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Genetic Polymorphisms of 17 Y-chromosomal Short Tandem Repeat Loci in Atayal Population of Taiwan

Fang-Chin Wu[1,2], Chin-Wen Ho[2], Chang-En Pu[1], Kuang-Yu Hu[3], David Hwang Liu[1]

[1]Department of Forensic Science, Investigation Bureau, Ministry of Justice, Taipei County, Taiwan, R.O.C.

[2]Department of Bioengineering, Tatung University, Taipei City, Taiwan, R.O.C.

[3]Department of Biochemistry, National Defense Medical Center, Taipei City, Taiwan, R.O.C.

Aim To define the Y-chromosomal genetic structure in a sample of Atayal men from Taiwan.

Methods Buccal swab samples were collected from 170 unrelated healthy male volunteers from Taiwanese aboriginal Atayal population. Genomic DNA was extracted and 17 Y chromosome-specific short tandem repeat loci (DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438, and DYS448) were analyzed using the AmpFlSTR Yfiler Polymerase Chain Reaction Amplification Kit.

Results A total of 99 different haplotypes were identified, 69 (69.7%) of which were unique. Total haplotype diversity was 0.9887. The most common haplotype was shared by 9 individuals in the study sample. Gene diversities ranged from 0.0574 for DYS438 to 0.6749 for DYS456.

Conclusion Our results will help provide the molecular genetic evidence for human settlement of the Pacific.

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Correspondence to:
Chin-Wen Ho
Department of Bioengineering,
Tatung University
No. 40, Chungshan N. Rd., Sec. 3
Taipei City 104, Taiwan, R.O.C.
cwho@ttu.edu.tw

The Y chromosome is inherited only from father to son and remains generally unchanged over generations except for gradual accumulation of mutations. This unique mode of inheritance and the absence of recombination with the non-recombining portion of the X chromosome during meiosis lead to the maintenance of polymorphisms inherited through men of the same paternal lineage. This property can be exploited for forensic purposes and paternity testing. The polymorphisms of Y-chromosomal short tandem repeat (Y-STR) loci are a powerful tool for identification and confirmation of shared paternity and the relatedness of half-brothers or grandfather and grandson (1).

The population of Taiwan in 2008 was about 23 million, comprising 68.9% of Holo, 15.0% of Hakka, 14.0% of the mainlander population, and only 2.1% of indigenous population. There are 13 indigenous tribes with the total population of 488 700: Amis, Paiwan, Atayal, Bunun, Truku, Rukai, Puyuma, Tsou, Saisiyat, Yami, Kavalan, Thao, and Sakizaya. The population of the Atayal tribe amounts to 82 200. Traditionally, the Atayal tribe resides in the mid-northern mountain regions of Taiwan (Figure 1), including Wulai Township of Taipei County, Fuhsing Township of Taoyuan County, the Jianshih and Wufeng Townships of Hsinchu County, the Nanjuang and Taian Townships of Miaoli County, Heping Township of Taichung County, Renai Township of Nantou County, the Datong and Nanao Townships of Yilan County, and the Sioulin, Wanrung, and Juoshi Townships of Hualien County (2).

Figure 1.

Map of regions in Taiwan where the Atayal population resides (adapted from http://www.apc.gov.tw/).

The aim of this study was to analyze 17 Y-STR loci in the Taiwanese Atayal population in order to investigate the genetic relationship between the Atayal tribe and the neighboring populations. The results obtained from this study could provide molecular genetic evidence for human settlement of the Pacific.

MATERIALS AND METHODS

Population

Buccal swab samples were collected from 170 unrelated male aboriginal Atayal volunteers residing in the mid-northern regions of Taiwan, who provided written informed consent. DNA was purified from the buccal swab samples using a Genomic DNA Extraction Kit (Yeastern company, Taipei, Taiwan, ROC); DNA concentrations were determined using the 7300 Real Time PCR System and the Quantifiler Y Human Male DNA Quantification Kit (Applied Biosystems company, Foster City, CA, USA).

