also found at other types of genetic markers, probably as a result of the 19th century bottleneck. Because of their low MHC variation the North Brother Island tuatara may be less well-equipped to counter novel diseases, so the current conservation strategy of establishing new populations of this species is important to ensure its future survival.

In contrast to North Brother, the Stephens Island population of >30,000 tuatara has a highly variable MHC, as one would expect for a large population. We now aim to investigate what underlies this high diversity on Stephens Island by correlating MHC variation with mate choice and pathogen loads.
Love Thy Neighbour - and share their Diseases!
Social connectivity and parasite transmission in tuatara populations.

Wildlife disease is a major threat for the conservation of threatened species, with diseases such as chytridiomycosis the cause of widespread population declines in Australian frogs. Yet, as a consequence of their negative effects on host fitness, parasites can also play a key role in the evolution and ecology of their hosts. To aid management of wildlife disease, we need a better understanding of natural host-parasite interactions, and what factors influence parasite transmission. One potential factor is social connectivity of host populations.

If a close friend or someone you live with has a cold, there is usually a good chance you will catch their cold. Just as behaviour and social interactions can dictate disease transmission in human societies, similar principles can be applied to understanding transmission processes in wildlife populations. However, in the past, this has often been overlooked when it comes to understanding the evolution of host-parasite interactions, and in the broader context of managing wildlife disease outbreaks. At the Allan Wilson Centre at Victoria University of Wellington, and in collaboration with Flinders University (Adelaide, Australia), we are investigating how social connectivity influences parasite transmission dynamics in populations of tuatara (Sphenodon punctatus) on Stephens Island (NZ).

When epidemiologists first began to understand parasite transmission dynamics, individuals were assumed to randomly mix with one another. However, just like human societies, animal populations can form complex behavioural associations, which can vary from individuals defending their own territories, through to the formation of large social groups. These non-random contacts may play a central role in driving transmission dynamics. For instance, more dominant individuals may monopolise mating opportunities, and consequently increase their exposure to sexually transmitted diseases, whilst also facilitating their spread among sexual partners. One way of understanding how social organization can influence the dynamics of parasite transmission is through social network analysis.

An example of a social network

Social networks are essentially a map of social interactions within a population. Individuals are considered to be nodes, and interactions are the ties that link these nodes together to form a matrix or map of interactions within a population. Using social network analysis, we can calculate a number of properties of both the network as a whole, and the individuals within the network to measure social connectivity and flow. By viewing populations as a social network, we may determine how social connectivity drives the dynamics of parasite transmission, and whether some individuals may act as ‘superspreaders’ by driving disease transmission.

Although, little is currently known of the behavioural ecology of tuatara, a study by Jennifer Moore (Victoria University of Wellington) in parallel with this study is increasing our knowledge about the social structure of this species. Tuatara exhibit stable, long term territories, where individuals defend their own home range area. While females tend
to occupy a small home range area around their burrow, larger male territories are actively defended through aggressive encounters.

Tuatara are host to a number of parasites, including blood-sucking ticks (*Aponomma sphenodonti*), chigger mites that feed on tissue and lymph (*Neotrombicula sphenodonti*), blood parasites that live within the blood cells (*Haemogregarina tuatarae*), and intestinal worms (*Hatterianema hollandei*). We have been measuring parasite loads of tuatara within three study areas on Stephens Island over the past two years, whilst Jen Moore has obtained detailed observations of territory structure and mating behaviour of these individuals. Tick loads can vary from zero, through to extremely high levels, with over 500 ticks found on one tuatara! Similarly, the small mites that infest tuatara, are most abundant over the summer months when they can infest tuatara in their thousands, appearing as bright orange patches. We have found that these ectoparasite loads are higher on larger males, which may indicate some role for social dominance, as larger males are typically more dominant.

Social network analysis will allow us to examine the role of social connectivity and social position in the patterns of parasitism observed. By understanding what factors drive parasite transmission dynamics in socially structured populations, we may be better equipped to manage any future disease threats to tuatara, and also apply these principles to other species. By understanding how social structure influences parasite transmission, we can gain further insights into the role of parasites in the evolution and ecology of host social organization.

