Report on the prospects and potential value of Scientific research on human remains from New Zealand held in the British Museum

Phillip Endicott BA (Oxon), MA (UEA), MSc (Oxon)

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0.1 Science and the repatriation of human remains

This report marks an important stage in the movement to deaccession human remains held in British institutions. Decisions already taken to repatriate remains from various sources have been marked by a curious lack of interest in receiving detailed evidence of exactly what the potential loss to Science, the rest of humanity, and future generations of the claimant communities themselves, might be.

There appears to be a prevailing attitude amongst many people associated with promoting the process of repatriation that there is very little scientific potential in the human remains under consideration. The promulgation of this *opinion* has been assisted by the fact that some of the most critical developments in the field of molecular biology are so new that they have not yet reached the publication stage or are not widely known. So in the place of informed debate there tends to be a reflection on the history of physical anthropology, which is often seen as tainted by its 19^{th} century beginnings. This is lamentable because at the very moment in history that the future of these remains is being debated, science is just beginning to offer powerful methods to work with them to the potential benefit of everyone, including the claimant communities.

Perhaps the most useful information that science can generate from human remains, under the present circumstances, pertains to provenience. With techniques of isotopic analysis and molecular biology, it is possible to obtain many types of data concerning the life history of an individual, including their ultimate origin. Population genetics can show a general provenience for remains, important to deciding whether the individual has been correctly assigned in a museum catalogue. Having decided the correct geographical region, modern surveys of the local geology of that region, can provide isotopic analysis with sufficient information to circumscribe the range of their movements throughout life; for example, a close examination of local isotopic fingerprints was able to confine Otzi the European iceman to within 60km of his resting place (1). It is, therefore, surprising that this form of investigation is not utilised to decide whether human remains are what the labels say they are, prior to decisions to repatriate them.

This is a critical issue, because whatever the basis for a decision to repatriate human remains, it is of the utmost importance to ensure that remains are returned to the correct community. This is even more so if the basis of the decision to return them is their *sacred* status to the community concerned. To return human remains to another group would amount to sacrilege to the real potential claimants, and potentially to the recipients as well.

As genetics has the greatest potential to recover information from human remains, which can be both scientifically and morally (with regard to epidemiology) important, this report is heavily skewed towards this aspect of research. It does mention other aspects of research but expects these to be well covered already by more generalised and readily available literature.

The layout is intended to explain in some detail one current aspect of research using human remains (population genetics) that is already well established, but the principle applies to approaches for improving the epidemiology of disease,

which ultimately relates directly to human genetic diversity. This is followed by an assessment of the physical remains from New Zealand (Aotearoa), as to their suitability for research, contextualised in a brief history of Polynesia, and the conclusions.

0.2 Genetic Research

0.2.1 Introduction

0.2.1.1 Common assumptions in the age of meta-genomics

The field of human genetics based on sequence data, revealing the building blocks of amino acids rather than analysis of proteins created out of those components, is a very young discipline. The entire human genome was only sequenced for the first time at the turn of the century and much remains to be understood about the information it contains. Even when all the gene functions have been mapped, there will remain crucial lacuna to be filled concerning exactly how regulation of gene expression varies under particular circumstances. In other words, although we now have a complete blueprint of the genetic components contained within the human genome, we have very little understanding of how they all function, particular their interaction. Yet, a commonly held perception amongst non-geneticists is that this *decoding* means there is nothing left to discover about the human genome.

A related misconception is that if we have the complete picture from the sequencing of modern, pristine, DNA, there is little point in investigating *ancient* samples, by which we define anything that is degraded and damaged by post-mortem processes of decay. This misses the critical point that it is human genetic *diversity* that is important to understanding the history and future of our species, including our relationship to disease, both infectious and non-infectious.

The demographic perturbations associated with the start of the modern era means that critical components of that diversity are only preserved in the remains of humans of that time. And recovering that diversity may prove vital to understanding our past and future. Unlike other sources of ancient DNA, for example, Late Pleistocene megafauna which exist in large numbers in the permafrost regions of Canada, these human remains are a finite resource and they can never be replaced.

0.2.1.2 The moral importance of genetic diversity

A general principle for the right to study lost diversity contained in human remains comes from a need to comprehend the nature of the epidemiology of infectious disease. If we are not in a cosy co-existence with pathogens but rather an *arms race,* as many scientists believe, then we need to recover all the data possible about previous large-scale epidemics. In the case of viruses, whose evolution is extremely rapid, the time scale required for important information

is very short. In this way, the retrieval of genetic information about the 1918 flu pandemic from victims' remains is already informing scientists about how this virus mutated into a lethal variety, which killed millions of people worldwide. In the face of new strains of bird flu, lethal to humans, understanding how such viruses jump the species barrier may save tens of millions of lives.