DNA analysis

Target DNA (0.1 ng/μL) was amplified in a thermal cycler GeneAmp PCR System 9700 (Applied Biosystems) using the AmpFlSTR® Yfiler PCR Amplification Kit (Applied Biosystems) according to the manufacturers' instructions. Single-tube polymerase chain reaction (PCR) was used for co-amplification of multiple STR loci, and 4-color detection of the resulting length-variant STR alleles allowed typing of 17 Y chromosome markers: DYS456, DYS389I, DYS390, DYS389II, DYS458, DYS19, DYS385a/b, DYS393, DYS391, DYS439, DYS635, DYS392, Y GATA H4, DYS437, DYS438, and DYS448. These include a 9-marker European minimal haplotype (minHt, the haplotype set of DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393) and an 11-marker Scientific Working Group on DNA Analysis Methods (SWGDAM) core set (minHt plus DYS438 and DYS439). PCR thermocycling parameters were the following: polymerase initial hot start at 95°C for 11 minutes; 30 cycles of denaturation 94°C for 1 minute, annealing at 61°C for 1 minute, and extension at 72°C for 1 minute; final extension was performed at 60°C for 80 minutes. PCR reactions were carried out in a final volume of 25 μL – 10 μL of

target DNA, 5 μL of primer set, 9.2 μL of PCR reaction mix, and 0.8 μL of DNA polymerase. Electrophoresis of the PCR products, together with GeneScan-500 Internal Lane Size Standard (LIZ-500) for size determination, was performed on the ABI Prism® 3100 Avant genetic analyzer (Applied Biosystems) to separate Y-STR alleles. Data were analyzed using GeneMapper, version 3.1, software (Applied Biosystems) in conjunction with the Yfiler Allelic Ladder. Alleles were named as recommended by the DNA Commission of the International Society of Forensic Genetics (3).

Statistical analysis

Allele frequencies were determined by direct counting. Gene diversity and haplotype diversity were calculated according to Nei (4). Formulas applied were: gene diversity = $1-\Sigma P_i^2$, where P_i is the frequency of the i-th allele, and haplotype diversity = $n(1-\Sigma f_i^2)/(n-1)$, where n is the sample size and f_i is the frequency of the i-th haplotype. The standard error for haplotype diversity estimate was calculated according to the following equation (4): $SE = \{2[\Sigma f_i^3-(\Sigma f_i^2)^2]/n\}^{1/2}$. Comparisons between 2 populations were made by the analysis of molecular variance (AMOVA) test performed by Arlequin software, version 3.11 (5).

RESULTS

Y-STR loci allele frequencies in 170 Atayal men are shown in Table 1. The most common alleles of the 17 Y-chromosomal STR loci were DYS456*17, DYS389I*13, DYS390*23, DYS389II*29, DYS458*15, DYS19*15, DYS385a/b*13/13, DYS393*13, DYS391*10, DYS439*12, DYS635*22, DYS392*14, Y GATA H4*12, DYS437*14, DYS438*10, and DYS448*18. Gene diversity values of these loci ranged from 0.0574 (DYS438) to 0.6749 (DYS456). Allele frequencies above 0.9 were found in 6 loci (DYS390, DYS393, DYS392, DYS437, DYS438, and DYS448). The gene diversities of the 6 loci were all below 0.16.

A total of 99 haplotypes were identified in the Atayal population (Table 2), 69 of which were unique and 30 were present in 2 or more individuals. The 13, 7, 3, 3, 3, and 1

TABLE 1. Allele frequencies and gene diversities of 17 Y-chromosomal short tandem repeat loci in 170 unrelated Atayal men from Taiwan