**Acknowledgements:**

Thanks to the Holsworth Wildlife Endowment, ARC/NHMRC Network for Parasitology, Flinders University, Wildlife Disease Association (Australasian Section) and the Australian Society for Herpetology for financial support. Thanks to Ngati Koata and the Department of Conservation for their support.

**Stephanie Godfrey**
PhD
Victoria University of Wellington and Flinders University, South Australia
Stephanie.Godfrey@flinders.edu.au
Evolution and Neutral Theory

Sampling penguins in Antarctica

It is nine o’clock on a December morning, and as a glittering sun shifts in the Antarctic sky, a colony of Adélie penguins—Antarctica’s unofficial emblem—is helping New Zealand scientists come a step closer to solving one of biology’s most significant and controversial questions.

Dr Craig Millar of the Allan Wilson Centre for Molecular Ecology and Evolution is taking blood samples from the penguins in order to calculate their rate of DNA mutation—and whether it differs from the rate of molecular evolution. This is part of an ongoing project, which has already attracted substantial international interest, because it attempts to answer one of the central questions in biology: does the rate of evolution equal the rate of mutation?

The project – to determine what causes rapid DNA evolution – is ambitious. It involves using a combination of both modern and ancient penguin samples to directly measure their DNA mutation and evolutionary rates. This tests one of evolution’s central dogmas: neutral theory. Many people are familiar with the theory of evolution, which advocates survival of the fittest through selection of advantageous traits that arise from DNA mutations. Neutral theory, a component of evolutionary theory, proposes that many DNA mutations in non-coding DNA (DNA that does not produce a functional protein) occur randomly, and are not influenced by selection pressures. According to this theory, mutation rates and evolutionary rates are equal for non-coding genome regions. However, the Allan Wilson Centre’s previous research on Adélie penguins revealed an evolutionary rate that was eight times higher than other bird genera. So, what is the rate of evolution? Do different species have different evolutionary rates?

If these questions are to be answered, there is no better place than Antarctica. At Cape Bird in the subcontinent’s north-east corner, a set of conditions has combined to create ideal circumstances for measuring both mutation and evolution. In the Antarctic permafrost below existing Adélie penguin colonies are the serially preserved remains of their ancestors, some as old as 36 000 years. Because of the cold, dry, and constant conditions, and because these remains are stacked like clocks in a geological chronology, they contain well-preserved ancient DNA that can be extracted and screened for changes over defined time periods, giving the rate of evolution. In addition, the penguins’ living relatives return every year to breed, providing an abundant source of modern DNA. Blood samples taken from nesting penguins and their chicks can be screened for DNA changes to estimate the rate of molecular mutations over one generation.

The only drawback is accessibility: the penguins are in Antarctica, after all. To
get there, Allan Wilson Centre scientists fly to Scott Base on the northern side of Ross Island, where novices complete a two-day Antarctic field-training course before heading out into the field. Cape Bird hut is a 45-minute helicopter ride north from Scott Base, following the icy contours of the land. The field-site consists of an eight-person hut, tethered to the rocky shore above the beach that overlooks the penguin colony. The site is surrounded by glaciers, cliffs, and dense sea-ice.

According to Dr Millar, working in Antarctica is "not bad", although he is apprehensive before each visit. The success of the 20-day field trip is largely his responsibility, and although the trip is planned long in advance, certain factors cannot be predicted. "Sometimes, a lot of things are out of your control", he says.

Timing is crucial for every stage of the project. The Antarctic research season runs from November to February when daylight is almost unlimited and the sea-ice is at a minimum. For Dr Millar and his research team, however, this already short time is reduced further by the Adélie penguins’ breeding season. In addition, field-work is at the mercy of the weather. Transport from New Zealand to Antarctica via US aircraft, and within Antarctica via helicopter, can only occur in good conditions, and even a couple of days’ bad weather can delay field-work beyond the point of feasibility. Scientific equipment must be shipped to Scott Base one month before field-work begins, and any breakages jeopardise the success of the entire field season.

