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Research Article

Mitochondrial DNA Polymorphisms of the Saisiyat Indigenious Group of Taiwan, Search for a Negrito Signature

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Abstract

The genetic profile of Negritos of the Philippines differs from the non-Negrito groups with mitochondrial DNA haplogroups B4b1a2, B5, D6a, M, M52a, and N11b. Although Negritos are not seen in Taiwan, the strong genetic affinity between the Philippines and Taiwan Mountain Tribe Aborigines (TwMtA), and Folks tales of TwMtA, Saisiyat and Atayal recounting past contacts with Negritos, warrant the search for a Negrito signature in Taiwan.

Material and Method: Discriminant Analysis of Principal Component (DAPC) was used to determine the genetic relationship between TwMtA, Filipino and non-TwMtA groups.

Results: The deep coalescence of B4b1a2 in the Philippine Negritos, Saisiyat, Atayal, Island Southeast Asia, and SEA (Southeast Asia) suggested a deeply rooted common ancestry, but could not support a past Negrito presence in Taiwan. Conversely, the sharing of cultural components and mtDNA (mitochondrial DNA) haplogroup D6a2 in Saisiyat, Atayal and Philippine Negritos may characterize a Negrito signature in Taiwan. Although the molecular variation of D6a2 determines its presence in Taiwan back to middle Neolithic, other markers, Y-SNP haplogroups C-M146 and K-M9, warrant further analysis.

Conclusion: Most likely, the physical characteristics, languages, and the genetic makeup of the Negritos in Taiwan have been diluted as the result of heavy migration from the mainland in the last 400 years.

Keywords: Molecular Anthropology, Negrito, Austronesian, Population genetics, Saisiyat, Taiwan aborigines, Mitochondrial DNA.

Abbreviations: TwMtA-Taiwan Mountain Tribe Aborigines, DAPC-Discriminant Analysis of Principal Components, SEA-Southeast Asia, mtDNA-mitochondrial DNA, NRY-Non-Recombination Y-chromosome, BSP-Bayesian Skyline Plot, MMDA-Mismatch Distribution Analysis, Y-SNP-Y-chromosome Single Nucleotide Polymorphism, NTwMtA-North Taiwan Mountain Tribe Aborigines, MSEA-Mainland Southeast Asia, HVS-I-Hypervariable Segment I, STR-Short Tandem Repeat, SNP-Single Nucleotide Polymorphism, ISEA-Island Southeast Asia, CTwMtA-Central TwMtA, STwMtA-Southern TwMtA.

Introduction

The Saisiyat tribe is an Austronesian speaking group, a member of the Taiwan Mountain Tribe Aborigines. In the year 2018 April, the Saisiyat numbered 6,607, making them one of the third smallest indigenous groups on the island [1]. Its people live in the North West flank of the Taiwan mountain range, between Hsinchu and Miaoli (**Figure 1**). The geography of this region, which comprises the Egongji and Hengpingbei Mountains, forced Saisiyat to divide into two groups, the Sai-Kirapa in the north and the Sai-Maghahyobun in the south.

Historically Sai-Kirapa has had significant interaction with the northeastern Atayal tribe while the Sai-Maghahyobun has had more contacts with the Hakka who migrated there from East China in the last 400 years [2-6]. Similarly, Saisyat has two main dialects: the Taai Dialect in the North, and the Tungho Dialect in the south [7]. While Saisiyat has traditional views that mix aspects of ancestor worship and animism where all things are considered being alive and possess a distinct character, other Saisiyat people also practice Christianity [2].

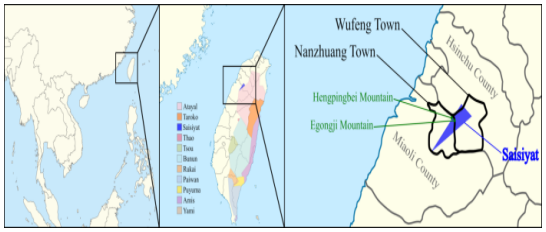

Figure 1: Saisiyat distribution map.

Most TwMtA tribes have kept folktales and myths that relate to past contacts with Negritos. In particular, Saisiyat is the only tribe in Taiwan that has rituals every two years honoring the memory of "the Short People or Pas-ta'ai" [8]. The Short People in these folktales are described as short-statured, dark-skinned and frizzy-haired and have the same anthropometric characteristics as Negritos in the Philippines. Some anthropologists believe these may have been Proto-Australoid people who possibly arrived from Africa during the early Southern Dispersal 60,000 years ago, but to this day, no archeological evidence has ever revealed the past presence of Negritos in Taiwan [9,10]. It now proposed that, instead of a shared ancestral phenotype from an ancient and well-distributed population, the resemblance of Negrito with other Negritos of Asia and Pygmies in Africa is the result of convergent evolution in the different parts of the word under equivalent environmental conditions [11,12]. This is supported by genetic evidence showing that Negritos of different parts of the world region have different genetic structures [13]. Further, other genetic studies observed that there is no simple dichotomy between Negrito and non-Negrito groups of the Philippines [14,15].

Most Negrito groups share genetic variations with neighbor populations while they have more deeply rooted variants that suggest a much earlier arrival in the region, isolation, and admixture with later arrivals [16]. Many studies using mitochondrial DNA (mtDNA) and Y-chromosome variation have established a significant common ancestry between the populations of Taiwan and the Philippines, it is therefore expected to find a Negrito signature in Taiwan[14,15,17-21]. Although Atayal and Saisiyat have a genetic profile that distinguishes them from the southern TwMtA, the polymorphism is homogenously distributed through all the tribes. [2,3,6,21-24].In this study, we analyze the mitochondrial genetic polymorphism of the Saisiyat tribe and search genetic evidence of the speculated presence of Negritos in all Taiwan indigenous groups.

The mitochondrial molecular clock is faster than the molecular clock of Non-Recombination Y-chromosome (NRY) haplogroups determined using Single Nucleotide Polymorphisms (SNPs) and slower for NRY haplotypes determined using Short Tandem Repeats (STRs) [25]. The rate of mtDNA is, therefore, most appropriate to measure and trace evolutionary human changes phylogenetically in time and space. Further, its short length (16,569 base pairs), its presence in both males and females, its high polymorphism and the higher concentration than genomic DNA, makes it a most effective material, practically and financially, to use in a small laboratory [26]. However, we will use NRY in our comparative analysis with the Philippines.

Results

Mitochondrial DNA Diversity

Compared to the mtDNA genetic diversity of all Taiwan groups (h=0.717 to 0.991), the Saisiyat tribe (h=0.864) was lower than in Fujian and Taiwan Han (Minnan and Hakka, TwH) (~ 0.99), and in range with other TwMtA (h=0.717 to 0.942) (**Table 1**) [27]. Similarly, the number of mtDNA haplogroups observed in Saisiyat (n=20) was in range with the number of haplogroups seen in other TwMtA (n=7 to 55) and contrasted strongly with the number seen in Fujian, Minnan and Hakka (n=87, 95 and 226 respectively). Further, the tests of neutrality for Saisiyat, Tajima's D (D=-0.438; p=0.365) and the more powerful Fu's Fs test (Fs=-24.275; p<0.0001) indicated a departure from neutrality expectation, and were in range with most value observed among other TwMtA groups (Data not shown).

