J Hum Genet (2002) 47:523–528

ORIGINAL ARTICLE

Ashraf A. Ewis · Juwon Lee · Yoko Kuroki
Toshikatsu Shinka · Yutaka Nakahori

Yfm1, a multicopy marker specific for the Y chromosome and beneficial for forensic, population, genetic, and spermatogenesis-related studies

Received: February 12, 2002 / Accepted: June 17, 2002

Abstract A recently developed microsatellite marker on the Y chromosome, Yfm1, which was originally cloned from a cosmid clone mapped near the DAZ (Deleted in AZoospermia) genes, was used to classify Y chromosomes using an automatic sequencer. Yfm1 could detect multicopies on Y chromosomes in a single polymerase chain reaction, showing four main classes, A, A*, B, and C, according to the number of copies and peak patterns. Compound haplotype analysis of the Y chromosome using the Yfm1 marker with three other biallelic markers on the Y chromosome, SRY, DXYS5Y, and YAP, resulted in nine different haplotypes among different populations, including Japanese. Haplotype II (defined by YAP insertion) observed in the Japanese population was consistently associated with Yfm1 class A or A*, which showed the lowest number of copies of Yfm1. Haplotypes III and IV were consistently associated with Yfm1 class B. On the other hand, haplotype I showed a variety of Yfm1 patterns that were dubbed class C when not appropriately classified as A, A*, or B. These relationships among Yfm1 microsatellite and Y-specific biallelic markers could supply useful population genetic information. Moreover, because we have already shown that men with haplotype II have significantly lower spermatogenic ability than those with other haplotypes, Yfm1 class A or A* with the least number of copies may be related to the haplotype II-specific structure of the Y chromosome, such as deletion of DAZ or DAZ repeats, reflecting the lower spermatogenic abilities of Japanese haplotype II men. Thus, Yfm1 represents a very useful marker for analysis of genetic structure in different populations and studies on Y chromosome lineage-specific genotype–phenotype correlations.

Key words Haplotypes · Yfm1 · Population · Japanese · Forensic · Spermatogenesis · Y chromosome

A.A. Ewis · J.W. Lee · Y. Kuroki · T. Shinka · Y. Nakahori (✉)
Department of Human Genetics and Public Health, Graduate School of Proteomics, Faculty of Medicine, The University of Tokushima, 3-18-15 Kuramoto-cho, Tokushima 770-8503, Japan
Tel. +81-88-633-7075; Fax +81-88-633-7453
e-mail: nakahori@basic.med.tokushima-u.ac.jp

A.A. Ewis
Department of Public Health and Occupational Medicine, School of Medicine, El-Minia University, El-Minia, Egypt

Y. Nakahori
CREST (Core Research for Evolutional Science and Technology), JST (Japan Science and Technology), Kawaguchi, Japan

Introduction

The Y chromosome has unique characteristics that distinguish it from all other segments of the genome. The major part of the Y chromosome, ~60 million base pairs, is transmitted exclusively from fathers to their sons. Because it is haploid with no recombination events except for the pseudoautosomal region, studies of human Y-linked polymorphisms have been proposed as tools for investigating the genetic structure of populations and male-specific gene flow between populations (Whitfield et al. 1995; Underhill et al. 1996, 2000; Jobling and Tyler-Smith 1995, 2000). We have previously classified Japanese men into four main haplotypes using a set of three biallelic DNA markers on the Y chromosome, DYS287 (YAP), DXYS5Y (47z/*StuI*), and SRY. Of these four haplotypes, I and II are commonly distributed in the world, whereas haplotypes III and IV are specific only to East Asian populations (Shinka et al. 1999). Furthermore, we developed three microsatellite markers, DXYS241, DXYS265, and DXYS266, on the Y chromosome that may help in detailed haplotype analysis and when studying the relationship between haplotypes constructed from the results of other Y chromosome biallelic markers (Lee et al. 2001).