And then there are the penguins themselves. Although they are an ideal source of both modern and ancient DNA, taking samples is not always easy. Every summer, the birds travel south across the thawing sea to Cape Bird. Unlike other penguin species, Adélie penguins will not nest on ice, preferring instead exposed ground where they build shallow, rock nests. Each female lays two eggs, and parents take turns incubating and feeding the chicks. As one penguin parent heads seaward across the 80-kilometre stretch of pack-ice to reach open water, the other stays with the nest. Eventually, they swap roles after performing an elaborate greeting ritual to re-establish identity. This ‘incubation routine’ is useful for the Allan Wilson Centre scientists, because it allows them to recognise family groups. Only blood from identified families can be used to measure the rate of DNA mutation over a generation. Thus, Dr Millar and his team observe the colony and its incubation routines from a distance of ten metres to identify parents and offspring for sampling. Families on the colony’s periphery, rather than the centre, are targeted to minimise disturbance.

Dr Millar and his team wait until they see an adult pair greet each other at their nest, before capturing both parents and their two chicks. All four birds are weighed and blood samples are taken from a vein in the leg or foot. The parents are banded to prevent re-sampling. The whole process must be...
done as quickly and as efficiently as possible to minimise distress to the penguins—and the researchers. Adult Adélie penguins weigh between four and six kilograms and are adept fighters if provoked. Gloves are not usually worn during the sampling process because they make sampling difficult. Unfortunately, bare arms do not provide much protection against bites and scratches from the penguins’ sharp beaks.

Once again, limited time is available for collecting DNA samples from the penguin colonies. By the time the chicks are four weeks old, they begin to stray from their nests and eventually group together to form a crèche. Once this happens, it is too late to continue taking blood samples because families can no longer be identified. If an adequate number of samples have not been taken, the project must wait until the next year.

Collecting ancient DNA samples is easier because, apart from the limits of the Antarctic field-season, there are no other time restrictions—and dead birds cannot bite. Bone samples are taken from the subfossil remains buried in layers of soil, ice, and guano beneath the Cape Bird and other colonies. To prevent geological and molecular contamination, bones must be excavated from the iron-like Antarctic permafrost without mixing layers. Gathering material to estimate the rate of evolution is a tiring process that requires energy, patience, and endurance in the harsh Antarctic conditions.

Despite the unpredictable weather, time constraints, and the sharp beaks of the penguins, the physical demands of working in Antarctica are outweighed by the mental challenges. According to Dr Millar, the continent’s sheer size and emptiness can be overpowering. “You have to become mentally used to it”, Dr Millar points out, “as well as getting used to the cold and five to ten kilograms of extra clothing”.

Perhaps the most difficult aspect of working in Antarctica is the isolation. Communication with the outside world—particularly while in the field at Cape Bird—is limited to a radio. Over Christmas, the time of each year’s field season, this sense of isolation can turn into loneliness.

Fortunately, the drawbacks of working in Antarctica are countered by the rewards, which are both scientific and personal. The continent’s grandeur is mirrored in the ground-breaking scientific research that occurs there. Several seasons of field-work will cumulate in mid-2005, when analysis of the ancient and modern penguin samples from the Allan Wilson Centre’s most recent field-trip will be completed. Six hundred and seventy penguin families have been sampled, making the study significantly larger than any other estimation of DNA mutation rates. So far, the penguins’ DNA mutation and evolution rates appear equal; however, both Dr Millar and Professor Lambert
stress that these results are preliminary and they are keeping an open mind about the possible implications. If the Adélie penguins’ rates of mutation and evolution are equivalent and neutral theory is correct, why does this particular penguin species evolve more quickly than other birds? Do evolutionary rates differ between species? Are they constant, or do they change over time? The Adelie penguin study may raise more questions that it can answer immediately, and this is precisely what makes it such valuable scientific research. This year, the project will be extended internationally to compare the rates of evolution in other species. An otherwise unlikely combination of slowly-evolving tuatara, ancient Peruvian mummies, and Antarctic silverfish found in snow petrel regurgitations will be used, among other species, for this purpose.

The applications of a calibrated molecular clock are diverse, and encompass both practical and theoretical uses. New or refined knowledge about the genetic and evolutionary relationships between organisms is germane to conservation genetics because of the increased understanding it can provide about the Earth’s biota. Applying the results to hominid bones may reveal human origins and global migration patterns. In forensic science, a reliable measure of DNA mutation rates would clarify whether mismatched DNA samples between family generations are, in fact, mutations, and thus identify parents and children more accurately.

