Mitochondrial DNA variation in the Fijian Archipelago

By

Diana A. Taylor

Submitted to the graduate degree program in Anthropology and the Graduate Faculty of the University of Kansas in partial fulfillment of the requirements for the degree of Master of Arts.

_____

Chairperson Dr. Alan J. Redd

_____

Dr. James H. Mielke

_____

Dr. Maria E. Orive

Date Defended: April 5, 2012

The Thesis Committee for Diana A. Taylor
certifies that this is the approved version of the following thesis:

Mitochondrial DNA variation in the Fijian Archipelago

_____
Chairperson Dr. Alan J. Redd

Date approved: April 18, 2012

ABSTRACT

The purpose of this thesis is to explore the evolutionary history of Fijians with respect to maternal ancestry. Geographically situated between Melanesia and Polynesia, Fiji has been a place of cultural exchange between Pacific Islanders for at least three thousand years. Traditionally, Fijians have been classified as Melanesians based on geography, culture, and skin pigmentation. However, Fijians share much in common linguistically, phenotypically, and genetically with Polynesians.

Four questions motivated my research. First, are Fijians more Melanesian or Polynesian genetically? Second, is there a relationship between geography and genetic variation? Third, are Rotumans more similar to Fijians or Polynesians? And lastly, are Lau Islanders more similar to Fijians or Tongans? I used maternally inherited mitochondrial DNA (mtDNA) as my tool of investigation. In addition, I used various lines of anthropological evidence to synthesize my conclusions. I examined a sample of over 100 Fijians from five island populations, namely: Viti Levu, Kadavu, Vanua Levu, the Lau Islands, and Rotuma. In addition, my sample included two Melanesian and two Polynesian island populations.

The results of the analyses place Fijian mtDNAs intermediate between Melanesians and Polynesians. However, the Fijians appear slightly more Polynesian than Melanesian based on a Multidimensional Scaling (MDS) plot and a comparison of frequencies of Near-Oceanic versus Asian mtDNA lineages. I did not detect a genetic-geographic association. Other factors besides geographic distance shaped maternal migration patterns. This is the first genetic study of Rotumans. The Rotumans are very similar to Polynesians genetically. The Rotuman sample has little genetic diversity suggesting that a maternal genetic bottleneck occurred at some point in their history. Finally, Lau Islanders are as diverse as the Fijian mainlanders, which supports a hypothesis that the Lau Group historically functioned as a crossroads for Fijians and Tongans. Lau Islanders are more similar to Tongans than they are to other Fijian Islanders (excluding Rotuma) based on a MDS plot and a comparison of frequencies of Near-Oceanic versus Asian mtDNA lineages.

This thesis is dedicated to my family, who support me through all the 'chutes and ladders' of life: My mother and grandmother for watching over me; my father and second mother, Vicky, for endless support and love; my brothers, Grant and Dane, for keeping their big sister in line; my aunts, Rita and Patricia, for taking me under their wings when I needed guidance; and finally, a special thanks to Steven and Michaela for helping me survive this thesis and graduate school in general. I love you all.

ACKNOWLEDGEMENTS

First and foremost, I thank the participants of this study; their curiosity to learn more about their maternal ancestry was refreshing and I hope the results from this project offer them personal insight. I would also like to sincerely thank Dr. Anand P. Tyagi, and The University of the South Pacific for making this study possible.

Two of my committee members, Dr. James H. Mielke and Dr. Maria E. Orive, helped to make this thesis a better product and I am incredibly thankful for their support. Special thanks to Dr. Geetanjali Tiwari for collecting biological samples and interviewing participants. Also, thanks to Michaela Beals for assisting with biological sample processing.

Finally, and most importantly, I would like to thank Dr. Alan J. Redd for guiding me and this project and providing an endless amount of support. Dr. Redd assisted me with all facets of this project and I am incredibly thankful to have had the privilege of working as his graduate student.

This project was partially funded by a Carol A. Clark award from the University of Kansas Department of Anthropology. Thank you to the members of the Carol A. Clark committee for offering support to this project.

Table of Contents

CHAPTER 1: INTRODUCTION 1
CHAPTER 2: BACKGROUND 5
2.1 ARCHEOLOGY IN THE FIJIAN ARCHIPELAGO 5
2.1.1 History of Near Oceania 5
2.1.2 History of the Lapita Expansion in Near Oceania 7
2.1.3 History of the Lapita Expansion in Remote Oceania 10
2.1.4 History of the Lapita Expansion in the Fijian Archipelago 13
2.1.5 Vanuatuan influence on the islands of Fiji 19
2.1.6 Polynesian influence on the islands of Fiji 21
2.2 LANGUAGE STUDIES IN THE FIJIAN ARCHIPELAGO 26
2.2.1 Papuan languages 26
2.2.2 Austronesian language expansion 27
2.2.3 Fijian language 28
2.3 KINSHIP ORGANIZATION IN THE FIJIAN ARCHIPELAGO 33
2.3.1 Post-marital residence rules in Oceanic populations 33
2.4 BIOLOGICAL ANTHROPOLOGY IN THE FIJIAN ARCHIPELAGO 35
2.4.1 Near-Oceanic mitochondrial DNA 35
2.4.2 Mitochondrial DNA associated with the Austronesian expansion 42
2.4.3 The Austronesian expansion: Evidence from the mitochondrial DNA 9 base pair deletion 47
2.4.4 Austronesian colonization of Remote Oceania 48
2.4.5 Sex-biased genetics in Austronesian-founded populations 50
2.4.6 Biological studies of the Fijian people 51
2.4.7 Fijian genetics 55
CHAPTER 3: MATERIALS AND METHODS 60
3.1 MATERIALS 60
3.1.1 Study participants 60
3.1.2 Island populations examined 60
3.2 LABORATORY METHODS 61
3.2.1 Protocol for mtDNA sample processing 61
3.2.2 MtDNA sequencing 62
3.2.3 MtDNA haplogroup assignment 63
3.3 METHODS OF ANALYSIS 64
3.3.1 Haplogroup frequency classification 64
3.3.2 Haplotype sharing 64
3.3.3 Measurements of diversity within populations 65
3.3.4 Measurement of diversity among populations 66
3.3.5 Measurement of multivariate distances 67
3.3.6 Tree phylogeny 68
CHAPTER 4: RESULTS 70
4.1 MITOCHONDRIAL DNA RESULTS 70
4.1.1 Mitochondrial DNA (mtDNA) haplogroup assignment 70
4.1.2 Haplogroup frequency visualization 75
4.1.3 Haplotype sharing 76
4.1.4 Measurements of diversity within populations 78

4.1.5 Measurements of diversity among populations 81
4.1.6 Measurement of multivariate distances 83
4.1.7 Tree phylogeny 85
4.1.7 Statistical evaluation of samples 88
CHAPTER 5: DISCUSSION 96
WORKS CITED 112

Table of Figures

Figure 1. Micronesian, Melanesian, and Polynesian islands (Kahuroa, 2010) *1*
Figure 2. Map of the Fijian Archipelago (Duerr, 2006) *2*
Figure 3. Near Oceanic (Kirch, 2000) *6*
Figure 4. Mount Witori Volcano of New Britain, Bismarck Archipelago (Jago and Boyd, 2005) *8*
Figure 5. Distribution of early Lapita sites in Near and Remote Oceania (Kirch, 1997) *11*
Figure 6. Near and Remote Oceania with Lapita sites highlighted (Irwin, 2009) *12*
Figure 7. Early Lapita sites in the Fijian Archipelago (About.com, 2012) *14*
Figure 8. Vanuatu and Lakeba Island of the Lau Islands (About.com, 2012) *20*
Figure 9. Vanua Levu, Fiji and the Mulifanua site in Samoa (About.com, 2012) *22*
Figure 10. The Lau Islands of Fiji and the Tongan Archipelago (About.com, 2012) *23*
Figure 11. Rotuma Island, Samoa, and Tonga (About.com, 2012) *25*
Figure 12. Distribution of mtDNA lineages in Oceania (Kayser et al., 2010) *36*
Figure 13. New Britain, Bougainville, and the Solomon Islands (About.com, 2012) *37*
Figure 14. New Britain, Santa Cruz Isl., Solomon Isl., Vanuatu, and Fiji (About.com, 2012) *39*
Figure 15. West NG Highlands, PNG Highlands, and Melamela (About.com, 2012) *40*
Figure 16. WNG High/Lowlands, Mussau, New Britain, and Bougainville (About.com, 2012) *41*
Figure 17. Distribution of B4a (PM included) and B4a1a1 (Friedlaender et al., 2007)* *45*
Figure 18. Tuvalu, Taiwan, and the Philippines (About.com, 2012) *47*
Figure 19. Evaluation of Stress *67*
Figure 20. Diversity values with geographic location (About.com, 2012) *80*
Figure 21. Population pairwise Fst values *82*
Figure 22. Two dimensional monotonic MDS plot of pairwise F_{ST} distances (Stress=0.03977) *82*
Figure 23. Mantel randomization test correlation plot using all nine island samples *84*
Figure 24. Mantel randomization test correlation plot using island sample subset *85*
Figure 25. Neighbor-joining tree *87*
Figure 26. MtDNA haplogroup frequency results for this project (n=13) *89*
Figure 27. Proportion of Asian and Near-Oceanic lineages present in Melanesian samples *89*
Figure 28. MtDNA haplogroup frequency results of the Solomon Island sample *90*
Figure 29. Haplogroup frequencies of Tonga *91*
Figure 30. Proportion of Asian and Near-Oceanic lineages present in Tonga *91*
Figure 31. Haplogroup frequencies of Samoa *92*
Figure 32. Proportion of Asian and Near-Oceanic lineages present in Samoa *93*
Figure 33. Haplogroup frequencies of Fijians *94*
Figure 34. Proportion of Asian and Near-Oceanic lineages present in Fijian sample *95*
Figure 35. Proportions of Asian & Near-Oceanic lineages *96*

Figure 36. Clinal increase in Asian mtDNA lineages from west to east (About.com, 2012) *97*
Figure 37. Proportion of Asian to Near-Oceanic mtDNA lineages *102*
Figure 38. MtDNA haplogroups frequencies from Rotuman sampling..... *103*
Figure 39. mtDNA haplogroup frequencies from Lau sample *107*

Table of Tables

Table 1. M27a & M27b haplogroup information..... *37*
Table 2. M28, M28a, & M28b haplogroup information *39*
Table 3. P1 haplogroup information..... *40*
Table 4. Q1 & Q2 haplogroup information..... *42*
Table 5. PM haplogroup information..... *46*
Table 6. B4a1a1 haplogroup information..... *46*
Table 7. B4b1 haplogroup information..... *47*
Table 8. Variable sites and haplogroup assignment for sequences..... *75*
Table 9. Haplogroup frequencies by count and percentage..... *76*
Table 10. Number of haplotypes shared between populations..... *77*
Table 11. Number of Near-Oceanic haplotypes shared between populations *78*
Table 12. Measurements of diversity..... *79*
Table 13. Significantly different pairs of populations (+): Population differentiation test *81*

CHAPTER 1: INTRODUCTION

The Fijian Archipelago is the ideal location to test Pacific Island human migration hypotheses. Fiji was one of the first homes to the Proto-Polynesian people (Kirch, 2000). Geographically situated between Melanesia and Polynesia, Fiji was and is today a place of exchange between neighboring island chains (Kirch, 2000) (See Fig. 1).

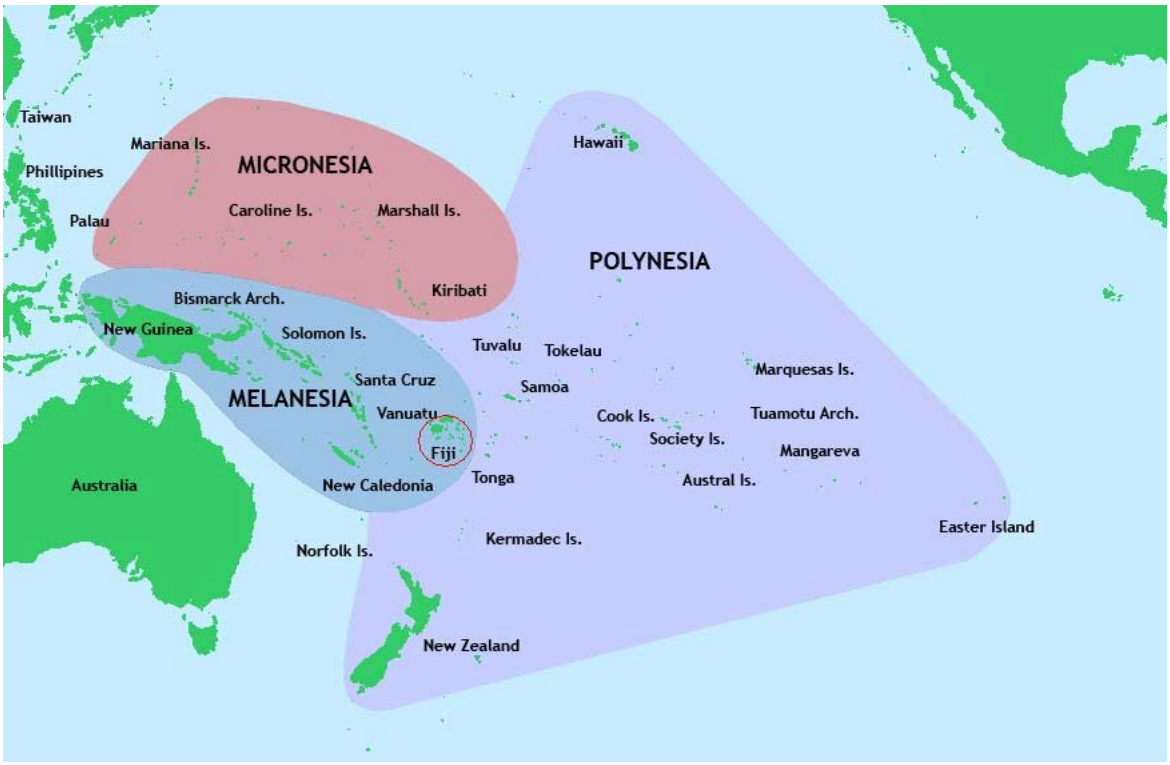


Figure 1. Micronesian, Melanesian, and Polynesian islands (Kahuroa, 2010)

Fijians have traditionally been classified as Melanesian based on their cultural practices and some morphological features (Spriggs, 1997). However, Fijians share much in common linguistically (Geraghty, 1983), phenotypically (Howells, 1933), and genetically (Kayser et al., 2006) with Polynesian populations. Despite all anthropological evidence

for variation, population geneticists have yet to focus attention exclusively on Fijian populations. As a result, there has been limited population genetics sampling within Fiji (Kayser et al., 2006; Sheppard, 2011). Fijian mitochondrial DNA (mtDNA) has been used for multiple population studies; however, sample sizes have been small (fewer than 60 sequences total) and generally limited geographically to Fiji's main island, Viti Levu (Kayser et al., 2006) (See Fig. 2).

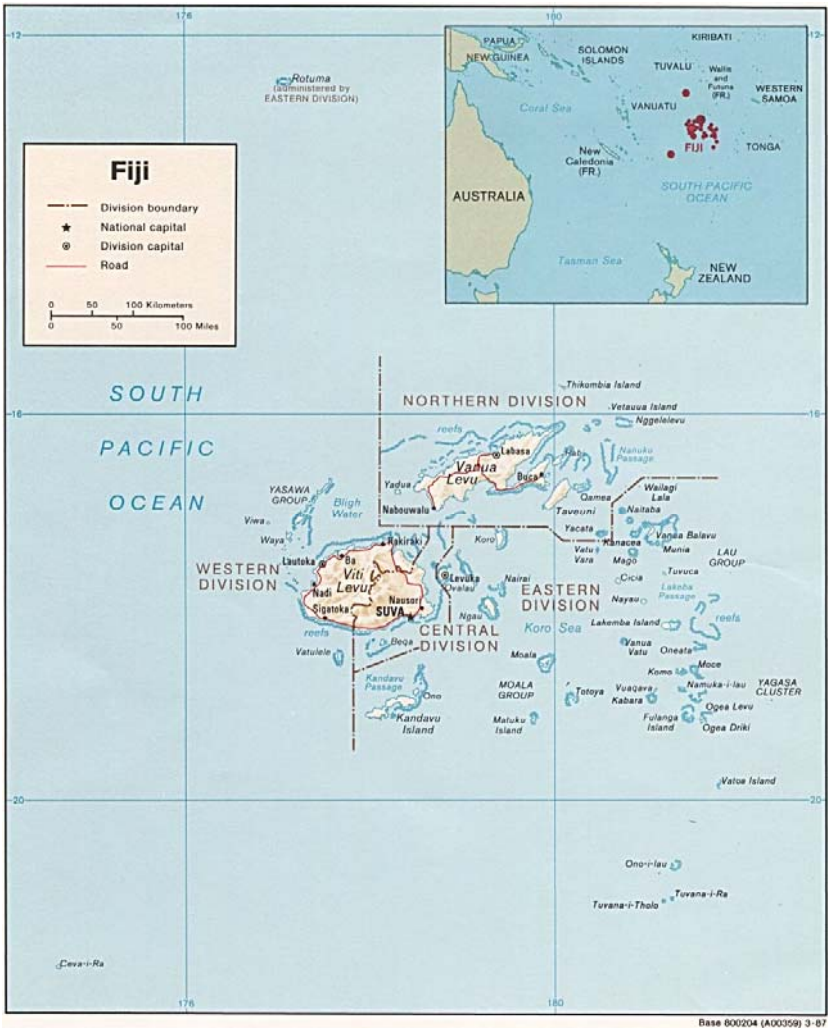


Figure 2. Map of the Fijian Archipelago (Duerr, 2006)

This thesis will examine human mitochondrial DNA variation among the major Fijian islands: Viti Levu, Kadavu, Vanua Levu, the Lau Islands, and Rotuma. This thesis will also reveal the genetic structure of Rotuma, a Fijian-Polynesian outlier. Taken together, this research will provide anthropologists with a better understanding of key human migration movements throughout Fiji and the Pacific Ocean in general.

This thesis proposes to answer the following questions:

1. **Are Fijian mtDNAs more Melanesian or Polynesian (i.e., where do they fit genetically)?**

Past sampling efforts with limited sample size indicate that Fijians are intermediate and share haplotypes common in both Melanesia and Polynesia (Kayser et al, 2006).

2. **Is there a relationship between genetic and geographic variation?**

This thesis will explore the relationship between geographic location and mtDNA population structure.

3. **Are Rotumans mtDNAs more Fijian or Polynesian? Does Rotuman mtDNA structure align with their origin myth?**

Rotumans believe that they are Samoan and Tongan derived (Howard, 1985). Linguists believe that Rotumans are Fijian derived (Geraghty, 1983; Pawley, 1996). In order to lend weight either way, the Rotuman population must be compared with local Fijian populations and Polynesian populations.

4. **Are Lau Islander mtDNAs more similar to Fijian or Tongan mtDNAs?**

The Lau islanders are the Fijian population predicted by linguists and archeologists to be most related to Polynesians (Geraghty, 1983; Kirch, 2000; Schutz, 1978). This population has a long history of working alongside Tongans in the sandalwood trade

industry (Kirch, 2000). Given the Lau Islander's close geographic proximity and historical ties to Tonga, we should expect to find that Lau Islanders are more genetically similar to Polynesians than Melanesians. Whether this relationship is reflected in their genetic structure has yet to be determined.

This thesis is organized into five additional chapters. Chapter 2 gives an overview of the archeological, linguistic, cultural, and biological research that has been performed by other researchers on the populations studied in this thesis. Chapter 3 provides details on the sampling efforts, laboratory protocols, and statistical analyses that were performed. Chapter 4 presents the results from all analyses. Chapter 5 discusses the results of the analyses and addresses each thesis question outlined above. Finally, Chapter 6 summarizes all conclusions reached.

CHAPTER 2: BACKGROUND

2.1 ARCHEOLOGY IN THE FIJIAN ARCHIPELAGO

2.1.1 History of Near Oceania

For at least 37,000 years, Near Oceania was sparsely inhabited by small human populations. This first colonization of the Pacific occurred during the Pleistocene when humans were able to access Sahul, a large continent joining Australia, New Guinea, and Tasmania (Birdsell, 1977; Kirch, 2000; Sheppard, 2011). Multiple independent migrations allowed humans to reach both the Bismarck and Solomon Archipelagos (Anderson & Clark, 1999; Redd & Stoneking, 1999). Today this large group of island chains is collectively referred to as 'Near Oceania' (See Figure 3) (Green, 1991).

AR Kirch PV. 2010.
Annu. Rev. Anthropol. 39:131–48

Figure 3. Near Oceanic (Kirch, 2000)

Humans continued to inhabit this region for at least 37,000 years while the other islands of the Pacific remained unoccupied (Sheppard, 2011). While little is known about the initial settlers of Near Oceania (Kirch, 2000; Spriggs, 1997), archeologists do know that the Pleistocene populations inhabiting this region were foragers who lived low-density lifestyles (Sheppard, 2011). These small populations preferred temporary living sites located inland (Kirch 2000). By the mid-Holocene, Near Oceanic populations mastered hunting local game and collecting forest products (Spriggs, 1997) and the Old World Melanesians even experimented with crop production (Kirch, 2000). Shell and stone were two important materials used in everyday life (Kirch, 2000; Spriggs, 1997). From these materials, adzes were constructed for forest clearance and woodworking, and fishhooks were produced for sea hunting (Kirch, 2000). The presence of obsidian, a

volcanic glass product used for tool production, found on islands where it does not naturally occur suggests that communication was established and maintained between populations hundreds of miles apart (Kirch 2000; Sheppard, 2011). The lifestyle that these populations became accustomed to, however, changed when an influx of Asian migrants entered the region. Old World Melanesia was a scarcely populated island playground for humans; but an Oceanic empire soon took over.

2.1.2 History of the Lapita Expansion in Near Oceania

A volcanic catastrophe in the Bismarck Archipelago may have facilitated the arrival of immigrants into Near Oceania. Mount Witori, an active volcano located in New Britain of the Bismarck Archipelago erupted violently 3,600 to 3,300 years B.P. (See Figure 4) (Kirch, 2000; Petrie and Torrence, 2008). This particular eruption,

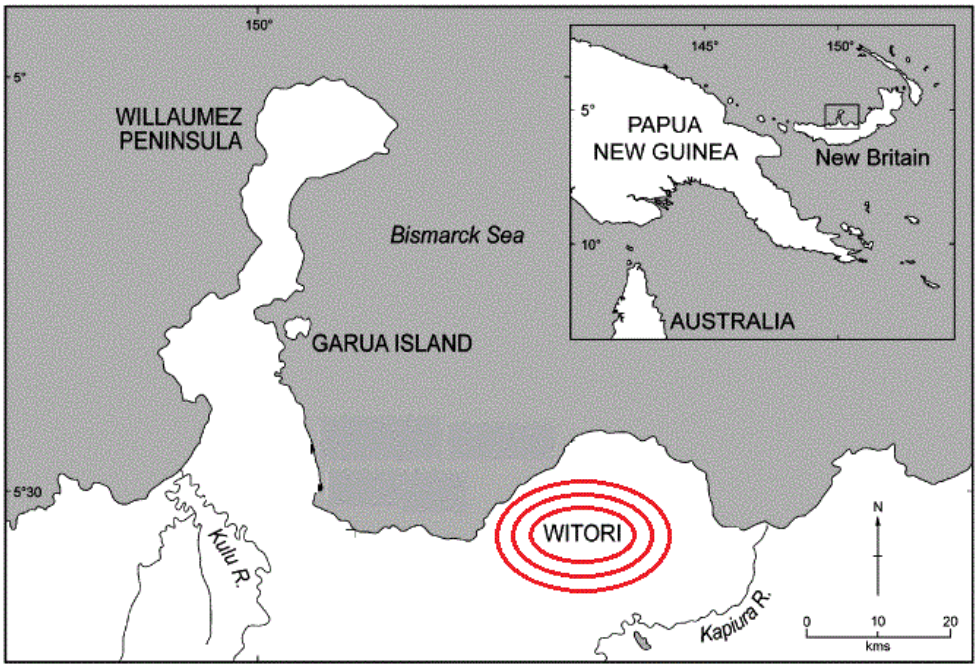


Figure 4. Mount Witori Volcano of New Britain, Bismarck Archipelago (Jago and Boyd, 2005)

also referred to as the W-K2 tephra stratiographic marker, was one of the largest to occur during the existence of modern humans (Spriggs, 1997). As a result, much of the Bismarck Archipelago was destroyed and it appears that many of the islands were abandoned (Kirch, 2000; Petrie and Torrence, 2008). Archeologists identified significantly different cultural material below and above the W-K2 tephra (Kirch, 2000). Whereas before the eruption, local populations were highly mobile; after the eruption, inhabitants took up permanent coastal settlement (Kirch, 2000). There was also minimal obsidian, or volcanic glass, exchange that took place in the region prior to the catastrophe (Torrence and Summerhayes, 1997). Moreover, the obsidian tools used by the earlier population of the Bismarck Archipelago were significantly different than the obsidian tools used by the replacement population (Kirch, 2000). To be specific, the pre-W-K2 obsidian tools were crafted with stemmed bases. The later inhabitants of this region used

a completely different style of tools. These new technologies included un-retouched flakes of obsidian and the sedimentary rock product, chert (Kirch, 2000). Remarkably, no pottery associated with these earlier populations has been found in the region. This is significant, because the replacement population produced and used a wide variety of ceramic materials (Kirch, 2000). This major catastrophic event and subsequent influx of immigrants forever changed 'Old World' Melanesia.

The arrival of Asian sailing migrants in Near Oceania resulted in the Lapita cultural complex. Between 3,500 to 3,400 years B.P., a population of Asian ocean navigators arrived and settled in the Bismarck Archipelgo (Kirch, 2000; Sheppard, 2011). The introduction of this group into Near Oceania resulted in rapid local change. Some of the most commonly found artifacts associated with the Lapita people, included earthenware ceramics that were plain and decorated, and sophisticated fish hooks (Bellwood, 1998; Kirch, 2000). In general, the materials used by the Lapita people showed more artistic and functional range than the artifacts used by the first inhabitants of Near Oceania (Kirch, 2000). The Lapita pottery found in the Bismarck Archipelago was related to contemporaneous and older pottery found in eastern Indonesia and the Philippines (Kirch, 1995). However, the Lapita pottery decorative style appears to have been invented in Near Oceania (Kirch, 2000). Archeologists believe that this distinctive Lapita style was a product of cultural fusion between the native islanders and the immigrant Asian population.

The Lapita culture is strongly associated with Lapita style pottery, but other cultural material and social behavior has been linked to this complex. Impressive outrigger canoes propelled by wind or containing paddles are associated with the Lapita

people (Kirch, 2000). Moreover, worked obsidian found on islands hundreds of miles apart, with less than 100 years discrepancy between the first Near-Oceanic sites, assures archeologists that the Lapita people were skilled ocean navigators. The Lapita people were also expert fishermen in both shallow and deep water as well as horticulturists (Kirch, 2000). Unlike the native Old World Melanesians, the Lapita people set up stilt-house settlements on beaches (Kirch, 2000). There was also evidence that the Lapita people kept domesticated animals including dogs, pigs, and chickens (Sheppard, 2011). The distinctive cultural material and social behaviors associated with the Lapita people have been tremendously helpful to archeologists in identifying settlements of the Lapita people across Near Oceania.