In 2000, Matsuki et al. reported the development of a new Y-specific microsatellite marker, Yfm1, which was originally identified from a cosmid clone that contained polymorphic CA repeats and was located near the DAZ (Deleted in AZoospermia) genes (Fig. 1). Interestingly, the Yfm1 locus can be amplified using a primer set consisting of a partial sequence of LINE1 and a Y-chromosome-specific

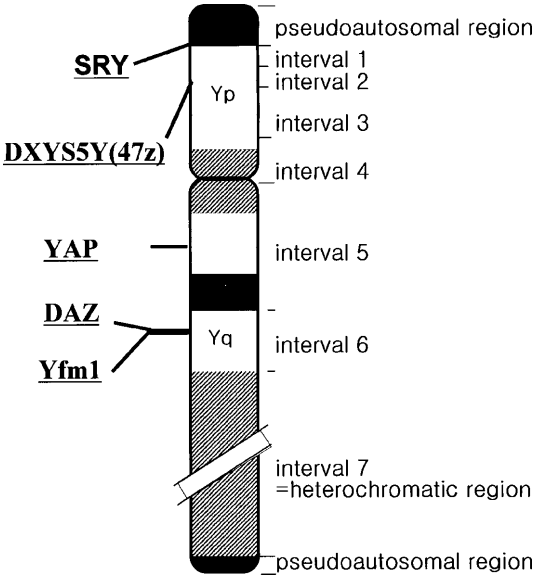

Fig. 1. A schematic diagram of the Y chromosome showing the location of the three biallelic loci used for haplotyping and the location of the Yfm1 near to the DAZ genes on interval 6 of the Y long arm, Yq11.2

sequence. Furthermore, the primer set for Yfm1 can detect multicopies on the Y chromosome in a single polymerase chain reaction (PCR), resulting in highly polymorphic patterns. This Yfm1 marker could be useful for various human genetic and forensic studies (Matsuki et al. 2000).

In the present study, we discuss the relationship between the polymorphic patterns of Yfm1 and the compound Y chromosome haplotypes that we have already reported. In addition, we show that Yfm1 is a very useful marker for the analysis of genetic structure in different populations and Y chromosome lineage-specific genotype–phenotype correlations.

Materials and methods

DNA samples

Genomic DNAs were prepared from peripheral leukocytes according to the standard method (Sambrook et al. 1989). Blood samples were collected from 209 Japanese men and 88 women. Male samples were used to study the Y-specific markers, whereas female samples served as negative controls. For the other ethnic groups, collaborating researchers provided a variable number of samples. DNA samples from 62 Bolivian men, 17 white American men, and 18 black American men were available. DNA samples of these American men were described elsewhere (Shinka et al. 1999). We also examined 26 Taiwanese and 28 Korean male samples. All samples were collected according to approved human subject protocols.

Y chromosome haplotyping

Y chromosome haplotyping was performed using a set of three biallelic polymorphic markers [DYS287 (YAP), DXYS5Y (47z/*StuI*) and SRY] as described previously (Shinka et al. 1999).

Development of Yfm1 marker

The Yfm1 microsatellite marker was developed on the Y chromosome and described previously (Matsuki et al. 2000).

Yfm1 microsatellite genotyping

Genotyping of the Y chromosomes from different populations for Yfm1 was done using an ABI 377 sequencer (Applied Biosystems Japan, Tokyo, Japan). The PCR reaction contained a primer pair, one of which was end labeled with a fluorescent dye, FAM. DNA samples were amplified by PCR in a volume of 10 µl containing 66 ng genomic DNA, 67 mM tris-HCl (pH 8.3), 3 mM $MgCl_2$, 16.6 mM $(NH_4)SO_4$, 0.1 mM deoxyribonucleoside triphosphates, 0.25 µM of each primer and 1 u Taq Gold DNA polymerase. Thermocycling was performed using a PE9600 thermocycler under the following conditions: initial denaturation at 95°C for 12 min, followed by 30 cycles of denaturation at 95°C for 30 s, ramping slowly to 60°C within 2 min, annealing at 60°C for 30 s, and extension at 72°C for 1 min. The final extension step was at 72°C for 30 min. PCR products were resolved with urea denaturing polyacrylamide gels on the ABI sequencer using an internal size standard in each lane. Raw genotype data were collected using Genescan software (ABI), and gel files were analyzed with the Genotyper software package (ABI).