So, at the most universal level there exist clear cut moral and ethical grounds for the use of human remains for genetic research, as the outcome may save millions of people, worldwide, from the indiscriminate effects of exposure to lethal pathogens. The key issue here is knowledge of human genetic diversity, in this case, how and why resistance arose, and what it means to the future of our species. But there are aspects of non-infectious disease regimes that are extremely pertinent to the people of Polynesia, who have a natural predisposition to obesity and its related problems, especially type II diabetes, amongst the highest rates in the world. The descendants of those Polynesians who did not succumb to the initial effects of European contact are now suffering serious problems from lifestyle changes of the last 100 years. Understanding why this problem should be so acute may benefit from genetic knowledge of the past to cast light on the disease schedules of the present and reduce the burden to future generations.

0.2.1.3 The potential role of human remains held in museums

This is where the human remains from the colonial era held in museums across the world come sharply into focus, because they represent a vital snapshot of human genetic diversity at or around the time of contact with the European colonial powers. With recorded rates of population loss as high as 99% of the early contact populations, human remains are the only record we have for some peoples; for example, the main populations of the Andaman Islands in the Bay of Bengal (2).

But perhaps, the most valuable potential contribution of genetics to the debate about human remains is that of provenience. It is one thing to say that something is from a group of people but quite another thing to prove it. But this is exactly what genetics can do. Given sufficiently detailed genetic data it is possible to demonstrate inter-generational connections; i.e. the genetic parents of a particular child. It is therefore surprising that many institutions have not sought advice on this subject, particularly where provenience may be uncertain. With human remains, this should be presumed to be the case until proved otherwise due to the propensity for the duping of collectors, wherever profit is concerned.

0.2.1.4 Technical considerations

The value of genetic information gained from human remains is dependent upon the amount and quality of information retrievable. It also depends on the spectrum of contemporary data available for comparative purposes, which is rapidly being compiled for many areas of the world in great detail. Moreover,

the recent development of rapid parallel sequencing machines (pyrosequencing) now make it feasible to characterize the entire genome of an individual in a single laboratory in a matter of weeks. The price of doing this will rapidly reduce to the point that it becomes quite routine in genetic research. This is a quantum leap, because the data from the entire human genome is capable of producing answers to any question conceivable.

Pyrosequencing can also be used to great effect on ancient DNA, and the genome of a Neanderthal is currently being reconstructed from a Croatian sample dating to the Upper Palaeolithic period of European prehistory (3). This is highly significant because it means that with some modifications the same technology can be used successfully on human remains also. With the quality of the DNA present in many colonial era remains being orders of magnitude better than the Neanderthal currently being sequenced, it is now possible to recover total genomic DNA from human remains held in museums. Of course, doing so would depend on the research agenda in hand, but the point is that, for suitable remains, there is no limitation on what can now be done.

The results of whole genome sequencing from contemporary samples can however already benefit research into ancient DNA. There wealth of genetic markers now available can be used to test hypotheses regarding health and ethnicity, linked to population history, which is in turn responsible for the genetic diversity underlying components of the disease schedules. Until recently, testing large numbers of genetic markers in ancient DNA was arduous and technically challenging. However, recent methodological developments make it possible to rapidly test up to 40 markers in a single assay with automated interpretation (4), permitting full integration with contemporary surveys.

The other technical problem that has held back human aDNA research is potential contamination of the samples from external sources. However, this is much less of an obstacle when working with populations with highly specific genetic markers, such as Polynesians, because contamination is much easier to filter out. Also, a novel methodology has recently been developed that can physically select for ancient DNA over modern contamination and which can retrieve DNA templates that would normally be beyond the reach of traditional molecular biology techniques (Brotherton et al., submitted).

0.2.1.5 An outline of the case for genetics

There follows a general explanation regarding the how and why human genetic diversity develops. The choice of human population genetics as an example is, to some extent, arbitrary, but the implications are clear and can be applied to the much larger subject of medical genetics just as readily. However, the subject of human migration history is of such general interest, its very inclusive nature raises issues of who represents the interests of other parties in this debate, including those indigenous peoples whose views are not necessarily the same as the political representatives acknowledged by the government of a particular country.

The natural extension of this theoretical explanation for the potential utility

of human remains is followed by a scientific assessment of the New Zealand (Aotearoa) holdings of the British Museum. This is set within the context of outstanding questions about the settlement and history of Polynesia that provide clear cut applications for the extant human remains, based on the current methodologies available to research into ancient bio molecules.

