

International Congress Series 1239 (2003) 117-120

# Allele distributions and genetic relationship with 13 CODIS core STR loci in various Asian populations in or near Japan

Toshimichi Yamamoto<sup>a,\*</sup>, Masaki Mizutani<sup>a</sup>, Rieko Uchihi<sup>a</sup>, Miwa Tanaka<sup>a</sup>, Takashi Yoshimoto<sup>a</sup>, Shogo Misawa<sup>b</sup>, Naruya Saitou<sup>c</sup>, Yoshinao Katsumata<sup>a</sup>

<sup>a</sup>Department of Legal Medicine and Bioethics, Graduate School of Medicine, Nagoya University, 65 Tsurumai-cho, Showa-ku, Nagoya, 466-8550, Japan <sup>b</sup>Department of Legal Medicine, Institute of Community Medicine, University of Tsukuba, Tennodai 1-1-1, Tsukuba-shi, 305-8575, Japan

<sup>c</sup>Laboratory of Evolutionary Genetics, National Institute of Genetics, 1111 Yata, Mishima-shi, 411-8540, Japan

# Abstract

We calculated allele frequencies for 13 Combined DNA Index System (CODIS) core short tandem repeat (STR) loci using each more than 100 DNA samples in two Japanese, six Chinese, one Korean, one Thai and one Burmese populations. We analyzed these allele frequency distributions by genetic distance DA to construct a tree based on the neighbor-joining method, and obtained one that is well coincident with their geographical distributions. We also present a genetic relationship including the published ethnic data in the world.

© 2003 Elsevier Science B.V. All rights reserved.

Keywords: STR polymorphism; Allele frequency; Genetic relationship; Asian; Japan

# 1. Introduction

Short tandem repeat (STR) polymorphisms are mainly used in the forensic field for paternity tests and personal identification at present. Multiplex PCR amplification and typing system with multi-colored fluorescent labeled primers have made it convenient to genotype STRs using commercially available kits. The FBI in the USA adopted the Combined DNA Index System (CODIS) core 13 STRs (D3S1358, vWA, FGA, D16S539,

<sup>\*</sup> Corresponding author. Tel.: +81-52-744-2119; fax: +81-52-744-2121.

E-mail address: yamachan@med.nagoya-u.ac.jp (T. Yamamoto).

TH01, TPOX, CSF1PO, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820) to construct a huge database for criminal investigations. As international crimes have increased, allele frequencies at these 13 STR loci are being been calculated all over the world. We investigated allele frequency distributions at these 13 STR loci using, for each, more than 100 DNA samples among Japanese (Hondo, Main Island and Ryukyu), Korean (Seoul), Chinese (Beijing, Shanxi, Hunan, Guangdong, Fujan and Jiangsu), Thai (Bangkok) and Burmese (Rangoon) subjects. We analyzed these samples by genetic distance,  $D_A$ , to construct a tree based on the neighbor-Joining method. We also compared the genetic relationship including published ethnic data from other parts the world.

# 2. Materials and methods

## 2.1. DNA samples

DNA samples were collected from Japan—207 in Hondo (Nagoya) and 194 from Ryukyu (Okinawa); 110 from South Korea (Soul); China—118 in Beijing, 108 in Shanxi province, 119 in Jiangsu province, 105 in Hunan province, 111 in Guangdong province, and 116 in Fujan province; 183 from Bangkok, Thailand; and 122 from Rangoon, Burma. These samples were obtained with informed consent.

## 2.2. PCR amplification and typing

The 13 CODIS core STRs were genotyped using the AmpFISTR Profiler plus and Cofiler. PCR amplification and typing were performed according to the kit protocol except for a reduced total PCR volume using the Genetic Analyzer 310 and the Genotyper software 2.1 or 2.5.

#### 2.3. Statistical analyses

Tests for Hardy–Weinberg equilibrium (HWE) were carried out using homozygosity test, a likelihood ratio test and an exact test. Observed and expected heterozygosities were also calculated.

#### 2.4. Construction of a phylogenetic tree

We calculated the  $D_A$  (genetic distance) according to Nei and constructed a tree based on the neighbor-joining method using the NJBAFD (neighbor-joining tree construction from allele frequency data) software package.

## 3. Results and discussion

We genotyped a total of 1493 people from 11 Asian populations and calculated the allele frequencies at these 13 STR loci in each population. For each allele distribution, we