The following primer set was used for PCR; the forward primer was labeled with FAM: CA-F: 5′-CACCATTTGTT GAAAAGAC-3′ CA-R: 5′-TATAGAGAGCCCAGAA AGAG-3′

Results

We typed 209 Y chromosomes from Japanese men for the Yfm1 microsatellite marker and three other Y-specific biallelic markers, DXYS5Y (47z/*StuI*), DYS287 (YAP), and SRY.

Haplotyping of the Y chromosomes was performed using the three polymorphic biallelic loci, DXYS5Y, YAP, and SRY (Shinka et al. 1999). The results showed that Japanese Y chromosomes are classified into four haplotypes: haplotype I (Y1, YAP- and C), haplotype II (Y1, YAP+ and C), haplotype III (Y1, YAP- and T), and haplotype IV (Y2, YAP- and T). The frequency distribution of the 209 Japanese men by haplotype compared with other populations is presented in Table 1.

All samples were typed for the new microsatellite marker, Yfm1, which showed four main classes: A, A*, B,

Table 1. Frequency distribution of Y chromosome haplotypes constructed by three (YAP, 47Z/*StuI*, and SRY) biallelic markers among men from different populations

	Japanese		Korean		Taiwanese		White American		Black American		Bolivian	
Y haplotype	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%	*n*	%
I	73	34.9	19	67.9	26	100.0	14	82.4	4	22.2	57	91.9
II	64	30.6	0	0.0	0	0.0	3	17.6	14	77.8	5	8.1
III	20	9.6	5	17.9	0	0.0	0	0.0	0	0.0	0	0.0
IV	52	24.9	4	14.2	0	0.0	0	0.0	0	0.0	0	0.0
Total	209	100.0	28	100.0	26	100.0	17	100.0	18	100.0	62	100.0

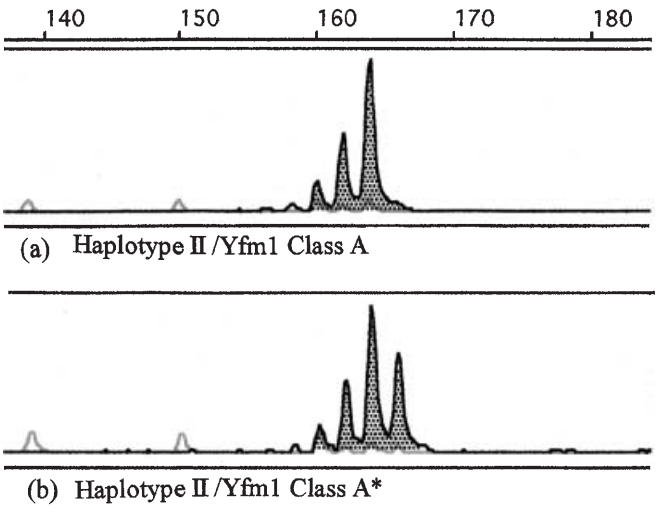

Fig. 2 **a** Yfm1 class A with its few peaks of 160, 162, and 164 bp. **b** Yfm1 class A* with its extra peak of 166 bp. Both classes are consistently associated with Japanese Y chromosomal haplotype II. The true Yfm1 peaks are *shadowed*. The *unshadowed* peaks are those of the size standard marker. The *horizontal scale* indicates size of Yfm1 peaks in base pairs