	East Asia	**Taiwan**													**Mainland Southeast Asia**	**Philippines**
		Taiwan Han		Taiwan Mountain Tribes Aborigines (TwMtA)												
	Fujian	Hakka	Minnan	Northern tribes			Central tribes			Southern tribes					Vietnam (n=58) Thailand (n=77) Akka (n=42)	Filipinos
				Atayal	Taroko	**Saisiyat**	Thao	Tsou	Bunun	Rukai	Paiwan	Puyuma	Amis	Yami		
Sample size	149	153	599	109	54	**88**	30	60	181	77	168	107	292	88	177	372
Total number of mtDNA haplogroups (n)	87	95	226	21	7	**20**	15	16	40	22	35	26	55	9	96	72
Haplogroup diversity (h) (Nei et al. 1987)	0.984	0.983	0.991	0.814	0.717	**0.864**	0.907	0.89	0.911	0.915	0.925	0.923	0.942	0.843	0.981	0.955
± SD	0.001	0.002	0	0.021	0.025	**0.013**	0.012	0.012	0.008	0.009	0.005	0.007	0.004	0.009	0.002	0.002

Table 1: Mitochondrial DNA diversity of the Taiwan groups.

Demographic Analysis

A bimodal curve was observed between 11 and 21 basepair differences in the mismatch distribution analysis of Saisiyat for 88 mtDNA sequences (**Figure 2**). The bimodal mismatch curve may have been the result of admixture. Further, in contrast with the Fu's Fs test, the plot did not support population sudden expansion [28]. Similarly, the hypothesis of sudden expansion was rejected by two demographic indexes, the Sum of Squared Deviation (SSD) test (SSD=0.008, P<0.001) and the raggedness (r=0.011, P<0.001) (Harpending 1994) indicating that the data deviated from the simulation expected under the model of expansion (Figure 2, blue line). The analysis (Number of pairs vs. Base pair differences) was obtained from 88 mtDNA Saisiyat sequences using nucleotide positions (nps) 8,000-9,000, nps 10,000-11,000, and hyper variable segment I (HVS-I) nps 16040-16390 [22,24]. Using the Bayesian Skyline method, patterns of historical demography can also be inferred from estimates of the effective population size over time.

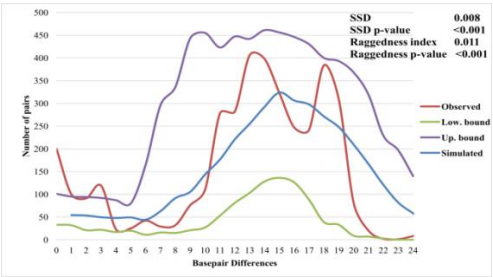

Figure 2: Mismatch Distribution Analysis (MMDA) of Saisiyat.

Accordingly, we constructed a Bayesian Skyline Plot (BSP) plot (**Figure 3**) from 88 Saisiyat sequences of the mtDNA hyper variable segment I (HVS-I) data, with 20 million Markov Chain Monte Carlo (MCMC) iterations, sampled every 3,000 steps, using a relaxed molecular clock and a mutation rate of 2.2964 x 10-7 mutations per site per year. The BSP showed an early Neolithic signature of population expansion, followed by a long phase of relatively constant population size and a sudden steep population reduction around 500 years BP. The Saisiyat present-day effective population obtained in Figure 3 is approximately 340 women (CI 100 to 1120 women) [29].

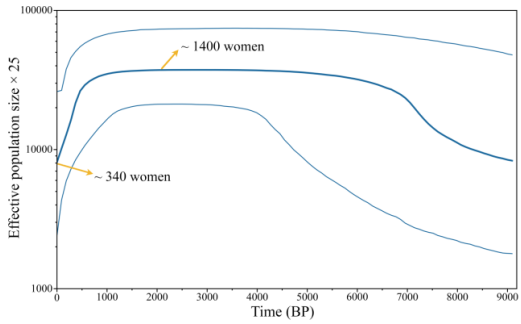

Figure3: Bayesian Coalescent Skyline analysis of the Saisiyat tribe.

Bayesian Skyline Plot (BSP) plot based on the mtDNA obtained from 88 Saisiyat sequences for the HVS-I control region. BSP was calculated using a relaxed molecular clock and a mutation rate of 2.2964×10^{-7} mutations per site per year and estimated with 20 million MCMC iterations sampled every 3,000 steps. The dark blue line represents the posterior median of the effective population size through Time (one generation=25 years). The light blue lines represent the 95% confidence interval.

MtDNA Haplogroup Distribution

Out of 20 mitochondrial haplogroups seen in Saisiyat (**Figure 4**), 15 were uniquely shared with the other the Austronesian speaking groups of Taiwan, and five haplogroups (B5a2a2a2, E1a1a1, F4b1', M7b1a2a and Y2) had a frequency greater than 8% representing 75% of the Saisiyat gene pool. Interestingly, haplogroups D6a2 was only seen in Saisiyat (1.1%), Atayal (4.6%), reported in a single individual of the Pazeh plain tribe, and the Mamanwa Negritos from the Philippines (3.3%) [14,24].

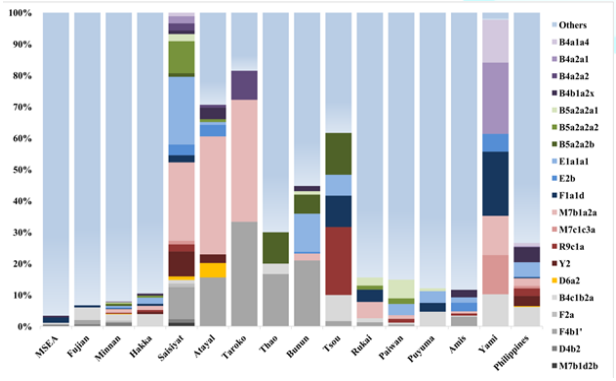

Figure 4: Haplogroup frequency in Saisiyat shared with other populations.

Distribution of shared mtDNA haplogroups of Saisiyat constructed using Taiwan data and other relevant populations [24]. Haplogroups with a shade of grey represent sharing with non-Indigenous groups of Taiwan (Minnan and Hakka). All haplogroups not seen in Saisiyat but present in other groups are represented by "other".

Population Differentiation

Discriminant Analysis of Principal Components (**Figure 5**) showed a clear geographic divide along the first Discriminant component (the X axis), which form a separates the Austronesian-speaking groups on the right, from the Han, the TwH, and MSEA (Indochina) on the left. Further, although individuals were not tightly grouped, the Northern and Central TwMtA form a cluster that clearly separates them from a lower cluster encompassing Southern TwMtA and the Philippines. Finally, we note that the Southern Austronesian cluster (Southern TwMtA and the Philippines) shows more admixtures with TwH than the Northern cluster.

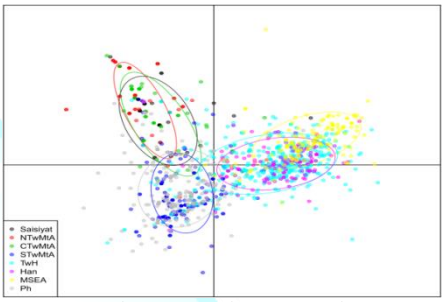

Figure 5: Scatter plot from DAPC from SNPs of mitochondrial DNA of Taiwan and the East Asian populations.

