Int J Legal Med (1995) 108: 165–166

SHORT COMMUNICATION

A. Piccinini · A. Jürling · A. Junge

Short tandem repeat (STR) system HumD21S11: Population genetic study on an Italian population

Received: 31 July 1995 / Accepted: 16 August 1995

Abstract Allele frequencies of the Short Tandem Repeat locus HumD21S11 were determined analysing 119 unrelated individuals from the area of Milano (Northern Italy). A total of 13 alleles was detected. One allele (< 26) was found which has never been observed in a wider German population sample. The system showed neither significant deviation from Hardy-Weinberg equilibrium nor significant differences with a German population sample.

Key words Short tandem repeats · HumD21S11 · Population studies · Northern Italy

Introduction

Typing of polymorphic DNA systems has become routine over the last 10 years in human identification (Edwards et al. 1991). Because of the high degree of polymorphism and information content of the system HumD21S11 (Sharma and Litt 1992; Möller et al. 1994), population genetic studies were carried on a Northern Italian population sample.

Materials and methods

DNA was extracted from air dried blood on sterile cotton fabric from 119 unrelated Caucasian individuals residing in the Milano area.

The extraction procedure was carried out as previously described (Wiegand et al. 1993). The polymerase chain reaction assay and electrophoresis conditions were according to Möller et al. (1994). Bands were visualized by silver staining (Budowle et al. 1991). Alleles were designated by comparison with a specific allelic ladder consisting out of 9 sequenced alleles (Möller et al. 1994).

The statistical analysis was performed using the HWE-Analysis software, Version 3.0, provided by C. Puers (C. Puers, Münster, Germany). The comparison of observed and expected numbers of heterozygotes (gene diversity) was calculated according to Nei (1978), the mean exclusion chance according to Krüger et al. (1968), the mean paternity exclusion probability according to Brenner and Morris (1989), the polymorphic information content according to Botstein et al. (1980), the probability of match and the discrimination power according to Jones et al. (1972) and the distinct heterozygous and homozygous genotypes according to Chakraborty et al. (1993).

The frequency profile comparison between Italian and German populations was carried out using a test for genetic heterogeneity (R × C contingency table; G. Carmody, Ottawa, Canada).

Results and discussion

A total of 13 alleles was observed for an Italian population sample (Table 1). Allele 33, also very rare in the German survey, was not observed in the Italian population study. However a very low molecular weight allele (< 26)

Table 1 Allele frequency distribution for HumD21S11 in an Italian population (n = 119 unrelated individuals) compared to a German population survey (n = 572 unrelated individuals). Designation of the alleles according to Möller et al. (1994)

Allele	Allele frequencies	
	Italians (n = 119)	Germans (n = 572)
< 26	0.0042	–
26	0.0084	0.0026
27	0.0294	0.0367
28	0.1681	0.1723
29	0.2185	0.2054
30	0.1849	0.2256
30.2	0.0504	0.0323
31	0.1135	0.0830
31.2	0.0882	0.1032
32	0.0042	0.0122
32.2	0.0882	0.0909
33	–	0.0009
33.2	0.0336	0.0297
> 33.2	0.0084	0.0052

A. Piccinini
Istituto di Medicina Legale, Universita' degli Studi di Milano,
Via L. Mangiagalli 37, I-20133 Milano, Italy

A. Jürling · A. Junge (✉)
Institute of Legal Medicine, Westfälische-Wilhelms-Universität,
Von-Esmarch-Strasse 86, D-48149 Münster, Germany

Table 2 Statistical data for HumD21S11. H_{obs}=observed heterozygosity; H_{exp} = expected heterozygosity; SE = standard error; MEC = mean exclusion chance; MEP = mean exclusion probability; PIC = polymorphic information content; pM = match probability; D = discrimination power

H_{obs}	0.8103
H_{exp}	0.8596 +/– 0.0632
MEC	0.7074
MEP	0.7138
PIC	0.8397
pM	0.0427
D	0.9573

was detected in the Italian population which was not found in the German population so far.

The population data at locus HumD21S11 showed no significant differences between the Italian and German populations ($p > 0.05$) and no significant deviation from Hardy-Weinberg equilibrium ($p > 0.05$; Table 2).

The high polymorphism of the HumD21S11 locus represents a good reference point in forensic investigations as well as a useful tool for further genetic studies on other Italian populations.

References

Botstein D, White RL, Skolnick M, Davis RW (1980) Construction of a genetic linkage map in man using restriction fragment length polymorphism. Am J Hum Genet 32:314–331

Brenner C, Morris J (1990) Paternity index calculations in single locus hypervariable DNA probes: validation and other studies. In: Proceedings of the International Symposium on human identification 1989, Promega Corporation, pp. 21–53

Budowle B, Chakraborty R, Giusti AM, Eisenberg AJ, Allen RC (1991) Analysis of the variable number of tandem repeat locus D1S80 by the polymerase chain reaction followed by high resolution polyacrylamide gel electrophoresis. Am J Hum Genet 48:137–144

Chakraborty R (1993) A class of population genetic questions formulated as the generalized occupancy problem. Genetics 134: 953–958

Edwards A, Civitello A, Hammond HA, Caskey CT (1991) DNA typing and genetic mapping with trimeric and tetrameric tandem repeats. Am J Hum Genet 49:746–756

Jones DA (1972) Blood samples: Probabilities of discriminations. J Forensic Sci Soc 12:355–359

Krüger J, Fuhrmann W, Lichte KH, Steffens C (1968) Zur Verwendung des Polymorphismus der sauren Erythrocytenphosphatase bei der Vaterschaftsbegutachtung. Dtsch Z Gerichtl Med 64:127–146

Möller A, Meyer E, Brinkmann B (1994) Different types of structural variation in STRs: HumFES/FPS, HumVWA and HumD21S11. Int J Legal Med 106:319–323

Nei KM (1978) Estimation of average heterozygosity and genetic distance from a small number of individuals. Genetics 89: 583–590

Sharma V, Litt M (1992) Tetranucleotide repeat polymorphism at the D21S11 locus. Hum Mol Genet 1:67

Wiegand P, Budowle B, Rand S, Brinkmann B (1993) Forensic validation of the STR systems SE33 and TC11. Int J Legal Med 105:315–320