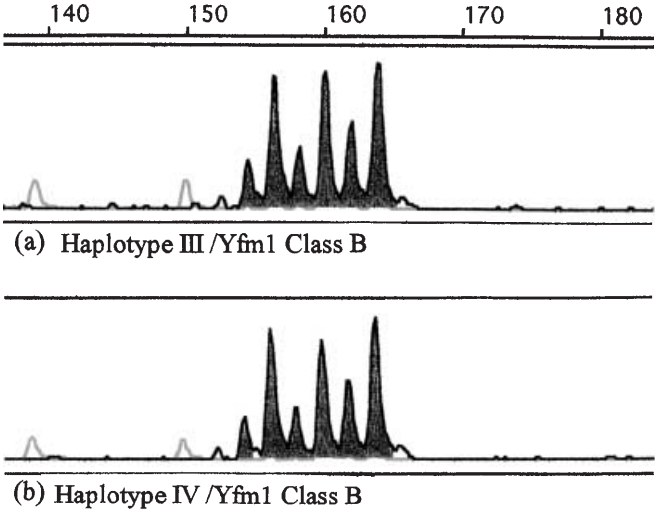

Fig. 3a,b. Yfm1 class B with its characteristic peak pattern. Peaks are shown at 154, 156, 158, 160, 162, and 164 bp. Yfm1 class B is consistently associated with Japanese Y chromosomal haplotypes III (**a**) and haplotype IV (**b**). The true Yfm1 peaks are *shadowed*. The *unshadowed* peaks are those of the size standard marker. The *horizontal scale* indicates size of Yfm1 peaks in base pairs

and C. Class A was very characteristic among the four classes in having the least number of copies, as indicated by the peak pattern, which showed few peaks ranging between 160 and 164 bp (Fig. 2a). Some men with Yfm1 class A showed an extra peak (copy) of 166 bp that we named class A* (Fig. 2b). Class B was unique in having a fixed pattern with a fixed number of peaks ranging from 154 to 164 bp (Fig. 3). Although class A contained a 164-bp fragment only, and class A* contained two fragments of 164 and 166 bp, class B showed three fragments with 156, 160, and 164 bp, indicating the polymorphic pattern of the Yfm1 marker (Figs. 2 and 3). Any results other than the preceding three classes were described as class C, which included any other Yfm1 patterns with different copy numbers that did not fit in class A, A*, or B (Fig. 4).

We studied the relationship between Yfm1 classes and Y chromosome haplotypes. Yfm1 classes showed constant associations with Y-specific haplotypes. Haplotype II was consistently associated with class A or A*, whereas both haplotypes III and IV were consistently associated with class B. On the other hand, haplotype I showed different peak patterns of Yfm1, mostly of class C, and less frequently of class A, A*, or B. The Yfm1 relations with Y-chromosomal haplotypes in Japanese and other populations are presented in Table 2.

Discussion

Genetically, Japanese men are classified into four haplotypes according to three polymorphic loci, DXYS5Y, YAP, and SRY, on the Y chromosome (Shinka et al. 1999). To elucidate the diversity of Y chromosomes in the Japanese population and the relationships among different populations, we constructed haplotypes using these three biallelic markers and a newly developed microsatellite marker on the Y chromosome, named Yfm1 (Matsuki et al. 2000). Yfm1 consists of multicopies on the Y chromosome and shows highly polymorphic patterns in the Japanese population. Although Yfm1, which shows complex and highly polymorphic patterns, has not yet been completely

Table 2. Distribution of men from different populations by their Y chromosome haplotypes (YAP, 47Z/StuI, and SRY) of biallelic markers and the Yfm1 microsatellite marker classes

Haplotype	I				II				III				IV				
Yfm1 class	A	A*	B	C	A	A*	B	C	A	A*	B	C	A	A*	B	C	Total
Japanese	7	15	4	47	53	11	—	—	—	—	20	—	—	—	52	—	209
Korean	2	4	1	12	—	—	—	—	—	—	5	—	—	—	4	—	28
Taiwanese	2	14	—	10	—	—	—	—	—	—	—	—	—	—	—	—	26
White American	—	9	—	5	—	—	—	3	—	—	—	—	—	—	—	—	17
Black American	—	2	—	3	—	1	—	12	—	—	—	—	—	—	—	—	18
Bolivian	3	45	—	9	—	3	—	2	—	—	—	—	—	—	—	—	62