	Locus																
Allele	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS393	DYS391	DYS439	DYS635	DYS392	Y GATA H4	DYS437	DYS438	DYS448	Genotype	DYS385a/b
10								0.747				0.006		0.971		11,11	0.006
11		0.006						0.253	0.053		0.006	0.171		0.024		12,13	0.035
12		0.135					0.035		0.882		0.012	0.594		0.006		12,14	0.006
13		0.806					0.947		0.059		0.035	0.229				12,19	0.006
14	0.018	0.053			0.006	0.024	0.018		0.006		0.947		0.965			12,20	0.006
15	0.065				0.665	0.818							0.035			13,13	0.629
16	0.118				0.253	0.141										13,14	0.265
17	0.406				0.029	0.018									0.029	13,15	0.006
18	0.376				0.029										0.918	13,18	0.012
19	0.018				0.018					0.012					0.024	14,14	0.006
20										0.029					0.024	14,20	0.006
21										0.182					0.006	15,18	0.012
22			0.012							0.629						15,19	0.006
23			0.935							0.129							
24			0.024							0.018							
25			0.029														
26				0.006													
27				0.024													
28				0.129													
29				0.424													
30				0.394													
31				0.024													
Gene diversity	0.6749	0.3294	0.1237	0.6474	0.4921	0.3107	0.1015	0.3779	0.2152	0.5525	0.1017	0.5653	0.0681	0.0574	0.1559		0.5320

TABLE 2. Haplotypes observed of 17 Y-chromosomal short tandem repeat loci in 170 unrelated Atayal men from Taiwan