Just as important as the scientific benefits of Antarctic research are the personal rewards for the scientists who work there. The beauty and emptiness of Antarctica is impossible appreciate by viewing photographs or listening to second-hand descriptions. “Just seeing the size and vastness of the place is one of the best bits of the research”, Dr Millar says.

The Allan Wilson Centre’s Adélie penguin research project takes place in one of the Earth’s most extreme environments and uses extraordinary material to answer questions that are critical to our understanding of evolution and the fundamentals of life. This outcome justifies the amount of preparation that is necessary to achieve it; however, Antarctic field-work is not without its frustrations and difficulties. Rising temperatures, increased atmospheric and marine pollution, and depleting ozone levels are already evident in Antarctica, and have caused changes to the Adélie penguins’ breeding patterns. Consequently, Antarctic field-work is becoming increasingly recognised as an endeavour with global scientific importance, rather than simply a romantic adventure into an unconquerable, frozen land.

Meg Heaslop
Science Journalist
Massey University, Albany, Auckland

Further reading:


Canine DNA Profiling

For many people, the words ‘DNA identification testing’ are synonymous with police work, forensics, and private investigation. Now, dog pedigrees and lost pets can be added to the list. A new service offering paternity tests for dogs will safeguard prospective buyers from spending thousands of dollars on non-pedigree animals, and will also help owners identify lost pets.

Molecular biologists at Massey University are developing a consultancy program that will create canine DNA profiles from a simple cheek swab to establish the paternity of pure-bred dogs.

When canine paternity testing was introduced in America in 1998, 10% of dogs claimed to be purebred were found to be of mixed pedigree, emphasising the need for a conclusive identification system. Genetic pedigree verification is now becoming common practice in many countries, and has been mandatory for all purebred dogs in Australia from January 2006.

In New Zealand, The Allan Wilson Centre Genome Service will allow breeders to verify the pedigree status of their stud dogs, and help buyers to avoid the problem of false pedigree claims. “Sometimes accidents happen even in the most stringent breeding programs,” Canine Services coordinator Jennifer Anderson said. “This test can verify the true sire, so buyers can be sure that they’re getting what they pay for,” she said.

The test will use a combination of genetic markers, or signature DNA sequences, found within the genome of each dog. These genetic markers have two versions of a DNA sequence (called alleles) at each locus, with one inherited from each parent. Using buccal swabs of cheek cells, the markers will be extracted and analysed according to their molecular size to create a profile of the dog’s genotype. The combination of these alleles is unique to individual dogs and can be used to distinguish the animal from others, as well as to trace the lineage of pedigrees. Unlike tags, tattoos, and other identification methods, DNA is present in all living cells and cannot be removed, lost, or altered, allowing for an unambiguous identification to be made.

The Massey team has successfully tested their methods by genotyping 100 animals of different breeds, including full families of Dalmatians, Samoyeds, and Golden Retrievers.

The service will also create a database of all genotyped dogs, reducing the need for multiple testing and saving time and money, and a website will allow owners to check the genotyping results. Costs will be further reduced through the use of a new “state-of-the-art sequencing machine”, which will provide a high-throughput service within one to two weeks, Ms Anderson said. “Our new machines not only offer quality results from the smallest samples but they also run at a fraction of the cost of the older machines,” she said. The profits from this service will be put back into research programs in the Allan Wilson Centre, with a long-term goal of funding genetic testing of inherited diseases in pedigree dogs.

The service has been operational since February 2005.

Meg Heaslop
Science Journalist
Massey University
Albany, Auckland

An example of a canine genetic analysis test form.
Recent Publications


Stevens, M.I., and Hogg, I.D. (2006), Contrasting levels of mitochondrial DNA variability between mites (Penthalodidae) and springtails (Hypogastruridae) from the Trans-Antarctic Mountains suggest long-term effects of glaciation and life history on substitution rates, and speciation processes. *Soil Biology & Biochemistry*, 38: 3171-3180


(Recent publications can be viewed by visiting the Allan Wilson Centre: [http://awcmee.massey.ac.nz/publications.htm](http://awcmee.massey.ac.nz/publications.htm))