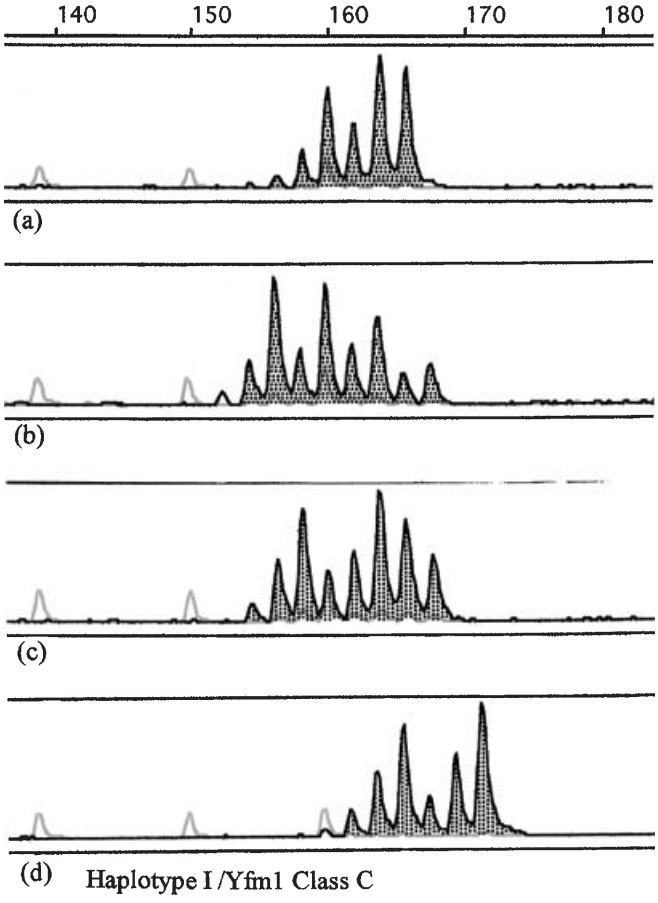

Fig. 4a–d. Yfm1 class C with its variable peak patterns (**a**, **b**, **c**, and **d**). Japanese Y chromosomes with haplotype I show consistent association with Yfm1 class C. The true Yfm1 peaks are *shadowed*. The *unshadowed* peaks are those of the size standard marker. The *horizontal* scale indicates size of Yfm1 peaks in base pairs

described, this marker can provide a useful tool for pursuing the origin of the Japanese population and studying the relationships between different populations.

On the basis of haplotyping using the three biallelic loci, DXYS5Y, YAP, and SRY, it is assumed that haplotype I is the ancestral haplotype from which other haplotypes diverged. When the YAP element was inserted at the DYS287 locus, haplotype II arose, and in haplotype I another separate mutation in the SRY gene (C→T) occurred, producing the T allele and giving origin to a new lineage of haplotype III, which was further divided by a polymorphism at the DXYS5Y locus into haplotypes III or IV (Shinka et al. 1999).

By combination haplotype analysis using the new Yfm1 marker together with the three biallelic markers, nine haplotypes were found among the studied populations: IA, IA*, IB, IC, IIA, IIA*, IIC, IIIB, and IVB (Table 2). Eight haplotypes were found in the Japanese population and the hypothesis that haplotype I is the ancestral haplotype has been confirmed. Haplotype I showed the most varied peak patterns of Yfm1 among the four haplotypes, suggesting that haplotype I is the ancestral haplotype. Haplotype II showed only two patterns of peaks, with the least number of copies that we described here as class A and A*. Both haplotypes III and IV shared the same characteristic pattern of Yfm1 class B. Haplotypes III and IV are specific to Japan, Korea, and narrow areas of China around the Yellow River (Harihara et al. 1988; Horai et al. 1996; Hong et al. 1998). Because Yfm1 class B was associated with haplotypes III and IV, it was not found in any population other than those of East Asia. The geographical distribution found for haplotypes III and IV with Yfm1 class B suggests a shared genetic background among the Japanese, Korean, and confined Chinese populations.

Yfm1 class A, which associates with about 9.6% of haplotype I in Japanese men, was also found in a number of YAP samples of Taiwanese men (haplotype I), indicating its common origin with Korean and Japanese men who shared the same class.