0.2.2 The application of human remains to tracing human migration

0.2.2.1 Theoretical background

Evidence of ancient human dispersal and settlement is preserved in the genomes of its inhabitants, in the form of randomly accumulating mutations, which are passed down through the generations. Provided that there has been limited long range movement of people since the initial settlement of distinct geographic regions it is possible to differentiate, genetically, between the populations of these regions by the arrays of mutations arising locally. Besides the ongoing differentiation driven by mutation, random genetic drift, whereby population expansions and contractions will tend to catalyze the random sorting of genetic frequencies in populations, induces and exaggerates further differences between them. When considering mutations that have strictly maternal or paternal modes of inheritance (mitochondrial and Y-chromosomal DNA, respectively), individuals sharing identical combinations of mutations at any single locus are grouped under the same haplotype (from the Greek haplo for single). When haplotypes are grouped together (into haplo-groups) by their likeliest descent order they form a tree because successive generations of mutations can be traced back to root types, which due to random chance have been preserved in the current population.

Using a high enough number of informative molecular markers it is possible to find a geographic separation between different branches of trees constructed in this way. This phylogeographic approach can in principle provide clues regarding both the peopling of a region of interest and about subsequent population movements into it, as well as bearing witness to demographic processes of the past, such as bottlenecks and expansions. By examining the mitochondrial or Y chromosomal genomes of individuals representing different positions on the tree inferences can be made about the movements of women and men in both space and time, respectively. The resolution obtained is dependent upon the amount of informative markers available and tested.

As a daughter population occupies a new territory local region-specific variations arise on the background of those gene alleles that were randomly taken by the migrating unit. More technically speaking, haplo-groups that have reached different world regions randomly accumulate additional mutations, which identify new region specific sub-clades. Applying a phylogeographic approach, it is then possible, with certain limitations, to reconstruct common ancestors between populations to reveal information about their origin and spread (see Fig. 1).

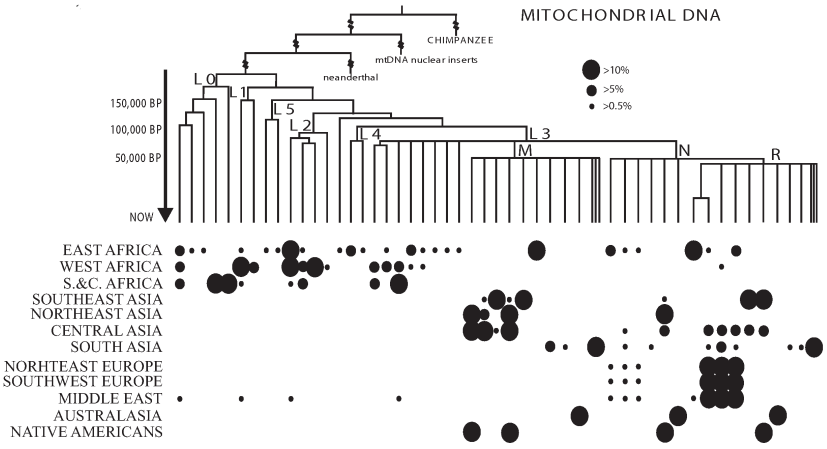

Figure 1: Phylogeography of main haplogroups of human mtDNA, showing the strong regional groupings. Most of the mtDNA of Polynesia shares an origin in East Asia with those components of the Native American mtDNA deriving from haplogroup R. This pattern reflects the migration of humans from Africa, eastwards, around 40-60kya. The general principle is that moving eastwards from Africa the mtDNA clades vary according to geographical distance, reflecting a single rapid expansion of humans, followed by local differentiation. This strength of this pattern is due to the limited subsequent movement between regions. The origin of the dominant lineage in Polynesia has now been identified, and to date has only been found in Taiwan (5).

0.2.2.2 Example 1: Population history of the Andaman Islands

Using human remains from the Natural History Museum in London, a recent study (6) of the Andaman Islanders recovered sufficient genetic diversity to reveal a contiguity between culture, genetics and linguistics in the archipelago that separates the main tribal groups (Fig. 2). The largest group (Greater Andamanese) was studied entirely from human remains due to a total extinction of most tribes by disease during the first 50 years of occupation (2). In other words, the contemporary data for the Andamans does not contain sufficient diversity to represent these important insights into prehistory, which show that the various groups have been living, side by side, but separately for thousands of years. Estimates from genetics for the dates of separation will now provide a unique insight into the rate and direction of language shift amongst these populations whose dialects are Palaeolithic in origin. The surprise was to find that some of the mtDNA of the Andaman Islanders also exists in East India, and appears to have been taken there by a back migration ~25,000 years ago (see Fig. 3) .