			Locus																
Haplotype	n*	f†	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	Y GATA H4	DYS437	DYS438	DYS448
H01	1	0.006	14	12	25	28	15	16	12,19	12	10	12	20	13	12	15	10	19
H02	1	0.006	14	12	25	28	17	16	12,20	12	10	11	21	14	12	14	10	19
H03	1	0.006	14	13	24	29	16	16	12,14	13	11	12	22	14	12	14	10	18
H04	1	0.006	15	11	25	29	19	16	13,18	13	11	11	22	13	11	14	10	18
H05	1	0.006	15	12	22	27	18	16	13,13	13	10	11	19	14	11	14	10	18
H06	1	0.006	15	12	23	27	18	16	13,14	13	10	12	21	14	12	14	10	17
H07	1	0.006	15	12	23	28	18	14	15,18	12	10	12	20	14	12	15	12	20
H08	1	0.006	15	12	23	28	19	14	15,18	12	10	12	20	14	12	15	11	20
H09	1	0.006	15	12	23	29	17	14	15,19	12	10	12	20	14	12	15	11	20
H10	1	0.006	15	12	24	26	18	14	13,18	13	10	13	21	14	12	15	11	20
H11	1	0.006	15	12	24	28	16	16	13,15	14	11	12	21	13	12	14	10	19
H12	1	0.006	15	12	24	29	16	15	13,13	13	10	11	20	14	12	14	10	18
H13	1	0.006	15	13	23	30	15	15	11,11	14	10	11	22	11	11	14	10	21
H14	1	0.006	15	14	23	30	15	15	13,13	13	10	12	21	14	12	14	10	18
H15	1	0.006	16	12	23	27	18	16	13,14	13	10	12	21	14	12	14	10	17
H16	1	0.006	16	12	23	27	19	16	13,14	13	10	12	21	14	12	14	10	17
H17	1	0.006	16	12	25	29	17	15	12,13	12	11	12	19	12	12	15	10	17
H18	1	0.006	16	12	25	29	17	15	14,20	14	10	11	23	13	10	14	10	18
H19	2	0.012	16	13	23	29	15	15	13,13	13	10	12	22	14	13	14	10	18
H20	3	0.018	16	13	23	29	15	15	13,13	13	10	12	23	14	13	14	10	18
H21	1	0.006	16	13	23	29	15	15	12,13	13	10	12	22	14	13	14	10	18
H22	1	0.006	16	13	23	29	15	17	13,13	13	10	12	21	14	11	14	10	18
H23	6	0.035	16	13	23	29	16	15	13,14	13	10	12	22	14	12	14	10	18
H24	2	0.012	16	13	23	29	16	16	13,14	13	10	12	22	14	11	14	10	18
H25	1	0.006	16	13	23	30	15	15	13,14	13	11	12	22	14	12	14	10	18
H26	1	0.006	17	12	23	28	15	15	13,13	13	10	13	21	14	12	14	10	18
H27	5	0.029	17	13	23	28	16	15	13,14	13	10	12	22	14	12	14	10	18
H28	1	0.006	17	13	23	28	16	15	14,14	13	10	12	22	14	12	14	10	18
H29	1	0.006	17	13	23	28	16	16	13,13	13	10	12	22	14	12	14	10	18
H30	1	0.006	17	13	23	29	15	15	13,13	13	10	12	22	14	13	14	10	17
H31	2	0.012	17	13	23	29	15	15	12,13	13	10	12	22	14	13	14	10	18
H32	6	0.035	17	13	23	29	15	15	13,13	13	10	12	22	14	13	14	10	18
H33	6	0.035	17	13	23	29	15	15	13,13	13	10	12	23	14	13	14	10	18
H34	1	0.006	17	13	23	29	15	15	13,13	13	11	12	22	14	12	14	10	18
H35	2	0.012	17	13	23	29	15	17	13,13	13	10	12	22	14	13	14	10	18
H36	1	0.006	17	13	23	29	16	15	12,13	13	10	12	22	14	13	14	10	18
H37	5	0.029	17	13	23	29	16	15	13,13	13	10	12	22	14	13	14	10	18
H38	1	0.006	17	13	23	29	16	15	13,14	13	10	11	21	14	12	14	10	18
H39	1	0.006	17	13	23	29	16	15	13,14	13	10	11	23	14	12	14	10	18
H40	2	0.012	17	13	23	29	16	15	13,14	13	10	12	21	14	12	14	10	18
H41	3	0.018	17	13	23	29	16	15	13,14	13	10	12	22	14	12	14	10	18
H42	2	0.012	17	13	23	29	16	16	13,14	13	10	12	23	14	11	14	10	18
H43	3	0.018	17	13	23	29	16	16	13,14	13	10	12	24	14	11	14	10	18
H44	1	0.006	17	13	23	29	17	15	13,14	13	10	12	21	14	12	14	10	18
H45	1	0.006	17	13	23	30	15	15	13,13	13	10	12	21	14	12	14	10	18
H46	1	0.006	17	13	23	30	15	15	13,13	13	10	12	21	14	13	14	10	18
H47	2	0.012	17	13	23	30	15	15	13,13	13	10	12	22	14	12	14	10	18
H48	4	0.024	17	13	23	30	15	15	13,13	13	10	12	23	14	13	14	10	18
H49	1	0.006	17	13	23	30	15	15	13,13	13	11	12	22	14	11	14	10	18
H50	5	0.029	17	13	23	30	15	15	13,13	13	11	12	22	14	12	14	10	18
H51	1	0.006	17	13	23	30	15	15	13,14	13	11	13	22	14	12	14	10	18
H52	1	0.006	17	13	23	30	15	16	13,13	13	11	12	22	14	12	14	10	18
H53	1	0.006	17	13	23	30	16	15	13,13	13	11	12	22	14	12	14	10	18
H54	2	0.012	17	14	23	30	15	15	13,13	13	10	12	22	14	12	14	10	18
H55	1	0.006	17	14	23	30	16	15	13,13	13	10	12	22	14	12	14	10	18
H56	2	0.012	17	14	23	30	16	15	13,13	13	10	12	22	14	13	14	10	18
H57	1	0.006	17	14	23	31	15	15	13,13	13	10	12	22	14	12	14	10	18
H58	1	0.006	17	14	23	31	16	15	13,13	13	10	12	22	13	13	14	10	18
H59	1	0.006	18	12	22	28	15	15	13,13	13	10	13	22	14	12	14	10	18
H60	1	0.006	18	12	23	28	15	15	13,13	13	10	12	21	14	12	14	10	18
H61	2	0.012	18	12	23	28	15	15	13,13	13	10	12	22	14	12	14	10	18
H62	1	0.006	18	12	23	28	15	15	13,13	13	10	13	21	14	12	14	10	18
H63	1	0.006	18	12	23	28	15	15	13,13	13	10	13	22	14	12	14	10	18

TABLE 2. Haplotypes observed of 17 Y-chromosomal short tandem repeat loci in 170 unrelated Atayal men from Taiwan – continued