The dots represents individual from eight different groups and locations whose inertia ellipses are characterized by a color as indicated in the insert on the left. Sampling locations are: NTwMtA: North Taiwan Mountain Tribe Aborigines (TwMtA); CTwMtA: Central TwMtA; STwMtA: Southern TwMtA; TwH: Taiwan Han (Minnan and Hakka); MSEA: Mainland Southeast Asia (Indochina); Ph: Philippines; Han: Fujian.

Phylogenetic Analysis

A maximum-likelihood tree using mtDNA haplogroup frequencies was inferred with the TreeMix software (Figure 6A). The tree was consistent with the geographical distribution of populations in Taiwan; it places Saisiyat in a strong relationship with the Northern tribes (Atayal and Taroko). Further, migration arrows were first limited to 20 migration events in the analysis and only the three most significant gene flow events were retained for clarity of (Figure 6B). The relationship delineated between Saisiyat and the central TwMtA (Thao and Bunun) was expected from the DAPC clustering shown in Figure 5. More interesting, was a significant input from the Philippines to Taiwan, consistent with a previous study [20]. And here seen as gene flow to Saisiyat with a migration weight of ~ 0.65 (**Figure 6**). Most likely, this result is the effect of the sharing of haplogroups B4a2a, E2b, M7b1a2a, D6a2, R9c1a and Y2 between Saisiyat and the Philippines (Figure 4).

6A: Maximum-Likelihood tree inferred by TreeMix for all Taiwan and SEA populations assuming 20 significant gene-flow events, only the three most significant gene-flow events are shown for clarity, they are colored according to their weight on a zero to one scale [30]. 6B: Residual fit from A. Shaded colored cells represent Standard error for admixture events across all pairs of populations. Population pairs with a residual above zero are more closely related and more likely to correspond to an admixture event.

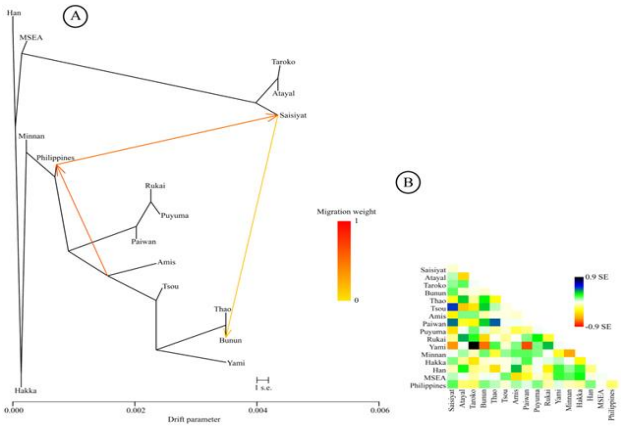

Figure6: Derived origin of admixture for Taiwan populations using TreeMix.

Discussion

In the first stage of this work, we examined the genetic variability using mitochondrial nucleotide positions (nps) 8000 to 9000 and nps 10,000 to 11,000 of the coding regions, and the HVS-I segment of the D-loop region to determine the genetic diversity and origin of the Saisiyat tribe of Taiwan. In the second stage, we investigated the general believed that Negrito groups predating the Lower Glacial Maximum period were associated with the first settlers of Sunderland/Island Southeast Asia (ISEA) [9].

Although there are some Chinese accounts of small, dark-skinned people with curly hair in Taiwan, to date, Taiwan has no archeological human remains supporting this hypothesis. Interestingly, most Taiwan Mountain tribes have kept folk tales describing past contacts with Negrito groups, most particularly the Saisiyat tribe of Hsinchu and Miaoli (Figure 1) who still perform solemn rites to commemorate this past. On the other hand, the presence of Negrito is still existent in the Philippines and other parts of peninsular East Asia, but not in Taiwan. If there is any truth in these TwMtA folk tales, then a small number of Negrito in Taiwan must have interacted with Neolithic agriculturalist migrants from the Southeast Asian mainland and most likely shaped their genetic diversity. In this regard, it is sensible to expect that these early contacts must have left some genetic traces. Here, our analysis of mtDNA polymorphisms tries to provide new insights into the history of the Saisiyat tribe [31,32].

Genetic Structure of Saisiyat

To investigate the mtDNA structure of Saisiyat, we first generated a mismatch distribution (Figure 3). A bimodal curve was obtained, and the two demographic indexes, the SSD test (SSD=0.008, P<0.001) and the raggedness (r=0.011, P<0.001) were significantly different to expectation. These results did not support expansion. Further, the Bayesian Skyline plot (Figure 4) along with previous results from Ko's research group did not reveal sufficient structure to visualize a recent population expansion. These results were in contrast with a highly significant Fu's Fs test for the Saisiyat tribe [22,28,33].

It possible these results are revealing a sign that the Saisiyat tribe experienced prehistorically a rapid population growth from an ancestral population with a small effective population size. Alternatively, the excess of rare mutations indicated by the significant negative Fu's Fs test could be the result of recent gene flow introduced by non-indigenous groups of Taiwan, such as the Minnan and Hakka. Finally, The BSP indicated an effective population of approximately 1400 women. This number may actually be inflated since our data set was collected by LM in 2004, but does not conflict with previously published BPSs, nor with the actual present-day number of Saisiyat women indicated in the last Census from the Taiwan Council of Indigenous Peoples [1,2,22].

Distribution

The mtDNA composition of the Saisiyat: Out of 21 different mtDNA haplogroups, 15 haplogroups were characterized as northern TwMtA haplogroups. Four haplogroups, F2a, E1a1a1, M7b1a2a and Y2 (Figure 4), constituted 75% of the Saisiyat genome. Consistent with other extant Taiwan Mountain tribes, the Saisiyat tribe 29% of its mtDNA genome was shared with Non-Taiwan Aborigines (Supplementary Table S1) and were most likely acquired from migrants of Mainland East Asia in the last 400 years.

Most of the remaining haplogroups were commonly seen throughout Taiwan Northern tribes. Among them, B4a2a, E2b, M7b1a2a, R9c1a, and Y2 were also seen in the Philippines. They are thought to represent a plausible signal for a mid-Holocene out-of-Taiwan expansion or a signal for a bidirectional migration between Taiwan and the Philippines [18,20,22,24,34-37]. The distribution of haplogroup D6 was intriguing. With a coalescence time of 14,390 years BP (Supplementary Table S1 and Figure S1) haplogroup D6 was seen at low frequency as D6c in East Asia and Southeast Asia (SEA). The presence of D6a2 as a single individual in the Pazeh plain tribe, in Saisiyat (1.1%), in Atayal (4.6%) and in the Mamanwa Negrito group of Mindanao in the Philippines (3.03%) could represent a genetic indicator of a past Negrito presence in Taiwan. However, a coalescence age estimate of D6a2 (2,626 years BP, CI 0-5,850) makes this supposition doubtful. It is possible the sharing of D6a2 between Saisiyat/Atayal and the Mamanwa must be the result of more recent gene flow.