0.2.2.3 Example 2: Provenience of Tasmanian human remains

In the case of the Tasmanians held at the NHM in London the author was able to demonstrate that one cranium belonged to an individual with East Asian mtDNA (Phillip Endicott, unpublished data). This does not necessarily mean the individual is wrongly assigned, as it is conceivable that this mtDNA relates to a phase of human migration that has left no genetic evidence in Australia. Alternatively, it is also possible that an Asian woman entered into the aboriginal community, from a Japanese or Chinese fishing vessel, who are known to have frequented Tasmanian waters prior to European contact. This form of miscegenation is not unknown in Australia where European mtDNA is found amongst the surviving contemporary indigenous people (7).

A second collection of Tasmanian remains have been investigated with surprising results. The mtDNA of these displays a clear link to that found today in the islands of New Britain (Phillip Endicott, unpublished data). However, their position on the phylogenetic tree is ancestral to the contemporary mtDNA of Melanesia, suggesting a deep separation of the two related lineages. These results would benefit from finding a match in another collection, but in the current climate of repatriation this may never be possible. Resolution would be most important because the results suggests either a hitherto unknown period of human migration to Tasmania (akin to the Andamans and East India), or the remains are not from Tasmania after all. Whatever their true identity, the conundrum highlights the need for scientific investigation of all human remains prior to decisions concerning repatriation.

0.2.2.4 An irreplaceable resource

These examples show how important a resource human remains are for the study of human population genetics. The examples used are drawn from work

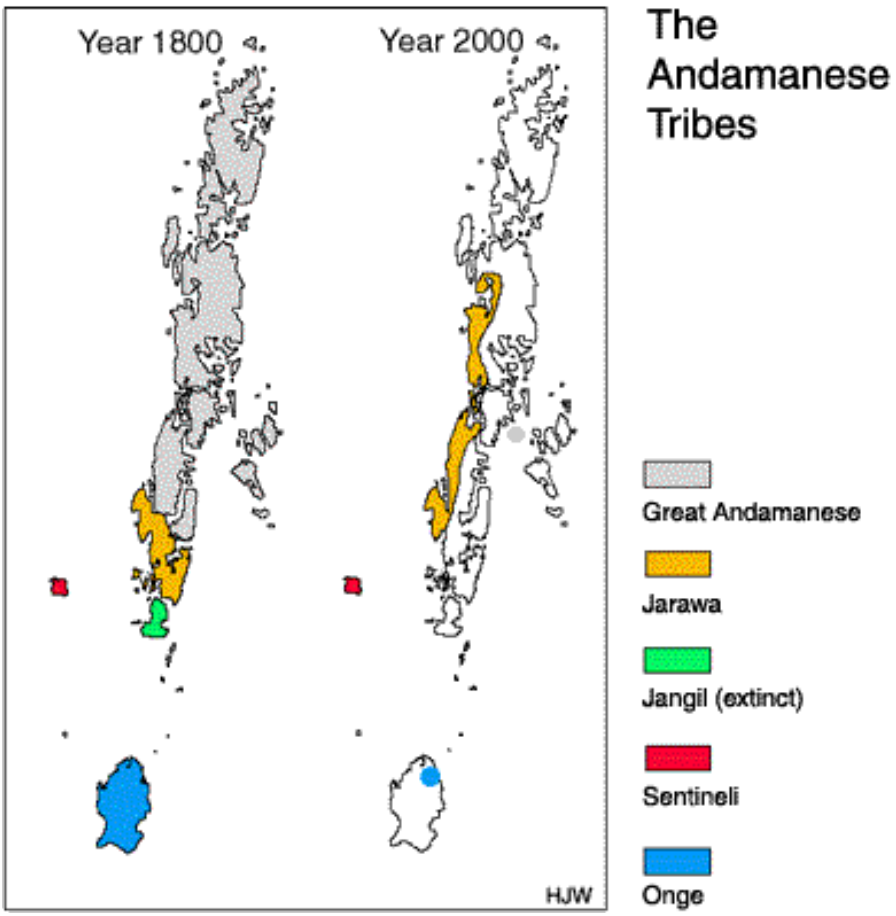

Figure 2: Map of the various ethnic groups in the Andaman Islands at the time of permanent European settlement and at the beginning of the 20^{th}century. Note the disappearance of the majority Greater Andaman populations, destroyed mainly by infectious disease. Without the use of human remains, the true history of these peoples would be lost forever.