			Locus																
Haplotype	n*	f†	DYS456	DYS389I	DYS390	DYS389II	DYS458	DYS19	DYS385a/b	DYS393	DYS391	DYS439	DYS635	DYS392	Y GATA H4	DYS437	DYS438	DYS448
H64	1	0.006	18	12	23	29	15	16	13,13	13	10	13	22	14	12	14	10	18
H65	1	0.006	18	12	23	29	15	16	13,14	13	10	13	22	14	12	14	10	18
H66	1	0.006	18	13	23	28	15	15	13,13	13	10	13	22	14	13	14	10	18
H67	1	0.006	18	13	23	28	15	15	13,13	13	10	14	22	14	13	14	10	18
H68	1	0.006	18	13	23	28	16	15	13,14	13	10	12	22	14	12	14	10	18
H69	1	0.006	18	13	23	29	15	15	13,13	13	10	12	22	14	11	14	10	18
H70	1	0.006	18	13	23	29	15	15	13,13	13	10	12	22	14	12	14	10	18
H71	3	0.018	18	13	23	29	15	15	13,13	13	11	12	21	14	12	14	10	18
H72	1	0.006	18	13	23	29	15	15	13,13	13	11	12	22	14	12	14	10	19
H73	1	0.006	18	13	23	29	15	15	13,13	13	11	12	23	14	12	14	11	18
H74	3	0.018	18	13	23	29	15	15	13,14	13	11	12	22	14	12	14	10	18
H75	2	0.012	18	13	23	29	15	16	13,13	13	10	12	22	14	12	14	10	18
H76	1	0.006	18	13	23	30	14	15	13,13	13	11	12	21	14	12	14	10	18
H77	1	0.006	18	13	23	30	15	15	13,13	13	10	12	21	14	11	14	10	18
H78	4	0.024	18	13	23	30	15	15	13,13	13	10	12	21	14	12	14	10	18
H79	9	0.053	18	13	23	30	15	15	13,13	13	10	12	22	14	11	14	10	18
H80	1	0.006	18	13	23	30	15	15	13,13	13	10	12	22	14	12	14	10	18
H81	1	0.006	18	13	23	30	15	15	13,13	13	11	11	22	14	12	14	10	18
H82	3	0.018	18	13	23	30	15	15	13,13	13	11	12	21	14	12	14	10	18
H83	1	0.006	18	13	23	30	15	15	13,13	13	11	12	22	12	12	14	10	18
H84	1	0.006	18	13	23	30	15	15	13,13	13	11	12	22	13	12	14	10	18
H85	2	0.012	18	13	23	30	15	15	13,13	13	11	12	22	14	11	14	10	18
H86	4	0.024	18	13	23	30	15	15	13,13	13	11	12	22	14	12	14	10	18
H87	1	0.006	18	13	23	30	15	15	12,13	13	10	12	22	14	11	14	10	18
H88	1	0.006	18	13	23	30	15	15	13,14	13	10	12	22	14	12	14	10	18
H89	2	0.012	18	13	23	30	15	15	13,14	13	10	12	23	14	12	14	10	18
H90	1	0.006	18	13	23	30	15	15	13,14	13	11	12	21	14	12	14	10	18
H91	1	0.006	18	13	23	30	15	15	13,14	13	11	12	22	14	11	14	10	18
H92	3	0.018	18	13	23	30	15	15	13,14	13	11	12	22	14	12	14	10	18
H93	1	0.006	18	13	23	30	15	16	13,13	13	10	12	22	14	11	14	10	18
H94	1	0.006	18	13	23	30	15	16	13,13	13	10	12	23	14	12	14	10	18
H95	1	0.006	18	13	23	31	15	15	13,13	13	10	12	22	14	11	14	10	18
H96	1	0.006	18	14	23	30	16	15	13,13	13	10	12	22	14	12	14	10	18
H97	1	0.006	19	13	23	30	15	15	13,13	13	10	12	23	14	12	14	10	18
H98	1	0.006	19	13	23	30	15	15	13,13	13	11	13	21	14	12	14	10	18
H99	1	0.006	19	13	23	31	15	15	13,14	13	11	12	22	14	12	14	10	18

*Number of individuals.
†Haplotype frequency.

