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Letter to the Editor

Allele frequencies of nine non-CODIS STR loci in Chinese Uyghur ethnic minority group

Dear Editor,

We investigated the genetic polymorphisms of nine non-combined DNA index system (CODIS) short tandem repeat (STR) loci for 252 healthy unrelated autochthonous individuals of Chinese Uyghur ethnic minority group in Xingjiang. The 9 STR loci included in STRtyper10G/F^{TM} kit (D18S1364, D12S391, D13S325, D6S1043, D2S1772, D11S2368, GATA198B05, D8S1132, and D7S3048) were highly polymorphic markers and reliable tools for forensic casework [1,2]. These markers are probably unlinked to common STRs included in commercially available kits (e.g., PowerPlex 16 system) and powerful to obtain additional information in STR analysis for complicated cases [1].

The Chinese Uyghurs, with a population of 9,870,000, mostly live in the Xinjiang Uyghur autonomy region of China. They are a Turkic ethnic group and believe in Islam. Their language belongs to the Uyghur Turkic branch of the Turkic language family, which is controversially a branch of the Altaic language family.

DNA samples from 252 healthy unrelated Chinese Uyghur individuals were extracted using the Chelex-100 protocol [3]. PCR amplifications were performed with the STRtyper10G/F^{TM} kit (CODON, Zhuhai, Guangdong, China). The PCR products were analyzed with ABI 3130 Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) and GeneMapper ID Version 3.2 software (Applied Biosystems, Foster City, CA, USA). Hardy–Weinberg equilibrium analysis and heterozygosity were performed with the Arlequin Software Version 3.11, and other forensic parameters were performed with Powerstats Version 1.2 software package (Promega, Madison, WI, USA). Exact test differentiation of allele frequency distribution between populations was carried out by Arlequin Software ver 3.11. Minimum allele frequencies (MAF) for PCR-based loci, based on statistical and population genetics theory [4] were determined. The level of significance was 0.05 for all statistical tests. The allele frequencies and statistical parameters of the studied loci of Chinese Uyghur ethnic minority group are given in Supplementary Table 1.

109 alleles and 383 genotypes were observed in the 9 STR loci, and all loci were found to be highly polymorphic. Only the locus D7S3048 showed a departure form Hardy–Weinberg equilibrium in the present research ($P = 0.0285$). Population substructure and selection may be the possible reasons. The power of discrimination (PD) ranged from 0.9299 to 0.9695, and it showed the value of 0.999999 for combined power of discrimination (CPD). The power of exclusion (PE) ranged from 0.5873 to 0.7567, and the value of combined power of exclusion (CPE) was 0.999958.

Comparison of the allele frequencies from the studied population with other ethnic minority group, Asian populations and the European for which the data were available was performed. The results showed significant differences between Chinese Uyghur ethnic minority group and Chinese Guangdong Han population [1] at all 9 loci except DS325 ($P = 0.25$). On the other hand, only the distribution of alleles for DS1043, DS2368, and DS1132 showed significant differences ($P < 0.05$) between our data and Chinese Tibetan population at all 9 loci [2]. For D12S391, two intermediate alleles designated 17.3 and 18.3 which have been found previously in population samples from Germany [5] and Poland [6] were also detected in Uyghur population. The distribution of alleles for D12S391 versus the German [5], Poland [6], and Italy and Egypt populations [7] indicated statistically significant differences ($P < 0.05$). Frequencies of the alleles of D13S325 versus the Thai population [8] showed significant difference ($P < 0.05$). The Uyghur group differed significantly from the Japanese population in D8S1132 [9], and from Korean population in D6S1043 [10] ($P < 0.05$).

In conclusion, the nine STRs proved to be valuable for differentiation of individuals and parentage testing of Chinese Uyghur ethnic minority group. They are also useful tools for the research of human genetics and anthropology.

This paper follows the guidelines for the publication of population genetic papers in the journal [11], and the ISFG and EDNAP recommendations concerning STR nomenclature and working practices [12].

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at doi:10.1016/j.fsigen.2010.12.005.