We could not determine whether the YAP element was inserted on a haplotype I Y chromosome with Yfm1 class A or A*. Y chromosomes with haplotype II (YAP+) and Yfm1 class A* were observed in Japanese as well as other populations, whereas those with haplotype II and Yfm1 class A were not found in any other population except for the Japanese (Table 2). Therefore, it is likely that the YAP insertion event occurred on a haplotype I Y chromosome with Yfm1 class A*, and then after the YAP insertion the Y chromosome branched off into another lineage of haplotype II with Yfm1 class A. Based on this hypothesis, the alleles of Yfm1 class A found on Y chromosomes with haplotype I and haplotype II may have arisen independently. More samples from different lineages, including

those of East Asians, should be analyzed to confirm our hypothesis.

Haplotype II "YAP+" Y chromosomes were not found in any of the examined Korean or Taiwanese samples, supporting Hammer's reports that YAP+ chromosomes are rare in Asia, except for Japanese populations who show rates of about 30% (Hammer 1994; Hammer and Horai 1995). However, some reports showed a very low percentage (up to 1.3%) of YAP+ chromosomes in Korea, and this may have resulted from migrations back into Korea from Japan (Kim et al. 1998, 2000). However, the YAP+ chromosomes from Africa and Japan are believed to be identical by descent (Hammer and Horai 1995; Hammer 1995). Our results regarding the Yfm1 marker suggest that Japanese YAP+ chromosomes are different from YAP+ chromosomes from Bolivian, African-American, and white American men. Moreover, we studied different population samples for a polymorphism found in the DFFRY gene, Arg 211 Cys, which was reported by Shen et al. (2000). Among the studied populations, a C→T substitution polymorphism in the Arg 211 Cys starting from the initial methionine amino acid of the DFFRY gene was found in all Japanese haplotype II men, whereas it was absent in all Japanese other haplotypes, as well as American YAP+ and all Bolivian YAP+ men (Ewis et al. 2002). In addition, our data from studying the deletion polymorphism of the 12f2 amplicon indicates that YAP+ Japanese men are different from other YAP+ men from different geographical areas in that about 50% of them have deletion of the 12f2 88 bp amplicon. That 12f2 deletion was not detected in any of the other three Japanese haplotypes or YAP+ chromosomes of Bolivian, white American, or black American men. Hence, Y chromosomes with haplotype II in the Japanese population are relatively homogeneous, but have many structural differences compared with YAP+ chromosomes from other populations. In other words, the YAP+ chromosomes of Japanese men are characteristically different from those of men from other geographical areas (Ewis et al. 2002).

Other than analysis of genetic structure among different populations, Yfm1 can contribute to other studies that analyze Y chromosome lineage-specific phenotypes.

Interestingly, Yfm1 was originally cloned from a cosmid clone mapped near to the DAZ genes (Matsuki et al. 2000), and DAZ repeats that are located as clusters consisted of more than four mutually highly homologous copies and are a very strong candidate for Azoospermic factor (AZF) (Saxena et al. 2000). Because all the azoospermic and oligospermic men who have interstitial deletions in the AZFc, including the DAZ genes, showed deletions of all Yfm1 copies, we suggested that the Yfm1 copies should be located on interval 6 of the long arm of the Y chromosome (A.A. Ewis, J.W. Lee, T. Shinka, and Y. Nakahori, unpublished work). Searching the draft sequence of the human genome revealed that at least three loci of Yfm1 are located in interval 6 on the long arm of the Y chromosome (Yq11.2), and each locus is located distant from the nearest DAZ gene by nearly 25–30 kbp. The exact copy number of DAZ remains unknown because the surrounding interval 6 contains many repetitive sequences, which complicates the structural analysis of the human Y chromosome. Giacalone et al. (2000) have shown, using an optical mapping method, that there are four copies of DAZ genes on the Y chromosome. Yen et al. (1997) have reported that there are at least seven copies of DAZ genes from analysis of DAZ cDNA and genomic structure of AZFc. Recently, the structure of AZFc, which contains DAZ genes and many repetitive sequences over its entire region, has been reported by Kuroda-Kawaguchi et al. (2001). Because Yfm1 consists of multiple loci, which have different numbers of (CA) repeats and are located near the DAZ gene in AZFc, Yfm1 may be useful for discriminating similar genomic clones mapped in AZFc and for producing a correct map for AZFc.