It is conceivable that the bearers of D6a have experienced a bottleneck between 2,600 and 12,000 years BP, as suggested by the long stretch of nucleotide variation between D6a and D6a2 in their mtDNA genome (Supplementary Table S1 and Supplementary Figure S1). Lastly, mtDNA haplogroup Y2 is also shared between the Mamanwa and the Saisiyat and Atayal tribes. Nonetheless, its distribution in the Philippines (Negritos and non-Negritos) and its coalescence age estimate (5216 years BP, CI: 529-10046), characterize Y2 as a signature of the Neolithic expansion of Austronesian agriculturists in insular East Asia rather than a Negrito signature [14,15,17-21,24,34,38,39].

Principal Component Analysis

To characterize population structure across Saisiyat, other Taiwan groups, and their relationship with neighboring populations in MSEA and the Philippines, we performed a DAPC (Figure 5). The first component captured a clear geographical divide between Austronesian speaking groups and non-TwA groups including Fujian, Minnan, and Hakka. Component 2 in Figure 5 disclosed a strong affinity between Northern and Central TwMtA, and between the Philippines and the Southern TwMtA, suggesting that all these Austronesian-speaking populations have a common origin. However, the mtDNA composition of the Saisiyat suggested evidence supporting genetic affinity between Saisiyat and Negrito and non-Negrito groups of the Philippines.

Using Delfin mtDNA and our Taiwan data set we constructed a Multidimensional scaling plot to establish this relationship (Supplementary Figure S3). While the relationship between populations was the same as in the DAPC plot, the Aeta and Agta Negrito groups were outbound, most likely because of the conjoint results of drift, the presence of high frequency haplogroups such as P and M52 in Aeta and Agta, and long isolation [14]. On the other hand, haplogroup B4b1a2, E1a1a1, Y2, and D6a in the Mamawan group inferred strong affinity of the Mamanwa Negritos with other Austronesian groups, suggesting a more recent gene-flow of Austronesian-speakers in the Mamawa.

Maximum Likelihood Tree from TreeMix

TreeMix results inferred mtDNA gene-flow events (Figure 6) potentially summarizing patterns of population in the history of Taiwan such as bottlenecks, isolation, consanguinity within populations, here Saisiyat was characterized as a northern Taiwan tribe. Further, the gene-flow from Saisiyat (or the Northern TwMtA) to the Central TwMtA (Bunun, Thao, and Tsou) was previously foreseen in Figure 4 and 5, and is confirmed in Figure 6 [30]. Moreover, the strong migration event depicted by TreeMix from the Philippines to Saisiyat indicates genetic interflow. The mtDNA haplogroups possibly associated with this event, and seen in Saisiyat/Atayal and the Mamanwa Negrito group of the Philippines, can only be attributed to subtypes of haplogroups B4b1a2, E1a1a1, Y2, and D6a2.

These findings substantiate a possible past existence of Negritos in Taiwan. They suggest that the Mamanwa are intermediate between Austronesian and Negritos (Supplementary Figure S3**)** and possibly experienced several admixture events in the past. This option is nonetheless not supported by the age estimate of molecular variation obtained for any of the haplogroups of the same clade between Mamanwa and Saisiyat/Atayal. For example, D6a2 dates only to 2600 ± 1500 yrs BP (Supplementary figure S1) and Y2 dates 3956 ± 2455 yrs BP (Supplementary figure S2). One possible way to demonstrate a Negrito ancestry in Taiwan associated to D6 or Y2 would be to find sister branches of these haplogroups in Taiwan and/or the Philippines that would allow a coalescent node in the pre-Holocene period.

Other Gene Systems

Supporting this last observation, our previous Y chromosome analysis observed 4 Y-chromosome single nucleotide polymorphism (Y-SNP) haplogroups out of 24 unrelated Saisiyat males (Supplementary Table S1). Only one major haplogroup O1a1* (P203) had a frequency of 87.5%, while all other haplogroups (O1a2 (M50/110, O3a1* (KL1/122) and O3a2c1a (M133/M7/M134) were seen only once (4.2%) [21]. When compared to the Y haplogroup profile of the Philippines, O1a1* (P203) was prevalent in all Filipino ethnolinguistisc groups, Negritos and non-Negrito and its presence in any Negrito groups was regarded as an admixture with the former. Most interestingly, Negrito groups in the Philippines invariably possessed, to various levels, haplogroup haplogroups C-RPS4Y/M216, K-M9, and O3-M122 [15]. These haplogroups have not been seen in Saisiyat, but single observations of C-RPS4Y/M216 and K-M9 have been seen in the Taiwan plain tribes and could support a past presence of Negrito in Taiwan [15,21].

Lastly, to our knowledge, no previous studies associating the Filipino Negrito groups and the HLA gene system have yet been published; accordingly, no Negrito HLA inferences could be used for Taiwan. Nonetheless, several HLA*A-B-DRB1 haplotypes were unique to Saisiyat and 1/3 of Saisiyat haplotypes were shared with Atayal (Supplementary Table S1)**.** Lastly, the sharing of haplotype HLA A*34:01-B*56:01 or simply the sole presence of A*34:01 between Amis, Papua New Guinea highlanders, Maoris of New Zealand, and Australian Aborigines is intriguing. These findings suggest that HLA A*34:01 could be a genetic indicator of the pre-dispersal period of the Negrito throughout ISEA in the late Pleistocene era and should warrant further HLA analysis of the Philippines Negritos [3,6,40,41].

Summary

This investigation has contributed substantially more insights into the population groups in Taiwan and the Philippines. Further, while the physical appearance of Negritos has never been seen in Taiwan, few Taiwan Mountain tribes, such as the Saisiyat and the Atayal tribes, have conserved folktales inferring prehistoric co-habitation with them, and to this day, still celebrate this period bi-annually. Among the few mtDNA haplogroups shared between Taiwan Northern tribes and the Mamanwa Negritos (B4b1a2, E1a1a1, Y2 and D6a) only D6a may represent a common Negrito genetic legacy of the Saisiyat and Atayal tribes. This finding must be taken with caution, as the mid-Neolithic coalescence age estimate of D6a is too shallow. Further, no support was given from the Y chromosome analysis for Saisiyat and Atayal. Although the apparent affinity between the Taiwan Northern tribes and the Mamanwa Negritos of the southern Philippines could be the result of gene flow brought upon by bidirectional population movements at the time of the out of Taiwan, the presence of C-RPS4Y/M216 and K-M9 in Taiwan were scarce, and warrant more extensive studies of the Taiwan gene pool in the future.

Material and Method

Samples

Whole blood or saliva specimens were collected from 2704 unrelated individuals (**Table 2**) comprising Austronesian speaking groups from the Philippines (n=372), 251 TwMtA consisting of Saisiyat (n=88), Atayal (n=109) and Taroko (n=54), 271 central TwMtA consisting of Thao (n=30), Tsou (n=60) and Bunun (n=181), and 732 southern TwMtA consisting of Rukai (n=77), Paiwan (n=168), Puyuma (n=107), Amis (n=92) and the Yami islanders (n=88). The sampling also included 752 Taiwanese of Han descent (TwH) namely Minnan (n=599) and Hakka (n=153). Samples from neighbor populations included Han individuals from the east coast of China (Fujian, n=149), groups from Mainland Southeast Asia (MSEA, n=177), namely Vietnam (n=58), Thailand (n=77) and Akka (n=42), and finally 372 individuals from the Philippines as described in Tabbada. All samples above were collected from volunteers with individual written informed consent during the period of 2001 to 2004 by ML under approval of the Ethics Committee of the Mackay memorial hospital after giving information regarding the origins of their parents and grandparents [3,6,20].