References

[1] D.-j. Lu, Q.-l. Liu, H. Zhao, Genetic data of nine non-CODIS STRs in Chinese Han population from Guangdong Province, Southern China, Int. J. Legal Med. (2010), doi:10.1007/s00414-009-0388-x.
[2] X.-b. Song, MeiLangQuCuo, D.-j. Tang, R. Ren, J.-m. Liu, X. Hu, Y. Zhou, L. Zhang, X.-j. Lu, J. Wang, Y.-x. Ye, B.-w. Ying, L.-l. Wang, Genetic polymorphisms of 9 non-combined of DNA index system short tandem repeat loci of Chinese Tibetan ethnic minority group in Tibet, Forensic Sci. Int. Genet. (2010), doi:10.1016/j.fsigen.2010.02.005.
[3] P.S. Walsh, D.A. Metzger, R. Higuchi, Chelex 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material, Biotechniques 10 (1991) 506–513.
[4] B. Budowle, K.L. Monson, R. Chakraborty, Estimating minimum allele frequencies for DNA profile frequency estimates for PCR-based loci, Int. J. Legal Med. 108 (1996) 173–176.
[5] D. Schmid, K. Anslinger, B. Rolf, Allele frequencies of the ACTBP2 (=SE33), D18S51, D8S1132, D12S391, D2S1360, D3S1744, D5S2500, D7S1517, D10S2325 and D21S2055 loci in a German population sample, Forensic Sci. Int. 151 (2005) 303–305.
[6] P. Kuzniar, E. Jastrzebska, R. Ploski, Validation of nine non-CODIS STR loci for forensic use in a population from Central Poland, Forensic Sci. Int. 159 (2006) 258–260.

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doi:10.1016/j.fsigen.2010.12.005

[7] M. Klintschar, U. Ricci, N.A. Hammadi, B. Reichenpfader, A. Ebner, M.L.G. Uzielli, Genetic variation at the STR loci D12S391 and CSF1PO in four populations from Austria, Italy, Egypt and Yemen, Forensic Sci. Int. 97 (1998) 37–45.
[8] Z. Wang, Y. Wang, B. Zhou, B. Du, B. Zhang, G. Zhang, Y. Jia, Y. Zhu, Y.-s. Wei, L. Zhang, Allele frequency of D13S325 and D13S892 in two populations, J. Forensic Sci. 52 (2007) 226.
[9] H. Asamura, M. Ota, H. Fukushima, Population data on 10 non-CODIS STR loci in Japanese population using a newly developed multiplex PCR system, J. Forensic Legal Med. 15 (2008) 519–523.
[10] C.H. Shin, P. Jang, K.M. Hong, M.K. Paik, Allele frequencies of 10 STR loci in Koreans, Forensic Sci. Int. 140 (2004) 133–135.
[11] A. Carracedo, J.M. Butler, L. Gusmão, W. Parson, L. Roewer, P.M. Schneider, Publication of population data for forensic purposes, Forensic Sci. Int. Genet. 4 (2010) 145–147.
[12] P. Gill, B. Brinkmann, E. d'Aloja, J. Andersen, W. Bar, A. Carracedo, B. Dupuy, B. Eriksen, M. Jangblad, V. Johnsson, A.D. Kloosterman, P. Lincoln, N. Morling, S. Rand, M. Sabatier, R. Scheithauer, P. Schneider, M.C. Vide, Considerations from the European DNA profiling group (EDNAP) concerning STR nomenclature, Forensic Sci Int. 87 (1997) 185–192.

Siyue Li[1]
Yi Zhou[1]
Department of Laboratory Medicine, West China Hospital, Sichuan University, Chengdu 610041, Sichuan Province, PR China

Zhao Cheng[1]
Department of Laboratory Medicine, Kelamayi Central Hospital of Xinjiang, Kelamayi, Xinjiang, PR China

Jun Wang
Xingbo Song
Yuanxin Ye
BinWu Ying*
An Zhenmei*
Department of Laboratory Medicine, West China Hospital, Sichuan University, Chengdu 610041, Sichuan Province, PR China

*Corresponding authors. Tel.: +86 28 85423510; fax: +86 28 85423510
E-mail address: anzhenmei@gmail.com (A. Zhenmei)
docybw@gmail.com (B. Ying)
[1]These authors contributed equally to this work.

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