2.1.3 History of the Lapita Expansion in Remote Oceania

The Lapita expansion into Remote Oceania was rapid and widespread and the rise of this cultural complex in Near Oceania took only a few hundred years. Then for reasons unknown, there was roughly a 200 year window of time where expansion out of that region halted (Kirch, 2000). At 3,200 years B.P., however, the Lapita expansion commenced. This time the Lapita people reached islands in the Pacific with no current or previous inhabitants. The Lapita people were the first to colonize islands south and east of the main Solomon Islands (Kirch, 2000). The absence of early Lapita sites in the main Solomon Islands suggests that these islands were passed over by the Lapita people, perhaps due to the fact that a majority of the Solomon Islands were already inhabited by Old World Melanesians (Clark and Anderson, 2009). This idea is consistent with the

Lapita preference for colonization of uninhabited landmasses, which is well documented (Clark and Anderson, 2009; Kirch, 2000). The earliest radiocarbon dates from Lapita settlements in the Santa Cruz Group of the Solomon Islands are between 3,200 and 3,100 years B.P. (Green, 1976) (See figure 5). Likewise, the earliest radiocarbon dates in Vanuatu are between 3,100 and 3,000 years B.P. (Hedrick, 1971; Spriggs, 1990).

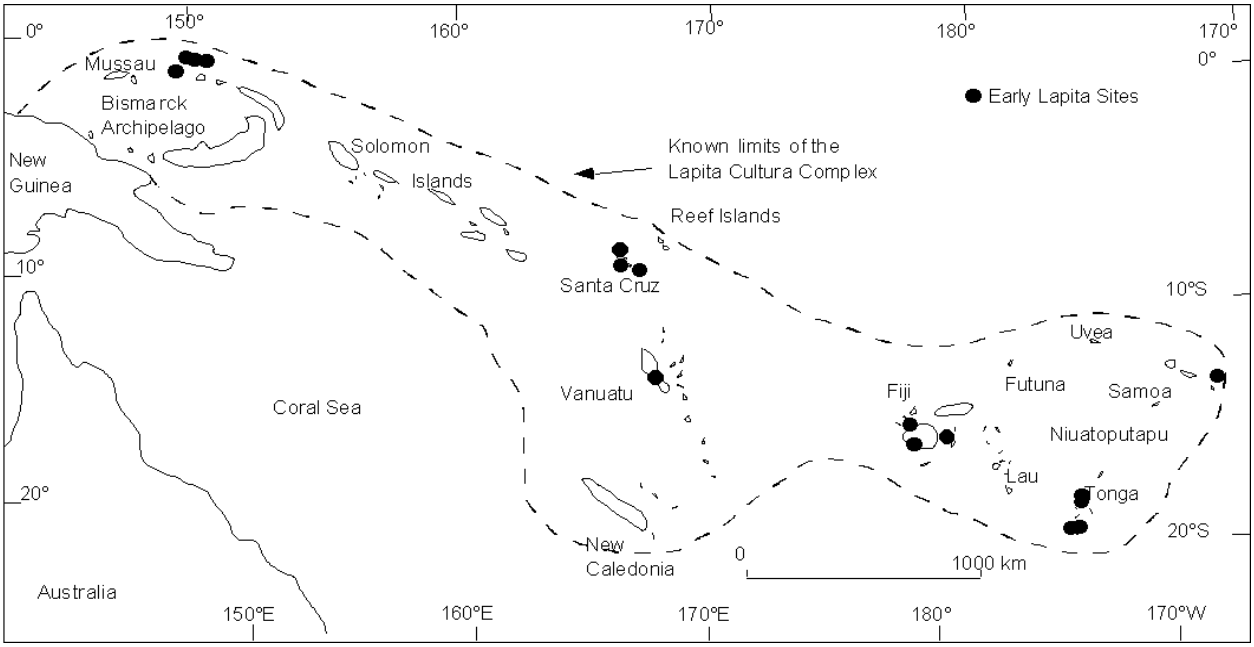


Figure 5. Distribution of early Lapita sites in Near and Remote Oceania (Kirch, 1997)

Vanuatu is argued to be the departure point for the Lapita settlement of Fiji (Anson, 1983; Bedford and Spriggs, 2008; Green, 1978). Given that the earliest Fijian sites date between 3,200 and 2,900 years B.P. (Anderson and Clark, 1999), this would make sense as the voyage from Vanuatu to Fiji, a distance of 500+ miles against the Pacific Ocean's wind and current patterns, was the largest inter-archipelagic voyage in the Lapita expansion (Clark and Anderson, 2009; Kirch, 2000). It is for this reason that

archeologists believed this route to be a significant barrier of Lapita movement in both volume and frequency (Green, 1991; Clark and Murray, 2006) (see Figure 6).

Figure 6. Near and Remote Oceania with Lapita sites highlighted (Irwin, 2009)

After Fiji was colonized, Lapita people continued eastward to Polynesia (Kirch, 2000). The earliest sites in the Tonga-Samoan chain date to 2,950 years B.P. (Kirch, 2000). The low number of early Lapita sites found in Fiji, Tonga, and Samoa are indicative of a slowing migration movement eastward (Clark and Anderson, 2009). The dates from all early Lapita sites combined give archeologists an idea of the approximate time it took these ancient voyagers to colonize Remote Oceania. Miraculously, in a period of 200 to 300 years the Lapita people had permanently colonized most Remote Oceanic islands within a range of 3000 miles.

2.1.4 History of the Lapita Expansion in the Fijian Archipelago

Rapid Lapita colonization of the Fijian Archipelago has been detected by archeologists. Radiocarbon dating of Lapita sites and associated pottery allowed archeologists to establish Lapita movement throughout the archipelago. Lapita pottery, the "chief characteristic of Fijian archaeology" was first discovered at Viti Levu, Fiji in 1951 by E.W. Gifford (Giford, 1951:189; Kirch, 2000). The earliest Lapita sites in the Fijian Archipelago contain pottery that radiocarbon dates to about 3,200 years B.P. (Kirch, 2000). Most of these early Fijian sites are located on or near Viti Levu (see Figure 5), though later Lapita sites can be found throughout the Fijian Archipelago. Based on ceramics stylistic change over time and radiocarbon dating, archeologists are able to establish a timeline of Lapita reign. Using these methods, it was argued that the reign of Lapita was relatively short in Fiji, lasting between 200-700 years (Anderson and Clark, 1999; Bedford, 2003; Clark and Anderson, 2009). This relatively short period of Fijian history firmly established this archipelago as a major portal of the Lapita expansion throughout Remote Oceania.

2.1.4.1 Lapita site preference

When the Lapita expansion moved throughout the Fijian Archipelago, Lapita people set up residence on small coastal sites. The earliest Lapita sites in Fiji were small, typically under 5,000 square meters (Best, 1984; Clark and Anderson, 2001; Nunn,

2007), which was a comparable size to Tongan (Burley, 1998) and other western Pacific sites (Sheppard and Green, 1991). One exception is the Lakeba Island site, which covered an estimated 15,000 square meters (Best, 2002) (see Figure 8). This Lau island

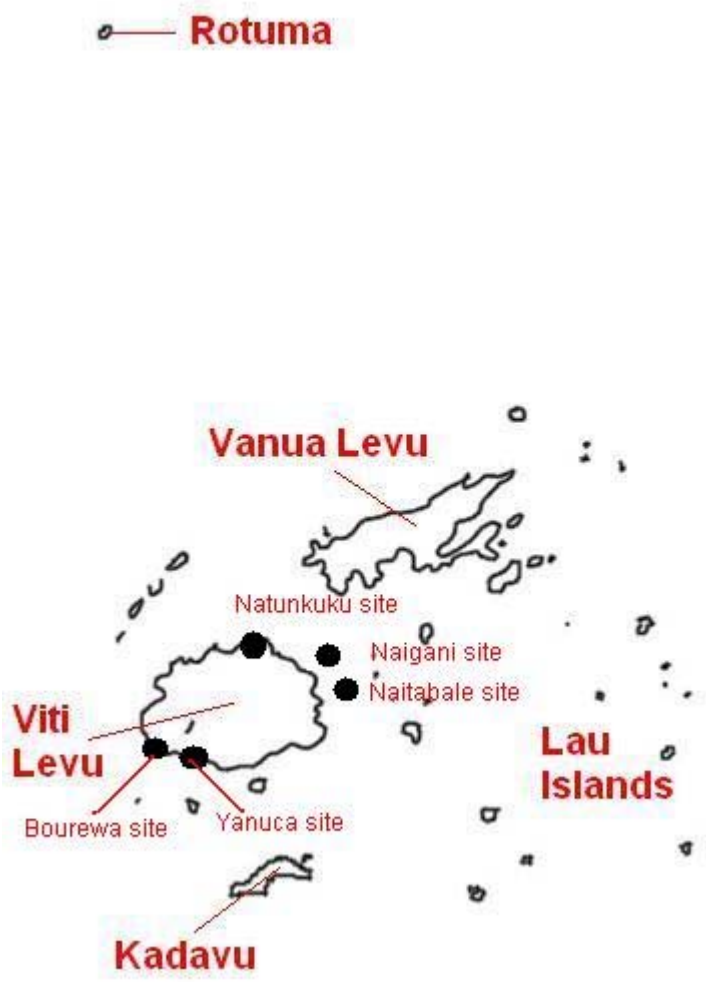


Figure 7. Early Lapita sites in the Fijian Archipelago (About.com, 2012)

may have been home to a larger sized population than the Viti Levu sites during the Lapita expansion because Lakeba may have served as a 'gateway' community. Gateway

communities provided staging points for migrants as they prepared for further expansion eastward (Hirth, 1978). To date, the Lakeba site is the largest found in all of Fiji and West Polynesia (Clark and Anderson, 2001). The Lapita people had a strong preference for habitation sites situated on sand plains near fringing reef. In fact, archeologists have only identified one early interior site in Fiji, located on Vanua Levu (Parke, 2000); though interior sites have been infrequently identified during the late Lapita period on both Viti Levu and Lakeba Islands. Lapita people are believed to have settled on coastal sites based on their subsistence patterns. Specifically, these people ate gregarious bivalves, fish, turtles, and birds (Clark and Anderson, 2009; Feld et al., 2009). For the Lapita people, wild resources were more important than proximity to horticultural land (Burley, 1998). Taken together, the Lapita settlement on coastal territory with budding off of Lapita groups to settle new land suggests that the founding populations of Fiji were migrant by nature.

2.1.4.2 Early Lapita pottery of Fiji

Viti Levu may have been the first Fijian island colonized by the Lapita people. The earliest Lapita pottery found in Fiji contains both dentate-stamping and incised design (Clark and Anderson, 2001; 2009; Kirch, 2000). Dentate-stamped ceramics production involved the pressing of stamps with intricate teeth patterns on the malleable surface of unfired clay. The stamp design was then pressed repetitively around the base of the object. Early Lapita dentate-stamping had a high density of toothed incisions and was very complex with great design variety between objects. It was also common to

incorporate three-dimensional elements such as nubbins, vertical bars, and transverse bars (Clark and Anderson, 2001). The only early Lapita sites found in Fiji are located on Viti Levu (Bourewa, Yanuca, and Natunuku sites) and nearby islands (Naigani and Naitabale sites) (see Figure 7). Ceramic shards with dentate stamping have also been found on Lakeba Island, one of the Lau islands; however, this site is not as early as the Viti Levu sites (Best, 2002; Clark and Anderson, 2009). In general, western Fiji has more early and potentially early Lapita sites than eastern Fiji (Clark and Anderson, 2001). The larger proportion of early sites on Viti Levu indicate that this large island was colonized first, followed by later colonization of Fiji's smaller islands.

2.1.4.3 Late Lapita pottery of Fiji

As Lapita people settled into Fijian habitation sites, there was a decline in the amount of decoration applied to ceramics. Lapita ceramics are known for their beautiful and complex decoration. Whereas the early Lapita pottery displays complex patterning with decoration covering most of the item, late Lapita pottery is a much more simplified version. For Fiji in general, the amount of decoration and number of vessel forms per Lapita assemblage declined over time (Clark and Anderson, 2009). Late Lapita dentate-stamping is simple, with one or two rows of lines and arcs surrounding the surface and there is generally a lot of unused space when compared to the earlier Lapita dentated-stamped pieces. The late works tend to have design only near the lip or rim, whereas the earlier works have design in many locations (Clark and Anderson, 2001). The relatively short-lived early to late Lapita pottery with dentate-stamping was replaced by the

simplified Sigatoka Phase very early on in Fijian history. This pattern of decline in early Fijian ceramics decoration has been thought of as a sign that the Lapita people had set up permanent residence in Fiji and over time lost connection to islands far away.

2.1.4.4 Post-Lapita pottery and warfare in Fiji

Post-Lapita ceramics in Fiji, like late Lapita ceramics, show a steady decline in overall decoration and number of vessel types; however, major stylistic change occurred at 900 years B.P. After initial Lapita colonization of the Fijian, Samoan, and Tongan Archipelagos, contact was maintained between island communities for several hundred years. Archeological evidence for this relationship is found in shared Lapita pottery techniques and residential patterns over time (Kirch, 2000). Between 3,200 and 900 years B.P., stylistic design was minimal on pottery. However, during this period of time, carved-paddle impressions appeared more frequently on globular pottery (Kirch, 2000). Fiji is unique in that it experienced a period of time where pottery was undecorated. Other Melanesian archipelagos like the Solomon Islands and Vanuatu transitioned directly from the Lapita dentate-stamped pottery to incised designs. Kirch (2000) suspects the reason why decoration on pottery ceased was because there was no or infrequent trade between Fiji and nearby archipelagos. His reasoning was that if ceramics were not sold for profit or exchanged, time spent on ornate decoration was wasted. Clark and Anderson (2009) agreed in principle with Kirch and they suggested that inter-island interaction declined when local population sizes grew and once population growth occurred, spouse exchange no longer required a long distance trek and

economic materials were locally produced by neighboring villages. While both of these hypotheses explain why stylistic design declined in Fijian pottery after the Lapita expansion ceased, there is a question as to why at 900 years B.P. there was a significant change in the way Fijians designed pottery. At 900 years B.P. and moving forward, a wide variety of incised designs are found on pottery. Archeologists have argued why this change occurred for a long time. There are two different possible explanations. The first, ceramic design changes were the result of local stylistic divergence. Rechtman (1992) argues that stylistic changes in pottery manufacture reflect internal socio-political change. Clark and Anderson (2009) also support this model that cultural change was the result of internal archipelagic processes. Others, however, argue that change in pottery style was due to an influx of new populations (Bellwood, 1979; Kirch, 2000). These new populations may have been transient or otherwise. Kirch (2000) believes that around 900 years B.P. there was a migratory influx of Melanesians, who brought incised ceramics to Fiji. While archeologists are able to speculate as to the many reasons why these changes occurred, it is important to note that there is uncertainty in stylistic change interpretation and alternative evidence is necessary to corroborate any hypothesis (Clark and Anderson, 2009). In addition to ceramics stylistic divergence, changes occurred with respect to warfare. Around 1,000 years B.P., fort construction began in Fiji and cannibalism was institutionalized (Best 1984; Kirch, 2000). Best argued that the construction of such forts and the practice of conquest warfare was the direct result of the population size reaching a maximum in Fiji. Excavation in both Viti Levu and the Lau Islands revealed that cannibalism was quite common and humans in particular were the most frequently consumed vertebrate animals (Gifford, 1951; Kirch, 2000). Some archeologists have

argued that intrusive populations brought about local warfare that led to fort building (Frost, 1974, 1979). Other archeologists, however, do not support the idea that external populations entered Fiji at this period of time (Parry 1981, 1987; Rechtman, 1992). To date, there has been no biological study to successfully confirm whether or not there was Melanesian migration into Fiji between 900 to 1,000 years ago.

2.1.5 Vanuatuan influence on the islands of Fiji

Archeologists have argued for intermittent contact and/or migration from Vanuatu to Fiji post Lapita Empire; however, there has been conflicting evidence. Most archeologists agree that there was some contact made between Vanuatuans and Fijians following the colonization of these two archipelagos (Bedford and Spriggs, 2008). This claim is supported by the distribution of the drug kava (*Piper methysticum*), the introduction of Oceanic rats (*Rattus praetor & Rattus exulans*), and a shared ceramic style (Bedford 2000; Bedford and Spriggs, 2008; Sand, 2000). The argument for major migratory events, however, has been strongly contended (Anderson and Clark, 2009; Bedford and Spriggs, 2008). For decades, archeologists believed that 1,700 year old obsidian tools found in Lakeba, a Lau Island of Fiji had been transported from northern Vanuatu (Best, 1987; 2002) (see Figure 8). A reanalysis of this study, though, revealed

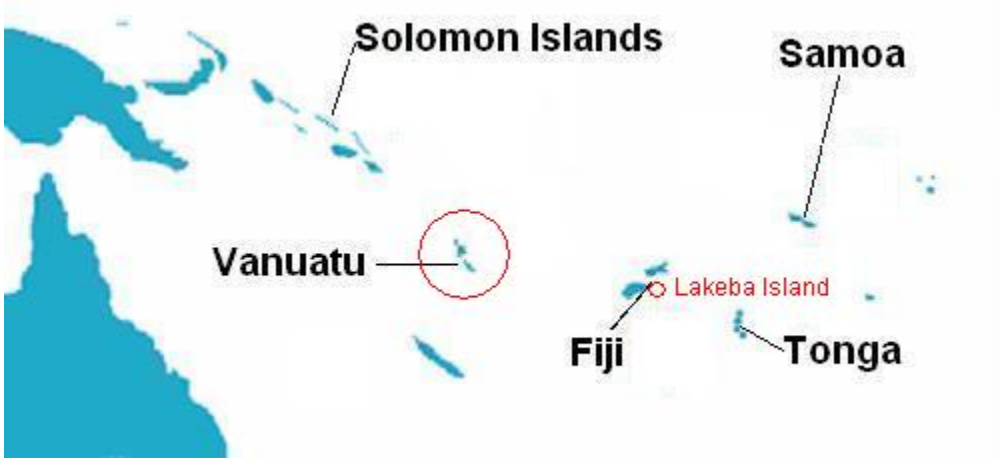


Figure 8. Vanuatu and Lakeba Island of the Lau Islands (About.com, 2012)

that the obsidian was most likely from a Fijian or Tongan source (Reepmeyer and Clark, 2010; Sheppard, 2011). Likewise, recent comparative analyses between contemporaneous Vanuatuan and Fijian ceramics (Bedford, 2000; 2006; Bedford and Clark, 2000; Bedford and Spriggs, 2008) have strongly challenged the argument for Vanuatuan influence on Fijian pottery (Best, 1984; Frost, 1979; Garanger, 1971). In 1971, Garanger claimed that the post Lapita pottery of Fiji was "exactly the same as the pottery of Mangaasi [Vanuatu]" (Clark and Anderson, 2009). In time, archeologists found that there were fewer similarities between Vanuatuan and Fijian ceramics. Best (2002) reduced the number of stylistic commonalities to three techniques. Then in 2008, after investigating northern Vanuatuan post-Lapita assemblages, Bedford and Spriggs declared that Vanuatu ceramics are not related to post-Lapita assemblages in Fiji (Clark and Anderson, 2009). Though one type of late Fijian ceramics sequence pot found in Fiji is similar to a style of bullet-shaped pots found in northern Vanuatu (Bedford, 2000; 2006). Nonetheless, limited surveying of northern Vanuatu remains a concern and

archeologists have yet to further establish any connections between Vanuatuan and Fijian ceramics (Bedford and Spriggs, 2008; Best, 2002; Clark and Anderson, 2009). Ceremonial parallels have been noted by archeologists (Frost, 1979; Bedford and Spriggs, 2008). Late Fijian ceremonial sites, called Naga, are very similar in appearance to north Vanuatuan ceremonial sites. These Fijian stone structures are unlike other local ceremonial sites in Fiji. Associated pottery includes elongated forms with pointed bases, not a style seen in other Fijian ceramics (Bedford and Spriggs, 2008). With all evidence taken into consideration, it is possible that contact was made between Vanuatu and Fiji, however, there is limited evidence that major migrational events between these archipelagos occurred.

2.1.6 Polynesian influence on the islands of Fiji

2.1.6.1 Contact between Vanua Levu of Fiji and Samoa

There has been limited archeological investigation on the island of Vanua Levu in Fiji and as a result, there is limited evidence of contact between this large island and Polynesia. The second largest island in Fiji, Vanua Levu surprisingly has not been the focus of many archeological surveys (Clark and Anderson, 2009) and thus far has only yielded one Lapita-era site (Parke, 2000). The early-Lapita pottery unearthed on this island came from an inland site (Parke, 2000), which is not typical of Lapita settlements (Kirch, 2000). All of the Lapita ceramics found on this island and identified by Parke (2000) displayed design patterns typical of East Fijian Lapita pottery, which is found in

Viti Levu. The pottery assemblages were also dated to different Lapita time periods, which suggests that contact was maintained between Lapita-era inhabitants of Vanua Levu and Viti Levu. Because Vanua Levu has been underrepresented in Fijian archeological surveys, there is not enough physical evidence available to argue for continuous contact outside of Fiji. There is only one study that has identified physical evidence of contact between Vanua Levu and a non-Fijian island (Dickinson, 2006). In 1995, Petchey found a quartz-bearing sherd from the Mulifanua site in Samoa (See Figure 9). Unlike other pottery sherds found at this Samoan site, this particular one was made up of materials derived from Vanua Levu in Fiji. To date, the Samoan sherd is the only physical evidence of non-Fijian contact made during the prehistory of Vanua Levu.

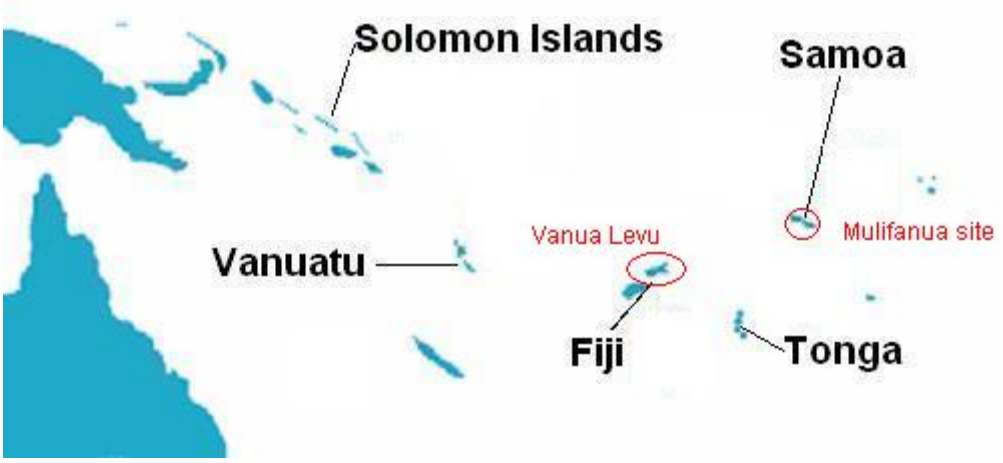


Figure 9. Vanua Levu, Fiji and the Mulifanua site in Samoa (About.com, 2012)

2.1.6.2 Contact between the Lau Islands of Fiji and Tonga

The largest island of the Lau Islands, Lakeba, served has historically served as a "crossroads of the sea" (Hage and Harary, 1996). The Lau Islands of Fiji are geographically situated between the larger main island of Fiji and the Tongan archipelago. Lakeba Island, the largest Lau island, situated among the southern Lau islands, has been extensively surveyed in recent years (Best, 1984, 2002; Reepmeyer and Clark, 2010) (see Figure 10). Lakeba Island is the only eastern Fijian island to yield early

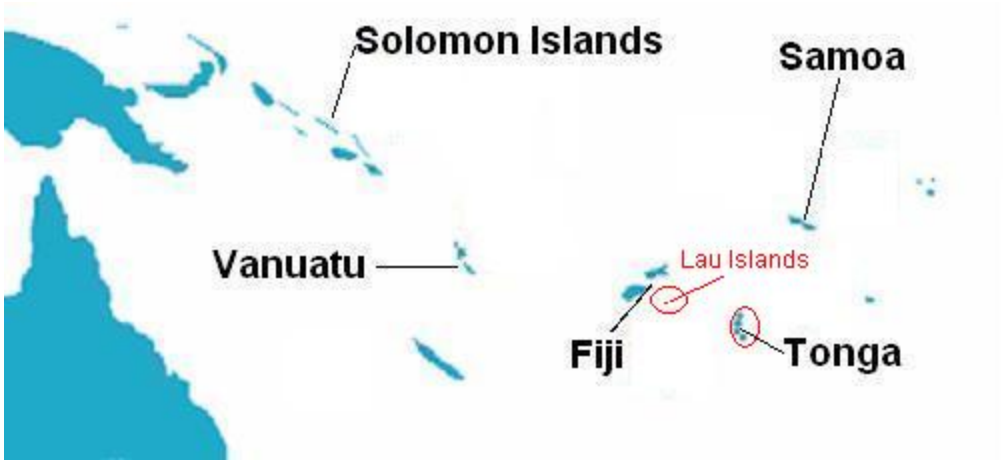


Figure 10. The Lau Islands of Fiji and the Tongan Archipelago (About.com, 2012)

Lapita pottery (Clark and Anderson, 2001, 2009). Lakeba Island is also unique in that it contains the largest Lapita site to be recorded in Fiji and West Polynesia (Best, 1984). The Wakea site (196) covers an estimated 15,000 square meters of coastal flat, significantly larger than typical Lapita sites which are generally under 5,000 square meters (Best, 1984; Clark and Anderson, 2001; Nunn, 2007). Based on Lakeba Island site dating, and ceramics and obsidian analyses, Clark and Anderson (2001) suggest that Lakeba Island was settled at a time when Lapita knowledge of the west Fijian territory

was complete. Of the early Lapita pottery found in Lakeba that was non-local, an estimated 30% of the ceramic tempers originated from other Lau Islands with a very small percentage originating from Viti Levu and Kadavu (Best, 1984; Clark and Anderson, 2001). The large volume of intra-archipelagic materials found on Lakeba Island support the idea that Lakeba was a gateway island to local Fijian territories and possibly beyond (Clark and Anderson, 2001).

Further evidence that Lakeba was a gateway island comes from Best (1984); A huge population expansion was identified around 2,500 years B.P. in Lakeba based on the number of shared date sites and expansion of villages inland. An island of extensive and thorough archeological investigation, Lakeba appears to have played a major part in the colonization of eastern Fiji and possibly beyond.

There is physical evidence that in addition to serving as a gateway community, Lakeba also served as a contact point between Fiji and Tonga. In 1984, Best unearthed three obsidian flakes at the Ulunikoro and Wakea sites of Lakeba Island. The obsidian flakes dated to 2500 cal. years B.P. and were identified as products of Tonga. These findings were supported by Reepmeyer and Clark's 2010 reanalysis of the 1984 study. In addition, Reepmeyer and Clark found that twelve obsidian flakes previously identified by Best as products of Northern Vanuatu were in fact products of a not-yet-identified source in the Fijian-Tongan region. However, further source analysis of the Fijian-Tongan region is required before any definitive conclusions can be made on the true origin of these twelve flakes. Nonetheless, the three obsidian flakes provide clear physical evidence of contact between prehistoric Lau Island and Tongan populations. The amount of obsidian transported from Tonga into Lakeba, however, was small when compared to

the amount of ceramic and stone material transported from northern Lau and Viti Levu (Best, 1984). This would suggest more external contact with local Fijian populations than with Polynesians. With this evidence taken into consideration, it appears that Lakeba was in fact a prehistoric point of contact between western Fiji and Tonga.

