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SHORT COMMUNICATION

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An investigation of the TH01 locus in a population from northern Thailand

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Abstract The STR locus HUMTH01 was studied in 110 unrelated Thais from the area of Chiang Mai in North Thailand. By using PCR and vertical PAGE, six alleles were identified and the frequencies ranged from 0.005 to 0.400. The allele frequency distribution in this population showed significant differences from a Japanese population and other ethnic populations but was similiar to Asians in the USA and Australia. The genotype distribution meets Hardy-Weinberg expectations. The average power of exclusion (in no-parent and one-parent cases) and the discriminating power (DP) were calculated to be 0.3020, 0.4761 and 0.8722 respectively.

Key words HUMTH01 · STR · PCR · Northern Thais · Population data

Introduction

Since the analysis of the polymorphism at the HUMTH01 locus appeared beneficial in human identification and paternity testing (Wiegand et al. 1993; Hochmeister et al. 1994; Kubat et al. 1995; Martin et al. 1995; Pfitzinger et al. 1995; Sjerps et al. 1995), allele and genotype data on this locus were explored in a northern Thai population.

Materials and methods

DNA was extracted from blood of 110 unrelated individuals living around Chiang Mai in North Thailand. The first 80 blood samples were extracted according to the method of Miller et al. (1988), the remaining other 30 samples according to Walsh et al. (1991). The primers used in PCR were those described by Gill et al. (1992), the cycling conditions as suggested by Puers et al. (1993). PAGE of PCR products was done according to Sajantila et al. (1994) and the gels were silver-stained (Budowle et al. 1991). Alleles were designated by comparison with an allelic ladder (consisting of alleles 6, 7, 8, 9, and 9.3/10) made by the "crush and soak" method (Sambrook et al. 1989). Alleles 9.3 and 10 were pooled and reassigned as allele 10. The discriminating power and power of exclusion were calculated according to Fisher (1951) and Garber and Morris (1983) respectively. The Hardy-Weinberg equilibrium (HWE) analysis was based on a comparison of observed and expected genotypes according to Dickinson-Gibbons (1976) and determination of the unbiased estimate of the expected heterozygosity (Nei and Roychoudhury 1974). The frequency profile comparison between different ethnic populations was carried out by using RxC contingency tables.

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Results and discussion

In this population sample from Thailand, six alleles were found with frequencies ranging from 0.005 to 0.40 (Table 1). Allele number 9 was the most frequent and 15 genotypes were observed in northern Thais. Genotype 7/9 was found to be the most common (f = 0.327). The population data for locus HUMTH01 showed no significant deviation from HWE ($0.10 > p > 0.05$, d.f. = 2) and were similar to Asians in USA (Puers et al. 1993) ($0.9 > p > 0.75$) and

Table 1 Allele frequencies at the TH01 locus in northern Thais, Japanese from central Japan, US-Caucasians, and US-Blacks

Allele	Northern Thais	Japanese[a]	US-Caucasians[b]	US-Blacks[b]
5	–	–	0.005	–
6	0.118	0.242	0.226	0.135
7	0.305	0.286	0.159	0.370
8	0.045	0.049	0.110	0.211
9	0.400	0.382	0.143	0.146
10 (9.3 + 10)	0.127	0.041	0.357	0.137
11	0.005	–	–	0.007

[a] Obtained from Nagai et al. (1996)
[b] Obtained from Puers et al. (1993)

Australia (van Oorschot et al. 1994) ($0.5 > p > 0.25$), but different from a central Japanese population ($p < 0.001$) (Nagai et al. 1996) and other major ethnic populations (US-Caucasians, $p < 0.001$; US-Blacks, $p < 0.001$).The discriminating power and the average power of exclusion were 0.8722, 0.3020 (no-parent case) and 0.4761 (one-parent case) respectively. This study shows that the TH01 system may have slightly less power for forensic purposes when used in the Thai population than in Caucasian populations (Puers et al. 1993; Hammond et al. 1994; Nellemann et al. 1994; Hochmeister et al. 1994; Pestoni et al. 1995; Sjerps et al. 1995). We suggest that local population data should be collected because there may be significant differences in allele distribution not only between major ethnic groups but even within Asian populations.

