

This document is a summary of the article prepared especially for the Rotuma Website by G.P. Shipley

G. P. Shipley, D. A. Taylor, A. Tyagi, G. Tiwari, & A. Redd. (2015). Genetic structure among Fijian island populations. *Journal of Human Genetics* 60(2):69–75.

Fiji has been characterized as the “Gateway to Polynesia”, yet while the peopling of Polynesia has received much attention, the peopling of Fiji remains unclear. Fiji was initially settled by the Lapitans approximately 3,100 years ago, but experienced subsequent immigration from both the east and west. As a group, Fijians have traditionally been classified as Melanesian, and treated as a single, homogenous population. But modern Fijians are a complex blend of Melanesian and Polynesian characteristics, and there is some support for splitting Fiji between Melanesia and Polynesia or including it altogether in Polynesia. This complexity of genetic, phenotypic, cultural, and linguistic variation found in Fiji reflects Fiji’s central role in Oceanic movements.

We sought to determine whether the Fijians are genetically homogenous, whether they exhibit the sex-biased genetic admixture commonly associated with areas settled by Austronesian-speaking peoples, and whether the Rotumans in the north and the Lau Islanders in the east are genetically more similar to Polynesians than is the rest of Fiji. To do this, we examined Y chromosome markers which are passed from fathers to sons and contain information about the paternal lineages of populations, and mitochondrial DNA (mtDNA) markers which are passed from mothers to their children (sons and daughters) and contain information about the maternal lineages of populations.

More specifically, we examined several Y chromosome short tandem repeats (Y-STRs) and the mtDNA hypervariable segment 1 (HVS1) region in samples from the Fijian island populations of Viti Levu, Vanua Levu, Kadavu, the Lau Islands, and Rotuma. As discussed in more detail below, we found that the Fijian island populations are not genetically homogenous as there is significant genetic structure among these populations for the Y-STRs, both with and without the Rotumans, but not for the mtDNA. We found that all five populations exhibited the sex-biased admixture associated with areas settled by Austronesian-speaking peoples, with paternal lineages more strongly associated with Melanesian populations and maternal lineages more strongly associated with Polynesian populations. And we found that the Rotumans in the north and the Lau Islanders in the east are genetically more similar to Polynesian populations than are the other Fijian populations, but only for the mtDNA. For the Y-STRs, the Rotumans and the Lau Islanders were genetically as similar to Melanesian populations as were the other three populations. Of the five populations, the Rotumans were the most different in almost every regard.

YDNA												
					Slatkin's Linearized F_{ST} Genetic Distances Values							
Population	N	Number of Haplotypes	Gene Diversity	Mean No. of Pairwise Differences	Viti Levu	Vanua Levu	Kadavu	Lau	Rotuma	Polynesia	Melanesia	
Viti Levu	47	35	0.98 +/-0.01	5.79 +/- 2.82								
Vanua Levu	17	16	0.99 +/-0.02	6.59 +/- 3.27	0.10							
Kadavu	10	10	1.00 +/-0.05	6.53 +/- 3.38	0.00	0.01						
Lau	18	16	0.98 +/-0.03	6.18 +/- 3.08	0.01	0.09	0.00					
Rotuma	10	8	0.93 +/-0.08	5.38 +/- 2.83	0.16	0.14	0.00	0.05				
Polynesia	58	37	0.96 +/- 0.01	5.13 +/- 2.52	0.14	0.32	0.22	0.17	0.55			
Melanesia	501	319	1.00 +/-0.00	6.06 +/- 2.89	0.18	0.15	0.01	0.12	0.06	0.25		

Table 1: Y-STR genetic diversity and genetic distance values for certain Fijian island populations, as well as for the centroids of Polynesia and Melanesia.

In Table 1, Y-STR data for the five individual Fijian island populations were compared to Polynesians as a group, to Melanesians as a group, and to each other. Again, this data represents the paternal lineages. The Rotumans were by far the least Polynesian-like and had the largest difference (the Rotuman-Polynesian distance is 0.55, while the Rotuman-Melanesian distance is 0.06). Within Fiji, the Rotumans were most different from the Viti Levuans and least different from the Kadavuans. Additionally, the Rotumans had the lowest number of different haplotypes, the lowest gene diversity, and the lowest mean number of pairwise differences.