2.1.6.3 Contact between Rotuma Island of Fiji and Polynesia

There is minimal archeological evidence for prehistoric interaction between Rotuman and other islands populations. To date, no early Lapita pottery has been unearthed on this small, isolated island located about 450 miles north of Viti Levu, 750 miles west of Samoa, and 780 miles northwest of Tonga (see Figure 11). The only

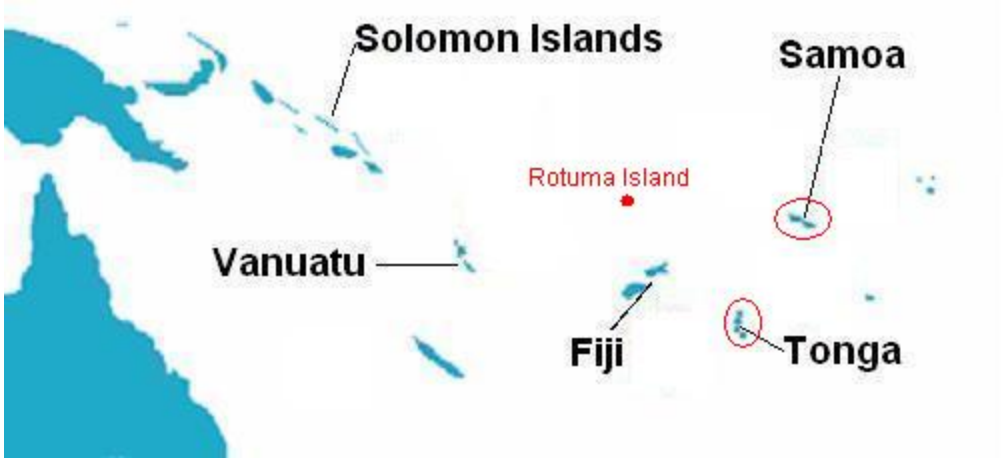


Figure 11. Rotuma Island, Samoa, and Tonga (About.com, 2012)

physical evidence that Rotumans made contact with Polynesians comes from prehistoric burial sites. A 1993 survey of 14 hilltop sites in Rotuma identified multiple pre-historic

burial sites. The largest burial complexes, called Langi, are very similar to chiefly burial mounds in Tonga. Specifically, they consist of large cut coral slab facings with an anterior fill of calcareous sand (Ladefoged, 1993). The geographical locations of Langi in Rotuma are exclusively in the northern and eastern districts. The location of these structures would have required significantly more energy and labor for construction. Because of this fact, it has been suggested that the pre-historic Rotumans buried their chiefs, like the Tongans, in Langi. Other evidence, linguistic (Pawley, 1996) and ethnographic (Howard, 1985), strongly support prehistoric Rotuman-Polynesian contact. Despite the limited archeological evidence in support of contact made between prehistoric Rotumans and Polynesians, an abundance of evidence exists in support of this claim in both linguistic and ethnographic form.

2.2 LANGUAGE STUDIES IN THE FIJIAN ARCHIPELAGO

2.2.1 Papuan languages

The first inhabitants of Near Oceania spoke languages that were related to today's Papuan language family. The two main language families spoken throughout the Pacific Islands are Austronesian and Papuan (Non-Austronesian). The Papuan language family is more diverse than the Austronesian language family and geographically confined to Melanesia and few islands west of New Guinea (Kirch, 2000). This high level of linguistic diversity found within the Papuan language family is not surprising, since Melanesian populations inhabited this region for at least 30,000 years (Kirch, 2000).

Papuan languages are assigned to 12 sub-families with each sub-family containing hundreds of different languages. Today, Papuan language use is concentrated within the New Guinea highlands and scattered throughout the Bismarck and Solomon archipelagoes of Melanesia, whereas Austronesian languages are dominant in the remainder of Near-Oceania and Remote Oceania.

2.2.2 Austronesian language expansion

Austronesian-speaking Asian migrants rapidly colonized parts of Near and all of Remote Oceania within a short period of time. Linguistic evidence suggests that Oceanic languages relate to each other and to the present-day languages of Taiwanese Aboriginals. Linguists named this group of languages 'Austronesian' (Kayser et al., 2006). The Austronesian language family is one of the largest in the world, containing around 1,200 languages with a geographic distribution spread from Taiwan to Madagascar and to Easter Island (Gray, Drummond, and Greenhill, 2009). Bayesian phylogenetic methods applied to Austronesian languages suggest that this language family came into existence roughly 5,200 years ago, likely in Taiwan. Language diversity is associated with population expansion, and diversity estimates among Austronesian languages suggests that there were three pulses, or expansions and two pauses, or periods of time where expansion halted (Gray, Drummond, and Greenhill, 2009). The first major expansion of Austronesian speaking people occurred in Taiwan around 5,200 years B.P., followed by a pause where there was no expansion from 3,800-4,500 years B.P. The second major pulse occurred when the Austronesian-speaking

people traveled from Taiwan to the Philippines and then spread rapidly throughout Near and Remote Oceania by 3,000 years B.P (Gray, Atkinson, and Greenhill, 2011). A final pause lasted in Western Polynesia for 1,000 to 1,500 years, and then a final pulse occurred as the Eastern Polynesian islands were colonized (Gray, Atkinson, and Greenhill, 2011). During the second expansion pulse, Austronesian-speakers spread over 7000 km from the Philippines to Western Polynesia. As these people traveled long distances over water, they encountered many different island populations. The emergence of the Lapita cultural complex was a product of such interactions. This cultural complex arose in the Bismarck Archipelago and was likely the product of the Austronesian speakers integrating with indigenous Near Oceanic populations (Green, 2002). After many Austronesian-speaking Lapita people left Near Oceania, they colonized all major island systems of Remote Oceania, including Fiji.

2.2.3 Fijian language

Fijian natives speak Fijian, an Oceanic Austronesian language. The people of Micronesia, Polynesia and much of Melanesia today speak languages classified as the Oceanic subgroup of the Austronesian language family (Kirch, 2000). Proto Oceanic society was characterized by Austronesian language usage and the Lapita Cultural Complex. Archeological evidence suggests that the founding population(s) of Fiji were members of this proto Oceanic society (Kirch, 2000). Linguists Geraghty (1983) and Pawley (1996) both argue that the first settlers of Fiji spoke a language ancestral to the present indigenous languages of Fiji, Rotuma and Polynesia. Geraghty (1986) coined this

ancestral language the proto Central Pacific dialect chain. As the early settlers spread across Fiji and into Polynesia, unity of speech was not maintained; however, transitional dialects emerged (Pawley 1996). In time, the proto Central Pacific dialect chain diverged into both the Western/Central Fijian dialects and proto Eastern Fijian/Polynesian dialects.

One commonly spoken Fijian dialect, the Bau dialect, has traditionally been used in linguistic analyses as a representation of all Fijian dialects. The Bau dialect of Vanua Levu is today spoken and written by most Fijians. It is also the official Fijian dialect used by religious, educational and governmental organizations (Schutz, 1978). Unfortunately, the Bau dialect has often been used to represent all of the Fijian language dialects and communalects. This is unfortunate, as linguistic variation within Fiji is hypothesized to be greater than any islands further east (Grace, 1964). Linguists agree that many dialects and hundreds of communalects, which are subdivisions of dialects, of Fijian are spoken throughout the Fiji islands (Geraghty, 1982; Pawley, 1996). Thus the Bau dialect does not represent the underlying linguistic variability in Fiji.

2.2.2.1 Lau Islander Fijian dialects

The Fijian communalects spoken by the Lau Islanders reflect the contact that was maintained between these Fijians and their Tongan neighbors over time. Interaction between Lau Islanders and Tongans was firmly established as early as the settlement of Tonga or as recently as the thirteenth century (Derrick, 1950; Geraghty, 1983). In the past 200-300 years there is much documented evidence of such relations. Lakeba, the largest Lau Island, played a prominent role in the shipbuilding industry (Couper, 2009).

For a long time, the province of Tui Lakeba was home to the best shipbuilders and navigators (Couper, 2009). Tongans traveling through Fiji had difficulty navigating through the Lau Islands during storms and often became shipwrecked. As a result, the powerful Tongan chiefdom offered the Lakeba chiefdom political and military alliance in exchange for aid in traveling emergencies. Missionaries from the 19th century documented that Tongans made extended visits to the Lau islands in order to work as sandalwood timber laborers and canoe builders (Kirch, 2000; Schutz, 1978). Often these Tongan laborers would take up Lau residence for months at a time. It has been documented that the native Lau Fijians spoke foreign language in order to interact with non-Fijian sandalwood traders. This tradition of 'foreigner talk' persists still today, as Fijians communicate with European traders in English and among local Indians in dialects of Hindi (Schutz, 1978). As a result of the Lau Islanders becoming familiar with the Tongan language, the Fijian communalects spoken in Lau contain more Polynesian loan words than most other East Fijian communalects. Upon comparison of Fijian language communalects with Polynesian languages, Pawley (1996) argued that the communalects spoken within the Lau Islands and eastern Vanua Levu were the Fijian communalects most similar to Polynesian languages. Taken together, there is no doubt that the Lau Islanders have strong historical ties to neighboring Tongans and it is expected that this relationship will also be reflected in Lau Islander mitochondrial DNA lineages.

2.2.2.2 Rotuman language

The Rotuman language reflects Rotuma's unique geographical position between multiple large island systems. Today, the Rotuman language is spoken by about 2,700 people living on the island of Rotuma and about 5,000 Rotumans living on the main islands of Fiji (Pawley, 1996). Rotuma island is geographically situated 350 miles North of Viti Levu, Fiji, 200 miles southwest of Niulaki, Tuvalu, 700 miles south of Kiribati, 700 miles west of Samoa, 800 miles northwest of Tonga, 700 miles north east of Vanuatu, and 700 miles east of the Solomon Islands. This small, 14 square mile island is thus isolated from multiple island systems that are hundreds of miles away. Interestingly, elements of different languages spoken by neighboring people have been detected within the Rotuman language.

The Rotuman language is classified as a Central Pacific Oceanic Austronesian language and it is most similar to the Fijian and Polynesian languages. An early linguistic study of the Rotuman language proposed that the Rotuman language is a fusion of Samoan, Tongan, Melanesian, Micronesian, and local language elements (Churchward, 1938). The Rotuman language may reflect multiple interactions between Rotumans and neighboring islands. Modern day linguists have argued that the Rotuman language is most similar to the Fijian and Polynesian languages (Geraghty, 1986; Pawley, 1996). Moreover, language studies have revealed that the Rotuman language likely derived from the proto Central Pacific Oceanic dialect chain of the Austronesian language family (Pawley, 1996). While linguists are in general agreement today that the Rotuman language is most like the other Central Pacific Oceanic languages, there is less agreement on whether Rotuman is a Fijian or Polynesian language.

Much of the Rotuman lexicon is shared with Fijian and Polynesian languages, which makes linguistic classification difficult. Traditionally, linguists have estimated Austronesian language relationships using lexicostatistical and comparative methods. These methods have produced trees in contrast with each other (Gray, Drummond, and Greenhill, 2009). Upon comparison of 200 cognates, or words that share a common meaning, between Austronesian languages, Dyen (1963) found that both the Rotuman and Fijian (Bau dialect) languages were descended from the same proto language as the Micronesian/Polynesian languages. Using a related lexicostatistical method, Grace (1961) compared the Rotuman, Fijian, Tongan, Maori (New Zealand), Mota (Vanuatu) and Sa'a (Solomon Islands) languages. The resultant tree placed the Rotuman language nearest to the Tongan language (26% commonality) and close to the Fijian language (20% commonality); however, the Rotuman language was not definitively classified as Fijian or Polynesian language. Grace (1964) and later Pawley (1996) offered an explanation as to why the lexicostatistic method had not been successful in classifying the Rotuman language: linguists had been comparing other Austronesian languages to the Bau dialect of Fijian.

Upon comparing the Rotuman language with many communalects of the Fijian language, it appears that Rotuman is derived from a Western Fijian dialect that was once spoken within Vanua Levu. Based on shared innovations, Geraghty and Pawley suggest that Rotuman diverged from the Western Fijian dialect chain at a somewhat later date then the divergence of the Proto Eastern Fijian/Polynesian dialect chain (Geraghty, 1983; Pawley 1996). Specifically, Rotuman shares roughly the same number of linguistic innovations with the Fijian dialects spoken in parts of Northwestern Vanua Levu

(Geraghty, 1996; Schmidt, 1999). Moreover, the similarity between the Rotuman and Polynesian languages can be explained as the result of massive borrowing that occurred more recently (Schmidt, 1999). According to Schmidt (1999), after a long period of isolation from other islands, Rotumans began to adopt linguistic and cultural innovations from the Polynesians who began to visit the island around 750 years ago. Schmidt (1999) argues that the Tongan language specifically was the most influential of these Polynesian languages. These conclusions are interesting considering that Rotuman oral records describe the first colonizers as Samoan. However, there is archeological evidence that supports Tongan influence on Rotuman burial mounds (Ladefoged, 1993). This would support Schmidt's argument that there was massive cultural and linguistic borrowing that occurred in Rotuma relatively recently. In conclusion, there is some evidence to suggest that the Rotuman language is derived from a dialect once spoken in Vanua Levu, and that Polynesian word borrowing occurred more recently.

2.3 KINSHIP ORGANIZATION IN THE FIJIAN ARCHIPELAGO

2.3.1 Post-marital residence rules in Oceanic populations

Historically, the Austronesian-speaking societies of the Pacific have tended to both practice matrilineal descent and possess matrilocal kinship structures, though it appears that for the Polynesian Islanders there was a gradual switch to a more patrilocal residence structure (Jordan et al., 2009). A couple takes up matrilocal residence when, after marriage, they move to the residence of the bride's maternal relatives. Likewise, a

couple takes up patrilocal residence when they move to the residence of the groom's paternal relatives. Matrilineal descent can be described as a system by which ancestry is traced through the maternal line. Patrilineal descent is the exact opposite system, where ancestry is traced through the paternal line. Matrilineal descent can be directly traced by the molecular marker, mtDNA; moreover, patrilineal descent can be directly traced by the molecular marker non-recombining Y (NRY). An understanding of social organization is vital when interpreting both mtDNA and NRY patterns in ancestral populations (Oota et al., 2001). It has been demonstrated that descent rules do not necessarily predict residence rules (Holy, 1996). Jordan et al. (2009) argued that this suggests post-marriage residence patterns and not descent regulate human dispersal. One general pattern that has been observed in Oceania, with respect to the proportions of mtDNA and NRY lineages, is that there is a predominance of Asian mtDNAs and also Melanesian NRYs that are found among Pacific Islanders (Hage and Marck, 2003). Because this pattern is so prevalent, some have suggested that the proto Polynesian founders of the Pacific Islands practiced matrilineal descent and took up matrilocal residence, thus the Asian females incorporated Melanesian men into their matrilocal residence (Hage and Marck, 2003). Other ethnographic lines of evidence such as kinship, social organization, ethnography, and language were also used to construct this evolutionary model. However, Jordan et al. (2009) found that Austronesian societies today showed great variation in post-marriage residence patterns. Among the populations examined by this thesis, Samoa was classified as ambilocal (both residence patterns were observed), Tonga and Fiji were classified as patrilocal, and Rotuma was classified as matrilocal. In general, Jordan et al. (2009) found that a many of the Polynesian societies practiced patrilocality, which is the opposite of

what Hage and Marck's hypothesis would have predicted. This may have been due to the decrease in long-distance voyaging once people had settled into communities. Males spending more time on their home island would translate into less need of a matrilocal support system for the women and children. It may also mean that with an increased presence of males within the home, there would be an increased power struggle between male and female leadership. Thus an explanation for why this occurred is that the founding proto-Polynesian populations practiced matrilineal descent and took up matrilocal residence, however, over time post-marriage residence patterns changed.

2.4 BIOLOGICAL ANTHROPOLOGY IN THE FIJIAN ARCHIPELAGO

2.4.1 Near-Oceanic mitochondrial DNA

Papuan speakers of Melanesia are believed to be the descendents of the Pleistocene colonizers of New Guinea ('Old World Melanesia') and their associated mitochondrial DNA (mtDNA) lineages (**M**, **P**, and **Q**) most likely arose in Near Oceania tens of thousands of years ago Near-Oceanic mtDNA lineages are most commonly found today in Near and Remote Oceania with exception (Kayser, 2010); specifically, the two mtDNA lineages, **P** and **Q**, have infrequently been found west of eastern Indonesia (Hill et al., 2007). The ancient **M**, **P**, and **Q** mtDNA lineages of Near Oceania today are fairly well understood; However, many Pacific islands have been insufficient sampled and as a result, geneticists have an incomplete understanding of the true diversity that exists among Pacific people. For this thesis project, the following Pacific populations were

sampled for mtDNA: Vanuatu, the Solomon Islands, Fiji, Samoa, and Tonga. In this next section, all Near-Oceanic mtDNA lineages positively identified in these human populations will be described. In the discussion section of this thesis, lineages **M**, **P**, and **Q,** the most ancient of all Pacific mtDNAs, will aid in tracking the prehistoric migratory movement of peoples across the above mentioned island territories.

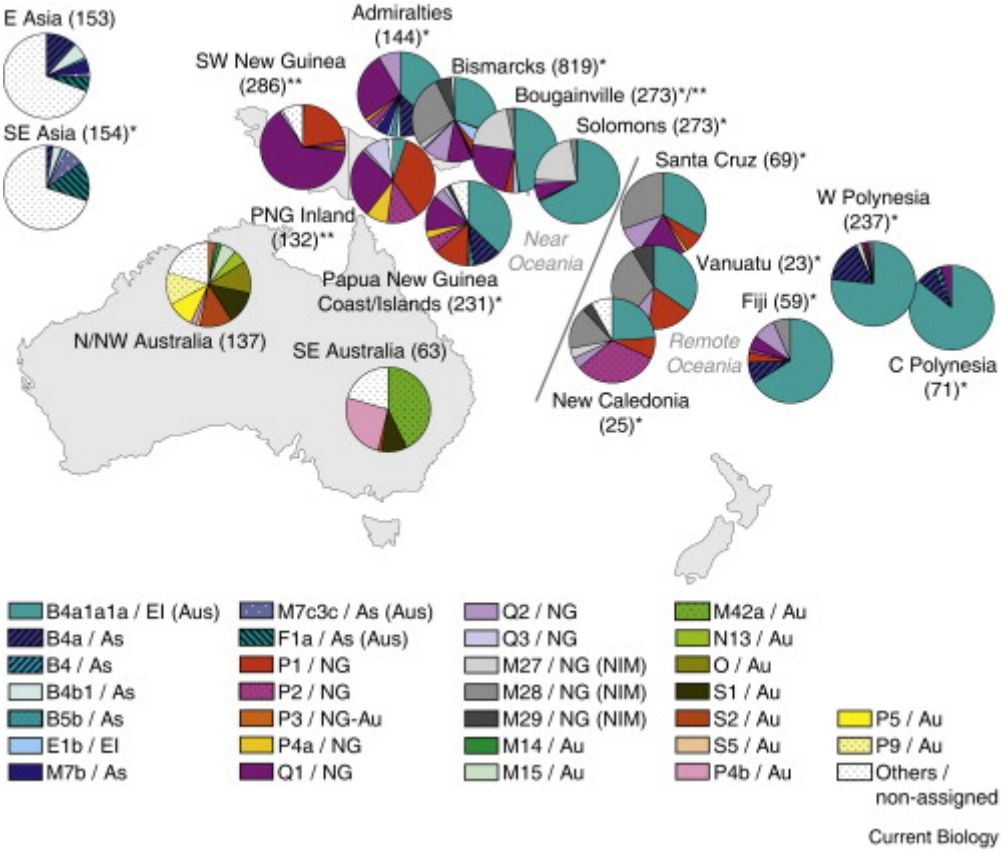


Figure 12. Distribution of mtDNA lineages in Oceania (Kayser et al., 2010)

2.4.1.2 MtDNA lineage M: Haplogroups M27a and M27b

Today, the highest frequencies of mtDNA haplogroups **M27a** & **M27b** are found among Solomon Islanders (see Figure 13 & Table 1). Haplogroup **M27a** is also found in

high frequencies in Bougainville, and elsewhere in the Pacific, this haplogroup is infrequently identified (see Figure 13 & Table 1). Haplogroup **M27b**, in addition to

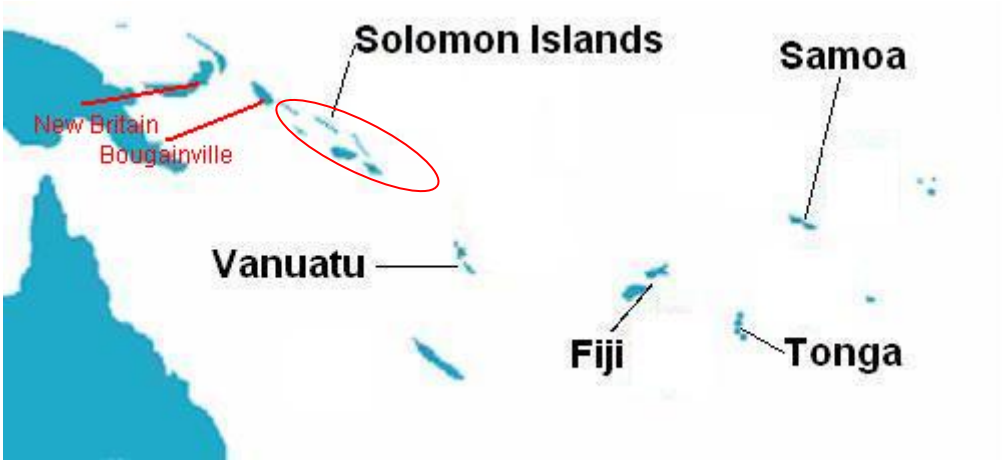


Figure 13. New Britain, Bougainville, and the Solomon Islands (About.com, 2012)

Haplogroup	M27a	
Highest frequency	Ranongga (Solomons)	0.292
High frequencies	Bougainville	0.179
Source	Delfin et al. 2012	
TMRCA	M27 = 40-70,000	
Source	Friedlaender et al., 2007	

Haplogroup	M27b	
Highest frequency	Malaita (Solomons)	0.274
High frequencies	Gela (Solomons)	0.250
High frequencies	Tolai (New Britain)	0.231
Source	Delfin et al. 2012	
TMRCA	M27 = 40-70,000	
Source	Friedlaender et al., 2007	

Table 1. M27a & M27b haplogroup information

being found in high frequencies among Solomon Islanders, it is also found in New Britain (See Figure 13 & Table 1). All mtDNA lineages are classified by a defined set of common substitutions. The time to most recent common ancestor (TMRCA), or the time

between today and the date when an ancestral lineage emerged, for the ancestral **M27** haplotype was estimated to be 40-70,000 years (Friedlaender et al., 2007).

2.4.1.3 MtDNA lineage M: Haplogroups M28, M28a, and M28b

MtDNA haplogroup **M28** is found more frequently among Pacific Islanders than haplorgoups **M28a** and **M28b**. Specifically, **M28** is mostly found in New Britain and the Santa Cruz Islands of the Solomons (see Figure 14 & Table 2). Elsewhere, it has been found in low frequencies. The TMRCA for haplogroup **M28** is 20-32,000 years (Friedlaender et al., 2007). A less common lineage than **M28** and a subgroup of **M28**, haplogroup **M28a** has been infrequently identified in Fiji, Vanuatu, and the Solomon Islands (see Figure 14 & Table 2). The TMRCA for this haplogroup is 11-17,000 years (Friedlaender et al., 2007), which means that this **M28a** may be the youngest of all haplogroups described in this section. Like **M28a**, haplogroup **M28b** is also less common among Pacific Islanders. The TMRCA estimation indicates that **M28b** is significantly older than **M28a**, with a TMCRA estimate of 27-41,000 years (Friedlaender et al., 2007) (see Table 2). M28b has only been identified in Vanuatu and the Solomon Islands (Friedlaender et al., 2007).

Figure 14. New Britain, Santa Cruz Isl., Solomon Isl., Vanuatu, and Fiji (About.com, 2012)

Haplogroup	M28	
Highest frequency	New Britain	0.474
High frequencies	Santa Cruz (Solomons)	0.191
Source	Delfin et al. 2012	
TMRCA	20-32,000	
Source	Friedlaender et al., 2007	

Haplogroup	M28a	
Highest frequency	Fiji	0.022
High frequencies	Vanuatu	-
High frequencies	Solomon Islands	-
Source	Delfin et al. 2012, Friedlaender et al., 2007	
TMRCA	11-17,000	
Source	Friedlaender et al., 2007	

Haplogroup	M28b	
High frequencies	Vanuatu	-
High frequencies	Solomon Islands	-
Source	Friedlaender et al., 2007	
TMRCA	27-41,000	
Source	Friedlaender et al., 2007	

Table 2. M28, M28a, & M28b haplogroup information

2.4.1.4 MtDNA lineage P: Haplogroup P1

The mtDNA haplogroup **P1** is very common among Pacific Islanders, however the highest frequencies of this old lineage are found in the Papua New Guinea (PNG) highlands, among the Melamela people of New Britain, and in the West New Guinea (NG) highlands (see Figure 15 and Table 3). **P1** can be found throughout Near Oceania, but it is also found in lesser frequencies within Remote Oceania. The TMRCA for this lineage is 30-50,000 years, which means this lineage is likely one of the oldest among Pacific Islanders (Friedlaender et al., 2007) (see Table 3).

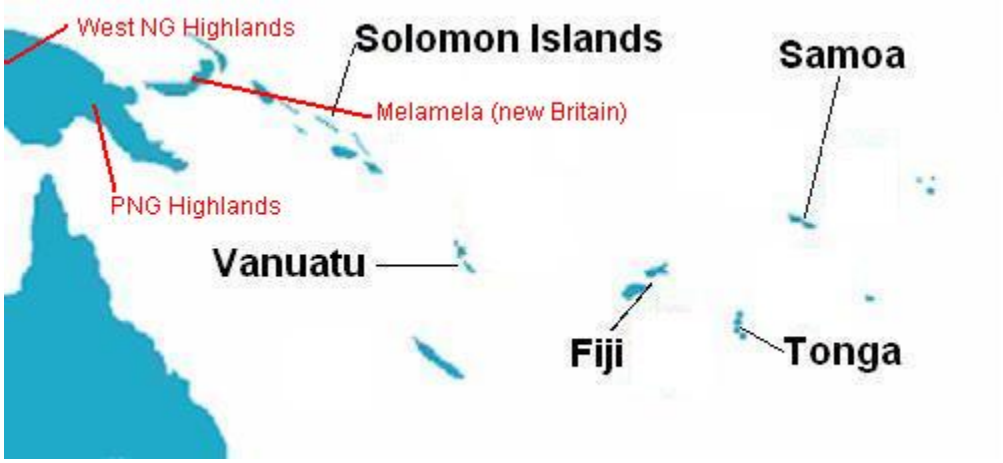


Figure 15. West NG Highlands, PNG Highlands, and Melamela (About.com, 2012)

Haplogroup	P1	%
Highest frequency	PNG Highlands	0.531
High frequencies	Melamela (New Britain)	0.500
High frequencies	West New Guinea Highlands	0.364
Source	Delfin et al. 2012	
TMRCA	30-50,000	
Source	Friedlaender et al., 2007	

Table 3. P1 haplogroup information

2.4.1.5 MtDNA lineage Q: Haplogroups Q1 & Q2

One of the most common haplogroups found in Near Oceania, **Q1**, is found commonly in Bougainville, the West NG high and lowlands, and New Britain (See Figure 16 and Table 4). **Q1** has also often been identified in most Remote Oceanic populations, including Vanuatu, Fiji, Samoa, and Tonga (Friedlaender et al., 2007; Kayser et al., 2006). The TMRCA for **Q1** is 21-27,000 years, which is moderately old for Near Oceanic mtDNA lineages (Friedlaender et al., 2007) (see Table 4). Haplogroup **Q2**, like **Q1**, is also found in high frequencies among Near-Oceanic populations, though it has also been identified to a much lesser extent as far south and east as Fiji and Vanuatu

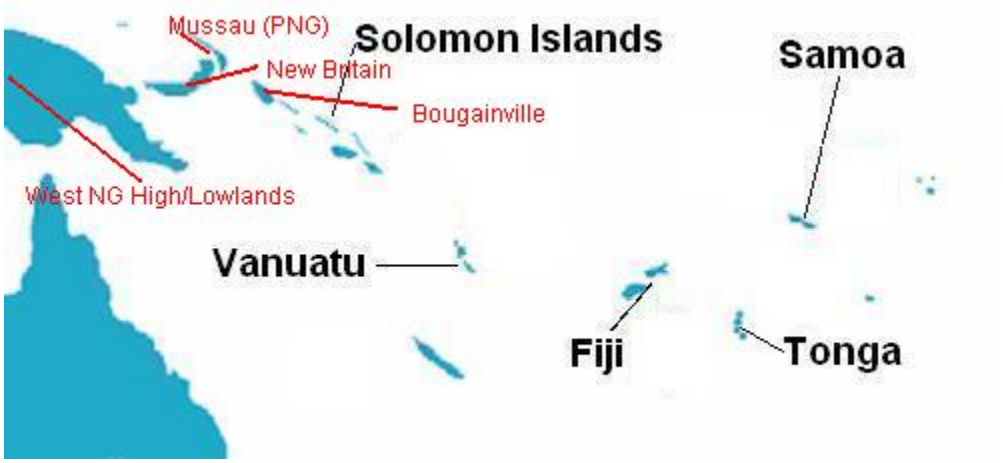


Figure 16. WNG High/Lowlands, Mussau, New Britain, and Bougainville (About.com, 2012)

Haplogroup	Q1	%
Highest frequency	Aita (Bougainville)	0.788

High frequencies	West New Guinea Low/Highlands	0.618
High frequencies	Loso (New Britain)	0.533
Source	Delfin et al. 2012	
TMRCA	21-27,000	
Source	Friedlaender et al., 2007	

Haplogroup	Q2	%
Highest frequency	Mussau (PNG)	0.500
High frequencies	Ata (New Britain)	0.485
High frequencies	Mali (New Britain)	0.362
Source	Delfin et al. 2012	
TMRCA	30-50,000	
Source	Friedlaender et al., 2007	

Table 4. Q1 & Q2 haplogroup information

(Friedlaender et al,2007; Kayser et al., 2006). **Q2** is found mainly in populations from Mussau Island (PNG) and New Britain (see Figure 16 and Table 4). The TMRCA for **Q2** is 30-50,000 years, making this lineage an old Near-Oceanic lineage (Friedlaender et al., 2007) (see Table 4).