Country	Population	Size	Groups	References
Taiwan	Saisiyat	88	Northern TwMtA[1]	Trejaut 2005; This study
Taiwan	Atayal	109	Northern TwMtA	Trejaut 2005
Taiwan	Taroko	54	Northern TwMtA	Trejaut 2005, Trejaut 2019
Taiwan	Thao	30	Central TwMtA	Trejaut 2005, Trejaut 2019
Taiwan	Tsou	60	Central TwMtA	Trejaut 2005
Taiwan	Bunun	181	Central TwMtA	Trejaut 2005
Taiwan	Rukai	77	Southern TwMtA	Trejaut 2005
Taiwan	Paiwan	168	Southern TwMtA	Trejaut 2005
Taiwan	Puyuma	107	Southern TwMtA	Trejaut 2005
Taiwan	Amis	292	Southern TwMtA	Trejaut 2005
Taiwan	Yami	88	Southern TwMtA	Trejaut 2005; Loo 2014
Taiwan	Minnan	599	TwH[2]	Trejaut 2005
Taiwan	Hakka	153	TwH	Trejaut 2005
China	Fujian	149	Han (EA[3])	Trejaut 2005
Vietnam	Vietnam	58	MSEA[4]	This study
Thailand	Thailand urban	77	MSEA	This study
Thailand	Akka	42	MSEA	This study
Philippines	Filipinos	372	Ph[5]	Tabbada and Trejaut 2010
Total		2704		

Note: [1]TwMtA: Taiwan Mountain Aborigines, [2]TwH-Taiwan Han, [3]EA-East Asia, [4]MSEA-Mainland Southeast Asia (Indochina) [5]Ph-Philippines.

Table 2: Population samples.

Data Analysis

All collected samples in our dataset were typed for Human leukocyte antigens (HLA-A, -B and -DRB1) and described in the Anthropology/HLA diversity component of the 13th international histocompatibility workshop. Specimen typed for mtDNA had haplogroups assigned according to Build 17 of Phylotree. Y haplogroups of the non-recombining part of the Y-chromosome (NRY) were determined using 81 Y-SNPs, and further analyzed using 17 Y-chromosome short tandem repeats (Y-STRs): DYS19, DYS385I, DYS385II, DYS389I, DYS389II, DYSS390, DYS391, DYS392, DYS393, DYS437, DYS438, DYS439, DYS448, DYS456, DYS458, DYS635, and Y GATA-H4. Additionally, we used corresponding mtDNA data from the literature including 24 complete mtDNA genome sequences representing Saisiyat [20-22,24,42,43].The partial mtDNA sequences are available in (Supplementary Table S2) The whole-mtDNA genome sequencing is available in Supplementary Text File S1. We deposited 12 new whole- mtDNA sequences in GenBank.

Statistical Analysis

In order to test for past population expansion of Saisiyat, we used two statistical tests Tajima's D and Fu's Fs [33,44]. The analyses were implemented in Arlequin 3.5.2.2, and p-values were generated using 1,000 simulations under a model of selective neutrality [45].

In addition, a mismatch frequency graph was plotted by using the mtDNA data from Arlequin 3.5.2.2 to determine whether the population of Saisiyat exhibited evidence of spatial range expansion or a stationary population history [44]. Demographic variation through time was obtained from a BSP using Beast with a relaxed molecular clock and a mutation rate of the mtDNA HVS-I data of 2.2964×10^{-7} mutations per site per year. Adegenet for R was used to perform DAPC with a number of Principal Components set to 273. The DAPC plot and inertia ellipses were produced using the poppr module of the R package. A maximum likelihood tree using mtDNA SNP frequencies was inferred with the TreeMix software. Admixture and direction of gene flow were inferred using the 20 most significant events [29,30,46-48].

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Author's contributions

The project was conceived and designed by JAT. JAT and LRC drafted the manuscript equally. LRC performed data analysis. The laboratory work was performed by ZSC and YHL. All authors have read and approved the final version of the manuscript.

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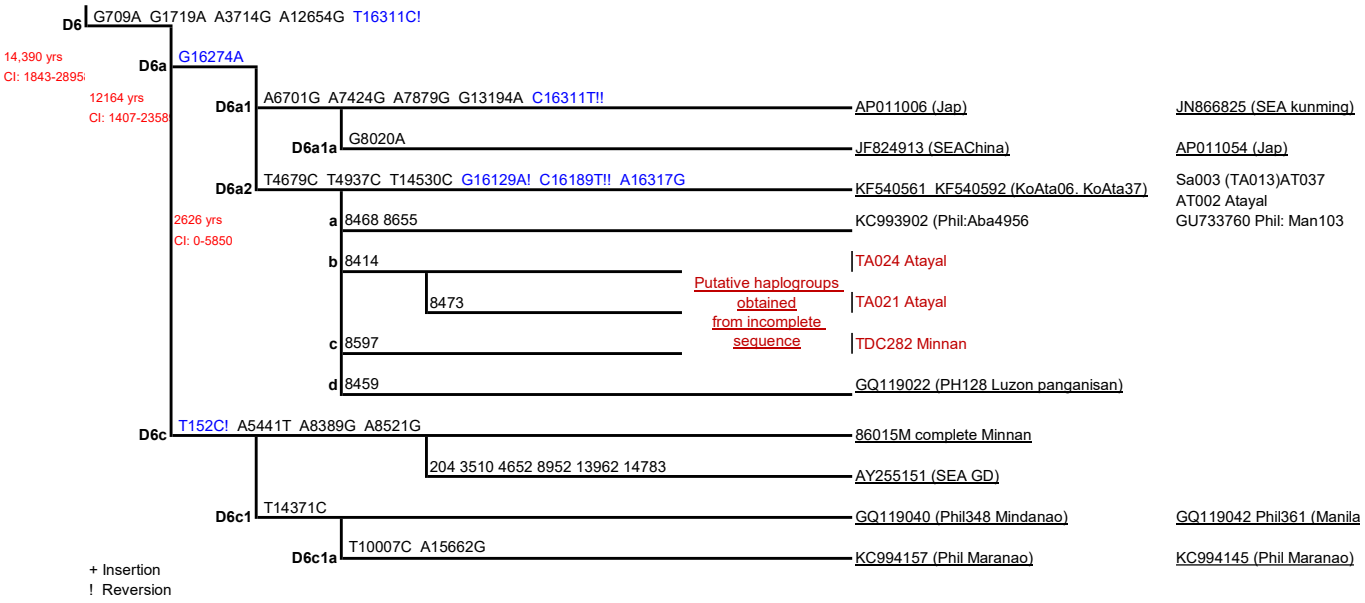
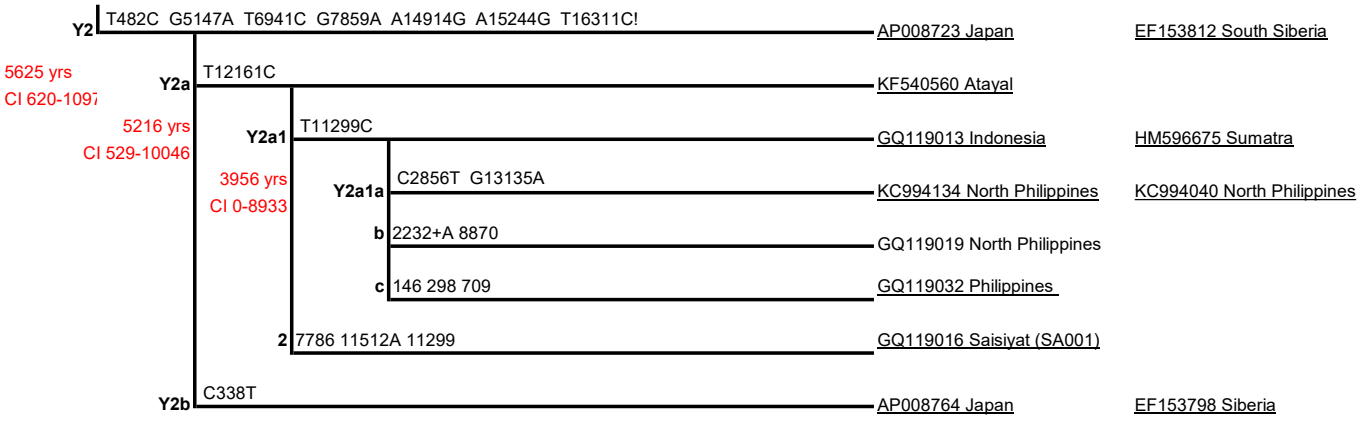
Supplementary Figure S1: Haplogroup D6