haplotypes were found in 2, 3, 4, 5, 6, and 9 individuals, respectively. Haplotype diversity was 0.9887 ± 0.0014 and the discrimination capacity was 0.5824 (99/170). The most frequent haplotype was H79, which was shared by 9 individuals. Alleles were 18 for DYS456, 13 for DYS389I, 23 for DYS390, 30 for DYS389II, 15 for DYS458, 15 for DYS19, 13-13 for DYS385a/b, 13 for DYS393, 10 for DYS391, 12 for DYS439, 22 for DYS635, 14 for DYS392, 11 for Y GATA H4, 14 for DYS437, 10 for DYS438, and 18 for DYS448.

These haplotype data were compared with the Y Chromosome Haplotype Reference Database (a worldwide population sample of 26 586 haplotypes in a set of 235 populations for the haplotype of an 11-marker SWGDAM core set, http://www.yhrd.org). This comparison found only 10 matches (Table 3), while 89 (89.9%) haplotypes were not previously recorded.

DISCUSSION

The gene diversity of DYS385a/b is usually highest among Y-chromosomal STR loci (6-11) but in this study the diversity of DYS456 (0.6749), DYS389II (0.6474), DYS635 (0.5525), and Y GATA H4 (0.5653) was higher than that of DYS385a/b (0.5320). The discrimination capacity of the Atayal population (0.5824) was lower than that of neighboring populations, shown by other studies on individuals that had some degree of relatedness (6-10). Such findings might result from the fact that the Atayal reside in mountains and rarely interact with other peoples in Taiwan.

The native language of the Atayal belongs to the Formosan subfamily of Austronesian languages (12,13). Besides linguistic studies, genetic analyses have also confirmed that Taiwan's aboriginal populations are close rela-

TABLE 3. Y-chromosomal short tandem repeat haplotypes of the Atayal found 10 matches of an 11-marker Scientific Working Group on DNA Analysis Methods core set at Y chromosome haplotype reference database

Haplotype of DYS19, 385, 389I, 389II, 390, 391, 392, 393, 438, and 439	Match with worldwide*	Match with Asian†	Match with European‡	Haplotype No. of Atayal
14-15,18-12-28-23-10-14-12-11-12	14	13	1	H02
14-15,19-12-29-23-10-14-12-11-12	2	1	1	H04
15-13,13-12-28-23-10-14-13-10-12	8	8		H12, H13
15-13,13-12-29-24-10-14-13-10-11	1	1		H17
15-13,13-13-30-23-11-14-13-10-11	1	1		H43
15-13,14-13-29-23-10-14-13-10-11	1	1		H62, H63
16-12,19-12-28-25-10-13-12-10-12	9	9		H80
16-13,13-12-29-23-10-14-13-10-13	1	1		H83

*Worldwide population sample of 26 586 haplotypes in a set of 235 populations.
†Asian population sample of 8334 haplotypes in a set of 72 populations.
‡European population sample of 11 213 haplotypes in a set of 100 populations.