2.4.2 Mitochondrial DNA associated with the Austronesian expansion

The Taiwanese migrants associated with the Austronesian expansion that began 5,500 years ago brought new mtDNA lineages into the Bismarck Archipelago and these lineages are today found throughout Near and Remote Oceania. Asian migrants associated with this expansion arrived at the Bismarck Archipelago by 3,400 years B.P. (Kirch, 2000). The Bismarcks are argued by many to be the birthplace of both the Lapita Cultural Complex and the proto-Oceanic language family (Kayser, 2010; Kirch, 2000; Spriggs, 2003). The Asian migrants brought new mtDNA lineages into the Bismarcks,

mainly **B4**. MtDNA haplogroups associated with this ancestral population and featured in this thesis project include: **B4a1a1**, **B4a1a1a** or the Polynesian Motif (**PM**), and **B4b1**.

2.4.2.1 MtDNA lineage B4: Haplogroup B4a1a1a, or the Polynesian Motif (PM)

Perhaps the most widely distributed Asian-derived mtDNA haplogroup associated with the Austronesian expansion throughout Near and Remote Oceania is the Polynesian Motif (**PM**) (see Figure X). The defining substitutions of **PM** are found in the Hyper Variable Region 1 (HVR-1) of the mitochondrial genome: a C at position 16217, a G at position 16247, and a T at position 16261 (Redd et al., 1995). This lineage is absent among the PNG highlanders and very common in areas of Near Oceania, Polynesia, and Micronesia (Friedlaender et al., 2007). Most Polynesian Islanders and many Melanesians possess the **PM** haplotype (see Figure 17 and Table 5). The **PM** is also present among Papuan-speaking island Melanesians and found at lower frequencies in central and eastern Indonesian populations (Redd et al., 1995) (see Table 5). The precursor to the **PM** (transition at position 14022), identified in Taiwanese aborigineal groups, was discovered by whole mtDNA sequencing (Trejaut et al., 2005). This finding contributes to the genetic and linguistic evidence that supports a Taiwanese origin of the proto-Polynesian/Austronesian-speaking people. The average divergence for the coalescent of the PM suggests that its defining substitution arose likely in Indonesia between 900 to 23,000 years ago (Redd et al., 1995). After the birth of the PM haplotype, Redd et al. (1995) estimated that there was a population expansion around 5,000 years ago, which

corresponds to the Austronesian expansion that moved from Indonesia eastward into Near Oceania.

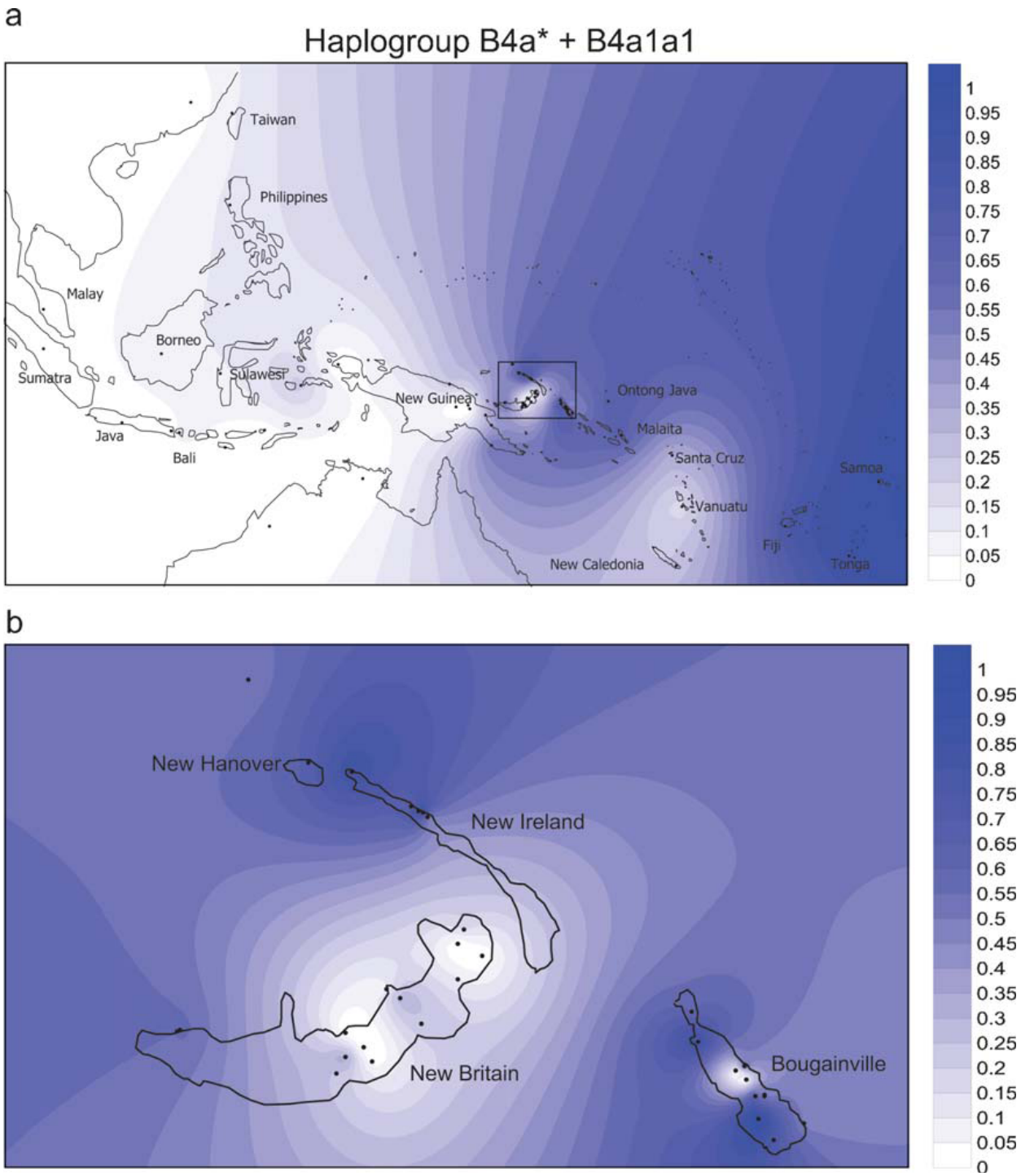


Figure 17. Distribution of B4a* (PM included) and B4a1a1 (Friedlaender et al., 2007)

Haplogroup	PM	%
Highest frequency	Remote Oceania	0.784
High frequencies	New Ireland	0.662
High frequencies	Solomons	0.592
Source	Delfin et al. 2012	

Table 5. PM haplogroup information

2.4.2.2 MtDNA lineage B4: Haplogroup B4a1a1

Like haplogroup **PM**, haplogroup **B4a1a1**, is rare in island southeast Asia, yet is found in high frequencies within Near-Oceanic and Remote Oceanic populations. **B4a1a1** is observed at near fixation in some Papuan-speaking populations such as New Ireland and Bougainville (Friedlaender et al., 2007) (see Figure 17 and Table 6). B4a1a1 is also found frequently in

Haplogroup	B4a1a1	%
Highest frequency	New Ireland	0.165
High frequencies	Solomons	0.145
High frequencies	Remote Oceania	0.136
Source	Delfin et al. 2012; Friedlaender et al., 2007	

Table 6. B4a1a1 haplogroup information

Polynesian populations and then at low frequencies in Vanuatuan and Fijian populations (Friedlaender et al, 2007; Kayser et al., 2006).

2.4.2.3 MtDNA lineage B4: Haplogroup B4b1

Asian-derived mtDNA haplogroup **B4b1** has been observed in Near Oceania and Remote Oceania, however, there is limited information on its origin and distribution (Friedlaender et al., 2007). A study in 2012 by Delfin et al. identified this haplogroup in low frequencies (under 13%) among populations from the Philippines, Taiwan (Aborigines), and Tuvalu (Polynesia) (see Figure 18 and Table 7). Other than its identification among these groups, there is little to no information available on haplogroup **B4b1**.

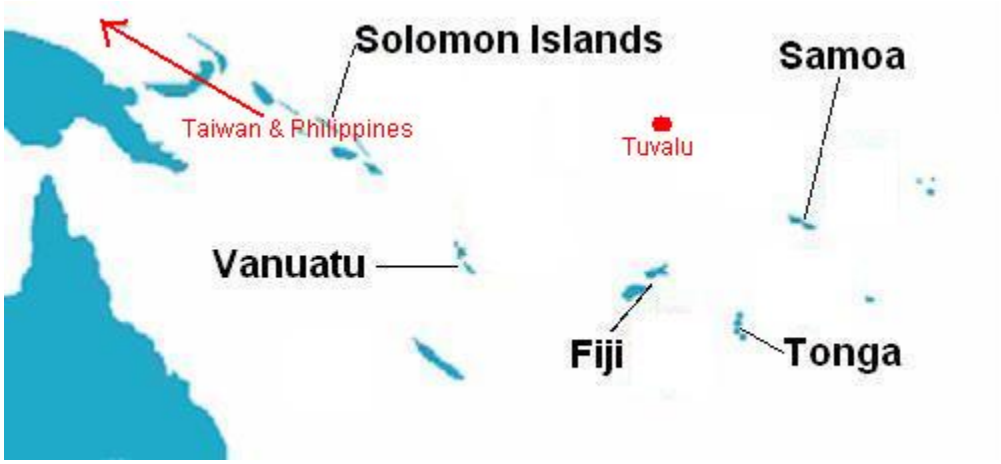


Figure 18. Tuvalu, Taiwan, and the Philippines (About.com, 2012)

Haplogroup	B4b1	%
Highest frequency	Philippines	0.133
High frequencies	Taiwan Aborigines	0.100
High frequencies	Tuvalu (Polynesia)	0.085
Source	Delfin et al. 2012	

Table 7. B4b1 haplogroup information

2.4.3 The Austronesian expansion: Evidence from the mitochondrial DNA 9 base pair deletion

The discovery of a 9 base pair (bp) deletion in southeast Asian-derived mtDNAs has been helpful in tracking the ancient movement of the people involved in the Austronesian expansion. The 9bp mtDNA deletion occurs between the COII and Lysine genes, and it has been valuable to those studying the Austronesian expansion throughout the Pacific because the proto Polynesians likely possessed this genetic signature that today allows anthropologists to track their ancient movements throughout the Pacific (Merriwether et. al. 1999; Redd et al., 1995). Most people possess two copies of the 9bp repeat segment, and this is likely the ancestral state (Horai et al., 1993). The 9bp deletion likely occurred when one repeated copy of the two repeated segments was mispaired during replication (Albertini et al., 1982; Levinson and Gutman, 1987). People outside of Southeast Asia and Polynesia typically have two repeated 9 bp segments, whereas most Southeast Asians and Polynesians do not have the second repeated segment (Redd et al., 1995). The 9bp deletion has been observed in 79% of Samoan (Polynesia) mtDNAs and 74% of coastal PNG (Melanesia) mtDNAs (Redd et al., 1995). Ohashi et al. (2006) estimated that the motif rapidly became incorporated in Melanesian and proto Polynesian mtDNA around 7,060 years ago. To date, geneticists have found that every Austronesian speaker sampled possessed the 9 bp deletion whereas non-Austronesian speakers did not (Redd et al., 1998; Merriwether, 1999). These results demonstrate that the deletion and the associated control region sequence data are very useful markers for tracking the movement of Austronesian speakers throughout the Pacific.

2.4.4 Austronesian colonization of Remote Oceania

Haplotype (gene) diversity (H) estimates support a west to east Austronesian colonization of the Pacific. In general, individuals from a population with low diversity are genetically very similar, whereas individuals from a population with high diversity are genetically more different from each other. MtDNA diversity among the islands of northern Melanesian is high when compared to islands further south and east. This variation reflects the antiquity of the populations inhabiting this region. Over a great period of time genetic drift, geographic isolation, internal population expansions, and the influx of Asian-derived mtDNA lineages all affected population structure in this region (Friedlaender et al., 2007). In 1995, Redd et al. examined mtDNA from three populations: Indonesian islanders, Papua New Guinea low and highlanders (Melanesian), and Samoans (Polynesian). The mtDNA pairwise diversity was calculated to be the greatest in Indonesia, intermediate in coastal PNG, then lowest in Samoa. This pattern suggests that the Austronesian speakers traveled from Indonesia, through Melanesia, then eastward to the Polynesian islands. A large-scale sampling of Pacific Island mtDNAs and NRYs provided further confirmation that haplotype diversity declines west to east for all Polynesian island populations (Kayser et al., 2006). This decrease in diversity is to be expected, as each founding population budded off an established island population, then headed westward. The resultant founder effect was also compounded by the geographic isolation each island population faced. Both variables contributed to the proliferation of founder mtDNA lineages that are today observed. Kayser (2006) identified Fiji as the founding population for all Polynesian islands. Moreover, Fiji's population was the most genetically diverse Near or Remote Oceanic population in terms of both mtDNA and

NRY haplotype diversity measures. These results support an Austronesian expansion eastward throughout Near and Remote Oceania, with the islands of Fiji playing a large role in the peopling of Polynesia.

2.4.5 Sex-biased genetics in Austronesian-founded populations

Genetic evidence suggests that the proto-Polynesians were likely traveling in matrilineal groups when they colonized Remote Oceania. Geneticists often utilize maternally and paternally-inherited markers for anthropological investigations. In addition to tracing ancestry, these markers possess the ability to reveal social information about the population to which they are being applied. For example, a population with high diversity of female lineages and only a few male lineages suggests that individuals within this population had taken up patrilocal residence and they most likely practiced patrilineal descent. Based on mtDNA and non-recombining Y chromosome (NRY) haplogroup distributions across Remote Oceania, geneticists have argued that the proto-Polynesians were matrilineal by descent and matrilocal in residence (Hage and Marck, 2003; Kayser, 2006, 2010). Today, matrilineal descent is widespread in Oceanic-speaking societies in Micronesia and in parts of Melanesia (Allen, 1984; Hage and Marck, 2003). In fact, the majority of Oceanic-speaking societies today display a matricentric orientation. Anthropologists interpret this observation as the historical residue of a matrilineal proto-Oceanic society (Hage and Marck, 2003). To further support this claim, a recent survey of Polynesian mtDNA and NRY lineages across Remote Oceania revealed that most Polynesian mtDNAs are Asian-derived (96%) and

most Polynesian NRYs are Near-Oceanic (62%) (Kayser et al., 2006). Kayser et al. (2000) proposed the 'Slow Boat' model to explain the high levels of male contribution to Polynesian founding populations. Under this model, the Austronesian-speaking ancestors of today's Polynesia "mixed extensively" with indigenous Papuan-speaking populations and the result was that Asian genetic signatures appeared in Near-Oceanic populations and Near-Oceanic genetic signatures appeared in Polynesian populations (Kayser et al., 2000). Because significantly more male than female lineages were incorporated into the proto-Polynesian populations, it is safe to say that outside men were entering this population but outside females were not. Furthermore, genome-wide SNP data analysis has also identified a higher Asian contribution to Polynesian X chromosomes than to the autosomes, confirming a sex-biased mating pattern (Wollstein et al., 2010). With all lines of evidence taken into consideration, it appears that matrilineal descent and matrilocal residence patterns were an integral part of proto-Polynesian societies.

2.4.6 Biological studies of the Fijian people

What makes the Fijian population so interesting from a biological standpoint is that depending on the biological marker used, Fijians may either be classified as Melanesian or Polynesian. An anthropologist looking solely at ABO blood frequencies would most likely cluster the Fijian population with Samoan and Tongan populations. Yet the anthropologist analyzing skin pigment notes that Fijians cluster with Melanesian populations. Various biological studies have demonstrated that Fijians are in some ways like Melanesians and in other ways like Polynesians.

In 1846, Horatio Hale examined the relationships between Polynesian language, geographic location, and physical appearance of island individuals. He concluded that Fiji was a melting pot for the darker Melanesian people and the lighter colored proto Polynesian people (Hale 1846; Kirch 2000). This idea that the Fijian islands functioning as a melting pot for Melanesian and Polynesian people is difficult to refute, as Fijians share so many biological features with both populations. Fijian people have dark skin and hair texture similar to Melanesians, yet a stature to body mass ratio similar to Polynesians (Houghton, 1996). Fijian's overall blood group frequencies are near identical to Samoan and Tongan populations, yet some anthropologists have argued that their cranial measurements are more Melanesian-like (Hunt, 1990; Pietrusewsky, 1983). Given that the Fijians present a heterogeneous mixture of many Melanesian and Polynesian biological traits, it is evident that Fijian history was complex, involving multiple interactions between neighboring island populations.

Stature and body mass measurements have often been used in biological studies and these measurements indicate that Fijians are more Polynesian-like than Melanesian-like. Early European voyagers described Fijians as possessing a "great variety of figures," but most were large and powerful in appearance (Williams, 1858). Like their Polynesian neighbors, Fijians were described as "well-formed" and of large stature (Erskine, 1967). Early stature estimates placed Fijians between average European height and average Tongan height, with the average 1850s European male about 5'6" and the average Polynesian male at this time 5'10" (Houghton, 1996). To date, the only morphological study to investigate inter-archipelagic variation in Fiji was the Gabel (1958) study. This research project used anthropometric measurements to identify

differences in stature and body mass between Viti Levu islanders and Lau islanders of Fiji (Gabel, 1958; Houghton, 1996). In general, stature was slightly greater in Viti Levu and body mass was much greater in the Lau Group. The average stature/body mass found among Lau Islanders was comparable to Tongan and Samoan results (Houghton, 1996). This is not surprising, as Lau Islanders are located geographically nearer to these islands and have a history of recent interaction via the sandalwood trade (Kirch, 2000). The people of Fiji, on average, share a comparable stature/body mass ratio with Polynesians and this is not surprising, as Fijians share a long and complex history of interaction with the Polynesian island systems.

Some anthropologists have argued that Fijians resemble Melanesian populations with respect to cranial features (Hunt, 1990; Pietrusewsky, 1983). Cluster analyses and Euclidean distance dendrograms both constructed from cranial measurement data placed Fijians closer to Melanesian populations than to Polynesian populations. These results stand in contrast to another biological study that focused on cranial and post cranial measurements. Howells and Moss (1933) found that averages of Fijian stature, head breadth, and facial height all fell within the limits of Polynesian population data. Only one averaged Fijian measurement, nasal index, fell within the limits of Melanesian population data. Four measurements were intermediate between the two populations. Howells and Moss concluded that the Fijians were metrically more Polynesian, though some morphological features like nasal index, hair texture, and skin color did not fit this notion.

Blood type testing of the Pacific Islanders from the 1950s to 1960s revealed that Fijians were more Tongan/Samoan-like than Melanesian-like (Simons, 1968). Decades

ago, physical anthropologists incorporated blood type testing into their research programs as a means to infer genetic population structure. Upon identifying overall frequencies of blood types (A, B, and O) within a population, anthropologists then compared results between populations (Houghton, 1996). This methodology enabled anthropologists to estimate genetic relatedness between populations and infer migration movements island to island in the Pacific. Using this method, the Fijian population was hypothesized to have been the founding population of both Tonga and Samoa (Simons, 1968). The B blood type, associated with Melanesians and Micronesians, was found more frequently in Fijian, Tongan, and Samoan populations than any other Polynesian populations. The authors suspected that the original founders of the Polynesian populations did not possess blood type B, but were most frequently type A and that recent gene flow from Melanesia and/or Micronesia explained why blood type B was commonly found in these three populations and rarely identified in other Polynesian populations (Simons, 1968). The high frequency of blood type B in the Fiji-Samoa-Tonga region explains why many Melanesian morphological features are present in the Fijian population.

Though there is mixed evidence for the classification of Fijians as Melanesian or Polynesian, it is evident that Fijians share a number of biological characteristics with the Polynesians (body size and some cranial features) and with the Melanesians (mainly skin color and hair texture, but also some cranial features). The Fijian population has historically been identified as a single population, but this may not be the best way to classify this grouping of individuals. The Gabel study (1958) comparing Viti Levi islander and Lau Islander stature to body mass ratios illustrates this problem. Each region of Fiji needs to be sampled for a more accurate description of the true biological

variation that exists. However, because these data do not exist to date, anthropologists must utilize what is available today. With all lines of evidence taken together, it appears that the Fijian people represent a mixture of both Polynesian and Melanesian features; however, inter-archipelagic biological variation exists in Fiji and this has not been satisfactorily addressed.

2.4.7 Fijian genetics

The people of Fiji are situated geographically and genetically intermediate between Melanesian and Polynesian populations. The Fijian population exhibits the highest diversity of mtDNA and NRY lineages when compared to Polynesian populations, with diversity decreasing eastward of Fiji, suggesting that the Lapita people colonized Fiji and then a subset continued to migrate out to the Polynesian islands (Kayser et al., 2006). Surprisingly, there have been relatively few genetic studies to include the Fijian population even though Fiji is one of the largest archipelagoes in the Pacific and it played a central role in the peopling of the Polynesian islands. Geneticists and archeologists have emphasized the need for more population sampling in Fiji in order to better understand Fiji's complex history (Kayser et al., 2006; Sheppard, 2011). Unfortunately, despite anthropologist demands for increased sampling of Fijian mtDNAs and NRYs, there has been no systematic investigation. Nonetheless, based on data currently available, Fijians appear genetically intermediate between Melanesians and Polynesians.

2.4.7.1 Fijian mitochondrial DNA studies

Fijian mtDNA diversity is high and Asian-derived lineages are more frequently observed than Near-Oceanic-derived lineages. Fiji is the only island population east of Vanuatu where all four major Near-Oceanic mtDNA haplogroups (**P**, **Q1**, **Q2**, and **M28**) are found (Kayser et al., 2006). Fiji also has the highest overall frequency of Near-Oceanic mtDNA lineages (20.5%) when compared to Polynesian populations (0-7.7%) (Kayser et al., 2006). Though population sampling has been small and limited in geographical range across the archipelago, the mtDNA haplogroups identified thus far in Fiji were: **PM**, **B4***, **P1**, **P2**, **Q1**, **Q2**, and **M28** (Friedlaender et al., 2007; Kayser et al., 2006). Unlike neighboring Vanuatu populations, Fijians possess more Asiatin-derived mtDNAs (60-80%) than Near-Oceanic mtDNAs (20-40%) (Friedlaender et al., 2007; Kayser et al., 2006). Fiji's high mtDNA diversity indicates that Fiji in fact played a central role in the peopling of Remote Oceania and the predominance of Asian-derived mtDNAs suggests that there was limited Melanesian migration into Fiji over the past 3,200 years.

2.4.7.1 Fijian Y chromosome studies

Fijian non-recombining Y (NRY) lineages show great diversity like the mtDNA lineages and the pattern of a high Asian contribution of mtDNAs coupled with a high contribution Near-Oceanic NRYs in Fiji aligns well with Hage and Marck's Matrilineality Hypothesis. All Near-Oceanic NRY lineages found in Polynesia are also

found in Fiji and Fijians display the highest diversity of Near-Oceanic NRY haplogroups when compared to Polynesian populations (Kayser et al., 2006). The following NRY haplotypes have been identified in Fiji: **C-RPS4Y**, **C-M38**, **C-M208**, **F-M89**, **K-M9**, **M-M4**, **M-M104**, **NO-M214**, **O-M119**, **O-M122**, **R-M173**, **K-M353** (Kayser et al., 2006). The NRY haplotype **M-M4** is more frequently observed in Fiji (24.3%) than anywhere else. **M-M4** is found in Melanesia with a frequency of 2%, and it likely arose in Near Oceania before reaching Fiji where it exploded in frequency. Interestingly, **M-M4**'s subgroup, **M-P34**, most likely arose after Fiji was founded, as it has not been identified in Fiji. Subgroup **M-P34** is observed at frequencies of 28-74% in Melanesia, whereas the high frequencies of **M-M4** found in Fiji suggest that Fiji was founded by the older haplogroup before a mutation occurred in **M-M4**. More NRY research in Fiji is needed to validate this observation. If **M-P34** is not found in Fijian populations, geneticists will have evidence that there was limited immigration to Fiji from Melanesia by at least the date of the P34 mutation. Nonetheless, the limited research focusing on the Fijian population has revealed a pattern that is consistent with many other Remote Oceanic island populations: more Fijians possess Asian-derived mtDNAs than Near-Oceanic-derived ones and the reverse is the case for Fijian NRYs. This finding supports Hage and Marck's Matrilineality Hypothesis which posits that Austronesian-speaking Lapita populations traveled in matrilineal groups, incorporating Melanesian men into their matrilocal residences. The evidence for this hypothesis is strong in Fiji, yet the high diversity of mtDNA and NRY lineages observed in Fiji suggests a more complex prehistory in Fiji than in the Polynesian islands.

2.4.7.1 Fijian autosomal study

Wollstein et al. (2010) argued that after Remote Oceania was colonized, Fiji, unlike the Polynesian islands, experienced subsequent contact with Near Oceania. Wollstein et al. used nearly one million genome-wide single nucleotide polymorphism (SNP) data from sub-Saharan Africans (n=60), Europeans (n=60), East Asian (n=90), Borneons (n=23), New Guineans (n=24), Fijians (n=25), and Polynesians (n=25) to investigate demographic models of Pacific prehistory. The results align well with previously reported date estimates for migration into the Pacific (Kirch, 2000). Specifically, the authors identified an ancestral Near-Oceanic divergence from Eurasians at about 27,000 year ago and genetic admixture between East Asians and Near Oceanians occurring around 3,000 years ago, preceding the Lapita expansion into Remote Oceania. In addition to testing well understood demographic models, Wollstein et al. focused on Fiji's prehistoric interactions with Near and Remote Oceania. Upon selecting the best fitting model of population history using approximate Bayesian computation simulations, the authors concluded that Fijians autosomes carry about two times more Near-Oceanic ancestry than Polynesians. The Polynesian sample was admixed with 87% Borneon and 13% New Guinean contribution, whereas the Fijian sample was admixed with 65% Polynesian and 35% New Guinean contribution. The authors argued that there was secondary admixture between Fijians and Near Oceanians after the colonization of Remote Oceania based on the admixture date estimation. However, Wollstein et al. did not feel this time estimate was reliable because the model used predicted Fiji's parental populations to be Near-Oceanic and Polynesian and not Near-Oceanic and Borneon (like

Polynesia). So, it is also possible that the founding populations of Fiji were admixed at the time of colonization. While this study has been useful in estimating autosomal admixture among Fijians, it has not been useful in dating or explaining the additional hypothesized Near-Oceanic admixture that may have occurred among Fijians.