Supplementary Table S2: mtDNA haplogroup Y2



\+ Insertion

! Reversion

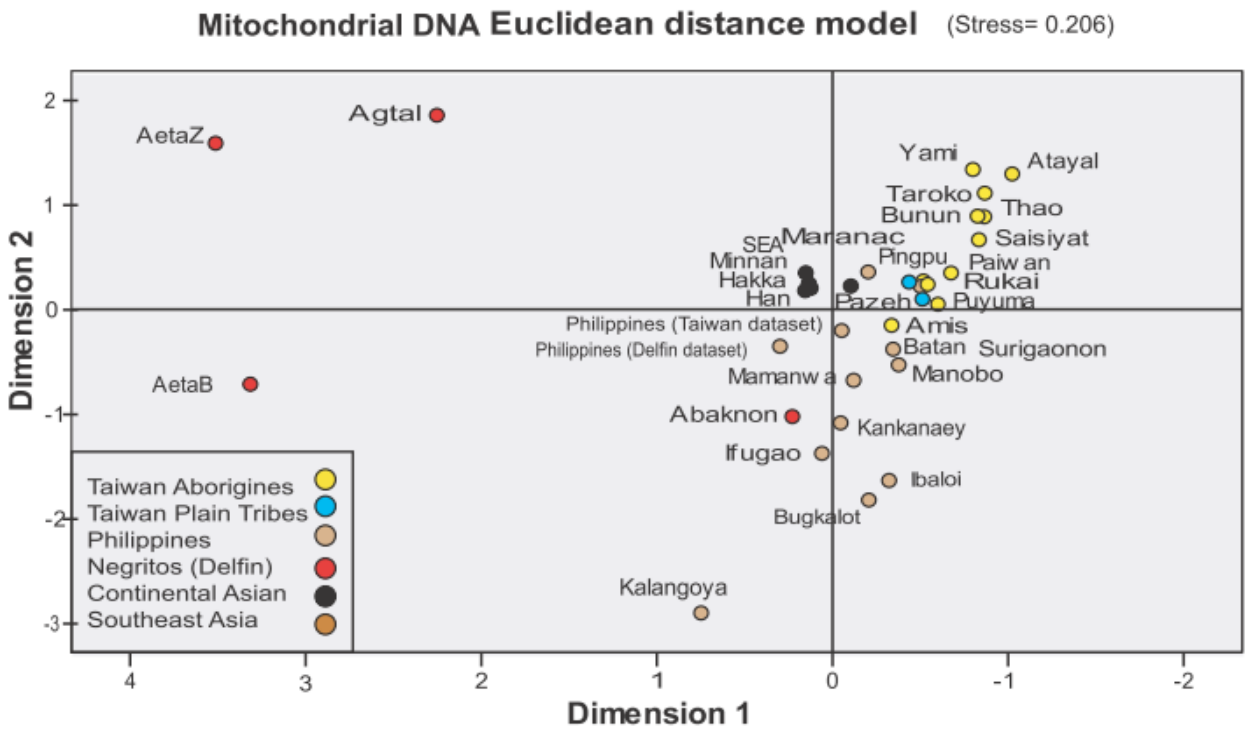

Mitochondrial DNA Euclidean distance model (Stress= 0.206)
Agtal
AetaZ
AetaB
Yami
Atayal
Taroko
Thao
Bunun
Saisiyat
Mananac
SEA
Minnan
Hakka
Han
Pingpu
Paiwan
Rukai
Pazeh
Puyuma
Philippines (Taiwan dataset)
Philippines (Delfin dataset)
Amis
Batan
Surigaonon
Manobo
Mamanwa
Abaknon
Kankanaey
Ifugao
Ibaloi
Bugkalot
Kalangoya
Taiwan Aborigines
Taiwan Plain Tribes
Philippines
Negritos (Delfin)
Continental Asian
Southeast Asia
Dimension 2
Dimension 1
2
1
0
-1
-2
-3
4
3
2
1
0
-1
-2