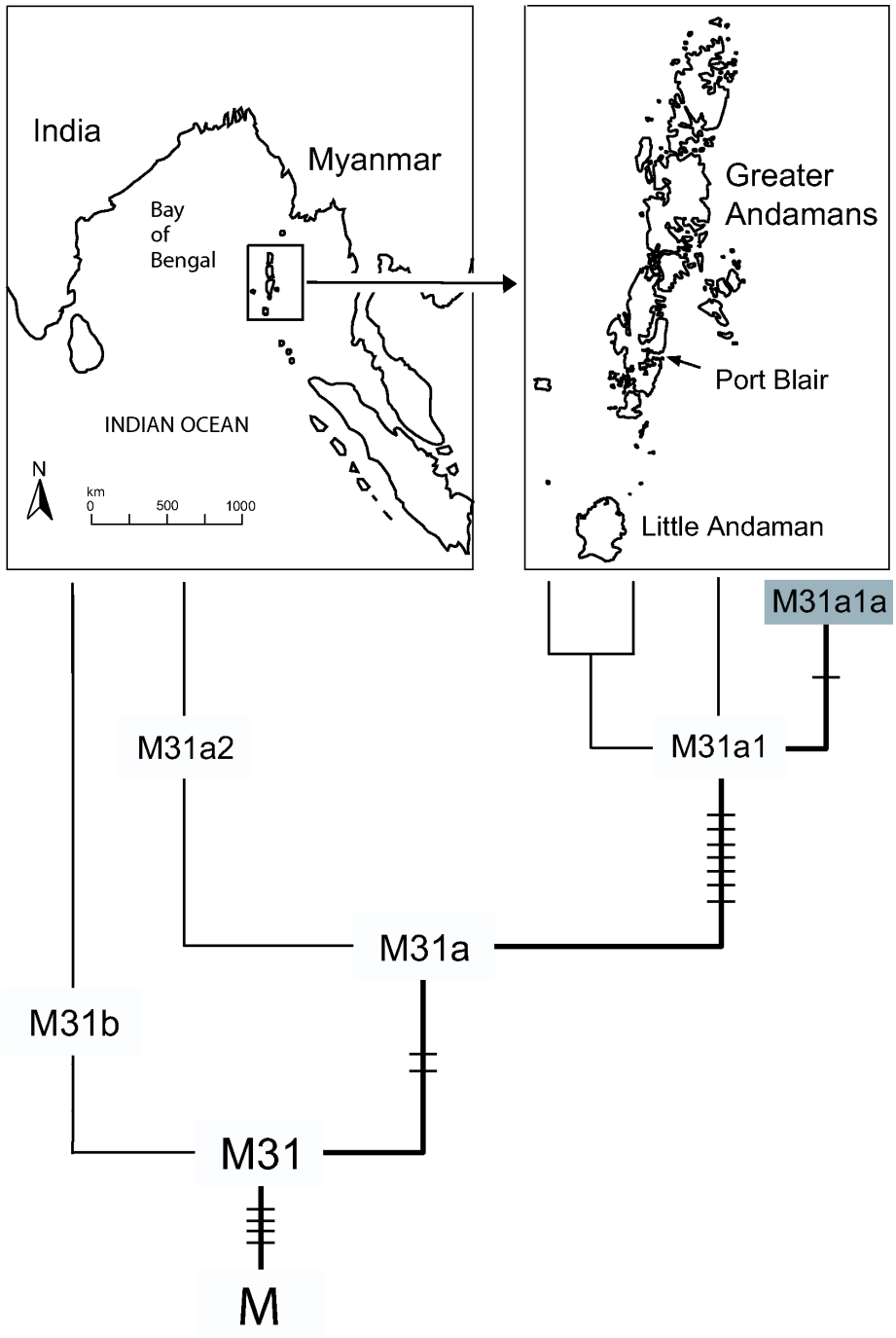

Figure 3: Details of phylogeography of mtDNA haplogroup M31 in India and the Andaman Islands. The parsimonious explanation for this distribution is that M31 in East India shares a common origin with that found in the Andamans, in South East Asia ~30,000 years ago. Within the Andamans different parts of M31 are located in the two main linguistic groups; Greater Andamanese and Onge/Jarawa.

on just one loci, mtDNA. However, the nuclear genome contains several orders of magnitude more information, which can provide much more detail on population histories, particularly over the longer term, as well as insights into the epidemiology of both infectious and non-infectious disease regimes.

The single most important take home message is that much of this evidence of human evolution has either been lost or become obscured since the demographic perturbations associated with the modern era. The only possible source for the recovery of this diversity are the human remains held in museums. This resource can never be replaced, and as the movements and mixture of peoples in the modern era accelerates, these genetic signals will be become ever more diluted. If these resources are put beyond use or compromised (for example, by heavy contamination by people with similar DNA) such that they become unsuitable for future research, the history of our species will never be complete, with large areas of a complex jigsaw permanently lost.

