J Forensic Sci, Jan. 2005, Vol. 50, No. 1
Paper ID JFS2004218
Published 15 Dec. 2004
Available online at: www.astm.org

FOR THE RECORD

Jian Tie,[1] M.D.; Yuka Suzuki,[1] B.Sc.; Etsuko Iwakami,[1] B.Sc.; Shigemi Oshida,[1] M.D.; and George Sensabaugh,[2] Ph.D.

The Polymorphisms of Four Y-Chromosome Short Tandem Repeat Loci in Chinese and Japanese Populations

POPULATION: A total of 155 unrelated healthy Chinese males living in Shenyang (Liaoning province) and 186 unrelated Japanese healthy males living in Tokyo.

KEYWORDS: forensic science, DNA typing, Y-chromosome, short tandem repeat, population genetics

The DNA was isolated from blood by the standard phenol/chloroform method and precipitated with ethanol. The PCR was carried out using a total reaction volume of 25 µl with the following conditions: an initial denaturation step at 95°C for 5 min followed by 30 cycles of denaturation at 94°C for 60 s, primer annealing at 60°C for 45 s and primer extension at 72°C for 60 s, with a final extension at 60°C for 40 min. For separating the PCR products of the multiplex in one gel, we redesigned the primers for GATA A4 (5′-TCT CGA GTT GTT ATG GTT TTA GGT C-3′ and GCC TGG CTT GGA ATT CTT TT-3′) and GATA A10 (5′-TCA TCC ATC CTC TTT CTT TCT CTC C-3′ and TGG AGA TAG TGG GTG GAT TG-3′) to allele sizes 205 ∼ 229 and 104 ∼ 128 bp. The primer sequences of GATA A7.2 and GATA C4 loci were according to White et al. (1). The PCR products were separated on 6.5% denaturing polyacrylamide gel (5% C) contains 7 M urea. The bands of allele fragments were visualized by silver staining. DNA typing was performed using allelic ladders that were constructed using the corresponding allele fragments identified by sequence analysis (ABI PRISM™ 310 Genetic Analyzer).

The observed allele frequencies are shown in Table 1. The most diverse loci were GATA C4, GATA A4 and GATA A10 in Chinese, and GATA A10 and GATA C4 in Japanese. Gene diversity was estimated according to Nei (2). Basically, higher gene diversity values were found in Chinese than in the Japanese at each locus. The allele frequency distributions at the four loci were not significantly different between the two populations (A4, A10 and C4, $p < 0.95$; A7.2, $p < 0.90$). These four Y-chromosome STR loci were combined to produce a total of 147 different haplotypes (93 in Chinese and 72 in Japanese; Table 2).

TABLE 1—*Allele frequency and gene diversity of four Y-STR loci in Chinese (Ch) and Japanese (Jp) population.*

	Y-A4		Y-A7.2		Y-A10		Y-C4	
Allele	Ch	Jp	Ch	Jp	Ch	Jp	Ch	Jp
7				0.013				
8		0.004	0.006	0.278				
9			0.142	0.616	0.006			
10	0.071	0.022	0.561	0.068	0.006	0.018	0.168	0.012
11	0.258	0.177	0.239	0.017	0.045	0.066	0.271	0.327
12	0.432	0.608	0.052	0.008	0.329	0.442	0.219	0.482
13	0.213	0.185			0.413	0.381	0.168	0.102
14	0.026	0.004			0.150	0.058	0.090	0.041
15					0.045	0.035	0.078	0.029
16					0.006		0.006	0.008
Gd*	0.700	0.567	0.609	0.541	0.700	0.654	0.813	0.651

* gene diversity.

All the alleles identified increased in regularly by 4 base pair increments. Sequencing results showed that the major repeat structure was simple GATA. The GATA C4 locus was only $(TCTA)_4$ $(TGTA)_2$ $(TCTA)_2$ (TGTA)n was observed in both populations. However, a different sequence structure $(TCTA)_4$ $(TGTA)_2$ $(TCTA)_2$ $(TGTA)_1$ $(TCTA)_{11}$ was found in two Japanese individuals. The common repeat structure of GATA C4 was $(GATA)_n$ based on White et al., it is allele 11. But Gonzālez-Neira et al. call it allele 20 (3). The PCR amplification efficiency for GATA A4 locus was poor using White's primers (3), but this problem was not happed by the newly designed primer in this study.

[1] Department of Legal Medicine, Nihon University School of Medicine, Tokyo, Japan.
[2] Forensic and biomedical science, Division of Public Health, University of California, Berkeley, CA.

TABLE 2—*Haplotype (H) of four Y-STR loci in Chinese (Ch) and Japanese (Jp) population.*