tives of the Polynesian peoples, because of the first colonizations of the Polynesian islands from Taiwan (14). Forster et al (15) typed 30 aboriginal Taiwanese, including the Amis, Atayal, Bunun, and Paiwan for 5 Y-STRs (DYS19, DXYS156-Y, DYS391, DYS392, and DYS393) and sequenced the DYS390 locus; these profiles were compared with aboriginal Australians and Papuans. The aboriginal Taiwanese had the highest frequency at DYS390*23 (0.67) among 15 populations. Hagelberg et al (16) and Hurles (17) analyzed 27 and 39 Taiwanese aboriginals from 4 tribes (Ami, Atayal, Bunun, and Paiwan) for polymorphisms at DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393 in order to find the genetic evidence for human settlement of the Pacific and to investigate the origins of the peoples speaking Austronesian languages. Hagelberg found that Taiwanese aboriginals were genetically closer to the populations of China, Java, Tolai, and Trobriands than to the populations of western Samoa, Papua New Guinea highlands, and Roro. Hurles found that among 11 populations Taiwan had the most similar population diversity to Papua New Guinea, based on the weighted mean intralineage mean pairwise difference. Kayser et al (14,18) investigated the Melanesian origin of the Polynesian peoples by typing 10 or 6 Atayal individuals and other globally dispersed human populations for Y chromosomal microsatellite polymorphisms at DYS19, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393. They found Polynesian ancestors originated from Asia/Taiwan but did not move rapidly through Melanesia; rather, they interacted with and mixed extensively with Melanesians, leaving behind their genes and incorporating many Melanesian genes before colonizing the Pacific. Su et al (19) screened 24 Atayal for 19 Y-chromosome biallelic loci and these were compared with Polynesian peoples: markers studied were M3 (C→T mutation), M5 (A→G mutation), M7 (C→G mutation), M9 (C→G mutation), M15 (9-bp insertion), M17 (1-bp deletion), DYS287 (YAP), M45 (G→A mutation), M50 (T→C mutation), M88 (A→G mutation), M89 (C→T mutation), M95 (C→T mutation), M103 (C→T mutation), M110 (T→C mutation), M111 (4-bp deletion), M119 (A→C mutation), M120 (T→C mutation), M122 (T→C mutation), and M134 (1 bp deletion). They found the Y-chromosome data did not favor Taiwanese origin of Polynesians. Capelli et al (20) screened 50 Atayal for 9 Y-chromosomal haplogroups (B, C, D, E, F, G, H, I, and L), 49 of which fell into haplogroup H and 1 into haplogroup L and found that the haplogroups of the Atayal were not shared by the populations of Irian Jaya and Madang of Melanesia. More recently, Li et al (21) used fluorescent-labeled primers to type 7 microsatellite markers (STR) on the Y-chromosome (DYS19, DYS388, DYS389I, DYS390, DYS391, DYS392, and DYS393) in 22 Atayal individuals and compared their haplotypes with western Austronesians and Daic populations, showing that Taiwan aborigines likely originated from the Daic populations based on their paternal lineages.

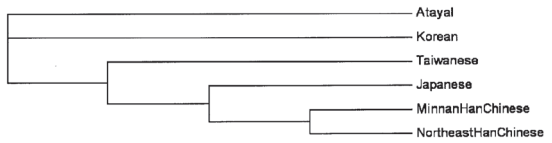
While previous studies of the Atayal people have analyzed fewer than 50 individuals and DNA typing has included HLA, mtDNA, Y-SNPs, and Y-STRs, the present study analyzed Y-STR polymorphisms in 170 male Atayal individuals. These data can be of considerable utility in ethnological studies and geographical genetics.

The Atayal reside in mid-northern mountain regions of Taiwan with little intercrossing with other Taiwanese peoples. The genetic structure of the Atayal has therefore been

largely conserved, and over half of 17 Y-STR loci typed contained high frequency alleles. At the DYS391 and DYS437 loci, only 2 alleles were recorded with little polymorphic variation.

The present data on Y-chromosome haplotypes in the Atayal and the data on minHt of Y-STR loci of Chinese population in Taiwan (monomorphic $[TCTG]_3$ at DYS389I and DYS389II including a repeat +3 compared with the available data) (6), Minnan Han Chinese (7), northeast Han Chinese (8), Korean (9), and Japanese (10) were analyzed using the Arlequin software package to determine the molecular variance between these populations. R_{ST} values were 0.318, 0.478, 0.448, 0.265, and 0.362, respectively, all of which were significant ($P < 0.001$). Neighbor-joining tree of the 6 populations (22,23) is shown as Figure 2.

Figure 2.



Neighbor-joining tree constructed from Slatkin's R_{ST} genetic distances based on the allelic frequencies of the minimal haplotype (minHt, the haplotype set of DYS19, DYS385a/b, DYS389I, DYS389II, DYS390, DYS391, DYS392, and DYS393) of Y-chromosomal short tandem repeat loci in 6 Asian populations.

A Y-STR haplotype database for Atayal population could be of great utility in determining the geographic origin of male individuals. In addition, because the Y chromosome haplotype has remained generally unchanged over the generations, this database can be used for determining the origin of different closely-related populations and contribute to better understaning of geographic effects and population migration.

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