0.3 Human remains from Aotearoa/New Zealand held in the British Museum

0.3.1 Suitability for Research

0.3.1.1 The survival of DNA

After death DNA is degraded by micro organisms and endonucleases within the body. The degradation is initially rapid, and then, once these actions associated with tissue decay have ceased, begins to slow. How long DNA survives in a stable condition in the longer term is largely determined by the mean temperature, acidity and humidity affecting the remains. If the remains have been buried the survival of usable DNA will be greatly determined by the conditions of the soil in which they are interred, which can lead to rapid deterioration, particularly where ground water comes repeatedly into contact with them. This is difficult to model retrospectively, but the effects of temperature are easier to predict (8).

The over-arching effect of temperature on DNA survival, means that in the hotter regions of the world, special conditions of preservation are required for successful recovery after as little as 100 years. Yet in exceptional conditions, bones from temperate climates have produced trace quantities from before the last ice age (3). This survival of bone and therefore DNA is enhanced in an alkaline environment, but adversely affected by an acid one. If, however, a body is defleshed shortly after death, or there exists some other method of arresting decay (for example, burial under hot ash), the survival of DNA will be greatly improved.

0.3.1.2 The special treatment of human remains

These obstacles to recovering DNA from archaeological contexts renders human remains stored in museums a unique source of genetic information. This is because they have been stored for most of their post-mortem existence in stable,

and temperate climatic conditions, thereby enhancing the survival of DNA. Moreover, many of the remains underwent special treatments relatively soon after death (e.g. the preservation of trophy heads), which will have substantially reduced the degradation of the endogenous DNA.

In general, therefore, the remains from museums are a prime resource for genetic research and, in many parts of the world (tropics and acidic environments), often represent the *only* access to past human genetic diversity. The author has conducted some preliminary work on teeth from Maori remains and the quantity of DNA surviving from the 19th century is the highest amongst 500 worldwide human samples processed so far (Phillip Endicott, unpublished data). This exceptional level of preservation is entirely consistent with the hypothesis that museum remains enhance the preservation of human DNA.

0.3.1.3 Preserved human heads (*mokomokai*)

The preservation of human heads is a special case in point, because the processes of decay have been arrested very quickly post-mortem by the removal of soft tissues, followed by drying and smoking. Similar trophy heads have been worked on by the author with success. These came from Torres Straits Islands, and despite many years spent in the Men's Houses in tropical conditions, have yielded good quality DNA offering important insights into the prehistory of this region (Phillip Endicott, unpublished data).

However, *mokomokai* are likely to be greatly superior in the quality of preserved DNA because they are in a much better condition, presumably due to the temperate climate from where they derive. This is borne out by the near pristine condition of the previous extractions of DNA from Aotearoa.

Visual examination can never be a substitute for a physical one, but experience of working on some hundreds of human remains facilitates an appraisal that all seven heads appear to be in an excellent state of preservation of an order of magnitude higher than those from Torres Straits. This suggests that the chances of recovering a full range of nuclear DNA markers are excellent. This level of information survival, in conjunction with the methods of recovery now available, would be capable of delivering a full genotype of each individual from mitochondrial, Y chromosomal and nuclear DNA.

In a randomly mating population, a sample of 30-40 individuals will be sufficient to recover the total genetic diversity of that group. If there are any substantial barriers, cultural or physical, to genetic interaction, then there will exist additional structure, requiring extra sampling. Therefore, the number of *mokomokai* in existence (~200) are an exceptional resource for research because they have the potential to provide a detailed picture of human genetic diversity in Aotearoa during the early colonial era, representing all the elements of the founding populations (*canoes*).

The presence of hair on these heads is useful for isotopic analysis of diet, because signatures can be obtained along the entire length of hair shafts, which can predict quite accurately, the type of food eaten during the time it took to grow. Other patterns of isotopic signatures can be found in both the bone and

teeth, some of which are laid down during the early years of life. In this way, it is possible to establish the main elements of dietary intake during childhood and adult life. This can show whether someone lived inland, on the coast, or was a seasonal perambulator. In the absence of written provenience for the *mokomokai* this data, combined with the genetic information, should be able to reconstruct some of the population structure of early colonial Aotearoa.

0.3.1.4 Unmodified skeletal remains

These comprise 9 pieces of bone in various states of preservation. The following list provides the UIN (unique identifying number) followed by an estimate, on a scale of 1-10, of the utility of the piece for scientific research. This is based on the density of the bone and general surface condition. The number is orientated around the likelihood of obtaining DNA, whereas it is assumed that generally the material will be useful for isotopic analysis, even when DNA is difficult to retrieve. For comparison, the equivalent score for *mokomokai* is 10.