	Japanese		Korean	Chinese						Thais	Burmese
	Hondo	Ryukyu	Soul	Beijing	Shanxi	Jiangsu	Fujan	Hunan	Guangdong	Bangkok	Yangon
D3S1358	0.72	0.71	0.67	0.73	0.72	0.72	0.72	0.73	0.72	0.74	0.73
vWA	0.80	0.79	0.80	0.80	0.79	0.78	0.78	0.79	0.79	0.78	0.81
FGA	0.86	0.86	0.85	0.85	0.84	0.85	0.85	0.85	0.86	0.89	0.89
D16S539	0.78	0.75	0.82	0.80	0.79	0.79	0.79	0.77	0.77	0.79	0.80
TH01	0.72	0.73	0.65	0.66	0.71	0.66	0.67	0.69	0.69	0.71	0.66
TPOX	0.67	0.71	0.65	0.62	0.63	0.65	0.61	0.64	0.60	0.62	0.60
CSF1PO	0.73	0.72	0.77	0.73	0.73	0.73	0.76	0.74	0.73	0.75	0.73
D8S1179	0.84	0.83	0.84	0.83	0.84	0.83	0.85	0.83	0.85	0.85	0.82
D21S11	0.79	0.74	0.81	0.84	0.80	0.80	0.82	0.81	0.84	0.83	0.81
D18S51	0.85	0.87	0.86	0.84	0.86	0.83	0.86	0.87	0.86	0.84	0.85
D5S818	0.80	0.80	0.78	0.76	0.78	0.75	0.77	0.77	0.78	0.76	0.77
D13S317	0.80	0.81	0.80	0.79	0.80	0.80	0.78	0.77	0.80	0.77	0.82
D7S820	0.77	0.78	0.77	0.78	0.79	0.76	0.73	0.76	0.76	0.78	0.79

Table 1 Expected heterozygosities at 13 STR loci in 11 Asian populations

carried out three tests for HWE. No significant deviations (p < 0.05) from HWE were observed in all three tests among four populations (Hondo and Ryukyu (Japan) and Beijing and Fujan (China)). For the rest, allele distributions at 1–3 loci were significantly deviated from HWE, and only in the Hunan population was the distribution at TH01 significantly deviated from HWE by all three tests (p = 0.0294, 0.0482 and 0.0332 for homozygosity, likelihood ratio and exact tests, respectively). However, since these values were mostly close to 0.05, the departures from HWE were not highly significant. From these allele frequencies, we calculated the expected heterozygosities (Table 1). In general, values at TH01 and TPOX were comparatively low among Asians.



Fig. 1. Neighbor-joining tree based on Nei's  $D_A$  genetic distance for 13 CODIS core STRs in 11 Asian populations.

The neighbor-joining tree was constructed based on Nei's  $D_A$  genetic distance for these 13 STRs in 11 Asian populations, as shown in Fig. 1. In this tree, two Japanese populations (Hondo and Ryukyu), three northern to middle Chinese (Beijing, Shanxi and Jiangsu), and three southern Chinese (Fujan, Guangdong and Hunan) populations comprised each cluster, and the obtained tree was well coincident with their geographical distributions. These bootstrap values were not exceedingly low, ranging from 27 to 100. We also constructed a similar tree, which includes published ethnic data [1–4] from other parts of the globe. These 11 populations, 4 African populations (Trinidadian, African-American, Jamaican and Bahamian) and 4 Caucasian populations (Portuguese, U.S. Caucasian, Swiss Caucasian and Italian) made each cluster formation. The Arabian and Hispanic populations are located between African and Caucasian and between Caucasian and Asian, respectively. The genetic relationship was almost similar to that described previously. It was suggested that STR markers lead to a phylogenetic tree with almost correct topology from more than 100 samples in each population using 13 tetranucleotide repeat loci.

#### Acknowledgements

We are grateful to Dr. Katsushi Tokunaga (Ryukyu), Dr. Park Kyung Sook (Korea), Dr. Song Chen (Beijing), Dr. Feng Jin (other Chinese population groups), Dr. Sirirurg Songsivilai (Thailand) and Dr. Hla Hla Htay (Burma) for providing various samples.

#### References

- L. Garofano, M. Pizzamiglio, C. Vecchio, G. Lago, T. Floris, G. D'Errico, G. Brembilla, A. Romano, B. Budowle, Italian population data on thirteen short tandem repeat loci: HUMTH01, D21S11, D18S51, HUMVWFA31, HUMFIBRA, D8S1189, HUMTPOX, HUMCSF1PO, D16S539, D7S820, D13S317, D5S818, D3S1358, Forensic Sci. Int. 97 (1998) 53–60.
- [2] C. Gehrig, M. Hochmeister, U.V. Borer, R. Dirnhofer, B. Budowle, Swiss Caucasian population data for 13 STR loci using AmpFISTR Profiler Plus and Cofiler PCR amplification kits, J. Forensic Sci. 44 (5) (1999) 1035–1038.
- [3] B. Budowle, T.R. Moretti, A.L. Baumstark, D.A. Defenbaugh, K.M. Keys, Population data on the thirteen CODIS core short tandem repeat loci in African American, U.S. Caucasians, Hispanics Bahamians, Jamaicans, and Trinidadians, J. Forensic Sci. 44 (6) (1999) 1277–1286.
- [4] A. Pérez-Lezaun, F. Calafell, J. Clarimón, E. Bosch, E. Mateu, L. Gusmão, A. Amorim, N. Benchemsi, J. Bertranpetit, Allele frequencies of 13 short tandem repeats in population samples from the Iberian Peninsula and Northern Africa, Int. J. Legal Med. 113 (2000) 208–214.

120