For primates other than human, the copy numbers of their DAZ genes are known to be different from those of humans (Reijo et al. 1995). Analyzing the Yfm1 on their Y chromosomes would be of interest for unveiling human evolution.

Using Southern blot analysis, we have already shown that Japanese Y chromosomes with haplotype II may possess a lower number of DAZ gene copies or DAZ repeats than those with other haplotypes. We showed the absence of a 15-kbp band from the blots of haplotype II but not from other haplotypes (J.W. Lee, A.A. Ewis, T. Shinka, Y. Nakahori, unpublished data). Moreover, we have already shown that Japanese men with haplotype II have significantly lower spermatogenic ability compared with men with other haplotypes (Kuroki et al. 1999). In this study, we showed that Y chromosomes with haplotype II have the lowest number of Yfm1 copies. Therefore, this low number of Yfm1 copies may reflect deletion of DAZ genes or DAZ repeats from Japanese Y chromosomes with haplotype II and may elucidate their lower spermatogenic ability.

In conclusion, there are consistent associations between Y chromosomal compound haplotypes of biallelic markers and the classes of the Yfm1 microsatellite marker. The haplotype analysis of Y chromosomes using biallelic markers together with Yfm1 may provide a useful tool for pursuing the origin of the Japanese population and the relationship between different populations. Furthermore, this DNA marker may be helpful for studies on Y chromosome lineage-specific genotype–phenotype correlations.

Acknowledgments The authors are grateful for useful discussions with Professor Takasumi Matsuki from the Department of Forensic Medicine, Fukui Medical University, Fukui, Japan, and for the excellent technical assistance of Miss K. Tsuji, Y. Unemi, and A. Endo. This work was supported by grants from the Ministry of Health, Welfare and Labor, and from the Ministry of Education, Science, Sports and Culture, Japan. Ashraf A. Ewis is supported by an Egyptian governmental scholarship offered by the Ministry of Higher Education, Egypt.

References

Ewis AA, Lee JW, Shinka T, Nakahori Y (2002) Two Y-chromosome-specific polymorphisms 12f2 and DFFRY in the Japanese population and their relations to other Y polymorphisms. J Med Invest 49:44–50

Giacalone J, Delobette S, Gibaja V, Ni L, Skiadas Y, Qi R, Edington J, Lai Z, Gebauer D, Zhao H, Anantharaman T, Mishra B, Brown LG, Saxena R, Page DC, Schwartz DC (2000) Optical mapping of BAC clones from the human Y chromosome DAZ locus. Genome Res 10:1421–1429

Hammer MF (1994) A recent insertion of an Alu element on the Y chromosome is a useful marker for human population studies. Mol Biol Evol 11:749–761

Hammer MF (1995) A recent common ancestry for human Y chromosomes. Nature 378:376–378

Hammer MF, Horai S (1995) Y chromosomal DNA variation and the peopling of Japan. Am J Hum Genet 56:951–962

Harihara S, Saitou N, Hirai M, Gojobori T, Park KS, Misawa S, Ellepola SB, Ishida T, Omoto K (1988) Mitochondrial DNA polymorphism among five Asian populations. Am J Hum Genet 43:134–143

Hong SS, Horai S, Lee CC (1998) Distribution of the 9-bp deletion in COII/tRNA^{Lys} intergenic region of mitochondrial DNA is relatively homogeneous in east Asian populations. Korean J Biol Sci 2:259–267

Horai S, Murayama K, Hayasaka K, Matsubayashi S, Hottori Y, Fucharoen G, Harihara S, Park KS, Omoto K, Pan IH (1996) mtDNA polymorphism in east Asian populations, with special reference to the peopling of Japan. Am J Hum Genet 59:579–590

Jobling M, Tyler-Smith C (1995) Father and sons — the Y chromosome and human evolution. Trends Genet 11:449–456

Jobling MA, Tyler-Smith C (2000) New uses for new haplotypes the human Y chromosome, disease and selection. Trends Genet 16:356–362