1. Oc1895,-396 length of bone (8)
2. Oc1895,-397 length of bone (8)
3. Oc1895,-627 length of bone (2)
4. Oc1895,-628 length of bone (6)
5. Oc1895.,629 length of bone (4)
6. Oc1895,-630 length of bone (0)
7. Oc1895,-631 length of bone (0)
8. Oc1895,-633 length of bone (2)
9. Oc1895,-634 length of bone (4)

Those pieces with a zero score have been subject to repeated wetting and drying and probably regular cycles of temperature difference too. This suggests that they have spent an extended period of time underground in a location that has seasonal changes in groundwater levels. Therefore, these are likely to be much older than the early colonial period. It is difficult to assess the way in which the bone has been cut without the use of a microscope and so it is not possible, by eye, to decide if the cutting of the lengths was a cultural modification or a utilitarian process.

0.3.1.5 Culturally modified skeletal remains

Although these items are not subject to a repatriation claim, they have been assessed on exactly the same basis as the unmodified remains, as follows:

1. Oc1850,-0206.1 bone flute (6)

2. Oc1896,-930 bone flute (6)
3. Oc1716 bone flute (6)
4. OcLMS.145 bone flute (6)
5. Oc1922,0607.1 bone tiki (8)
6. OcNZ.156 bone tiki (8)
7. OcNZ.157 bone tiki (8)
8. Oc1944,02.207 fish hook point (7)
9. Oc.2057 fish hook with bone point (8)
10. Oc.4317 fish hook with bone point (8)
11. Oc.NZ.188 bone fish hook (4)
12. Oc.NZ.189 bone fish hook (4)
13. Oc.NZ.190 bone fish hook (4)
14. Oc.NZ.191 bone fish hook (4)
15. Oc.NZ.192 bone fish hook (4)
16. Oc.NZ.193 bone fish hook (4)
17. Oc.NZ.195 bone fish hook (4)
18. Oc.NZ.196 bone fish hook (4)
19. Oc.4294 ear-ring of teeth (8)
20. Oc.4295 ear-ring of teeth (8)
21. Oc.NZ.162 ear-ornament of teeth (6)
22. Oc.1981,Q.1359 necklace of teeth (7)

0.3.2 Possible applications of research on the remains

0.3.2.1 The settlement of Remote Oceania

Archaeological evidence suggests that the settlement of Remote Oceania, including Polynesia, began ~3,500 years ago by people characterised by a distinct cultural assemblage known as the Lapita complex (9). This is surprising given the evidence for long-distance sailing in Island Melanesia dating back at least 20,000 years. It is unlikely that the islands of Polynesia were settled by chance, and such *events* were probably preceded by long periods of seasonal exploration (10). However, the evidence of early occupation is often too ephemeral to survive,

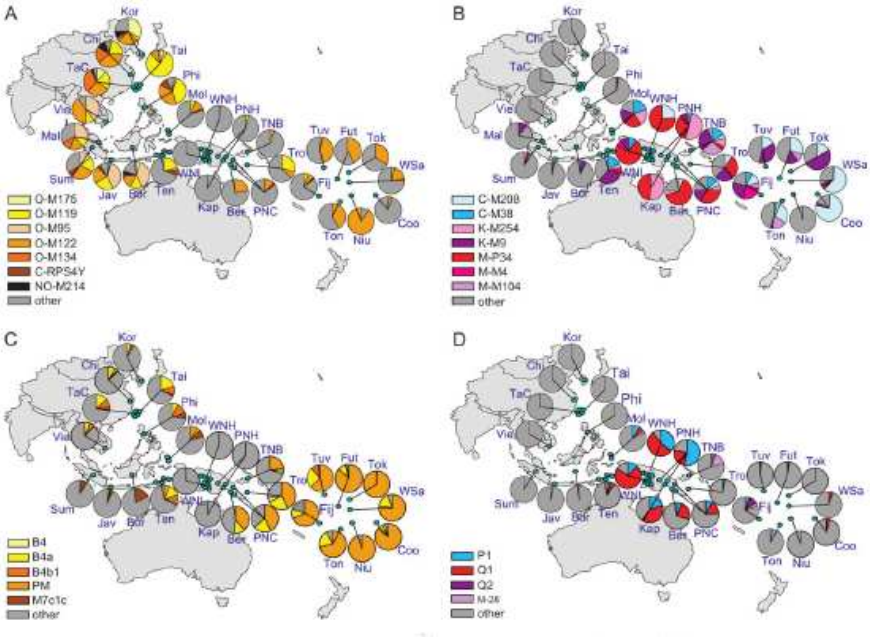

Figure 4: Gradients of frequencies of Y chromosome haplogroups (top) and mtDNA haplogroups (bottom) from Asia to Polynesia (from Kayser et al., 2006). For both mtDNA and Y chromosomal DNA, the left hand picture displays those haplogroups that have an origin in Asia, and the right hand one shows those with an origin in Melanesia. The paternal and maternal contributions are skewed towards Melanesia and Asia, respectively.

particularly where the settlement was coastal and took place at times of reduced sea level.