CHAPTER 3: MATERIALS AND METHODS

3.1 MATERIALS

This chapter provides information on the procedures used to perform the analyses in this project. The first section, Materials, will define the participants of this study and provide details on sampling methods. The second section, Laboratory Methods, provides the protocols used to process the mitochondrial DNA (mtDNA) samples. Finally, the third section, Methods of Analysis, explains each analytical technique used to explore the mtDNA dataset.

3.1.1 Study participants

A total of 162 individuals participated in this study. In addition to providing a buccal sample, each participant shared information regarding their maternal ancestry from as many generations back as they were able. Individuals claiming non-native Fijian decent were excluded from the study. All participants were able to identify the island of their mother's birthplace. Many paricipants were able to identify the island of their mother's mother's birthplace. All Fijian participants gave informed consent. Buccal samples from the participants were collected in 2008 by Geetanjali Tiwari, Alan J. Redd, and Anand P. Tyagi. This project was approved by the Human Subjects Committee of Lawrence (HSCL #17356).

3.1.2 Island populations examined

The following five Fijian island populations were represented: Viti Levu (n=22), Vanua Levu (n=21), Kadavu (n=21), Lau Islands (n=22), and Rotuma (n=21). Two Melanesian islands were represented: The Solomon Islands (n=20) and Vanuatu (n=13). Finally, two Polynesian islands were represented: Tonga (n=16) and Samoa (n=8).

3.2 LABORATORY METHODS

3.2.1 Protocol for mtDNA sample processing

The mtDNA used in this study came from buccal cells. MtDNA was extracted over a three day period using the phenol-chloroform method as described by Sambrook and Russell (2001). 100uL Low TE pH8 was added to the mtDNA pellets post extraction. All samples were tested for both mtDNA purity and concentration using a NanoDrop© Spectrophotometer.

A 405 base pair (bp) fragment from within the HVS1 region of the mitochondrial genome was selected for analysis. The light-chain (L) primer selected was L-15996 (5' ACTCCACCATTAGCACCCAAAGC 3') and the heavy-chain (H) primer selected was H-16401 (5' CACCATCCTCCGTGAAATCA 3'). The Polymerase Chain Reaction (PCR) buffer was produced by Takara© and contained a 10x buffer (2.5uL/sample), 2.5mM dNTPs (2uL/sample), 25mM MgCl2 (1.5uL/sample), and 5 units/uL Taq (0.2uL/sample). In addition to the master mix, 2uL of DNA, 15.4uL of sterile H2O, and 0.7uL of both 20uM primers made up the reaction mix. For the PCR reaction, a BioRad

MyCycler was used. The cycling profile was set to the following specifications: 1) Initial denature, 94°C for 3 minutes 2) Denaturation segment, 94°C for 45 minutes 3) Annealing segment, 55°C for 45 minutes 4) Elongation segment, 72°C for 45 minutes 5) Final extension, 72°C for 3 minutes. All PCR reactions were tested for success by running 2uL of the PCR product along with 4uL of a loading dye solution through a gel agarose plate while electrophoresing the products. The gels were then illuminated under a UV light and photographed for documentation. All successful PCR products were then cleaned using a QIAquick© PCR purification kit and protocol. All post PCR products were then re-tested for both DNA purity and concentration using a NanoDrop© Spectrophotometer. Finally, working solutions were prepared.

3.2.2 MtDNA sequencing

The sequencing of the HVS-1 fragments was performed by the University of Kansas DNA Sequencing Laboratory. After the sequence data were received, the forward and reverse fragments were visualized by the program SEQUENCHER®, version 4.8, (Gene Codes Corporation, 2007). Both fragments were aligned with the revised Cambridge Reference Sequence (CRS), which is a standardized sequence used by all scientists working with mitochondrial DNA. The sections of low quality sequence were removed. Each substitution within the sequence was inspected by viewing the chromatogram to ensure proper sequence calling. After the sequence was constructed by merging the two fragments, the ends were trimmed to fit the CR. The final mtDNA fragment length was 362 bp.

3.2.3 MtDNA haplogroup assignment

3.2.3.1 Identification of variable sites

All 162 sequences were aligned to the revised CRS using the program UltraEdit®, version 7.20a (IDM Computer Solutions Inc., 2000). The file was then opened in the program MEGA©, version 4, where the variable substitution sites were identified (Tamura et al., 2007). All substitutions for each sequence were identified and noted in Table 8, which is located in the Results chapter.

3.2.3.2 Defining mutations for mtDNA haplogroups and sequence assignment

In order to assign mtDNA haplogroups for the sequences, three haplotype defining sources were used: Friedlaender et al. (2005, 2007), and van Oven and Kayser (2009). All three sources have identified the defining substitutions for the mtDNA haplogroups of the Pacific people. For this study, a total of 41 unique, un-published haplotypes were observed. These unique haplotypes are shown in Table X of the Results chapter and later discussed in the Discussion chapter. In most instances, these haplotypes possessed at least one additional substitution outside of the defining substitutions for the haplotype. For this reason, all variable sites for each sequence have been identified in Table 8 (Results chapter). For sequences that possessed additional substitutions outside of the defining substitution list associated with a specific haplotype, or for those

sequences that had a possible reversal of a defining substitution, 'New Type' (NT) was denoted in the far right column of the table and the novel substitutions were highlighted white. Because there has been limited sampling in Fiji ($n < 70$) and that sampling has mainly been from the main island, Viti Levu, new haplotypes were expected to emerge from this project (Friedlaender et al., 2007; Kayser et al., 2006). Further classification of these new types is necessary, but unfortunately beyond the scope of this project.

3.3 METHODS OF ANALYSIS

3.3.1 Haplogroup frequency classification

Once haplogroups were assigned for all sequences, pie charts were constructed using Excel®, (Microsoft, 2003). The pie charts were created for two purposes: 1) they are simple tools that illustrate overall percentages of Asian and Near-Oceanic haplogroups that exist within each population sample, and 2) they provide a nice visualization of the mtDNA variation that exists between population samples. In addition to the pie charts, a two-part table were constructed to aid in the visualization of the haplogroup frequencies. The tables, like the pie charts, were also constructed in Excel®. The upper portion of Table 9 displays counts for each haplogroup found in each population and the lower portion displays haplogroup frequencies for each population.

3.3.2 Haplotype sharing

Haplotypes shared between samples were calculated using ARLEQUIN©, version 3.1 (Excoffier, 2006). Table 10 displays the overall number of shared haplotypes between samples and Table 11 displays the overall number of shared Near-Oceanic haplotypes between samples.

3.3.3 Measurements of diversity within populations

3.3.3.1 Nei's gene diversity statistic (H)

For populations with haplotype variation of mtDNAs, an unbiased estimate of gene diversity was calculated using Nei's gene diversity statistic (H). Haplotype diversity, or gene diversity, represents the probability that two randomly sampled haplotypes are different (Excoffier, 2006; Nei, 1987). This statistic describes the number and frequency of different haplotypes that exist in a given sample. For this study, *H* was calculated using the program ARLEQUIN©, version 3.1 (Excoffier, 2006). All nine populations were included in this calculation: Viti Levu, Vanua Levu, Rotuma, Kadavu, the Lau Islands, Tonga, Samoa, Vanuatu, and the Solomon Islands. The haplotype diversity values are shown in Table 12. The diversity values are also overlaid on a map in Figure 20.

3.3.3.2 Mean number of pairwise differences between all pairs of haplotypes within a sample (π)

The π statistic is defined as the mean number of base-pair differences between all pairs of haplotypes within a sample (Excoffier, 2006). Along with the gene diversity statistic (H), π is a classical molecular index that estimates within population diversity. For this study, π was calculated using the program ARLEQUIN©, version 3.1 (Excoffier, 2006). All nine population samples were included in this calculation. The pairwise differences (π) are shown in Table 12. The diversity values are also overlaid on a map in Figure 20.

3.3.3.3 Number of haplotypes

Measuring the number of mtDNA haplotypes within a population sample is a simple measure of diversity. The number of haplotypes identified for each population are shown in Table 12.

3.3.4 Measurement of diversity among populations

3.3.4.1 Non-Metric Multidimensional Scaling (MDS)

Using a table of genetic distances between items (in this case populations), multidimensional scaling (MDS) programs construct maps that show relationships between the items (Manly, 2005). This diagram may be in one, two, three or more dimensions depending on the nature of the dataset and the wishes of the user. MDS is useful for situations where the underlying relationship between items is unknown, but a

distance matrix can be estimated (Manly, 2005). Thus, MDS provides the dataset with a 'picture' or 'map' of the underlying relationship with similar items shown close together and dissimilar items shown far apart (Manly, 2005).

For this research project, a distance matrix was constructed from calculated population pairwise F_{ST} values using the program ARLEQUIN©, version 3.1 (Excoffier, 2006). F_{ST} was selected as the genetic distance measure because it is a classically used index of dissimilarity between pairs of populations (Excoffier, 2006). F_{ST} values range from 0 to 1, with $F_{ST} = 0$ indicating that the two populations are genetically identical and $F_{ST} = 1$ indicating that the two populations are genetically dissimilar. All nine populations of this study were included in various MDS plots constructed. The resultant population pairwise F_{ST} matrix was then uploaded into the program NTSYSpc©, version 2.02h, where a two-dimensional monotonic MDS plot was constructed. Goodness-of-fit between the monotone function of the original distances and the distances present in the plot was tested using Kruskal's Stress statistic. Kruskal gave the following verbal descriptions for various levels of fit:

Stress	*- Goodness of fit*
0.40	Poor
0.20	Fair
0.10	Good
0.05	Excellent
0.00	"Perfect"

Figure 19. Evaluation of Stress

3.3.5 Measurement of multivariate distances

3.3.5.1 Mantel randomization test

The Mantel randomization test is useful for comparing two different distance matrices to test for an association between two variables. The test assesses whether or not the elements between the two matrices show significant correlation between corresponding items (Manly, 2005). The statistic's product is compared with the Z distribution, which is produced by taking the objects in a random order for one of the matrices (Manly, 2005). The correlation, r, lies in the range of -1 to +1, with r = -1 indicating a perfect, negative correlation between the two distance measures and r = 1 indicating a perfect, positive correlation. An r value equal to 0 indicates no correlation (Manly, 2005).

For this project, the Mantel randomization test was employed to test for a relationship between an island's geographic location and its people's mtDNA population structure. A Euclidean distance matrix was constructed in Excel®. For all nine islands represented in this study, a geographical measurement was taken by capturing the latitude and longitude of the center of each island in decimal degrees. The distance between pairs of points was then calculated in Excel® using the Pythagorean Theorem. For the genetic distance matrix, pairwise Fst values previously calculated were used. Both matrices were uploaded to NTSYSpc©, where a Mantel randomization test was performed using 1,000 randomization runs.

3.3.6 Tree phylogeny

3.3.6.1 Neighbor-joining tree

The neighbor-joining (NJ) method transforms a genetic distance matrix into a phylogenetic tree. This method is ideal for large datasets, such as the dataset for this thesis, because the algorithm is fast. The NJ method also does not assume that all lineages possess the same evolutionary rate, so it produced an unrooted tree (Tamura et al., 2007). For this project, a NJ tree was constructed under a maximum composite likelihood model using the program MEGA©, version 4. One thousand replicates were performed. The tree was constructed to assess haplotype assignment success. The results are presented as Figure 25.

CHAPTER 4: RESULTS

4.1 MITOCHONDRIAL DNA RESULTS

This chapter displays the results of the analyses performed on the mitochondrial DNA (mtDNA) sequences used in this project. The first section highlights the substitutions found within each mtDNA sequence and lists the haplogroup assignment. The second section displays the haplogroup frequencies for each population. The third section provides the within-population diversity results and the between-population diversity results. Finally, the last section details the multivariate results.

4.1.1 Mitochondrial DNA (mtDNA) haplogroup assignment

Table X displays the mtDNA haplogroup assignments for each mtDNA sequence. ID refers to the identification of each individual that participated in the study. Each individual's name has been changed to a unique ID that combines both the name of the population where his or her maternal lineage originated and a number from 1 to n that identifies the individual within his or her population. The variable sites for each sequences are identified in columns 1-10, with the three digit number referring to the location of that particular base pair in the mitochondrial genome (add 16,000 to each three digit value) and the letter referring to the new base pair (bp) substitution. Under these same columns, the defining substitutions for each respective haplogroup, are highlighted in yellow, and new substitutions are highlighted in white. Column HG stands for 'Haplogroup Assignment' and this column displays the haplogroup assignment that

best defines each mtDNA sequence. Column NT stands for 'New Type,' referring to a unique haplotype that is a new discovery. The haplogroup counts and frequencies for each population are displayed in Table 9. In total, 13 different haplogroups were identified, with 51 different haplotypes falling under these groups. In addition, a total of 41 sequences were identified to be novel haplotypes with unique substitutions (some new haplotypes are shared between individuals, so the number of new haplotypes reflected in the column 'NT' does not reflect the actual number of newly discovered haplotypes)

KEY - Table X

ID – Identification of Islander (island population name & within population identifier)
HG – Haplogroup assigned to individual
NT – Denotes a unique haplotype that was novel

ID	1	2	3	4	5	6	7	8	9	10	HG	NT
Lau Islander 1	086 C	148 T	223 T	239 T	311 C	318 T					Q1	NT
Lau Islander 2	189 C	217 C	247 G	258 C	261 T						PM	NT
Lau Islander 3	189 C	217 C	247 G	261 T							PM	
Lau Islander 4	129 A	148 T	223 T	362 T							M28	NT
Lau Islander 5	066 G	129 A	223 T	241 G	294 T	352 C					Q2	NT
Lau Islander 6	189 C	217 C	247 G	261 T							PM	
Lau Islander 7	189 C	217 C	247 G	261 T							PM	
Lau Islander 8	189 C	217 C	247 G	261 T							PM	
Lau Islander 9	104 T	189 C	217 C	247 G	261 T	362 C					PM	NT
Lau Islander 10	189 C	217 C	247 G	261 T							PM	
Lau Islander 11	189 C	217 C	247 G	261 T							PM	
Lau Islander 12	189 C	217 C	247 G	261 T	311 C						PM	NT
Lau Islander 13	189 C	217 C	261 T								B4a1a1	
Lau Islander 14	066 G	129 A	223 T	241 G	294 T	352 C					Q2	NT
Lau Islander 15	189 C	217 C	247 G	261 T							PM	
Lau Islander 16	189 C	217 C	247 G	261 T	292 T						PM	NT
Lau Islander 17	189 C	217 C	247 G	261 T							PM	
Lau Islander 18	189 C	217 C	247 G	261 T							PM	
Lau Islander 19	189 C	217 C	247 G	261 T							PM	

Lau Islander 20	189 C	217 C	261 T								B4a1a1	
Lau Islander 21	189 C	217 C	261 T	270 T							B4a1a1	NT
Lau Islander 22	189 C	217 C	247 G	261 T							PM	
Rotuman 1	189 C	217 C	247 G	261 T							PM	
Rotuman 2	189 C	217 C	247 G	261 T							PM	
Rotuman 3	189 C	217 C	247 G	261 T							PM	
Rotuman 4	189 C	217 C	247 G	261 T							PM	
Rotuman 5	189 C	217 C	247 G	261 T							PM	
Rotuman 6	189 C	217 C	247 G	261 T							PM	
Rotuman 7	189 C	217 C	247 G	261 T							PM	
Rotuman 8	189 C	217 C	247 G	261 T							PM	
Rotuman 9	189 C	217 C	247 G	261 T							PM	
Rotuman 10	189 C	217 C	247 G	261 T							PM	
Rotuman 11	189 C	217 C	261 T								B4a1a1	
Rotuman 12	189 C	217 C	247 G	261 T							PM	
Rotuman 13	189 C	217 C	261 T								B4a1a1	
Rotuman 14	189 C	217 C	247 G	261 T							PM	
Rotuman 15	189 C	217 C	247 G	261 T							PM	
Rotuman 16	189 C	217 C	247 G	261 T							PM	
Rotuman 17	189 C	217 C	247 G	261 T							PM	
Rotuman 18	189 C	217 C	247 G	261 T							PM	
Rotuman 19	189 C	217 C	247 G	261 T							PM	
Rotuman 20	189 C	217 C	247 G	261 T							PM	
Rotuman 21	067 T	136 C	189 C	217 C							B4b1	NT
Vanua Levuan 1	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 2	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 3	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 4	176 T	209 C	266 T	357 C							P1e	
Vanua Levuan 5	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 6	086 C	189 C	217 C	247 G	261 T						PM	NT
Vanua Levuan 7	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 8	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 9	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 10	066 G	129 A	223 T	232 T	241 G						Q2	NT
Vanua Levuan 11	209 C	266 T	304 C	357 C							P1e	NT
Vanua Levuan 12	129 A	144 C	148 T	223 T	241 G	265 C	311 C	343 G			Q1	
Vanua Levuan 13	155 G	189 C	217 C	247 G	261 T						PM	NT
Vanua Levuan 14	163 G	189 C	217 C	247 G	261 T						PM	NT
Vanua Levuan 15	093 C	129 A	144 C	148 T	241 G	263 C	265 C	311 C	342 C	343 G	Q1	NT

Vanua Levuan 16	189 C	217 C	247 G	261 T	311 C						PM	NT
Vanua Levuan 17	189 C	217 C	247 G	261 T	341 C						PM	NT
Vanua Levuan 18	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 19	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 20	189 C	217 C	247 G	261 T							PM	
Vanua Levuan 21	189 C	217 C	247 G	261 T							PM	
Viti Levuan 1	189 C	217 C	247 G	261 T							PM	
Viti Levuan 2	066 G	129 A	223 T	241 G	294 T	253 C					Q2	NT
Viti Levuan 3	189 C	217 C	247 G	261 T							PM	
Viti Levuan 4	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT
Viti Levuan 5	189 C	217 C	261 T								B4a1a1	
Viti Levuan 6	075 C	129 A	144 C	148 T	223 T	241 G	265 C	311 C	343 G	362 C	Q1a2	
Viti Levuan 7	189 C	217 C	247 G	261 T							PM	
Viti Levuan 8	189 C	217 C	247 G	261 T							PM	
Viti Levuan 9	189 C	217 C	247 G	261 T							PM	
Viti Levuan 10	189 C	217 C	247 G	261 T							PM	
Viti Levuan 11	189 C	217 C	247 G	261 T	311 C						PM	NT
Viti Levuan 12	189 C	217 C	247 G	261 T							PM	
Viti Levuan 13	066 G	129 A	189 C	217 C	247 G	261 T					PM	NT
Viti Levuan 14	066 G	129 A	189 C	223 T	241 G						Q2	NT
Viti Levuan 15	189 C	217 C	247 G	249 C	261 T	280 G					PM	NT
Viti Levuan 16	066 G	129 A	189 C	223 T	241 G						Q2	NT
Viti Levuan 17	189 C	217 C	261 T	311 C							B4a1a1	NT
Viti Levuan 18	189 C	217 C	247 G	261 T							PM	
Viti Levuan 19	189 C	217 C	247 G	261 T							PM	
Viti Levuan 20	189 C	217 C	247 G	261 T							PM	
Viti Levuan 21	189 C	217 C	261 T	311 C							B4a1a1	NT
Viti Levuan 22	189 C	217 C	247 G	261 T							PM	
Kadavuan 1	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT
Kadavuan 2	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT
Kadavuan 3	189 C	217 C	247 G	261 T							PM	
Kadavuan 4	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT
Kadavuan 5	189 C	217 C	247 G	261 T							PM	
Kadavuan 6	189 C	217 C	247 G	261 T							PM	
Kadavuan 7	189 C	217 C	247 G	261 T							PM	
Kadavuan 8	189 C	217 C	247 G	261 T	311 C						PM	NT
Kadavuan 9	189 C	217 C	234 T	261 T							B4a1a1	NT
Kadavuan 10	189 C	217 C	247 G	261 T							PM	
Kadavuan 11	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT

Kadavuan 12	086 C	189 C	217 C	247 G	261 T						PM	NT
Kadavuan 13	051 G	086 C	129 A	148 T	223 T	362 C					M28a	NT
Kadavuan 14	086 C	129 A	148 T	189 C	223 T	293 G	362 C				M28a	NT
Kadavuan 15	189 C	217 C	247 G	261 T							PM	
Kadavuan 16	189 C	217 C	261 T								B4a1a1	
Kadavuan 17	180 G	189 C	217 C	247 G	261 T	311 C					PM	NT
Kadavuan 18	189 C	217 C	247 G	261 T							PM	
Kadavuan 19	189 C	217 C	247 G	261 T	311 C						PM	NT
Kadavuan 20	189 C	217 C	247 G	261 T	328 T						PM	NT
Kadavuan 21	189 C	217 C	247 G	261 T							PM	
Tongan 1	129 A	189 C	217 C	247 G	261 T						PM	NT
Tongan 2	189 C	217 C	261 T								B4a1a1	
Tongan 3	093 C	189 C	217 C	261 T							B4a1a1	NT
Tongan 4	189 C	217 C	261 T								B4a1a1	
Tongan 5	189 C	217 C	261 T								B4a1a1	
Tongan 6	189 C	217 C	247 G	261 T							PM	
Tongan 7	189 C	217 C	247 G	261 T							PM	
Tongan 8	189 C	217 C	247 G	261 T							PM	
Tongan 9	066 G	129 A	189 C	241 G	325 C						Q2	NT
Tongan 10	189 C	217 C	247 G	261 T							PM	
Tongan 11	189 C	217 C	247 G	261 T							PM	
Tongan 12	189 C	217 C	247 G	261 T							PM	
Tongan 13	093 C	189 C	217 C	247 G	261 T						PM	NT
Tongan 14	189 C	217 C	247 G	261 T							PM	
Tongan 15	189 C	217 C	247 G	261 T							PM	
Tongan 16	189 C	217 C	247 G	261 T							PM	
Samoan 1	189 C	217 C	247 G	261 T							PM	
Samoan 2	189 C	217 C	247 G	261 T							PM	
Samoan 3	189 C	217 C	247 G	261 T							PM	
Samoan 4	189 C	217 C	247 G	261 T	291 T						PM	NT
Samoan 5	189 C	217 C	247 G	261 T							PM	
Samoan 6	189 C	217 C	247 G	261 T							PM	
Samoan 7	067 T	136 C	189 C	217 C							B4b1	NT
Samoan 8	189 C	217 C	247 G	261 T							PM	
Solomon Islander 1	048 A	093 C	129 A	189 C	290 A	325 C	368 C	374 C			other	NT
Solomon Islander 2	129 A	189 C	217 C	247 G	261 T						PM	NT
Solomon Islander 3	129 A	144 C	148 T	176 T	223 T	265 C	311 C	343 G			Q1	NT
Solomon Islander 4	189 C	217 C	247 G	261 T							PM	

Solomon Islander 5	129 A	144 C	148 T	174 T	223 T	234 T	241 G	265 C	274 A	311 C	Q1	NT
Solomon Islander 6	189 C	217 C	247 G	261 T							PM	
Solomon Islander 7	189 C	217 C	261 T	318 G							B4a1a1	NT
Solomon Islander 8	189 C	217 C	247 G	261 T							PM	
Solomon Islander 9	048 A	077 T	172 C	223 T	311 C						M27a	NT
Solomon Islander 10	086 C	209 C	223 T	299 G							M27b	NT
Solomon Islander 11	086 C	209 C	223 T	295 T	299 G						M27b	NT
Solomon Islander 12	086 C	209 C	223 T	299 G							M27b	NT
Solomon Islander 13	189 C	217 C	247 G	261 T							PM	
Solomon Islander 14	189 C	217 C	247 G	261 T							PM	
Solomon Islander 15	189 C	217 C	247 G	261 T	291 T						PM	NT
Solomon Islander 16	189 C	217 C	261 T								B4a1a1	
Solomon Islander 17	129 A	189 C	290 A	368 C							other	NT
Solomon Islander 18	189 C	217 C	247 G	261 T							PM	
Solomon Islander 19	189 C	217 C	247 G	261 T							PM	
Solomon Islander 20	189 C	217 C	261 T								B4a1a1	
Vanuatuan 1	129 A	148 T	223 T	362 C							M28a	NT
Vanuatuan 2	086 C	129 A	148 T	223 T	362 C						M28a	
Vanuatuan 3	086 C	129 A	148 T	223 T	362 C						M28a	
Vanuatuan 4	148 T	223 T	254 G	291 T	311 C	318 C	362 C				M28b	NT
Vanuatuan 5	086 C	129 A	148 T	223 T	362 C						M28a	
Vanuatuan 6	086 C	209 C	223 T	299 G							M27b	NT
Vanuatuan 7	189 C	217 C	247 G	261 T							PM	
Vanuatuan 8	189 C	217 C	247 G	261 T							PM	
Vanuatuan 9	051 G	189 C	217 C	247 G	261 T						PM	NT
Vanuatuan 10	189 C	217 C	247 G	261 T							PM	
Vanuatuan 11	145 A	176 T	209 C	266 T	311 C	357 C					P1	NT
Vanuatuan 12	189 C	217 C	247 G	261 T							PM	
Vanuatuan 13	189 C	217 C	247 G	261 T							PM	

Table 8. Variable sites and haplogroup assignment for sequences

4.1.2 Haplogroup frequency visualization

A table was constructed to aid in visualization of the haplogroup frequencies. Table 9 displays both the number of individuals from each population (n) and the counts and frequencies of the haplogroups found within each population.

Population	n	B4b1	B4a1a1	PM	P1	P1e	Q1	Q1a2	Q2	M27a	M27b	M28	M28a	M28b
Viti Levu	22		3	14				1	3				1	
Vanua Levu	21			16		2	2		1					
Lau Islands	22		3	15			1		2			1		
Kadavu	21		2	13									6	
Rotuma	21	1	2	18										
Vanuatu	13			6	1						1		4	1
Solomon Islands	20		3	9			2		2	1	3			
Tonga	16		4	11					1					
Samoa	8	1		7										

Viti Levu	22		0.14	0.64				0.05	0.14				0.05	
Vanua Levu	21			0.76		0.10	0.10		0.05					
Lau Islands	22		0.14	0.68			0.05		0.09			0.05		
Kadavu	21		0.10	0.62									0.29	
Rotuma	21	0.05	0.10	0.86										
Vanua Levu	13			0.46	0.08						0.08		0.31	0.08
Solomon Islands	20		0.15	0.45			0.10		0.10	0.05	0.15			
Tonga	16		0.25	0.69					0.06					
Samoa	8	0.13		0.88										

Table 9. Haplogroup frequencies by count and percentage

4.1.3 Haplotype sharing

The three island samples with the most shared haplotypes were the Lau Islands, Viti Levu, and Kadavu (see Table 10). The Solomon Islanders also shared three

haplotypes with the Vanuatuans. The three island samples with the fewest shared haplotypes include Vanua Levu, Vanuatu, and Samoa. In total, there are 126 shared haplotypes between these population samples.

	Lau	Rotm	Vanl	Viti	Kadv	Tnga	Samo	Vanu	Solm
Lau Islands									
Rotuma	2								
Vanua Levu	2	1							
Viti Levu	4	2	2						
Kadavu	3	2	2	4					
Tonga	2	2	1	2	2				
Samoa	1	2	1	1	1	1			
Vanuatu	2	1	1	1	1	1	1		
Solomon Islands	2	2	1	2	2	2	1	3	

Table 10. Number of haplotypes shared between populations

Interestingly, there are only four Near-Oceanic shared haplotypes. Vanuatu, Viti Levu, and the Lau Group shared two of these four (see Table 11). One individual from Vanuatu shared a novel **M28a** haplotype with a single Lau individual. Moreover, one Vanuatuan shared a novel **M27b** haplotype with two Solomon Islanders. One Viti Levu individual shared a novel **M28a** haplotype with five individuals from Kadavu. Finally, one Viti Levu individual shared a novel **Q2** haplotype with two Lau individuals. These data suggest that there was little evidence for recent female migration events from Melanesia into Fiji.