Kim W, Shin DJ, You SA, Kim YJ (1998) Y-specific DNA polymorphisms of the YAP element and the locus DYS19 in the Korean population. J Hum Genet 43:195–198

Kim W, Shin DJ, Harihara S, Kim YJ (2000) Y chromosomal DNA variation in East Asian populations and its potential for inferring the peopling of Korea. J Hum Genet 45:76–83

Kuroda-Kawaguchi T, Skaletsky H, Brown LG, Minx PJ, Cordum HS, Waterston RH, Wilson RK, Silber S, Oates R, Rozen S, Page DC (2001) The AZFc region of the Y chromosome features massive palindromes and uniform recurrent deletions in infertile men. Nat Genet 29:279–286

Kuroki Y, Iwamoto T, Lee JW, Yoshike M, Nozawa S, Nishida T, Ewis AA, Nakamura H, Toda T, Tokunaga K, Kotliarova S, Kondoh N, Koh E, Namiki M, Shinka T, Nakahori Y (1999) Spermatogenic ability is different among males in different Y chromosome lineage. J Hum Genet 44:289–292

Lee J, Kotliarova SE, Ewis AA, Hida A, Shinka T, Kuroki Y, Tokunaga K, Nakahori Y (2001) Y chromosome compound haplotypes with the microsatellite markers DXYS265, DXYS266 and DXYS241. J Hum Genet 46:80–84

Matsuki T, Iida R, Sawazaki K (2000) Development of new DNA polymorphic marker on human Y chromosome. Nippon Hoigaku Zasshi 54:83

Reijo R, Lee TY, Salo P, Alagappan R, Brown LG, Rosenberg M, Rozen S, Jaffe T, Straus D, Hovatta O, de la Chapelle A, Silber S, and Page DC (1995) Diverse spermatogenic defects in humans caused by Y chromosome deletions encompassing a novel RNA-binding protein gene. Nat Genet 10:383–393

Sambrook F, Fritsch EF, Maniathis T (1989) Molecular cloning: a laboratory manual, 2nd edn. Cold Spring Harbor Laboratory, New York

Saxena R, de Vries JW, Repping S, Alagappan RK, Skaletsky H, Brown LG, Ma P, Chen E, Hoovers JM, Page DC (2000) Four DAZ genes in two clusters found in the AZFc region of the human Y chromosome. Genomics 67:256–267

Shen P, Wang F, Underhill PA, Franco C, Yang W-H, Roxas A, Sung R, Lin AA, Hyman RW, Vollrath D, Davis RW, Cavalli-Sforza LL, Oefner PJ (2000) Population genetic implications from sequence variation in four Y chromosome genes. Proc Natl Acad Sci USA 97:7354–7359

Shinka T, Tomita K, Toda T, Kotliarova SE, Lee J, Kuroki Y, Jin DK, Tokunaga K, Nakamura H, Nakahori Y (1999) Genetic variations on the Y chromosome in the Japanese population and implications for modern human Y chromosome lineage. J Hum Genet 44:240–245

Underhill PA, Jin L, Zemans R, Oefner PJ, Cavalli-Sforza LL (1996) A pre-Columbian Y chromosome-specific transition and its implications for human evolutionary history. Proc Natl Acad Sci USA 93:196–200

Underhill PA, Shen P, Lin AA, Jin L, Passarino G, Yang WH, Kauffman E, Tamir BB, Bertranpetit J, Francalacci P, Ibrahim M, Jenkins T, Kidd JR, Mehdi Q, Seielstad MT, Wells RS, Piazza A, Davis RW, Feldman MW, Cavalli-Sforza LL, Oefner PJ (2000) Y chromosome sequence variation and the history of human population. Nat Genet 26:358–361

Whitfield LS, Sulston JE, Goodfellow PN (1995) Sequence variation of the human Y chromosome. Nature 378:379–380

Yen PH, Chai NN, Salido EC (1997) The human DAZ genes, a putative male infertility factor on the Y chromosome, are highly polymorphic in the DAZ repeat regions. Mamm Genome 8:756–759