Table S1: Saisiyat distribution profile of HLA, mtDNA and NRY gene systemes

		East Asia	Taiwan													Philippines
			Taiwan Han		Taiwan Mountain Tribes Aborigines (TwMtA)											
					Northern tribes			Central tribes			Southern tribes					
		Fujian	Hakka	Minnan	Atayal	Taroko	**Saisiyat**	Thao	Tsou	Bunun	Rukai	Paiwan	Puyuma	Amis	Yami	Filipinos
Y haplogroups	O1a1* (P203)	0.231	0.029	0.200	0.904	0.950	**0.875**	0.875	0.902		0.690	0.400	0.478	0.410	0.500	0.156
	O1a2 (M50)		0.029		0.019		**0.042**	0.063	0.049	0.607	0.241	0.280	0.217	0.179		0.107
	O3a1* (KL1)		0.059				**0.042**									
	O3a2c1a (M133	0.135	0.294	0.200			**0.042**									0.025
Sample size		52	34	60	52	20	**24**	16	41	56	29	25	23	39	30	122
Total number of haplogroups (k)		13	16	16	3	2	**4**	3	3	3	3	5	5	5	5	26
Haplogroup diversity (*h*)		0.852	0.877	0.901	0.180	0.100	**0.239**	0.242	0.186	0.500	0.478	0.730	0.720	0.687	0.649	0.9021739
SD		0.018	0.028	0.004	0.048	0.062	**0.079**	0.095	0.056	0.025	0.060	0.029	0.048	0.025	0.040	0.008434
Number of haplotypes shared with Formosan speakers		6	11	4	3	2	**4**	3	3	3	3	5	5	5	5	9
Number of haplotypes Shared with Han		13	8	8	1	2	**2**	1	1	0	1	3	2	2	3	10
% contribution from Putative parent populations	from Formosan speakers	40.00%	66.51%	41.94%	0.813	59.09%	**0.743**	81.25%	81.25%	100.00%	81.25%	70.65%	78.31%	0.783	70.65%	56.52%
	from Han	60.00%	33.49%	58.06%	0.188	40.91%	**0.257**	18.75%	18.75%	0.00%	18.75%	29.35%	21.69%	0.217	29.35%	43.48%
HLA A,B,DRB1 haplotypes	A_0201_B_3901_DRB1_0803	0.008					**0.015**									
	A_0201_B_4001_DRB1_0405						**0.010**									
	A_0201_B_4001_DRB1_1401						**0.015**									0.009
	A_0201_B_4001_DRB1_1405						**0.010**									
	A_0201_B_4001_DRB1_1602						**0.010**									
	A_0201_B_4801_DRB1_0405				0.005		**0.010**	0.239								
	A_0201_B_4801_DRB1_1101				0.012	0.073	**0.010**					0.010	0.010			
	A_0201_B_5101_DRB1_1501						**0.020**									
	A_0201_B_5502_DRB1_1101				0.019	0.045	**0.010**	0.050								
	A_0203_B_3802_DRB1_0901						**0.010**									
	A_0206_B_4801_DRB1_1101						**0.005**									
	A_0206_B_4801_DRB1_1401				0.071	0.045	**0.015**	0.033						0.010		
	A_1101_B_3901_DRB1_1202		0.009		0.005		**0.015**									
	A_1101_B_4001_DRB1_1101	0.033	0.009				**0.020**	0.017	0.029	0.005	0.010					
	A_1101_B_4001_DRB1_1401	0.008					**0.054**	0.017								
	A_1101_B_4002_DRB1_1201						**0.010**									
	A_1101_B_5502_DRB1_0901						**0.010**	0.017								
	A_1101_B_5603_DRB1_0901						**0.010**									
	A_1102_B_1301_DRB1_1202						**0.016**									
	A_1102_B_3901_DRB1_1202						**0.023**									
	A_1102_B_3901_DRB1_1401						**0.049**									
	A_1102_B_4001_DRB1_1101			0.005			**0.039**									
	A_2402_B_1301_DRB1_1501		0.009				**0.013**									
	A_2402_B_3901_DRB1_0803				0.036	0.018	**0.103**	0.133	0.216	0.056	0.048	0.029	0.020	0.005		
	A_2402_B_3901_DRB1_1101						**0.015**				0.016					
	A_2402_B_3901_DRB1_1202						**0.083**			0.022	0.010					
	A_2402_B_3901_DRB1_1401						**0.044**									
	A_2402_B_3901_DRB1_1501						**0.036**									
	A_2402_B_4001_DRB1_0403	0.008			0.057	0.009	**0.020**	0.017	0.020	0.073		0.088	0.020			0.036
	A_2402_B_4001_DRB1_0901		0.027	0.014	0.066	0.018	**0.029**			0.015	0.030	0.010				
	A_2402_B_4001_DRB1_1401				0.090	0.082	**0.108**	0.050	0.078	0.025				0.010		
	A_2420_B_3901_DRB1_1202				0.076	0.018	**0.118**									
	A_2601_B_3901_DRB1_0803			0.005	0.029	0.027	**0.049**			0.035	0.019					
Sample size		60	56	101	105	55	**51**	30	51	101	50	51	50	98	50	55
Total Number of HLA(HLA* A-B-DRB1 haplotypes (k)		82	79	123	59	38	**33**	23	26	48	33	27	39	44	0	76
Haplotype diversity (*h*)		0.997	1.000	0.996	0.966	0.976	**0.958**	0.939	0.918	0.944	0.945	0.917	0.977	0.909	0.8749	0.998
± SD		0.003	0.002	0.002	0.004	0.004	**0.008**	0.017	0.015	0.009	0.014	0.017	0.006	0.010	0.0188	0.003
Number of haplotypes shared with Formosan speakers		18	12	25	59	38	**16**	23	26	48	33	27	39	44	19	10
Number of haplotypes shared with Han		81	11	10	3	4	**3**	6	5	7	3	6	6	3	3	5
% contribution from Putative parent populations	from Formosan speakers	8.33%	30.86%	50.56%	88.94%	79.53%	**68.57%**	61.06%	68.02%	73.72%	81.82%	64.80%	72.67%	85.71%	72.15%	45.00%
	from Han	91.67%	69.14%	49.44%	11.06%	20.47%	**31.43%**	38.94%	31.98%	26.28%	18.18%	35.20%	27.33%	14.29%	27.85%	55.00%
Mitochondrial DNA	B4a1a4	0.0087	0.0208	0.0015	0.0063	0.0204	**0.0114**		0.0370	0.0043	0.0157	0.0138			0.1364	0.0093
	B4a2a1		0.0052		0.0127	0.0306	**0.0227**				0.0236		0.0137		0.2273	
	B4a2a2				0.0063	0.0510	**0.0227**									
	B4b1a2x			0.0015	0.0253	0.0204	**0.0114**		0.0370	0.0130	0.0079			0.0322		0.0559
	B4c1b2a	0.0262	0.0313	0.0184		0.1020	**0.0114**	0.0333	0.0463		0.0236	0.0046	0.0616	0.0029	0.1023	0.0497
	B5a2a2a1		0.0052	0.0031			**0.0227**			0.0130	0.0315	0.0642	0.0137	0.0029		
	B5a2a2a2		0.0052	0.0031	0.0063		**0.1023**				0.0079	0.0138				
	B5a2a2b			0.0046			**0.0114**	0.1000	0.0833	0.0736						
	D4b2	0.0131	0.0104	0.0092			**0.0114**									
	D6a2			0.0015	0.0443		**0.0114**									0.0031
	E1a1a1		0.0156	0.0046	0.0253		**0.2159**		0.0463	0.1039		0.0275	0.0411	0.0205		0.0435
	E2b			0.0031	0.0506	0.0204	**0.0341**			0.0087		0.0092	0.0137	0.0263	0.0568	0.0031
	F1a1d	0.0087	0.0104	0.0046		0.1327	**0.0227**		0.0926	0.0087	0.0315	0.0046	0.0274		0.2045	0.0031
	F2a			0.0046			**0.0114**									
	F4b1'	0.0087		0.0015	0.1266	0.1837	**0.1023**	0.1667	0.0278	0.1948	0.0079	0.0092		0.0322		
	M7b1a2a		0.0104	0.0123	0.3861	0.2143	**0.2500**			0.0173	0.0315	0.0321	0.0068	0.0058	0.1250	0.0280
	M7b1d2b						**0.0114**									
	M7c1c3a					0.0102	**0.0114**								0.1250	0.0093
	R9c1a		0.0052	0.0031		0.0204	**0.0227**		0.2222	0.0043	0.0394	0.0092	0.0068	0.0058		0.0280
	Y2	0.0044	0.0052		0.0316		**0.0795**									0.0373
Sample size		149	153	599	109	54	**88**	30	60	181	77	168	107	292	88	372
Total number of haplogroups (k)		87	95	225	21	7	**21**	15	16	40	22	35	26	55	9	72
Haplogroup diversity (*h*)		0.990	0.989	0.992	0.821	0.730	**0.874**	0.938	0.905	0.916	0.927	0.931	0.932	0.945	0.852	0.958
SD		0.001	0.002	0.000	0.021	0.025	**0.013**	0.012	0.012	0.008	0.009	0.005	0.007	0.004	0.009	0.002
Number of haplotypes shared with Formosan speakers		15	27	57	21	7	**21**	15	16	40	22	35	26	55	9	37
Number of haplotypes Shared with Han		22	24	54	3	2	**6**	1	3	3	3	5	5	12	2	17
% contribution from Putative parent populations	from Formosan speakers	31.50%	43.14%	41.58%	82.52%	70.24%	**70.24%**	91.00%	78.25%	89.99%	83.18%	82.52%	77.81%	75.56%	75.22%	59.48%
	from Han	68.50%	56.86%	58.42%	17.48%	29.76%	**29.76%**	9.00%	21.75%	10.01%	16.82%	17.48%	22.19%	24.44%	24.78%	40.52%