	Lau	Rotm	Vanl	Viti	Kadv	Tnga	Samo	Vanu	Solm
Lau Islands									
Rotuma	-								
Vanua Levu	-	-							

Viti Levu	1	-	-						
Kadavu	-	-	-	1					
Tonga	-	-	-	-	-				
Samoa	-	-	-	-	-	-			
Vanuatu	1	-	-	-	-	-	-		
Solomon Islands	-	-	-	-	-	-	-	1	

Table 11. Number of Near-Oceanic haplotypes shared between populations

4.1.4 Measurements of diversity within populations

4.1.4.1 Nei's gene diversity statistic (H)

The haplotype diversity (H) values for each population reveal that the Melanesians (Vanuatu & Solomon Islands) are the most diverse and the Polynesians (Tonga & Samoa) are the least diverse (see Table 11). Fijian values were mostly intermediate between Melanesia and Polynesia, although Kadavu and Rotuma were exceptions. There is an overall decrease in HVS1 diversity from Melanesia to Fiji and then to Polynesia that likely reflects both the founding effects that took place during the colonization of Remote Oceania and the subsequent limited interaction between the Remote Oceania and Near Oceania that was due to geographic distance. Interestingly, Rotumans, have the lowest overall H value in this study. The Rotuman haplotype diversity is even much lower than the Polynesian diversity estimates. There were only three haplotypes observed here, with one type, the **PM**, accounting for 86% of the haplotypes. This situation would decrease the probability of difference between haplotype pairs, as most were one haplotype. The low diversity measure and high proportion of **PM** individuals suggests that the Rotuman population either experienced a

genetic bottleneck or founder effect. Kadavu is also unique in that it does not fit to the typical Fijian pattern of possessing intermediate H values. Kadavu has an H value that is more Melanesian-like than Fijian-like. Kadavu's H value is slightly higher than Vanuatu's value. This is likely explained by the fact that there were two frequently observed haplotypes, **PM** (n=8) and **M28a*** (n=5) with seven other haplotypes possessed mainly by single individuals. This situation would increase the probability of difference between haplotype pairs.

Population	n	Number of haplotypes	Gene diversity (H)	±	Mean no. pairwise differences (π)	±
Viti Levu	22	10	0.7576	0.0975	5.9048	2.9307
Vanua Levu	21	11	0.7381	0.1060	6.3143	3.1194
Kadavu	21	9	0.8476	0.0588	6.6381	3.2640
Lau Islands	22	10	0.7532	0.0960	5.1169	2.5788
Rotuma	21	3	0.3476	0.1276	0.7286	0.5650
Tonga	16	6	0.6750	0.1174	1.6750	1.0362
Samoa	8	3	0.6429	0.1841	2.0000	1.2562
Vanuatu	13	7	0.8333	0.0861	8.7436	4.3170
Solomon Islands	20	12	0.8789	0.0654	8.2526	3.9930

Table 12. Measurements of diversity

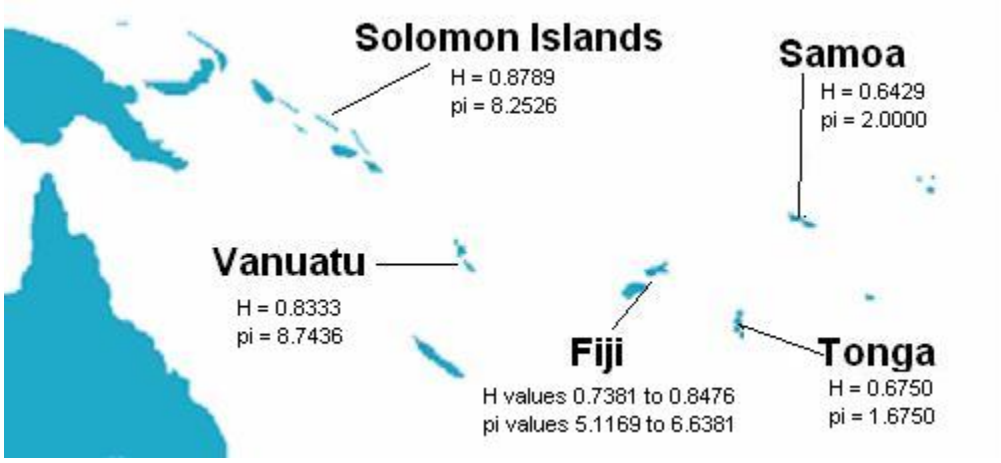


Figure 20. Diversity values with geographic location (About.com, 2012)

4.1.4.2 Mean number of pairwise differences between all pairs of haplotypes within a sample (π)

Whereas diversity was estimated to be highest in the Solomon Islands for H, the mean number of pairwise differences estimate of diversity was greatest in the Vanuatuan sample with the Solomon Islander sample the second highest (see Table 11). This is not surprising because both samples contain many different haplotypes and there are greater proportions of Near-Oceanic lineages, which contain many different substitutions away from the **B4** lineages. Like the values for H, the values for π show that diversity is greatest in Melanesia, intermediate in Fiji (Rotuma is still an exception) and lowest in Polynesia. It must be noted that although the Fijian values were intermediate between Melanesian and Polynesian values, they were closer as a whole to Melanesian values. This is likely because Fijians possess more Near-Oceanic haplotypes than Polynesians

and these Near-Oceanic types, in turn, contain very different substitution signatures than the **B4** lineages most frequently found among Polynesians.

4.1.5 Measurements of diversity among populations

4.1.5.1 Population differentiation test

After the population differentiation test was performed, several significant p-values were identified (0.05 level of significance), indicating significant genetic differentiation between the following pairs of populations. A '+' denotes significant difference between a pair of populations. The results displayed in Table 12 were not surprising because the Vanuatuan sample contains the most mtDNA haplotype variation and the Rotuman sample contains the least mtDNA haplotype variation. Moreover, Kadavu and the Solomon Island samples both contain higher amounts of haplotype variation; whereas the Tongan sampling contains less haplotype variation.

	Vanu	Solm	Viti	Kadv	Vanl	Lau	Rotm	Tnga	Samo
Vanuatu									
Solomon Islands									
Viti Levu	+								
Kadavu									
Vanua Levu	+								
Lau Islands	+								
Rotuma	+	+	+	+	+				
Tonga	+	+		+					
Samoa	+								

Table 13. Significantly different pairs of populations (+): Population differentiation test

With respect to the population pairwise Fst values, the populations exhibiting the least amount of mtDNA haplotype differentiation between pairs were:

Lau Islands & Viti Levu	(F_{ST} = 0.00000, p= 0.815 +- 0.002)
Lau Islands & Vanua Levu	(F_{ST} = 0.00000, p= 0.583 +- 0.002)
Samoa & Rotuma	(F_{ST} = 0.00000, p= 0.564 +- 0.002)
Samoa & Tonga	(F_{ST} = 0.00070, p= 0.345 +- 0.002)

Figure 21. Population pairwise Fst values

4.1.5.2 MDS plot of all nine populations represented

The non-metric MDS plot (monotonic in two dimensions) shows three distinct clusters with two outliers on either extreme of the x-axis: (from the left) Outlier Vanuatu, Cluster 1 (Solomon Islands & Kadavu), Cluster 2 (Viti Levu, Vanua Levu, & Lau Islands), Cluster 3 (Samoa & Tonga), Outlier Rotuma (see Figure 22). For this

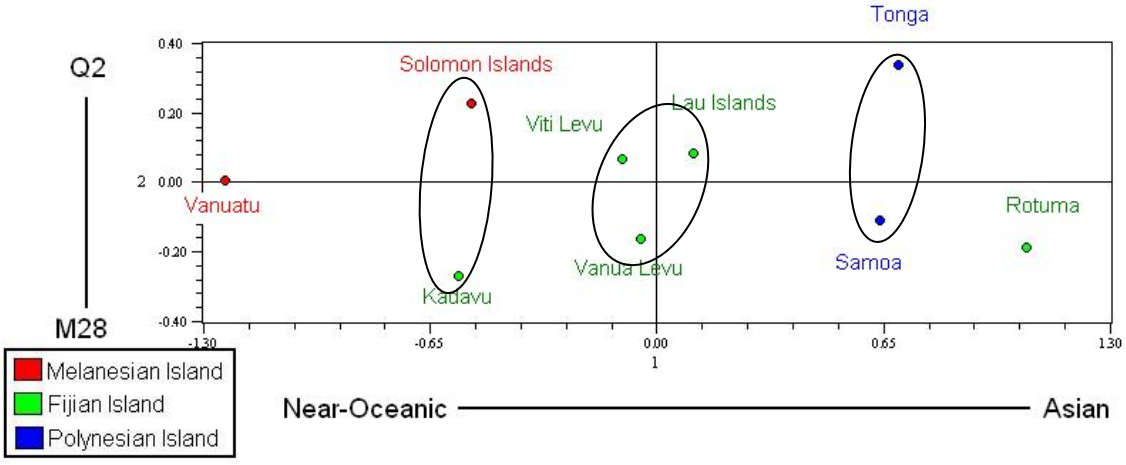


Figure 22. Two dimensional monotonic MDS plot of pairwise F_{ST} distances (Stress=0.03977)

particular MDS plot, 92.8% of the variation was captured in the first dimension (x-axis). Upon examination, the x-axis was determined to represent the ratio of Near-Oceanic to Asian mtDNA lineages, with populations presenting the most Near-Oceanic lineages on the left and populations presenting the most Asian lineage on the right. The second dimension (y-axis) only describes 7.2% of the variation and was determined to represent the ratio of Q2 to M28 mtDNA lineages, with populations presenting the most Q2 lineages at the top of the y-axis and populations presenting the most M28 lineages at the bottom. Because so much of the total variation is described by the first dimension, sample positioning will be described in terms of the x-axis.

Interestingly, the Fijian islands do not all cluster together. Kadavu, a Fijian island, clusters with the Solomon Islands, and Rotuma, an outlier, lies beyond the Samoan sample. Viti Levu, Vanua Levu, and the Lau Islands are both centrally located on the plot, nearly equidistant between the Melanesian and Polynesian samples. Vanuatu is a Melanesian outlier when compared to the other Melanesian islands (Fiji and Solomon Islands). The Stress value was 0.03977, which indicated that the goodness of fit was between **excellent** and **perfect**.

4.1.6 Measurement of multivariate distances

4.1.6.1 Mantel randomization test

Two mantel randomization tests were performed to test for association between an island's geographic location and its people's mtDNA population structure. Pairwise

Fst values and geographic coordinates were used to construct the two matrices compared. The first mantel randomization test that included all nine island populations produced a plot that was not significant with r = 0.05486 and p = 0.5927 (see Figure 23).

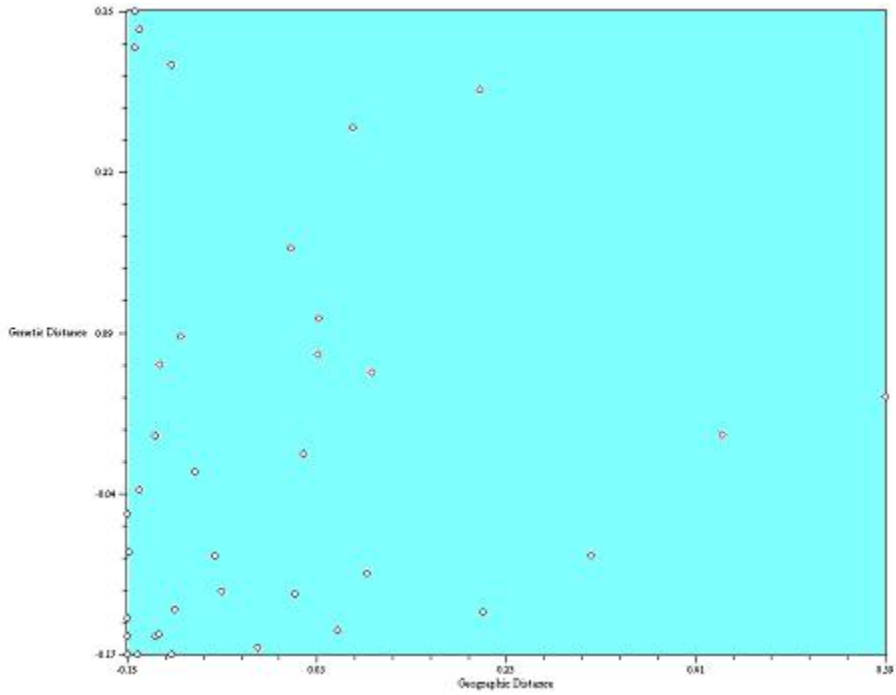


Figure 23. Mantel randomization test correlation plot using all nine island samples

Therefore, no direct relationship between mtDNA population structure and an island's geographic location could be validated. However, when the MDS plot was compared to a map of the region, there were several islands that appeared associated, and these islands were: Tonga, Samoa, Lau Islands, Viti Levu, and Vanua Levu. Their respective locations on both maps were near identical. A second mantel randomization test was then performed using genetic and geographic distances from only these five island populations (see Figure 24). The plot produced was not significant with

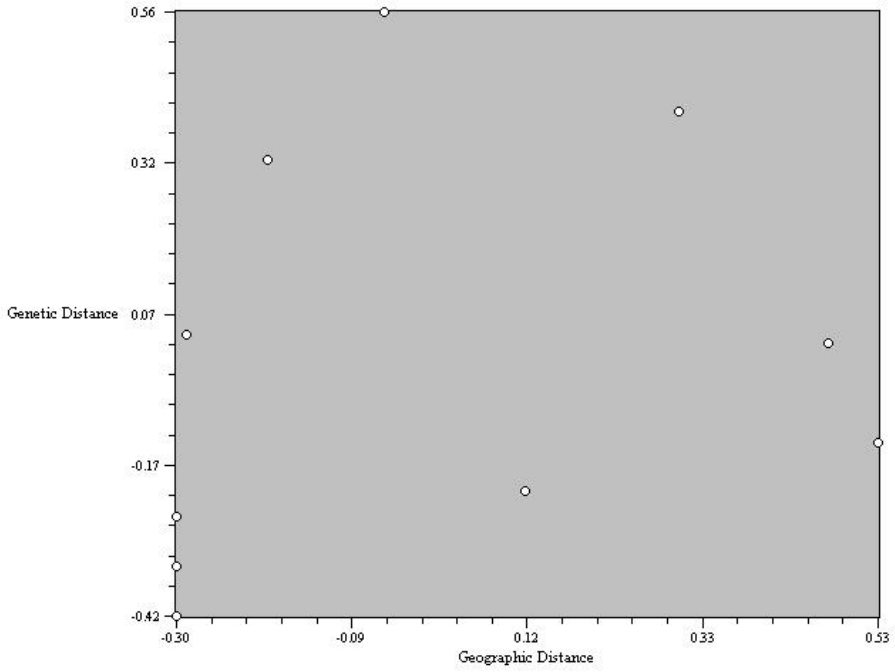


Figure 24. Mantel randomization test correlation plot using island sample subset

r = 0.2335 and p = 0.7605. Therefore, no direct relationship between mtDNA population structure and an island's geographic location could be validated even among the islands where a correlation seemed possible.

4.1.7 Tree phylogeny

4.1.7.1 Neighbor-joining tree

A neighbor-joining tree was produced using a maximum composite likelihood model (see Figure 25). The resultant tree neatly separated the haplogroups. Asian mtDNA lineages and Near-Oceanic mtDNA lineages separated to opposite ends of the

tree, demonstrating that the Asian lineages were more similar to other Asian lineages and the same was observed for the Near-Oceanic lineages. It appears that my classification of each individual haplotype was accurate, as all the major lineages (**B4, Q1, Q2, P1, M27**, and **M28**) gave rise to the haplotypes I had predicted. There were two single exceptions, a **Q1**-like individual and an **M28**-like individual. Both sequences were a challenge to classify, however, their location on the tree suggests that my efforts to classify them had been fairly accurate. They both arose from a common node, with the **Q1**-like sequence next to the **Q1** lineages and the **M28**-like sequence next to the **M28a** lineages.

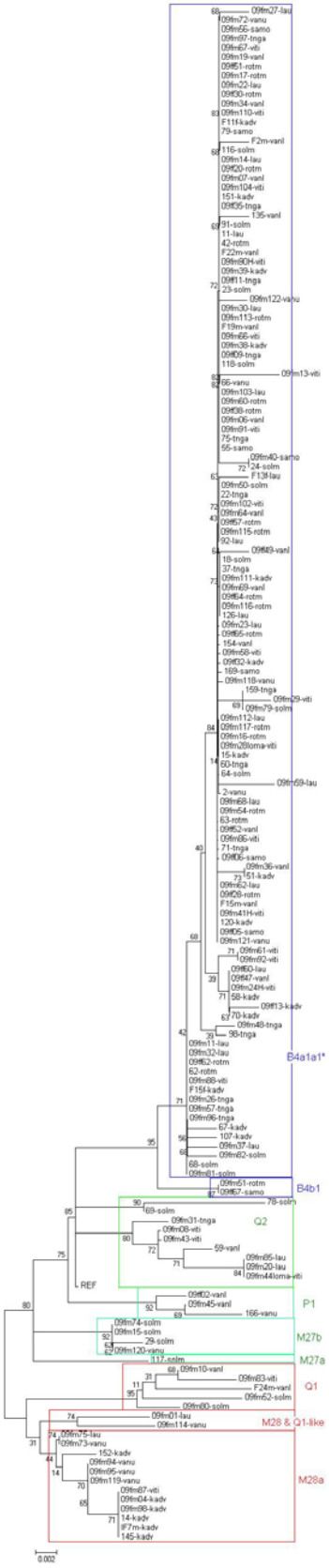


Figure 25. Neighbor-joining tree

4.1.7 Statistical evaluation of samples

This section statistically compares the sample variability of this study with previously published samples. Two tests were performed. First, I compared the lineage distributions. Next, I compared the proportion of Near Oceanian versus Asian lineages between the samples in this study with previously published studies. Both tests were performed using the χ^2 contingency table test.

4.1.7.1 Melanesian populations: Vanuatu & the Solomon Islands

In this project, the following mtDNA lineages were identified in Vanuatu: **B4**, **P1**, **M27**, and **M28** (n=13) (see Figure 25). Our results were not significantly different from previous samples ($p>0.05$) (Friedlaender et al., 2007; Pierson, 2006). Our study found that 46% of Vanuatuan mtDNAs were Asian-derived and 54% were Near-Oceanic (see Figure 26). Our Near-Oceanic to Asian mtDNA lineage ratios were not significantly different from previous samples ($p>0.05$) (Friedlaender et al., 2007; Pierson, 2006).

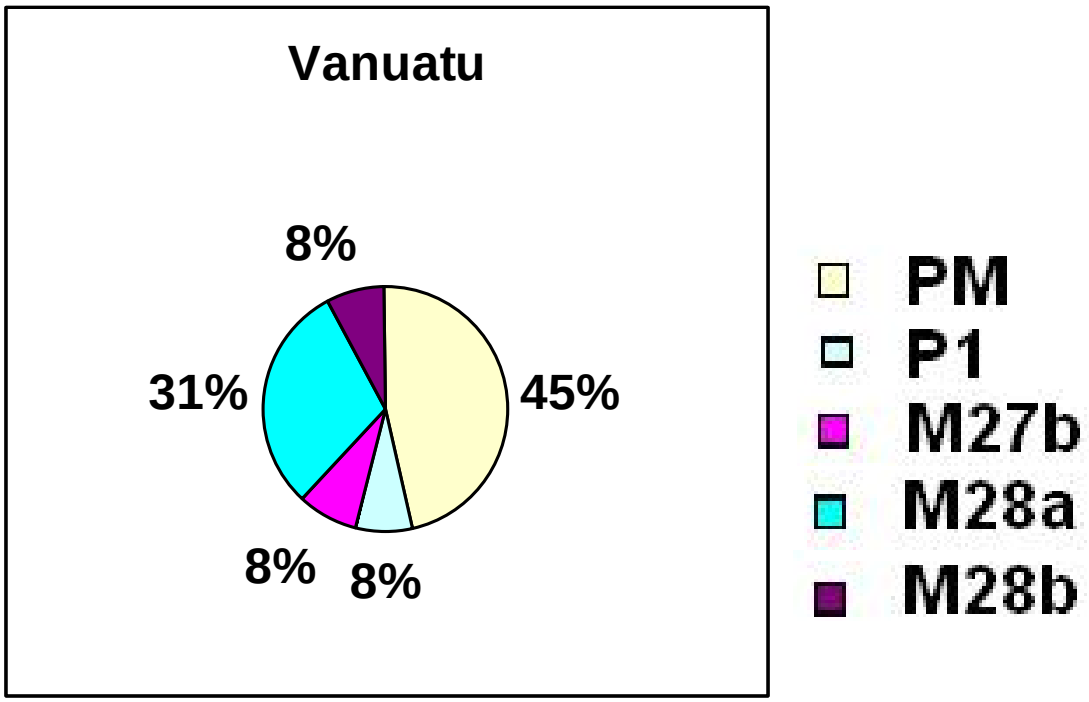


Figure 26. MtDNA haplogroup frequency results for this project (n=13)

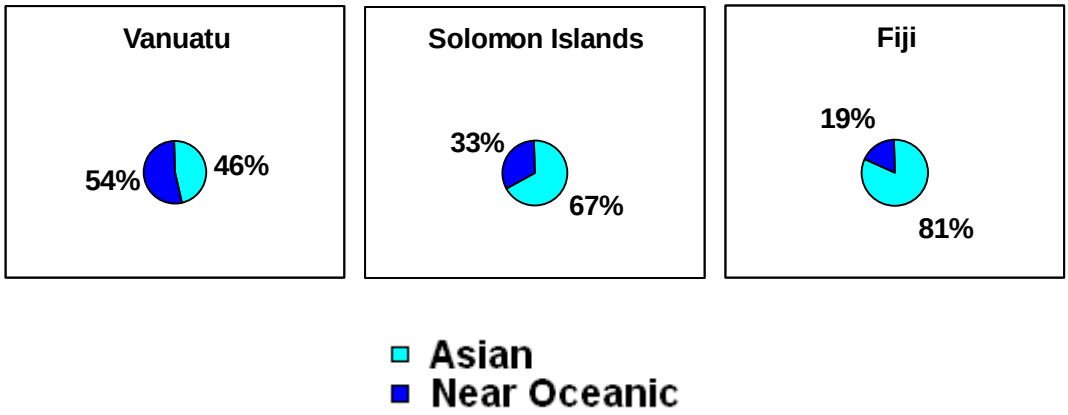


Figure 27. Proportion of Asian and Near-Oceanic lineages present in Melanesian samples

We identified the following lineages in the Solomon Islander sample: **B4**, **Q1**, **Q2**, and **M27** (see Figure 27). Our results were found to be significantly different than

previous samples ($p<0.001$). Specifically, a higher proportion of **PM** lineages were identified among Solomon Islanders sampled by Delfin et al., 2012. However, Delfin et al. included Polynesian outlier groups inhabiting the main Solomon Islands, which made up over 20% of that sample. For our study, we included only a single individual from a Polynesian outlier group (Tikopia). The remainder of our participants (n=19) claimed maternal ancestry from indigenous Solomon populations. Even though the Delfin et al. (2012) sample found a higher proportion of **PM** lineages among the Solomon Islanders than did this sample, the overall proportion of Asian to Near-Oceanic mtDNA lineages from our sample was not significantly different than what Delfin et al. found ($p>0.05$) (see Figure 26).

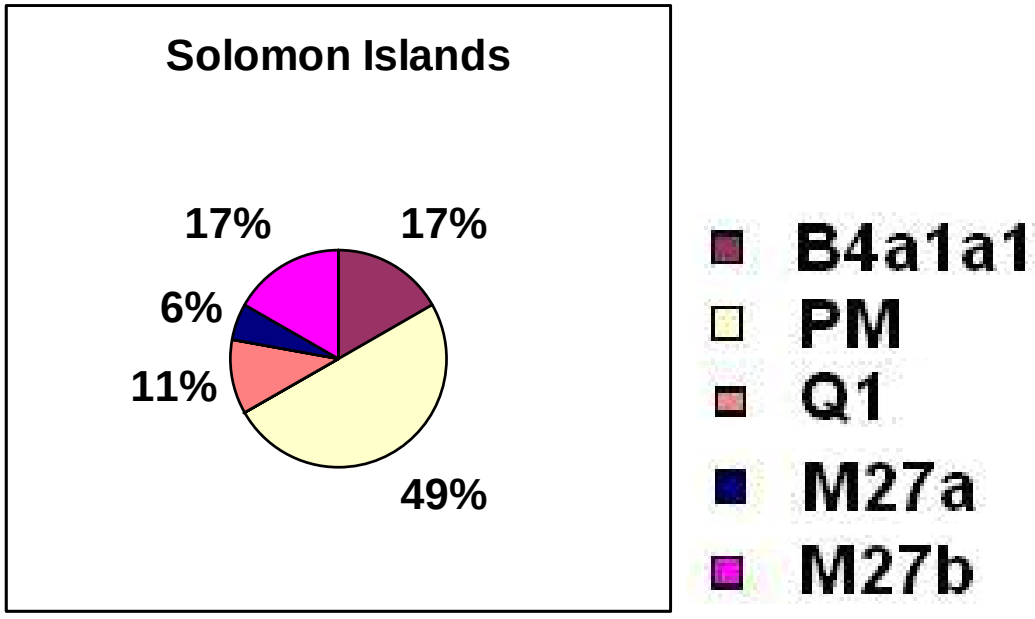


Figure 28. MtDNA haplogroup frequency results of the Solomon Island sample

4.1.7.2 Polynesian populations: Tonga & Samoa

In this project, **B4** and **Q2** mtDNA lineages were identified within the Tongan sample (see Figure 28). Our results were not significantly different from previous samples ($p>0.05$) (Kayser et al., 2006; Sykes et al., 1995). We also found that 94% of Tongan mtDNAs were Asian-derived and 6% were Near-Oceanic (see Figure 29). A statistical comparison of means between our sample and previous ones found no significant difference ($p>0.05$) (Kayser et al., 2006; Sykes et al., 1995).

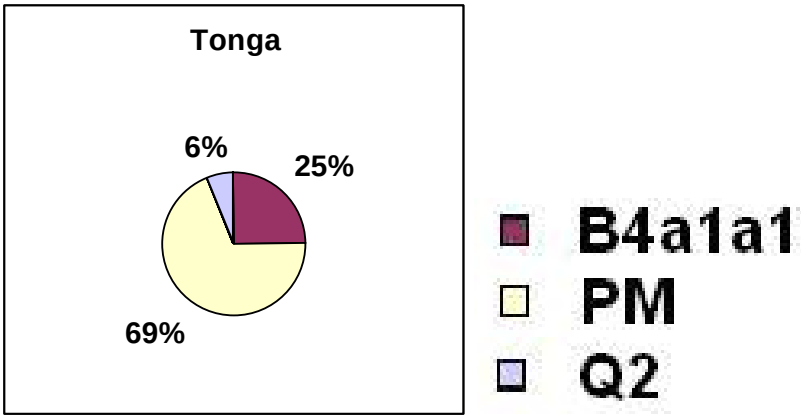


Figure 29. Haplogroup frequencies of Tonga

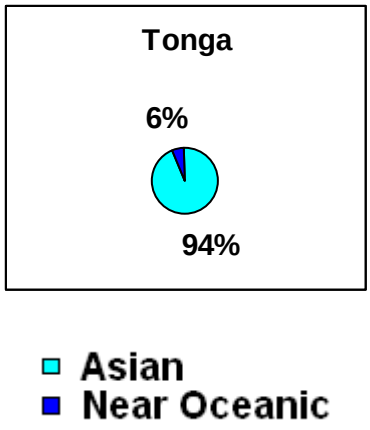


Figure 30. Proportion of Asian and Near-Oceanic lineages present in Tonga

For the Samoan sample, we only identified **B4** mtDNA lineages (see Figure 30). The results from this project were not significantly different from previous samples ($p>0.05$) (Kayser et al., 2006; Pierson et al., 2006; Redd et al., 1995; Sykes et al., 1995). Our study found that 100% of Samoan mtDNAs were Asian-derived (see Figure 31). A statistical comparison of means between our sample and previous ones found no significant difference ($p>0.05$) (Kayser et al., 2006; Pierson et al., 2006; Redd et al., 1995; Sykes et al., 1995).