Key to the debate concerning the settlement of Polynesia from a genetic perspective is whether it was a single rapid process of people coming from Asia (home of Austronesian languages spoken throughout Polynesia), the so-called *fast train* hypothesis (11), or a result of a much slower process involving intermediate stopping points along the way, resulting in the genomes representing an admixture with populations from Melanesia (12) (13).

The genetic interpretation for the settlement of Polynesia relies on the contemporary populations only, and therefore may be skewed in as yet unknown directions. However, the overall picture is fairly well constructed, and the conclusions are striking: ~94% of mtDNA found in Polynesia derives from Asian sources, whilst 66% of Y chromosomes are from Melanesia (14), thereby providing support for elements of both hypotheses.

The dates from archaeology for the settlement of Polynesia, however, do not fit particularly well with those from genetics. Those from mtDNA are broadly

consistent because the origin of the Polynesian specific clade (haplogroup B4a1a1) is calculated to be 6,400-11,800 years ago (5). There is though, a disagreement from dates made from the Y chromosome, which suggest a consistently older origin for the Melanesian paternal lineages *within* Polynesia (14). This is surprising, and suggests that the demographic history of the region is more complex than previously thought.

Increased sampling can only assist the resolution of these debates because additional diversity will help assess if the rate of mutation in the Pacific Islanders is sufficiently different to account for these disparities, and will certainly reduce the confidence margins.

0.3.2.2 The late settlement of Aotearoa/New Zealand

Aotearoa is a special case in Polynesia because there is no evidence of permanent settlement until ~800-1200 years ago (9), making it the last major landmass to be settled. Although there are stories of human remains collected in early colonial days that have a different morphology to the that of Polynesians, there has been no solid evidence provided. If there were different waves of settlement, followed, by genetic admixture, a survey of early contact human remains may find evidence of it, because a rare type will more likely be lost in a demographic reduction.

The genetic heritage of the population of New Zealand is less well known than the rest of Polynesia but due to the recent date of settlement, with sufficient genetic information it will be possible to identify the population(s) of origin for migrants and estimate whether this was an event or a process involving sustained movements back and forward to the place of origin.

The loss of genetic diversity since the European presence in the region limits the accuracy for reconstruction of times and patterns of settlement. The effect of this is illustrated by a moderate increase in sample size in a recent study of mtDNA, resulting in a doubling of the estimate of founding females to ~190 (15).

The most incisive approach to population genetics is to sample mitochondrial, Y-chromosomal, and autosomal DNA together. In particular, the use of neutral markers on the main pairs of chromosomes (autosomes) can reconstruct the number and location of populations supplying the founders. This is usually a much better representation of the real picture because markers such as mtDNA and Y chromosome can be adversely affected by non-random mating. For example, a single 4^{th}century Irish chieftain is thought to be responsible for the majority of Y chromosomes in one province of Ulster. Research with autosomal DNA can only be conducted with the better preserved human remains, for which purpose *mokomokai* seem perfectly suited.

0.4 Conclusions

The overwhelming majority of human remains from New Zealand held in the British Museum are suitable for investigation with the techniques of isotopic analysis of diet and molecular biology. Of those subject to a claim for repatriation, only 4 out of 16 items appear to be marginal in quality. The 7 preserved heads are all in an excellent condition and likely to provide outstanding quality of DNA. Naturally, this can neither be proven nor refuted without a pilot study on these particular items, but the combination of the climate of place of origin, long-term museum curation, and evidence from less well-preserved trophy heads already investigated by the author, suggests that the assessment would be borne out in the event of genetic analysis taking place on these particular *mokomokai*.

The prospects for the quantity and quality of data retrievable from these human remains are greatly enhanced by recent methodological developments in ancient DNA, which now allow for routine retrieval of nuclear and mtDNA from reasonably well preserved remains. These important advances mean that extremely detailed population histories can be reconstructed from a resource such as *mokomokai*. The wider framework of research possible in the future includes the epidemiology of the recent increase in type II diabetes in Polynesia, which has ramifications for present-day Polynesians and the wider global community.

Therefore, the importance of these and other human remains for genetic research cannot be over-emphasized. The genetic structure of the world at the commencement of European colonial contact contained a history of our species, since the time it evolved in Africa, tracing the migrations out of African and across the entire globe. The last of these adventures was the settlement of Polynesia, which makes it particularly amenable to study, and of considerable importance. Large numbers of indigenous peoples succumbed to a combination of pathogens and aggression, and those that survived were assimilated and or relocated from their traditional lands. This process has erased much of the genetic signature in place at the start of the modern era, which can never be recovered without the help of these extant and irreplaceable human remains.

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