Supplementary Table S2: MtDNA raw data

Saisiyat ID	mtDNA Haplogroup	Complete Sequence available	HVS1 (16040 to 16390) or Comple sequence	HVS2 (1 to 350) or complete sequence	9800 to 11000	8001 to 9000	1400 to 1500	Other SNP tested
SA001	Y2	Yes	16126 16231 16311	73 263 309+C 315+C	10398	8392 8860	14178 14693 14766 14914	338-ve
Sa002	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	73 93 210 263 315+C	9950 9962 10398	9bp 8584 8614 8860		
SA003	D6a2	Yes	16129 16223 16274 16311 16317 16362	73 204 207 263 309+CC 315+C	10398 10400 10873	8701 8860	14530 14766 14783	
SA004	M7b1a2a	Yes	16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860	14115 14766 14783	
SA005	B4a2a2	No	16154 16189 16217 16261	73 263 315+C	CRS	9bp 8860		6719-ve
SA006	F2a	Yes	16203 16291 16304 16311 16335	73 249d 263 309+C 315+C	10310 10535 10586	8860	14766	
SA007	Y2	No	16126 16231 16311	73 263 309+C 315+C	10398	8392 8860		338-ve
SA008	E1a1a1	No	16093 16223 16291 16362 16390	73 263 309+C 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SA009	M7b1a2a	No	16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SA010	E1a1a1	No	16093 16223 16291 16362 16390	73 204 263 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SA011	E1a1a1	Yes	16140 16223 16291 16362 16390	73 146 263 309insC 315insC 489 750	10398 10400 10834 10873	8701 8860	14577 14783	6719-ve 7598+ve
SA012	E1a1a1	No	16093 16223 16291 16362 16390	73 263 309+C 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SA013	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SA014	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SA015	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SA016	Y2	No	16126 16231 16311	73 263 309+C 315+C	10398	8392 8860		338-ve
Sa017	M7b1a2a	No	16086 16129 16192 16224 16297 16324	73 150 199 263 309+C 315+C	9824 10398 10400 10497 10873	8860		
SA018	Y2	No	16126 16231 16311	73 263 309+C 315+C	10398	8392 8860		338-ve
SA019	E1a1a1	No	16093 16223 16291 16362 16390	73 263 309+C 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SA020	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SA021	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SA022	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SA023	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SA024	E2b	No	16051 16086 16223 16362 16390	73 195 263 315+C	10398 10400 10873	8440 8701 8860		7598+ve
SA025	E1a1a1	No	16093 16223 16291 16362 16390	73 263 309+C 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SA026	M7b1a2a	No	16086 16129 16297 16324	73 199 263 309+C 315+C	9824 10398 10400 10497 10873	8701 8860		
SA027	M7b1d2b	Yes	16129 16223 16297	73 150 199 263 309+C 315+C	9824 10398 10400 10873	8251 8701 8860	14766 14783	5351+ve 6719-ve 12405+ve
SA028	B4b1a2x	No	16136 16189 16217	73 207 263 309+CC 315+C	CRS	8860	14000	
SA029	M7b1a2a	No	16086 16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SA030	B4a2a2	Yes	16154 16189 16217 16261 16324	73 263 309+CC 315+C	CRS	9bp 8860	14766	6719-ve
SA031	Y2	No	16126 16231 16311	73 263 309+CC 315+C	10398	8392 8860		338-ve
SA032	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SA033	B5a2a2a2 n	No	16140 16189 16245 16266G 16362	not done	9950 9962 10398	9bp 8584 8860		
SA034	M7b3a	No	16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB002	E1a1a1	No	16093 16223 16291 16362 16390	73 263 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SB003	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB004	M7b1a2a	No	16086 16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB005	E1a1a1	No	16223 16291 16362 16390	73 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB006	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB007	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB008	M7b1a2a	No	16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB009	M7b1a2a	No	16086 16129 16192 16224 16297 16324	73 150 199 263 309+CC 315+C	9824 10398 10400 10497 10873	8860		
SB010	M7b1a2a	No	16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB011	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB012	M7b1a2a	No	16086 16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB013	M7b1a2a	No	16086 16129 16192 16224 16297 16324	73 150 199 263 309+CC 315+C	9824 10398 10400 10497 10873	8860		
SB014	E1a1a1	No	16223 16291 16295 16362 16390	73 263 309+CC 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB015	B5a2a2a2	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SB016	E1a1a1	No	16093 16223 16291 16362 16390	73 204 263 315+C	10003 10398 10400 10834 10873	8701 8860		7598+ve
SB017	E1a1a1	No	16223 16291 16295 16362 16390	73 263 309+CC 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB018	M7b1a2a	No	16086 16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB019	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB020	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+CC 315+C	10097C 10310	8020 8575 8603 8860		
SB021	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB022	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB023	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 309+C 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB024	E2b	No	16051 16086 16223 16362 16390	73 195 263 315+C	10398 10400 10873	8440 8701 8860		7598+ve
SB025	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		
SB026	M7b1a2a	No	16086 16129 16297 16324	73 199 263 315+C	9824 10398 10400 10497 10873	8701 8860		
SB027	E1a1a1	No	16140 16223 16291 16362 16390	73 146 263 315+C	10398 10400 10834 10873	8701 8860		7598+ve
SB028	B5a2a2a2	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SB029	B5a2a2a2	No	16140 16189 16245 16266G 16362	73 93 210 263 315iC	9950 9962 10398	9bp 8584 8614 8860		
SB030	Y2a	No	16126 16231 16311	73 263 309+C 315+C	10398	8392 8860		
SB031	F4b1a'd-f	No	16218 16304 16311	73 249d 263 309+C 315+C	10097C 10310	8020 8575 8603 8860		

CRS = same as Cambridge reference sequence
' = or
9bp = 9 base pairs deletion
d = deletion
No Complete mtDNA sequencing not done
Yes Complete sequencing available in supplementary Text file S1