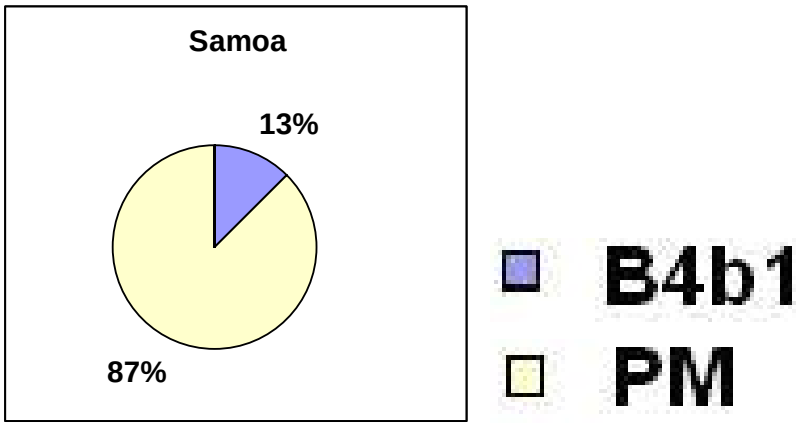
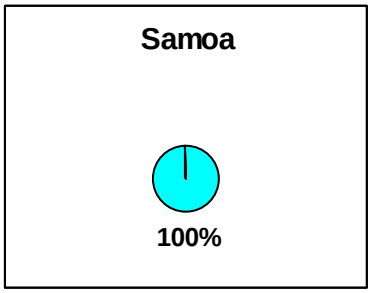


Figure 31. Haplogroup frequencies of Samoa



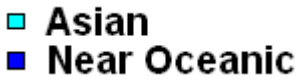


Figure 32. Proportion of Asian and Near-Oceanic lineages present in Samoa

4.1.7.3 Fijian population

In this project, mtDNA lineages **B4**, **P1**, **Q1**, **Q2**, and **M28** were identified among the 107 Fijians (see Figure 32). While the percentages of these lineages were not found to be significantly different from previous samples, the proportion of Asian to Near-Oceanic mtDNA lineages was significantly different between samples ($p<0.05$) (Friedlaender et al., 2007; Kayser et al., 2006). Whereas one previous sample found that 60% of Fijian mtDNAs were Asian-derived (Friedlaender et al., 2007), we found that 81% of the mtDNA lineages were Asian-derived, which is consistent with the results from the 2007 Kayser et al. sample (80% Asian-derived lineages).

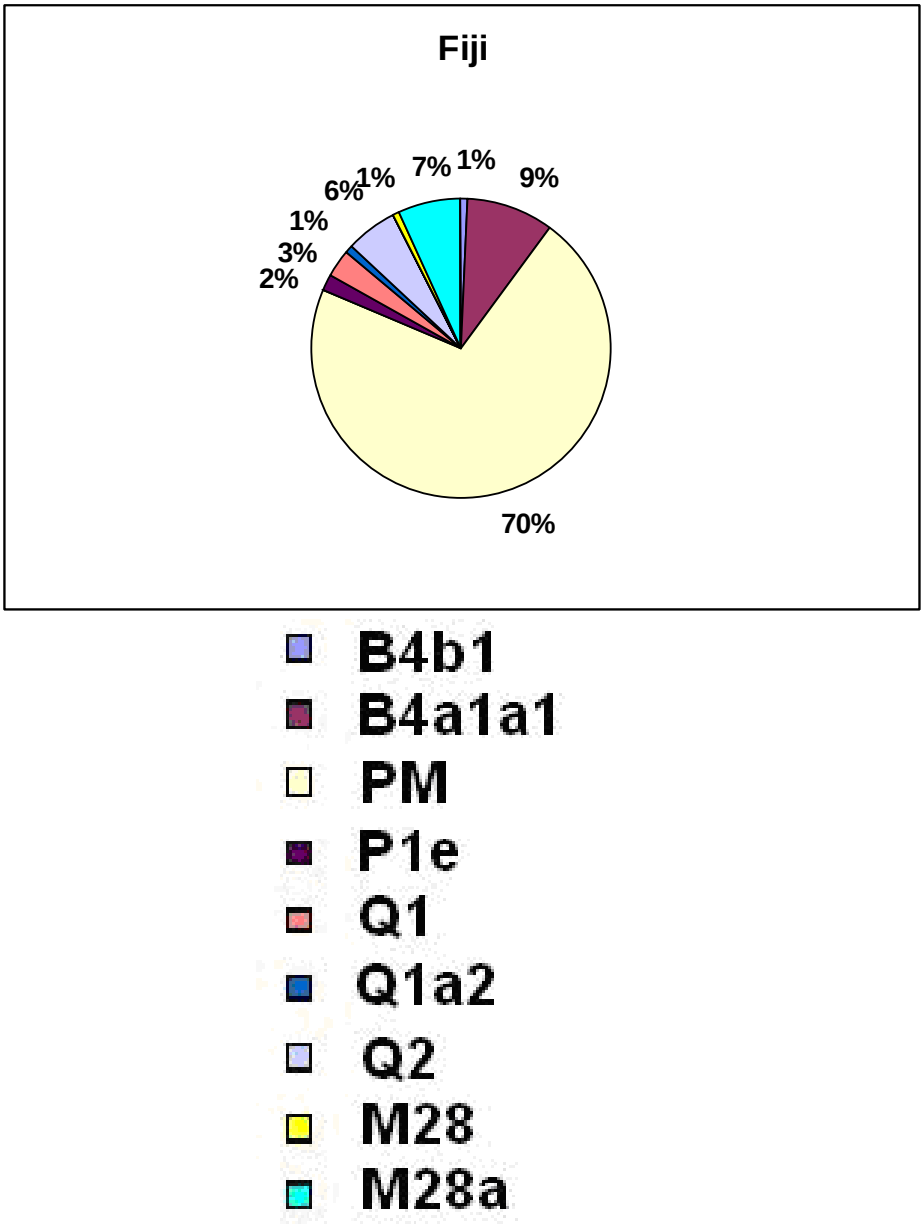


Figure 33. Haplogroup frequencies of Fijians

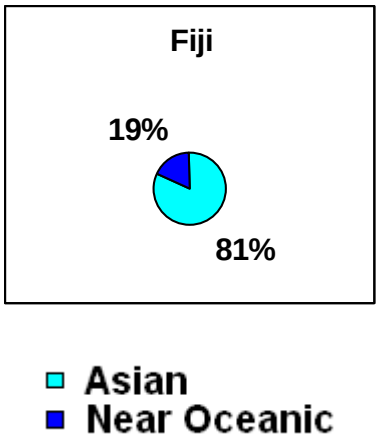


Figure 34. Proportion of Asian and Near-Oceanic lineages present in Fijian sample

CHAPTER 5: DISCUSSION

This chapter addresses the five questions outlined in the introductory chapter. The format for this chapter is an introduction to each question, followed by an interpretation of the mtDNA results, and finally a synthesis of all lines of evidence leading to a conclusion.

QUESTION 1:

Are Fijian mtDNAs more Melanesian or Polynesian?

With respect to overall Asian and Near-Oceanic mtDNA lineage ratios, the Fijian sample lies intermediate between Melanesian and Polynesian populations, slightly closer to the Polynesians (see Figures 35 & 36). Vanuatu had the highest proportion of

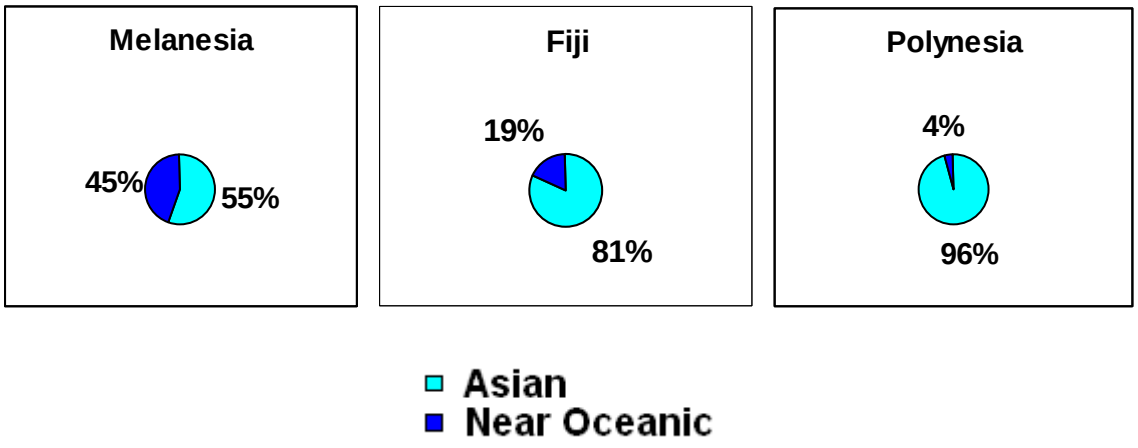


Figure 35. Proportions of Asian & Near-Oceanic lineages

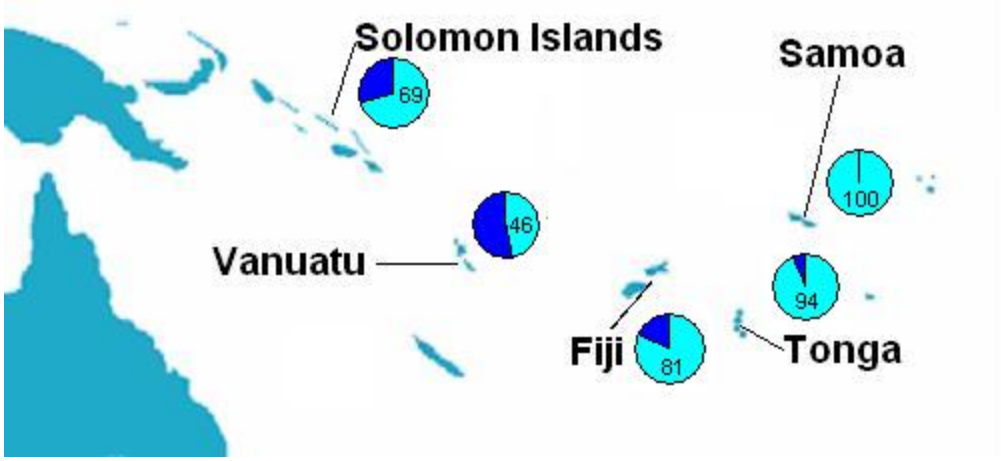


Figure 36. Clinal increase in Asian mtDNA lineages from west to east (About.com, 2012)

Near-Oceanic lineages followed by the Solomon Islands, Fiji, Tonga, and Samoa. Based on geographic proximity to Near Oceania, one would predict the Solomon Island sample to contain more Near-Oceanic mtDNA lineages than all other samples. This, however, is not observed and is likely due to the fact that there has been much Polynesian (back) migration into the Solomons in more recent times (Delfin et al., 2012). Looking to the other samples and with respect to Asian-derived mtDNA lineages, there is a pattern of clinal increase from Melanesia to Fiji to Polynesia (see Figure 36). Likewise, there is a clinal decrease in Near-Oceanic lineages that exists as one moves east. This is consistent with archeological evidence suggesting that the route of the Austronesian-speaking Lapita people was from Near Oceania and out to Remote Oceania (Kirch, 2000).

One interesting question that remains is: does the high prevalence of Near-Oceanic mtDNA lineages in Fiji suggest that there was female Melanesian migration into

Fiji after the colonization of the Lapita people, OR does this suggest that some Near-Oceanic lineages were incorporated into the matriliocal Lapita groups as the Lapita people left the Bismarks, resulting in decreased subsets of this diversity as the Lapita people island-hopped in an eastern direction? The very limited Near Oceanic haplotype sharing does not support a recent female Melanesian migration into Fiji.

The haplotype diversity values (H) for each sample reveal that the Melanesians (Vanuatu & Solomon Islands) are the most diverse group and the Polynesians (Tonga & Samoa) are the least diverse group (see Table 12– Results chapter). Fijian values were mostly intermediate between Melanesia and Polynesia, although Kadavu and Rotuma were exceptions. There is a general decrease in mtDNA diversity from Melanesia to Fiji to Polynesia that likely reflects both the founding effects that took place during the colonization of Remote Oceania and the subsequent limited interaction between Near and Remote Oceania that was due to geographic distance boundaries.

Like the values for haplotype diversity (H), the values for average pairwise distance (π) show that diversity is greatest in Melanesia, intermediate in Fiji (Rotuma is still an exception) and lowest in Polynesia. It must be noted that although the Fijian pairwise distance values were intermediate between Melanesian and Polynesian values, they were closer as a whole to Melanesian values. This is likely because Fijians possess more Near-Oceanic haplotypes than Polynesians and these Near-Oceanic types, in turn, contain very difference substitution signatures than the B4 lineages most frequently found among Polynesians. Taken together, both the H and π results suggest that Fijian mtDNAs are intermediate between Melanesian and Polynesian populations; although the π values place Fijians slightly closer to Melanesians.

The non-metric MDS plot revealed that three of Fiji's island samples (Viti Levu, Vanua Levu, and the Lau Islands) cluster with each other and are intermediate as a whole between Melanesian and Polynesian populations. Moreover, these three clustering Fijian samples are positioned slightly closer to the Polynesian cluster than to the Vanuatu and Solomon Island (Melanesian) samples (see Figure 22 – Results chapter). Interestingly, Kadavu clusters more closely with the Solomon Islands. The first dimension of the plot represents the ratio of Near-Oceanic to Asian mtDNA lineages. Kadavu has more Near-Oceanic mtDNA lineages than the other Fijian islands, particularly **M28a,** which is pulling this sample further left of the large islands. However, Kadavu is still intermediate between Polynesia and Vanuatu. Rotuma, appears to be a Polynesian outlier. Because there were no Near-Oceanic mtDNA lineages identified here, the Rotuman sample is pulled completely to the right on the x-axis. These results further confirm that Fijians, with respect to mtDNA, are genetically intermediate between Melanesian and Polynesian populations.

One special consideration worth mentioning is that the Fijian mtDNAs may be more Polynesian-like than the MDS plot revealed. This is due to the fact that there has been much Polynesian immigration into the Solomons via Polynesian outlier populations. Vanuatu pulls to one extreme of the MDS plot, far beyond even the Solomons. Based on geographic proximity to Near Oceania, the Solomons would be the sample expected to be located farthest to the left and that is not what is observed. The population differentiation test (see Table 13) revealed that the Vanuatu sample was significantly different from most island samples. The Solomon Islands and Kadavu were the only samples Vanuatu was not significantly different from. The fact that the Vanuatu sample is significantly

different from the largest island samples in Fiji (Viti Levu, Vanua Levu, and the Lau Islands) is interesting. Tonga and Samoa were not significantly different from these three major island samples.

Based on the between population comparison results from Near-Oceanic to Asian mtDNA ratios, mtDNA diversity measures (H & π), an MDS plot, and population differentiation test, it is apparent that Fijian mtDNAs are intermediately situated between Melanesian and Polynesian clusters. Though Fijian mtDNAs are slightly more Polynesian-like than Melanesian-like, as indicated by the mtDNA lineage ratio comparison, MDS plot, and population differentiation test. Additionally, the high amount of recent Polynesian admixture that has occurred in the Solomons may exaggerate Fiji's Melanesian ancestry.

QUESTION 2:

Is there a relationship between geography and genetic variation?

To investigate whether or not there is an association between geographical distance in island populations and genetic distance with respect to mtDNA, a Mantel randomization test was performed. Pairwise genetic distances and geographic distances were used to construct the two matrices which were then compared (see Figure 23 – Results chapter). The result was not significant with $r = 0.05486$ and $p = 0.5927$. Therefore, no direct relationship between mtDNA population structure and an island's geographic location could be detected using the full set of population samples. However, a number of populations in the genetic map are mirrored in location on the geographic

map: Tonga, Samoa, Lau Islands, Viti Levu, and Vanua Levu. Unfortunately, this subset of samples also produced a non significant mantel randomization test result with r = 0.2335 and p = 0.7605 (see Figure 24 – Results chapter).

Based on the Mantel randomization test results, geographical distance in island populations was not associated with mtDNA genetic distance. The lack of a correlation may be caused by scale effects: short distance migration versus long distance migration. Migration may also have been affected by wind and water currents; some islands may have been easier to reach than others. Whatever the reasons, it is evident that there were discordant genetic and geographic patterns in gene flow and migration with respect to mtDNA. Women moved in an unpredictable fashion with respect to geography. It is also possible that a genetic-geographic association will be detected using Y chromosome or autosomal data.

QUESTION 3:

Are Rotuman mtDNAs more similar to Fijian or Polynesian mtDNAs? Does Rotuman mtDNA structure align with the Rotuman origin myth?

The origins of the Rotuman people have yet to be determined. Linguists have argued that the Rotuman language derived from a Fijian dialect once spoken in Vanua Levu, even though over 40% of the Rotuman language includes Polynesian loan words (Geraghty, 1983; Schmidt, 1999). Archeological research within Rotuma has not revealed any Lapita sites (Ladefoged, 1993), possibly indicating a later colonization date than other Fijian islands. One archeologist (Ladefoged, 1993), however, did note that

some prehistoric burial mounds of Rotuma were similar in style to Tongan chiefly burials mounds, called Langi. Moreover, Rotumans physically appear to be very similar to Polynesians (and Micronesians). Their skin pigmentation is much lighter than typical Fijian pigmentation and their hair texture is typical of the Polynesian people. Ethnographic accounts (Howard, 1985) have documented that Rotumans believe they are Samoan and Tongan descended. Rotuman oral records indicate that the first inhabitants of the small, isolated island were from Samoa and they were ruled by a king named Rao. Later, there was intrusion by Tongan people (Howard, 1985). To date, there has been no genetic investigation to assess Rotuman origins. The results from this thesis project are the first.

We found that Rotuman mtDNAs were more Polynesian-like than Fijian-like with respect to the proportions of Asian-derived mtDNA lineages to Near-Oceanic mtDNA lineages (see Figure 37.). When comparing these proportions between Rotuma and Fiji, they were

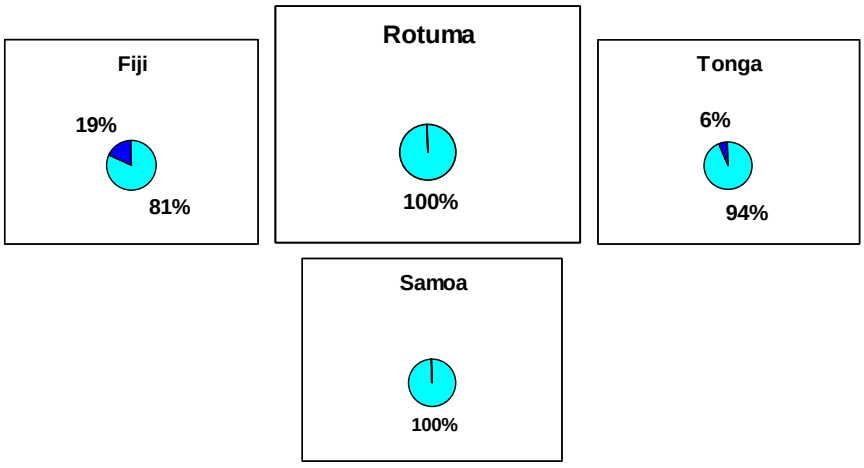


Figure 37. Proportion of Asian to Near-Oceanic mtDNA lineages

found to be significantly different ($p<0.05$). However, when Rotuma was compared to Tonga and Samoa separately, there were no significant differences ($p>0.05$ for both tests). The Rotuman sample was so Polynesian-like that we did not identify a single Near-Oceanic mtDNA haplotype. We did identify haplogroups **B4b1**, **B4a1a1**, and **PM** (see Figure 37). Moreover, unlike the other Fijian

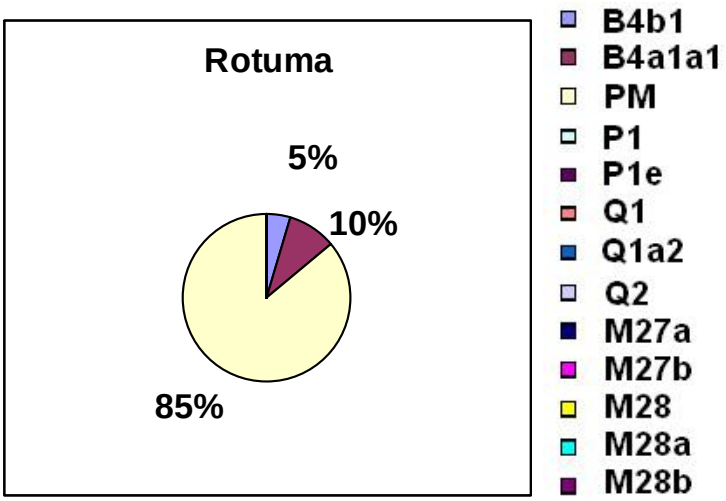


Figure 38. MtDNA haplogroups frequencies from Rotuman sampling

Island samples where multiple new haplotypes were discovered, we found only a single new haplotype in Rotuma. This novel haplotype is **B4b1**-like and contains an additional substitution at 16067 (T). We also identified this haplotype in another individual from Rotuma that claimed maternal ancestry from Samoa: "mother's mother's mother was 100% Samoan". While this finding is rather intriguing and suggests that it is possible Rotuma was in fact founded by Samoans, further molecular investigation is needed to test this hypothesis. The **B4b1** lineage is rare outside of Taiwan and the Philippines, yet it has been identified in Tuvalu, a Polynesian archipelago containing islands geographically

located only 200 miles northeast of Rotuma. Sufficient sampling of neighboring islands is needed before firmer conclusions on Rotuman origins can be made.

The Rotuman sample presented the lowest overall haplotype diversity (H) and average pairwise difference (π) values among all populations examined in this study. The Rotuman haplotype diversity was even lower than the Polynesian diversity estimates. There were only three haplotypes observed in the Rotuman sample, with one type, the **PM**, accounting for 86% of the haplotypes. The low diversity measures and high proportion of **PM** individuals indicate that the Rotuman population likely underwent a bottleneck event at some time in their history. This lack of genetic diversity may also suggest a founder effect and subsequent genetic drift. Furthermore, geographic isolation from other island populations likely contributed to the lack of additional mtDNA lineages.

The MDS plot constructed from pairwise F_{ST} values indicates that Rotumans are Polynesian outliers (see Figure 22 – Results chapter). Moreover, the Rotuman sample is closer to Samoa than any other population. The population differentiation test also revealed that, with respect to mtDNA, Rotumans exhibit the least amount of haplotype differentiation with Samoans (Fst= 0.00000, p= 0.564 +- 0.002). However, this was not true when the Rotuman sample was compared with the Tongan sample. Nonetheless, these results suggest that not only are Rotumans more Polynesian-like than Fijian-like, but they are also genetically indistinguishable from Samoans using the population differentiation test. This result aligns well with Rotuman oral records suggesting Samoan descent (Howard, 1985). However, it is important to stress that just because the Rotuman sample appears to be most like the Samoan sample does not mean Rotuma was founded

by Samoans. In fact, there are many other Polynesian and Micronesian islands located near Rotuma that we did not sample in this project. Within one Polynesian archipelago, Tuvalu, mtDNA **B4b1** lineages have been identified by other researchers (Friedlaender et al., 2007). Moreover, the study only examined maternally-inherited mtDNA. It is possible that alternative molecular tools reveal a different pattern than what this maternal marker is revealing.

Linguists have argued for years that Rotumans originated from Vanua Levu, Fiji (Geraghty, 1983; Schmidt, 1999). Interestingly, we found that Rotumans only shared one mtDNA haplotype in common with the Vanua Levu sample (see Table 10); whereas the Rotumans shared two haplotypes in common with all other Fijian island samples. Moreover, the population differentiation test revealed that the Rotuma and Vanua Levu samples were significantly different (see Table 13). Both analyses seem to suggest that Rotuma was not likely founded by a Vanua Levu population. However, as mentioned before, this project only used mtDNA to investigate Rotuman origins and it is possible that a different genetic marker will paint a different picture.

In conclusion, Rotumans appear to be most genetically related to Samoans and were possibly founded by a neighboring Polynesian population. The Rotuman mtDNA sample was extremely low in diversity. This finding indicates that this island population was genetically bottlenecked at some point in time, with a founding event being the most likely explanation. An MDS plot placed the Rotuman sample close to the Samoan population and revealed that Rotumans are more Polynesian-like than Fijian-like. A population differentiation test supported the close genetic ties between Rotuma

and Samoa. Taken together, all these lines of anthropological evidence reveal that Rotumans were likely founded by Polynesians.

QUESTION 4:

Are Lau Islander mtDNAs more similar to Fijian or Tongan mtDNAs?

Historically, the Lau Islands have served as a meeting place for people from different islands (Hage and Harary, 1996). Based on Lapita site dating, it has been suggested that the migration route of the Lapita people through Fiji was first around the main island, Viti Levu, then later through the Lau Islands and out to Polynesia (Kirch, 2000). One particular Lapita site, found on the island of Lakeba (Lau Island) is estimated to have covered 15,000 square meters of coastal flat, significantly larger than typical Lapita sites which were generally less than 5,000 square meters. This Lapita site likely served as the platform of a gateway community in the Lau Islands. Groups of people would meet and disperse from this site, as is evident by the many material artifacts found here that originate from other Fijian and Polynesian islands (see Chapter 2: Archeology for more description).

In more recent years, continuous interaction between Lau Islanders and Tongans has emerged as a result of the sandalwood trade industry that was established in colonial times (Kirch, 2000). Linguistic analysis has also revealed that the Fijian language communalects spoken among the Lau Islanders are more similar than other Fijian communalects to the Tongan language (Geraghty, 1983). Given that the Lau Islanders

share a rich history with neighboring island populations that began thousands of years ago, one would expect to find high levels of diversity among their mtDNAs.

We found haplogroups **B4a1a1**, **PM**, **Q1**, **Q2**, and **M28** (see Figure 38) within the Lau Island sample. These haplogroups all belong to the same mtDNA lineages that

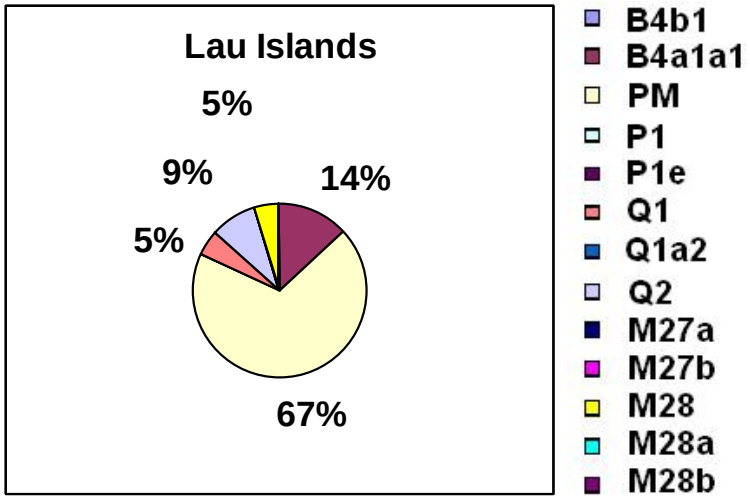


Figure 39. mtDNA haplogroup frequencies from Lau sample

we identified in the Viti Levu sample. This was not a surprise, as both island populations have historically served as a meeting ground for all Fijians.