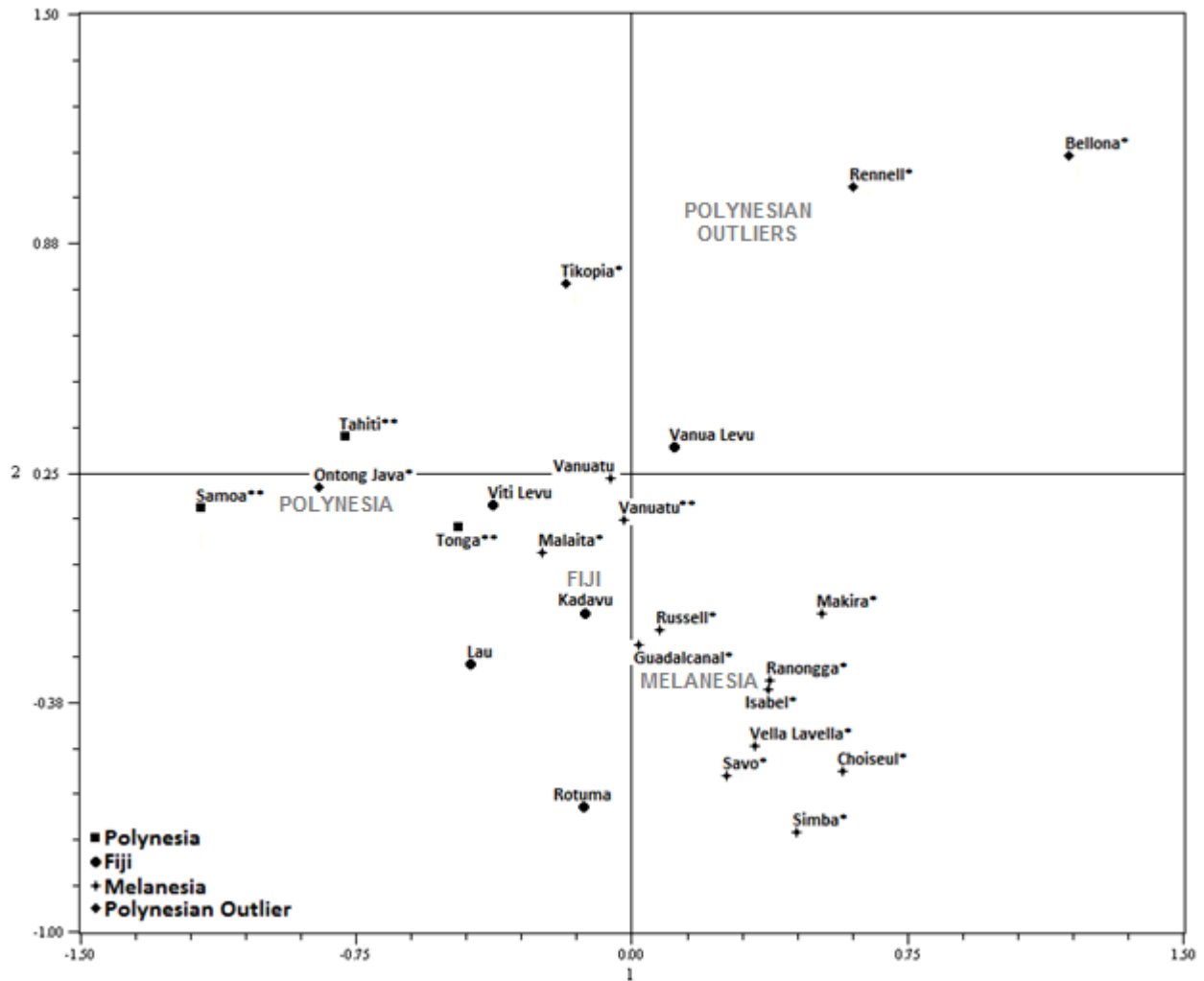


Figure 2: Two-dimensional plot of genetic distance values based on nine Y-STRs.

In Figure 2, Y-STR genetic distance data were plotted for the five Fijian island populations and several the Polynesian and Melanesian island populations. Surprisingly, the Rotumans grouped with the Melanesians, but this is likely due to increased genetic drift associated with the Y chromosome (as evidenced by the positions of the Polynesian Outliers), rather than to a strong genetic connection between Rotuma and Melanesia.

Population	N	Asian Haplogroups			Melanesian Haplogroups									
		B4b1	B4a1a1	B4a1a1a	P1	P1e	Q1	Q1a2	Q2	M27a	M27b	M28	M28a	M28b
<i>Fiji</i>	107	0.009	0.093	0.710		0.019	0.028	0.009	0.056			0.009	0.065	
Viti Levu	22		0.136	0.636				0.045	0.136				0.045	
Vanua Levu	21			0.762		0.095	0.095		0.048					
Kadavu	21		0.095	0.619									0.286	
Lau	22		0.136	0.682			0.045		0.091			0.045		
Rotuma	21	0.048	0.095	0.857										

Table 2: MtDNA haplogroup frequencies for certain Fijian island populations.