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References

Budowle B, Chakraborty R, Giusti AM, Eisenberg AJ, Allen RC (1991) Analysis of the VNTR locus D1S80 by PCR followed by high-resolution PAGE. Am J Hum Genet 48:137–144

Dickinson-Gibbons J (1976) Non-parametric methods for quantitative analysis. Holt, Rinehart and Winston, New York

Fisher RA (1951) Standard calculations for evaluating a blood group system. Heredity 5:95–102

Garber RA, Morris JW (1983) General equations for the average power of exclusion for genetic systems of n codominant alleles in one-parent and no-parent cases of disputed parentage. In: RH Walker (ed) Inclusion probability in parentage testing. American Association of Blood Banks, Arlington, Va, pp 277–280

Gill P, Kimpton CP, Sullivan K (1992) A rapid polymerase chain reaction method for identifying fixed specimens. Electrophoresis 13:173–175

Hammond HA, Jin L, Zhong Y, Caskey CT, Chakraborty R (1994) Evaluation of 13 short tandem repeat loci for use in personal identification applications. Am J Hum Genet 55:175–189

Hochmeister MN, Jung JM, Budowle B, Borer UV, Dirnhofer R (1994) Swiss population data on three tetrameric short tandem repeat loci – VWA, HUMTH01, and F13A1 – derived using multiplex PCR and laser fluorescence detection. Int J Legal Med 107:34–36

Kubat M, Wiegand P, Brinkmann B (1995) Population genetic study from the Zagreb area using 3 STR systems. Int J Legal Med 107:219–221

Martin P, Alonso A, Budowle B, Albarran C, Garcia O, Sancho M (1995) Spanish population data on 7 tetrameric short tandem repeat loci. Int J Legal Med 108:145–149

Miller SA, Dykes DD, Polesky HF (1988) A simple salting out procedure for extracting DNA from human nucleated cells. Nucleic Acids Res 16:1215

Nagai A, Yamada S, Watanabe Y, Bunai Y, Ohya I (1996) Analysis of the STR loci HUMF13A01, HUMFXIIIB, HUMLIPOL, HUMTH01, HUMTPOX and HUMVWFA31 in a Japanese population. Int J Legal Med 109:34–36

Nei M, Roychoudhury AK (1974) Sampling variances of heterzygosity and genetic distance. Genetics 76:379–390

Nellemann LJ, Moller A, Morling N (1994) PCR typing of DNA fragments of the short tandem repeat (STR) system HUMTH01 in Danes and Greenland Eskimos. Forensic Sci Int 68:45–51

Pestoni C, Lareu MV, Rodriguez MS, Munoz I, Barros F, Carracedo A (1995) The use of the STRs HUMTH01, HUMVWA31/A, HUMF13A1, HUMFES/FPS, HUMLPL in forensic application: validation studies and population data for Galicia (NW Spain). Int J Legal Med 107:283–290

Pfitzinger H, Ludes B, Kintz P, Tracqui A, Mangin P (1995) French Caucasian population data for HUMTH01 and HUMFES/FPS short tandem repeat (STR) systems. J Forensic Sci 40:270–274

Puers C, Hammond HA, Jin L, Caskey CT, Schumm JW (1993) Identification of repeat sequence heterogeneity at the polymorphic short tandem repeat locus HUMTH01 (AATG)n and reassignment of alleles in population analysis by using a locus-specific allelic ladder. Am J Hum Genet 53:953–958

Sajantila A, Pacek P, Lukka M, Syvanen AN, Nokelainen P, Sistonen P, Peltonen L, Budowle B (1994) A microsatellite polymorphism in the von Willebrand factor gene: comparison of allele frequencies in different population samples and evaluation for forensic medicine. Forensic Sci Int 68:91–102

Sambrook J, Fritsch EF, Maniatis T (1989) Molecular cloning: a laboratory manual, Cold Spring Harbor Laboratories Press, Cold Spring Harbor

Sjerps M, van der Geest N, Pieron C, Gajadhar M, Kloosterman A (1995) A Dutch population study of the STR loci HUMTH01, HUMFES/FPS, HUMVWA31/1 and HUMF13A1, conducted for forensic purposes. Int J Legal Med 108:127–134

van Oorschot RAH, Gutowski SJ, Robinson SL (1994) HUMTH01: amplification, species specificity, population genetics and forensic applications. Int J Legal Med 107:121–126

Walsh PS, Metzger DA, Higuchi R (1991) Chelex-100 as a medium for simple extraction of DNA for PCR based typing from forensic material. Biotechniques 10:506–513

Wiegand P, Bajanowski T, Brinkmann (1993) DNA typing of debris from fingernails. Int J Legal Med 106:81–83