In addition to the common Fijian haplogroups identified in the Lau Island sample, eight new haplotypes were discovered. Five of the new, different haplotypes were **PM**-like and **B4a1a1**-like. One unique **PM** haplotype was shared between a Lau Islander, an individual from Vanua Levu, an individual from Viti Levu, and two individuals from Kadavu. A substitution at 311(C) was found among all five of these Fijians. This lineage is likely a Fijian one, based on the geographic distribution of this type found only among

Fijians. This also suggests that the geographic isolation inherent within island living has not affected the movement of people throughout the Fijian Archipelago.

Anthropologists have described the Lau Islands as home to "gateway communities," and the results of this project support this conclusion. MtDNA diversity estimates (H, π, and overall number of haplotypes) indicated that the Lau Islander mtDNAs were as diverse as the other Fijian group mtDNAs, excluding Rotuma. This aligns well with the idea that the Lau Islands serve as a meeting place for all Fijians.

The Lau Islands are geographically situated closer to the Polynesian islands than the other Fijian groups (excluding Rotuma), suggesting closer genetic affinities with Polynesians than other Fijian populations. Moreover, the Lau Islanders have historically maintained relations (political, economical, and probably reproductive) with the neighboring island Tonga, as is evident through shared words with Polynesian languages in the Lau communalects of the Fijian language. For all these reasons, one would expect the Lau Islanders to be more genetically similar to Polynesians than other Fijians would be. Lau Islander mtDNA reveals that this population is in fact more genetically similar to Polynesians than other Fijians (excluding Rotuma). The results from the MDS plot place Lau Islanders closest to the Polynesian cluster, nearly equidistant between Samoa and Tonga (see Figure 22 – Results chapter). This may reflect the Lau Islander's continuous contact with both island communities or may also suggest that the founding populations of both Samoa and Tonga budded off the Lau Islands, as archeological evidence indicates.

Based on diversity measures, the Lau Island group was found to be as diverse as the other main Fijian island populations in spite of the fact that the Lau Islands

are geographically isolated from the main lands of Fiji, thus supporting the notion that this region has historically served as a gateway community. The Lau Islanders were also found to be more genetically similar, with respect to their mtDNA, to the Polynesian populations than were other Fijian groups. This finding corroborates other anthropological research supporting a continuous relationship between Lau Islanders and the Polynesians.

CHAPTER 6 : CONCLUSION

I found that with respect to maternally-inherited mitochondrial DNA (mtDNA), Fijian mtDNAs are intermediate between Melanesian and Polynesian mtDNAs, though on average they were slightly more Polynesian. Moreover, the Fijian samples were more similar on average to the Solomon Island sample than they were to the Vanuatu sample. This is surprising, given that Vanuatu is geographically situated closer to Fiji than are the Solomon Islands. Among the five Fijian island populations sampled, three were most similar to each other : Viti Levu, Vanua Levu, and the Lau Islands. These three shared the most haplotypes, clustered with each other on the MDS plot, and presented similar diversity values. Kadavu was the only Fijian island sample that was not significantly different from the Vanuatu sample. It was also found to be significantly different from the Polynesian samples. The presence of a novel **M28a** haplotype among five Kadavu individuals made the sample appear more Melanesian-like than Polynesian-like. One Viti Levu individual also shared this novel haplotype with the five Kadavu individuals. Future research could investigate a possible connection between Kadavu and Melanesia, although the M28a haplotypes found in Fiji are rather distantly related to the M28 haplotypes found further west.

The fifth Fijian sample, Rotuma, is a Polynesian outlier. Only Asian-derived **B4** lineages were identified within this sample and diversity values were lower than for the Polynesian samples. We identified a novel haplotype that was **B4b1**-like among two Rotumans, one of these individuals claimed Samoan ancestry on the maternal line. **B4b1** is found most frequently among Taiwanese aborigines and Philippinos, though it has also

been identified in Tuvalu, which is a close Polynesian neighbor to Rotuma. Most of the statistical analyses performed in this project placed the Rotuman sample nearest to the Samoan sample. Given that Rotuma is genetically bottlenecked and appears to be genetically indistinguishable from the Samoan sample, it is likely that Rotuma was founded by a Polynesian population. Because we only sampled two Polynesian islands near Rotuma and given that there are Polynesian islands geographically nearer to Rotuman that we did not sample, there is insufficient genetic evidence to conclude that Rotuma was founded by Samoans as their oral record suggests. Multiple linguists who research the Fijian language have argued that Rotuma was founded by a Vanua Levu population and not a Polynesian population. With respect to mtDNA, we did not find a high degree of similarity between samples to corroborate this hypothesis. In fact, we found that Rotuman mtDNAs were significanly different than Vanua Levuan mtDNAs. Further investigation is needed, however, to rule Vanua Levu out as a possible founding population for Rotuma, as mitochondrial DNA is only one molecular tool among others.

To test for an association between geography and genetics, a mantel randomization test was performed. However, no association was identified and this suggests that factors other than simple geographic distance affected female migration within Fiji. Wind and wave patterns may have made travel between certain islands more difficicult or easy than others. It is possible that other genetic systems, such as the Y chromosome or the autosomes, will show a genetic-geographic association.

WORKS CITED

About.com (2012). Fijian map. Retrieved April 17, 2012 from www.geography.about.com.

About.com (2012). Oceania map. Retrieved April 17, 2012 from www.geography.about.com

Albertini, A.M., Hofer, M., Calos, M.P. and Miller, J.H. (1982). On the formation of spontaneous deletions: The importance of short sequence homologies in the generation of large deletions. *Cell*, 29, 319-328.

Anderson, A. & Clark, G. (1999). The age of Lapita Settlement in Fiji. *Archaeology in Oceania*, 34(1), 31-39.

Anson, D. (1983). Lapita pottery of the Bickmark Archipelago and its affinities. Unpublished Ph.D. dissertation. University of Sidney.

Bedford, S. (2000). Pieces of the Vanuatu puzzle: Archaeology of the north, south, and centre. Vol. 2, Ph.D. dissertation. Canberra: Australian National University.

Bedford, S. (2006). Pieces of the Vanuatu puzzle: Archaeology of the north, south and centre. *Terra Australis*, 23. Canberra: Pandanus Books.

Bedford, S. and Clark, G. (2001). The rise of the incised and applied relief tradition: A review and reassessment. In G. Clark, A. Anderson and T. Sorovi-Vunidilo (eds), The archaeology of Lapita dispersal in Oceania: Papers from the fourth Lapita conference, June 2000, 61-74. Canberra: Centre for Archaeological Research and Department of Archaeology and Natural History, Australian National University.

Bedford, D. and Spriggs, M. (2008). Northern Vanuatu as a Pacific crossroads. The archaeology of discovery, interaction, and the emergence of the ethnographic present. *Asian Perspectives*, 47(1), 95-120.

Bellwood, P. (1979). *Man's conquest of the Pacific: The prehistory of Southeast Asia and Oceania.* New York: Oxford University Press.

Bellwood, P. (1998). The archaeology of Papuan and Austronesian prehistory in the Northern Moluccas, Eastern Indonesia. In R. Blench and M. Spriggs (eds), Archaeologu and language II: Correlating archaeological and linguistic hypotheses, 128-140. London: Routledge.

Best, S. (1984). Lakeba: The prehistory of a Fijian island. Ph.D. dissertation. Department of Anthropology, University of Auckland.

Best, S. (1987). Long-distance obsidian travel and possible implications for the settlement of Fiji. *Archaeology in Oceania*, 22, 31-32.

Best, S. (2002). Lapita: a view from the east. *New Zealand Archaeological Association Monographs,* 24. Auckland: New Zealand Archaeological Association.

Birdsell, J.B. (1977). The recalibration of a paradigm for the first peopling of Greater Australia. In J. Allen, J. Golson and R. Jones (eds), *Sunda and Sahul. Prehistoric Studies in Southeast Asia, Melanesia and Australia*, 113–67. London: Academic Press.

Burley, D. (1998). Tongan archaeology and the Tongan past, 2850-150 B.P. *Journal of World Prehistory*, 12(3), 337-392.

Burton, M.L., Moore, C.C., Whiting, W.M., and Romney, A.K. (1996). Regions based on social structure. *Current Anthropology*, 37(1), 87-123.

Churchward, C.M. (1938). Rotuman legends. *Oceania*, 8.

Clark, G. and Anderson, A. (2001). The pattern of Lapita settlement in Fiji. *Archaeology in Oceania*, 36, 77-88.

Clark, G. and Murray, T. (2006). Decay characteristics of the eastern Lapita design system. *Archaeology in Oceania,* 41, 107-117.

Couper, A. (2009). Sailors and traders. Honolulu: University of Hawai'i Press.

Cox, M.P. (2003). Genetic patterning at Austronesian contact zones. Doctoral dissertation. Dunedin: University of Otago.

Cox, M.P. (2007). Extreme patterns of variance in small populations: Placing limits on human Y-chromosome diversity through time in the Vanuatu Archipelago. Annals of Human Genetics, 71, 390-406.

Delfin, F., Myles, S., Choi, Y., Hughes, D., Illek, R., van Oven, M., Pakendorf, B., Kayser, M., Stoneking, M. (2012). Bridging Near and Remote Oceania: mtDNA and NRY variation in the Solomon Islands. *Molecular Biology and Evolution*, 29(2), 545-564.

Deniker, J. (1900). *The races of man: An outline of anthropology and ethnography.* London: W. Scott Ltd.

Derrick, R.A. (1950). A history of Fiji. Suva: Suva Print and Stationary Department.

Dickinson, W.R. (2006). Temper sands in prehistoric Oceanian pottery: Geotectonics,

sedimentology, petrography, provenance. Boulder: The Geological Society of America, Inc.

Duerr, R. (2006). Fijian map. Retrieved April 17, 2012 from http://www.globetrip.ch/karten/

Dyen, I. (1963). The lexicostatistical classification of the Austronesian languages. New Haven: Isidore Dyen.

Eerskine, J.E. (1967). Journal *of a cruise among the islands of the western Pacific*. London: Dawson.

Excoffier, L. (2006). ARLEQUIN©: A software for population genetics data analysis version 3.1 [computer software]. Bern, Switzerland.

Field, J.S., Cochrane, E.E., and Greenlee, D.M. (2009). Dietary change in Fijian prehistory: Isotopic analyses of human and animal skeletal material. *Journal of Archaeological Science*, 36, 1547-1556.

Friedlaender, J.S., Friedlaender, F.R., Hodgson, J.A., Stoltz, M., Koki, G., Horvat, G., Zhadanov, S., Schurr, T.G., Merriwether, D.A. (2007). Melanesian mtDNA complexity. *PLoS ONE*, 2(2): e248, 1-13

Frost, E.L. (1979). Fiji. In J.D. Jennings (ed). *The prehistory of Polynesia*. Cambridge: Harvard University Press.

Gabel, N.E. (1958). A racial study of the Fijians. *University of California Anthropological Records*, 20.

Garanger, J. (1971). Incised and applied-relief pottery, its chronology and development in southeastern Melanesia, and extra areal comparisons. In R.C. Green and M. Kelly (eds) *Studies in Oceanic culture history volume 2,* 53-99.

Gene Codes Corporation. (2007). Sequencher® sequence analysis software version 5.0 [computer software]. Ann Arbor, Michigan.

Geraghty, P.A. (1983). The history of the Fijian languages. *Oceanic Linguistics Special Publication*, 19, 1-483.

Geraghty, P.A. (1986). The sound system of Proto-Central-Pacific. In P. Geraghty, L. Carrington, and S.A. Wurm (eds.), *FOCAL II: papers from the fourth international conference on Austronesian linguistics*, 289-312. Canberra: Department of Linguistics, Research School of Pacific Studies, The Australian National University.

Gifford, E.W. (1951). Archaeological Excavations in Fiji. Anthropological Records 13:

189-288. Berkeley: University of California Press.

Gordon, R.G. Jr. (2005) *Ethnologue: Languages of the World*. Dallas: SIL International.

Grace, G.W. (1961). Lexicostatistical comparison of six Eastern Austronesian languages. *Anthropological Linguistics*, 3(9), 1-22.

Grace, G.W. (1964). The linguistic evidence. *Current Anthropology*, 5(5), 361-368.

Gray, R.D., Drummond, A.J., and Greenhill, S.J. (2009). Language phylogenies reveal expansion pulses and pauses in Pacific settlement. *Science*, 323(5913), 479-483.

Green, R.C. (1976). Lapita sites in the Santa Cruz group. In R.C. Green and M.M. Cresswell (eds), *Southeast Solomon Islands cultural history: A preliminary survey,* 133-147. Wellington: Royal Society of New Zealand.

Green, R.C. (1978). New sites with Lapita pottery and their implications for an understanding of the settlement of the Western Pacific. *Working papers in Anthropology, Archaeology and Maori Studies,* 51. Auckland: Department of Anthropology, University of Auckland.

Green, R.C. (1991). Near and Remote Oceania: disestablishing 'Melanesia' in culture history. In *Man and a half* (ed. A. Pawley), 491–502. Auckland: Polynesian Society.

Haddon, A.C. (1923). Migrations of peoples in the south west Pacific. *Proceedings of the Pan-Pacific Scientific Congress,* 1, 220-242.

Hale, H. (1846). Ethnography and philology. *The Report of the United States Exploring Expedition*, 6, 194.

Hedrick, J.D. (1971). Lapita-style pottery from Malo Island. *Journal of the Polynesian Society,* 80, 15-19.

Hill, C., Soares, P., Mormina, M., Macaulay, V., Clarke, D., Blumbach, P.B., Vizuete-Forster, M., Forster, P., Bulbeck, D., Oppenheimer, S., et al. (2007). A mitochondrial stratigraphy for island southeast Asia. *The American Journal of Human Genetics*, 80, 29-43.

Hirth, K.G. (1978). Interregional trade and the formation of gateway communities. *American Antuquity*, 43(1), 35-45.

Holy, L. (1996). Anthropological perspectives on kinship. UK: Pluto Press.

Horai, S., Kondo, R., Nakagawa-Hattori, Y., Hayashi, S., Sonoda, S. and Tajima, K.

(1993). Peopling of the Americas, founded by four major lineages of mitochondrial DNA. *Molecular Biology & Evolution*, 10, 23-47.

Houghton, P. (1996). *People of the great ocean*. Cambridge: Cambridge University Press.

Howard, A. (1985). History, myth and Polynesian chieftainship: The case of Rotuman kings. In A. Hooper and J. Huntsman (eds). *Transformation of Polynesian Culture.* Auckland: Polynesian Society.

Howells, W.W. and Moss, W.L. (1933). *Anthropometry and blood types in Fiji and the Solomon Islands*. New York: American Museum of Natural History.

Hudjashov, G., Kivisild, T., Underhill, P.A., Endicott, P., Sanchez, J.J., Lin, A.A., Shen, P., Oefner, P., Renfrew, C., Villems, R., et al. (2007). Revealing the prehistoric settlement of Australia by Y chromosome and mtDNA analysis. *Proceedings of the National Academy of Sciences USA*, 104, 8726-8730.

Hunt, T.L., and Graves, M.W. (1990). Some methodological issues in Oceanic prehistory. *Asian Perspectives*, 29, 107-115.

IDM Computer Solutions Inc. (2000). UltraEdit®-32 professional text/HEX editor version 7.20a. [computer software]. Hamilton, Ohio.

Irwin, G. (2009). Pacific migrations figure. Retrieved April 17, 2012 from http://www.TeAra.govt.nz/en/pacific-migrations/3/2

Jago, L.C.F. and Boyd, W.E. (2005). How a wet tropical rainforest copes with repeated volcanic destruction. *Quaternary Research*, 64(3), 399-406.

Jordan, F.M., Gray, R.D., Greenhill, S.J., and Mace, R. (2009). Matrilocal residence is ancestral in Austronesian societies. *Proceedings of the Royal Society of Biology*, 276, 1957-1964.

Kahuroa. (2010). Pacific culture areas map. Retrieved April 17, 2012, from http://en.wikipedia.org/wiki/File:Pacific_Culture_Areas.jpg.

Kayser, M., Brauer, S., Cordaux, R., Casto, A., Lao, O., Zhivotovsky, L.A., Moyse-Faurie, C., Rutledge, R.B., Schiefenhoevel, W., Gil, D., et al. (2006). Melanesian and Asian origins of Polynesians: mtDNA and Y chromosome gradients across the Pacific. *Journal of Molecular Biology and Evolution*, 23(11), 2234-2244.

Kayser, M., Lao, O., Saar, K., Brauer, S., Wang, X., Nürnberg, P., Trent, R.J., and Stoneking, M. (2008). Genome wide analysis indicates more Asian than Melanesian ancestry of Polynesians. *The American Journal of Human Genetics*, 82, 194-198.

Kayser, M. (2010). The human genetic history of Oceania: Near and remote views of dispersal. *Current Biology*, 20, R194-R201.

Kirch, P. (1997). The Lapita peoples. London: Blackwell.

Kirch, P. (2000). On the road of the winds. Berkeley: University of California press.

Ladefoged, T.N. (1993). Evolutionary process in an oceanic chiefdom: Intergroup aggression and political integration in traditional Rotuman society. Doctoral dissertation, Department of Anthropology, University of Hawai'i, Honolulu. Ann Arbor: University microfilms.

Ladefoged, T.N. (1995). The evolutionary ecology of Rotuman political integration. *Journal of Anthropological Archaeology*, 14, 341-358.

Levinson, G., and Gutman, G.A. (1987). Slipped-strand mispairing: A major mechanism for DNA sequence evolution. *Molecular Biology & Evolution*, 4, 203-221.

Lum, J.K. (1998). MtDNA and language support a common origin of Micronesians and Polynesians in Island Southeast Asia. *American Journal of Physical Anthropology*, 105, 105-119.

Manly, B.F.J. (2005). Multivariate statistical methods: A primer. New York: CRC Press.

Melton, T., Peterson, R., Redd, A.J., Saha, N., Sofro, A.S., Martinson, J., and Stoneking, M. (1995). Polynesian genetic affinities with SE Asian populations as identified by mtDNA analysis. *American Journal of Human Genetics*, 57, 403-414.

Merriwether, D.A. (1999). MtDNA variation is an indicator of Austronesian influence in island Melanesia. *American Journal of Physical Anthropology*, 110, 243-270.

Microsoft. (2003). Microsoft Excel® [computer software]. Redmond, Washington.

Mona, S., Grunz, K.E., Brauer, S., Pakendorf, B., Castri, L., Sudoyo, H., Marzuki, S., Barnes, R.H., Schmidtke, J., Stoneking, M., et al. (2009). Genetic admixture history of Eastern Indonesia as revealed by Y-chromosome and mitochondrial DNA analysis. *Journal of Molecular Biology & Evolution*, 26, 1865-1877.

Næss, A. and Boerger, B.H. (2008). Reefs-Santa Cruz as Oceanic: Evidence from the verb complex. *Oceanic Linguistics*, 47, 185-212.

Nei, M. (1987). Molecular evolutionary genetics. New York: Colombia University Press.

Nunn, P.D. (2007). Echoes from a distance: Research into the Lapita occupation of the

Rove Peninsula, southwest Viti Levu, Fiji. In S. Bedford, C. Sand, and S.P. Connaughton (eds). *Oceanic Explorations: Lapita and Western Pacific settlement*, 163-176. Australian National University: ANU E Press.

Ohashi, J., Naka, I., Tokunaga, K., Inaoka, T., Ataka, Y., Nakazawa, M., Matsumura, Y., and Ohtsuka, R. (2006). Brief communication: MtDNA variation suggests extensive gene flow from Polynesian ancestors to indigenous Melanesians in the Northwestern Bismarck Archipelago. *American Journal of Physical Anthropology*, 130, 551-556.

Oota, H., Settheetham-Ishida, W., Tiwawech, D., Ishida, T., and Stoneking, M. (2001). Human mtDNA and Y-chromosome variation is correlated with matrilocal versus patrilocal residence. *Nature Genetics*, 29, 20-21.

Parke, A.L. (2000). Coastal and inland Lapita sites in Vanua Levu, Fiji. *Archaeology in Oceania*, 35(3), 116-119.

Parry, J. (1987). The Sigatoka valley – pathways into prehistory. *Fiji Museum Bulletin, 9.*

Petchey, F.J. (1995). The archaeology of Kudon: Archaeological analysis of Lapita ceramics from Mulifanua, Samoa, and Sigatoka, Fiji. Auckland: University of Auckland.

Pierson, M.J., Martinez-Arias, R., Holland, B.R., Gemmell, N.J., Hurles, M.E., and Penny, D. (2006). Deciphering past human population movements in Oceania: Provably optimal trees of 127 mtDNA genomes. *Molecular Biology & Evolution*, 23(10), 1966-1975.

Pietrusewsky, M. (1983). Multivariate analysis of New Guinea and Melanesian skulls: A review. *Journal of Human Evolution*, 12, 61-76.

Pugach, I., Matveyev, R., Wollstein, A., Kayser, M., Stoneking, M. (2011). Dating the age of admixture via wavelet transform analysis of genome-wide data. *Genome Biology*, 12, R19.

Rechtman, R.B. (1992). The evolution of sociopolitical complexity in the Fiji islands. Los Angeles: University of California.

Redd, A.J., Takezaki, N., Sherry, S.T., McGarvey, S.T., Sofro, A.S., and Stoneking, M. (1995). Evolutionary history of the COII/tRNA-Lys intergenic 9 base pair deletion in human mtDNAs from the Pacific. *Journal of Molecular Biology and Evolution*, 12(4), 604-615.

Redd, A.J. & Stoneking, M. (1999). Peopling of Sahul: mtDNA variation in Aboriginal and Papua New Guinean populations. *American Journal of Human Genetics*, 65, 808-828.

Reepmeyer, C. (2008). Characterising volcanic glass sources in the Banks Islands, Vanuatu. *Archaeology in Oceania*, 43(2), 120-127.

Reepmeyer, C. and Clark, G. (2010). Post-colonization interaction between Vanuatu and Fiji reconsidered: The re-analysis of obsidian from Lakeba Island, Fiji. *Archaeometry*, 52, 1-18.

Ricaut, F-X., Thomas, T., Mormina, M., Cox, M.P., Bellatti, M., Foley, R.A., Mirazon-Lahr, M. (2010). Ancient Solomon Islands mtDNA: Assessing Holocene settlement and the impact of European contact. *Journal of Archaeological Science*, 37, 1161-1170.

Rodman, M. (1979). Following peace: Indigenous pacification of a northern New Hebridean society. In *The pacification of Melanesia.* Ann Arbor: University of Michigan press.

Rohlf, F.J. (1998). NTSYSpc©: Numerical taxonomy system version 2.02h [computer software]. Setauket, NY.

Ross, M. and Næss, A. (2007). An Oceanic origin for Aiwoo, the language of the Reef Islands? *Oceanic Linguistics,* 46, 456-498.

Sand, C. (2000). The specificities of the 'Southern Lapita Province': The new Caldonian case. *Archaeology in Oceania*, 35(1), 20-33.

Sand, C. (2001). Evolutions in the Lapita cultural complex: A view from the southern Lapita province. *Archaeology in Oceania,* 36, 65-76.

Schutz, A.J. (1978). Fijian Language Studies. *Bulletin of the Fiji Museum*, 4, 1-98.

Sheppard, P.J. (2011). Lapita colonization across the Near/Remote Oceania boundary. *Current Anthropology*, 52(6), 799-840.

Sheppard, P.J. and Green, R.C. (1991). Spatial analysis of Nenumbo (SE-RF-2) Lapita site, Solomon Islands. *Archaeology in Oceania*, 26, 89-101.

Spriggs, M. (1990). Dating Lapita: Another view. In M.Spriggs (ed), *Lapita design, form and composition*, 6-27. Occasional papers in prehistory No 19. Canberra: Department of Prehistory, Australian National University.

Spriggs, M. (1997). The island Melanesians. Oxford: Blackwell.

Spriggs, M. (2003). Post-Lapita evolutions in Island Melanesia. In C. Sand (ed.), *Pacific archaeology: assessments and prospects. Proceedings of the International Conference for the 50th anniversary of the first Lapita excavation, Kone-Noumea*,

213-220. Noumea: Les Cathiers de L'Archeologie en Nouvelle-Caledonie, Museum of New Caledonia.

Pawley, A. & Ross, M. (1993). Austronesian Historical Linguistics and Culture History. Annual Review of Anthropology, 22, 425-459.

Pawley, A. (1996). On the position of Rotuman. In *Nothofer*. 85-119.

Petrie, C.A. and Torrence, R. (2008). Assessing the effects of volcanic disasters on human settlement in the Wiallaumez Peninsula, Papua New Guinea: a Bayesian approach to radiocarbon calibration. *The Holocene*, 18(5), 729-744.

Sambrook, J. and Russell, D.W. (2001). Molecular cloning: A laboratory manual. Cold Spring Harbor: Cold Spring Harbor Laboratory Press.

Scheinfeldt, L., Friedlaender, F., Friedlaender, J., Latham, K., Koki, G., Karafet, T., Hammer, M., and Lorenz, J. (2006). Unexpected NRY chromosome variation in northern island Melanesia. *Molecular Biology & Evolution*, 23(8), 1628-1641.

Schmidt, H. (1999). Rotuma: Sprache und Geschichte. Ph.D. dissertation. University of Hamburg.

Schutz, A.J. (1978). Fijian Language Studies. *Bulletin of the Fiji Museum*, 4, 1-98.

Sheppard, P.J. (2011). Lapita colonization across the Near/Remote Oceania boundary. *Current Anthropology*, 52(6), 799-840.

Simons, R.T. (1968). Blood group genes in Polynesians and comparisons with other Pacific peoples. In A.P. Vayda (ed) *Peoples and cultures of the Pacific*. Garden City: The American Museum of Natural History.

Spriggs, M. (1997). The island Melanesians. Oxford: Blackwell.

Spriggs, M. (2003). Post-Lapita evolutions in Island Melanesia. In C. Sand (ed.), *Pacific archaeology: assessments and prospects. Proceedings of the International Conference for the 50th anniversary of the first Lapita excavation, Kone-Noumea*, 213-220. Noumea: Les Cathiers de L'Archeologie en Nouvelle-Caledonie, Museum of New Caledonia.

Swindler, D.R. (1968). Problems of Melanesian racial history. In A.P. Vayda (ed) *Peoples and cultures of the Pacific*. Garden City: The American Museum of Natural History.

Tamura, K., Dudley, J., Nei, M. and Kumar, S. (2007). MEGA©: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Molecular Biology and Evolution*. 24, 1596-1599.

Torrence, R. and Summerhayes, G.R. (1997). Sociality and the short distance trader: Intra-regional obsidian exchange in the Willaumez region, Papua New Guinea. *Archaeology in Oceania*, 32(1), 74-84.

Trejaut, J.A., Kivisild, T., Loo, J.H., Lee, C.L., He, C.L., Hsu, C.J., Li, Z.Y., and Lin, M. (2005). Traces of archaic mitochondrial lineages persist in Austronesian-speaking Formosan populations. *PLoS Biology*, 3, e247.

Van Oven, M., Kayser, M. (2009). Updated comprehensive phylogenetic tree of global human mitochondrial DNA variation. *Human Mutation*, 30(2), E386-E394.

Wickler, S., Spriggs, M. (1988). Pleistocene human occupation of the Solomon Islands, Melanesia. *Antiquity*, 62, 703-706.

Williams, T. (1858). *Fiji and the Fijians*. London: Alexander Heylin.

Wollstein, A., Lao, O., Becker, C., Brauer, S., Trent, R.J., Nurnberg, P., Stoneking, M., Kayser, M. (2010). Demographic history of Oceania inferred from genome-wide data. *Current Biology*, 20, 1983-1992.

Wrischnik, L., Higuichi, R.G., Stoneking, M., Erlich, H.A., Arnheim, N. and Wilson, A.C. (1987). Length mutations in human mitochondrial DNA: Direct sequencing of enzymatically amplified DNA. *Nucleic Acids Research*, *15, 529-542.*