In Table 2, we found that, as a group, Fijian mtDNA haplogroups were 81.2% Asian and 18.7% Melanesian. Again, this data represents the maternal lineages. The B4a1a1a mtDNA haplogroup, which has a very high frequency in Polynesia, had the highest frequency of any mtDNA haplogroup in all of the Fijian populations, and the highest frequency in Rotuma. Further, the Rotumans had exclusively (100%) Asian mtDNA haplogroups, which suggests they had a substantially different settlement or post-settlement experience than the other Fijian island populations.

MtDNA												
					Slatkin's Linearized F_{ST} Genetic Distance Values							
Population	N	Number of Haplogroups	Gene Diversity	Mean No. of Pairwise Differences	Viti Levu	Vanua Levu	Kadavu	Lau	Rotuma	Polynesia	Melanesia	
Viti Levu	22	10	0.76 +/- 0.10	5.91 +/- 2.93								
Vanua Levu	21	11	0.74 +/- 0.11	6.31 +/- 3.12	0.00							
Kadavu	21	9	0.85 +/- 0.06	6.64 +/- 3.26	0.01	0.03						
Lau Islands	22	10	0.75 +/- 0.10	5.12 +/- 2.58	0.00	0.00	0.02					
Rotuma	21	3	0.35 +/- 0.13	0.73 +/- 0.57	0.13	0.10	0.24	0.08				
Polynesia	24	---	---	1.78 +/- 1.07	0.08	0.07	0.19	0.04	0.00			
Melanesia	519	---	---	5.26 +/- 2.55	0.24	0.23	0.25	0.25	0.45	0.43		

Table 3: MtDNA HVS1 genetic diversity and genetic distance values for certain Fijian islands populations, as well as for the centroids of Polynesia and Melanesia.

In Table 3, mtDNA data for the five individual Fijian island populations were compared to the Polynesians as a group, to the Melanesians as a group, and to each other. Genetic distance values indicated that the Rotumans were the most Polynesian-like, though all five island populations were more Polynesian- than Melanesian-like. In contrast to the Y-STR data, the Rotumans were by far the least Melanesian-like and had the largest difference (the Rotuman-Polynesian distance is 0.00, while the Rotuman-Melanesian distance is 0.45). Within Fiji, the Rotumans were most different from the Kadavuans and least different from the Lau Islanders. As with the Y-STRs, but to a much greater extreme, the Rotumans had the lowest number of different haplotypes, the lowest gene diversity, and the lowest mean number of pairwise differences.

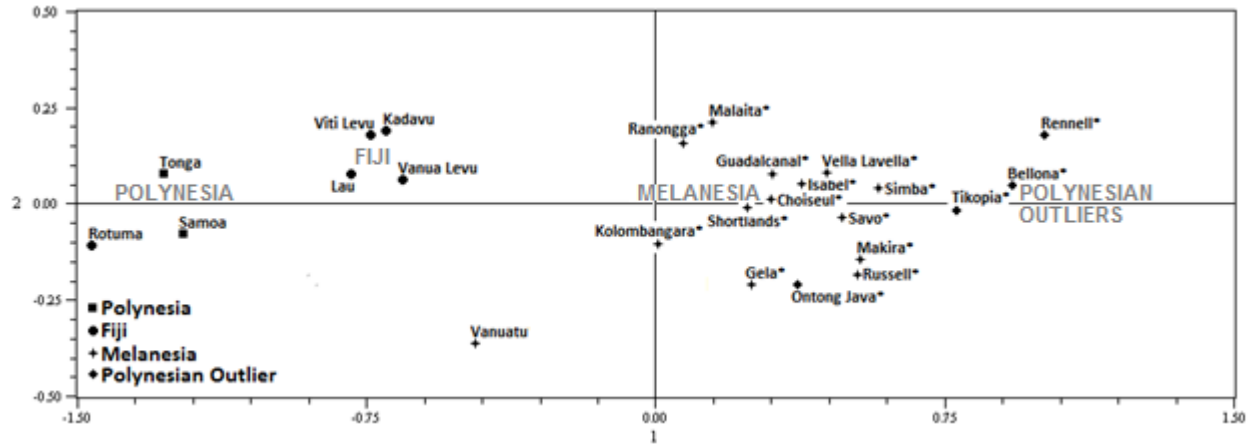


Figure 3: Two-dimensional plot of genetic distances based on the mtDNA HVS1 region.

In Figure 3, mtDNA HVS1 genetic distance data were plotted for the five Fijian island populations and several Polynesian and Melanesian island populations. Four of the five Fijian populations grouped clearly intermediate between the Polynesian and Melanesian clusters, while the Rotumans grouped much more closely with the Polynesians. As with the Y-STRs, the Rotumans did not associate with the Polynesian Outlier populations.