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SHORT COMMUNICATION

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North Italian population genetic data on the STR system HumFGA

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Abstract Frequency data for the STR system HumFGA were obtained from a North Italian population sample (Milano area) of 201 unrelated individuals. PCR products were detected by horizontal polyacrylamide gel electrophoresis and a total of 15 alleles were identified by side-by-side comparison with a commercially available sequenced allelic ladder. The observed genotype distribution showed no significant deviation from Hardy-Weinberg equilibrium. The high information content (discrimination power > 0.96, polymorphism information content > 0.84) render this system a useful tool in forensic routine casework both in criminal and paternity cases.

Key words STR · HumFGA · Population studies · North Italy

Introduction

HumFGA (Mills et al. 1992) is a complex repeat polymorphism showing regular 4 bp and sometimes 2 bp increments at the lower end of the observed size range, while a more complex structure is found at the upper end (Barber et al. 1996). However, very rare alleles differing by just one bp have also been described (Gill et al. 1996)

We performed the present study on a sample composed of 201 unrelated individuals in order to investigate the suitability and the usefulness of this system in combination with the detection system in use in our laboratory (horizontal polyacrylamide gel electrophoresis) in routine casework.

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Materials and methods

DNA extraction was carried out from air-dried blood on sterile cotton fabric and from fresh blood samples using the standard phenol-chloroform method.

Primer sequences and amplification conditions were according to Barber et al. (1996).

Horizontal polyacrylamide gel electrophoresis was carried out following previously described methods (e.g. Wiegand et al. 1993). PCR products were visualized by silver staining (Budowle et al. 1991) and alleles were compared to a sequenced allelic ladder consisting of 14 alleles (Serac, Bad Homburg-Germany). Isolation of stained fragments, Taq-cycle-sequencing and sequence analysis was performed as previously described (Möller and Brinkmann 1994).

Statistics

Statistical evaluations were performed using the HWE-Analysis software, Version 3.0, provided by C. Puers (C. Puers, Münster, Germany). These evaluations included the comparison of observed and expected numbers of heterozygotes (gene diversity) according to Nei (1978), the mean exclusion chance (MEC) according to Krüger et al. (1968), the mean paternity exclusion probability (MEP) according to Brenner and Morris (1990) the polymorphic informa-

Table 1 Allele frequencies for HumFGA (n = 201 individuals). MEC = 0.72404, MEP = 0.72541, PIC = 0.84799, pM = 0.03988, D = 0.96012. Observed and expected heterozygosities are 0.8507 and 0.8654 ± 0.0472 respectively (± 1.96 standard error)

Allele	Frequency
16	0.002
17	0.002
18	0.020
19	0.065
20	0.112
21	0.197
21.2	0.002
22	0.134
22.2	0.002
23	0.162
24	0.162
24.2	0.002
25	0.100
26	0.025
27	0.012

tion content (PIC) according to Botstein et al. (1980), the probability of match (pM) and the discrimination power (D) according to Jones (1972). These data are reported in Table 1.

Results and discussion

A total of 14 alleles was observed. Allele nomenclature was in accordance with Barber et al. (1996). The allele frequencies as detected in the North Italian population are summarized in Table 1.

No significant deviation from Hardy-Weinberg equilibrium could be detected ($P > 0.05$). Relevant statistical data are presented in Table 1.

In a population sample, consisting of more than 200 individuals, we observed 4 individuals each showing 3 different "interalleles" (21.2, 22.2, 24.2) and an allele with 16 repeats. The electrophoretic migration of this allele was compared to a sequenced 16 repeat allele (data not shown) kindly provided by B. Brinkmann (Münster-Germany). Sequence analysis was performed in order to verify the exact composition of these alleles (data not shown).

All data collected in this study confirmed the usefulness of this system in forensic routine casework even in association with an inexpensive resolution system like horizontal PAGE. This is due to the combination of the relatively low molecular weight of the alleles and their structure, which apparently shows only length microheterogeneities which are easily detectable. Nevertheless, further studies are required both on different Italian populations, as well as on other European and non-European populations, in order to increase the world database.

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