	Y-STR				n			Y-STR				n	
H	A4	A7.2	A10	C4	Ch	Jp	H	A4	A7.2	A10	C4	Ch	Jp
H1	9	9	13	15		1	H75	12	9	14	10	1	
H2	10	9	11	12		1	H76	12	9	14	11	1	18
H3	10	9	12	13	1		H77	12	9	14	12		3
H4	10	9	12	14	1		H78	12	9	15	10	1	
H5	10	9	13	13	1		H79	12	9	15	11		2
H6	10	9	13	14	1		H80	12	9	15	12		1
H7	10	10	12	11	2		H81	12	10	10	11	1	
H8	10	10	12	12	2	1	H82	12	10	11	11		1
H9	10	10	13	11	1		H83	12	10	11	12		1
H10	10	10	13	13	1		H84	12	10	11	14	1	
H11	10	10	14	14	1		H85	12	10	12	10	1	
H12	11	8	11	12		1	H86	12	10	12	11	3	1
H13	11	8	12	12		6	H87	12	10	12	12	5	1
H14	11	8	13	11		1	H88	12	10	12	13	3	
H15	11	8	13	12		1	H89	12	10	12	14	3	
H16	11	9	11	11	1		H90	12	10	13	10	3	
H17	11	9	11	12	1	1	H91	12	10	13	11	6	
H18	11	9	12	11		2	H92	12	10	13	12	1	2
H19	11	9	12	12		2	H93	12	10	13	13		2
H20	11	9	12	13		2	H94	12	10	14	10	3	
H21	11	9	12	14	1	2	H95	12	10	14	11	4	
H22	11	9	12	15	2		H96	12	10	14	12	1	
H23	11	9	13	11	1	1	H97	12	10	14	13	1	
H24	11	9	13	13		1	H98	12	10	15	12	1	
H25	11	9	13	15	1		H99	12	11	9	12	1	
H26	11	9	14	11		2	H100	12	11	12	12	1	
H27	11	10	11	11		1	H101	12	11	12	13	2	
H28	11	10	11	13	1		H102	12	11	13	10	2	
H29	11	10	11	15		1	H103	12	11	13	12	2	
H30	11	10	12	11	3	1	H104	12	11	13	13	4	
H31	11	10	12	12	3		H105	12	11	13	15	2	
H32	11	10	12	13	2	1	H106	12	11	14	11	1	
H33	11	10	12	14	2		H107	12	11	15	10	1	
H34	11	10	13	10	3		H108	12	11	15	12	1	
H35	11	10	13	11	4		H109	12	12	12	12		1
H36	11	10	13	12	2	5	H110	12	12	13	10	1	
H37	11	10	13	15	3		H111	12	12	13	12	2	
H38	11	11	12	12	2		H112	12	12	15	11		1
H39	11	11	12	13	1		H113	12	12	16	11	1	
H40	11	11	12	14	1		H114	13	8	11	12		1
H41	11	11	13	11	3		H115	13	8	12	12		7
H42	11	11	14	15	1		H116	13	8	12	13		1
H43	11	11	15	15	1		H117	13	8	15	12		1
H44	11	12	13	10	1		H118	13	9	11	11	1	
H45	12	8	11	14		1	H119	13	9	11	12		1
H46	12	8	12	11		1	H120	13	9	12	11		3
H47	12	8	12	12		13	H121	13	9	12	12		6
H48	12	8	12	14		1	H122	13	9	12	13	1	2
H49	12	8	12	15		1	H123	13	9	13	11		5
H50	12	8	13	11		1	H124	13	9	13	12		5
H51	12	8	13	12		6	H125	13	9	14	11		1
H52	12	8	13	13		2	H126	13	10	12	12	2	
H53	12	8	13	14		2	H127	13	10	12	13	3	
H54	12	8	13	15	1		H128	13	10	13	11	2	1
H55	12	8	14	11		3	H129	13	10	13	13	2	
H56	12	8	14	12		1	H130	13	10	13	16	1	
H57	12	8	14	15		1	H131	13	10	14	10	3	2
H58	12	8	15	12		1	H132	13	10	14	12	2	
H59	12	9	10	11		1	H133	13	10	15	10	1	
H60	12	9	10	12		2	H134	13	10	15	11	1	
H61	12	9	11	11	1	1	H135	13	11	11	11	1	
H62	12	9	11	12		1	H136	13	11	13	10	1	
H63	12	9	11	13		1	H137	13	11	13	11	2	
H64	12	9	12	11		2	H138	13	11	13	12	2	
H65	12	9	12	12		15	H139	13	11	13	13	1	
H66	12	9	12	13	1	4	H140	13	11	13	14	1	
H67	12	9	12	14	1	1	H141	13	11	14	10	1	
H68	12	9	12	15	1		H142	13	11	14	11	2	
H69	12	9	13	11		9	H143	13	12	12	12	1	
H70	12	9	13	12	1	7	H144	13	12	13	10	2	
H71	12	9	13	13		2	H145	14	10	13	13	1	
H72	12	9	13	14	1		H146	14	10	14	10	1	
H73	12	9	13	15		1	H147	14	11	13	10	1	
H74	12	9	13	16		1							

Haplotype diversity value was 0.992 for Chinese and 0.970 for Japanese.

The complete data set is available to any interested researcher at http://www.med.nihon-u.ac.jp/∼legalmed/jtie/Y-STR.doc.

References

1. White PS, Tatum OL, Deaven LL. New, male-specific microsatellite markers from the human Y chromosome. Genomics 1999;57:433–7. [PubMed]
2. Nei M. Molecular evolutionary genetics. New York: Columbia University Press, 1987.
3. Gonzalez-Neira A, Elmoznino M, Lareu MV. Sequence structure of 12 novel Y chromosome microsatellites and PCR amplification strategies. Forensic Sci Int 2001;122:19–26. [PubMed]

Additional information and reprint requests:
Jian Tie, M.D.
Department of Legal Medicine
Nihon University School of Medicine
30-1, Oyaguchi-kamimachi
Itabashi-ku, Tokyo 173-8610
Japan