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Southern Poland population study with the use of an AmpFISTR®SGM Plus™ kit

Introduction

Over the last ten years polymorphic microsatellite STR sequences have been often used for various forensic purposes. Analysis of STR loci is not only the quickest but also the most effective way of genetic typing of biological material in forensic practice. The commercially used AmpFISTR®SGM Plus™ kit allows carrying out a quick amplification of 10 microsatellite STR loci from different regions of human nuclear DNA.

Population studies on 10 autosomal STR loci were carried out in many regions of Europe, Asia, Australia and both Americas [1]. In Poland polymorphism of 10 STR loci was studied in: western Poland [2], central Poland (Łódź) [3, 4], central Poland [5, 6], Warmia and Mazury (north-eastern Poland) [7], Podlasie (north-eastern Poland) [8], southern Poland [9], Polish Roms [10] and Polish Tatars [11].

The aim of the research was: to study the distribution of allele frequencies of the following autosomal loci: D3S1358, VWA, D16S539, D2S1338, AMEL, D8S1179, D21S11, D18S51, D19S433, THO1 and FGA in a population sample from southern Poland, show their genetic balance with Hardy-Weinberg equilibrium as well as to calculate and compare statistical parameters (PD, PIC, MEC, PM, Ht and MEP) which could allow assessing the usefulness of these genetic markers for forensic purposes.

Materials and methods

The population sample consisted of 704 unrelated individuals (354 male and 350 female) of European origin living in a southern part of Poland. Total DNA was extracted from whole blood or buccal swabs using a Blood DNA Prep Plus kit (A&A Biotechnology) [12] and an EZ1 Tissue DNA kit in robotic station Biorobot EZ (Qiagen, Germany) [13]. Concentration of human DNA was measured using a NanoDrop ND-1000 spectrometer (ThermoFisher Scientific TK, Biotechnology, USA). PCR reactions were carried out according to the recommendations of the manufacturer of the AmpFISTR®SGM Plus™ kit [1] (Applied Biosystems, USA) on the GeneAmp®PCR System 2700 and 8700 (Applied Biosystems, USA). PCR products were separated and detected on the 3130 Genetic Analyzer (Applied Biosystems, USA). The DNA growth standard was

the GeneScan-500 LIZ marker (Applied Biosystems, USA). The obtained data were analyzed with GeneMapper®IDX v. 3.2 computer software (Applied Biosystems, USA). 10 autosomal loci: D3S1358, VWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, THO1, FGA and AMEL were determined. χ^2 and Exact tests as implemented in TEPGA computer software were used to test for significant deviations from Hardy-Weinberg equilibrium. FatRec software was applied for calculation of the forensically relevant statistical parameters (PD, PIC, MEC, PM, Ht and MEP).

Results and discussion

The distribution of allele frequencies of 10 autosomal STR loci in the examined population sample is presented in Table 1. Performed χ^2 and Exact tests did not indicate deviation from Hardy-Weinberg equilibrium (p > 0.005). Rare alleles were found in the following loci: D3S1358, VWA, D16S539, D2S1338, D8S1179, D18S51, D19S433, THO and FGA, however they had been previously found in other regions of Poland, too. Moreover, alleles 24.2 and 35.2 were found in locus D21S11 and 18.2 in D18S51 which have not been described in Polish literature yet.

No deviation was noted from the data concerning the examined STR loci reported in literature for populations from other parts of Poland, but statistically significant deviations were found in comparison with populations of Roms and Tatars. D8S1179, D19S433 and FGA locus constituted the exception.

Statistical parameters calculated for 10 STR loci are shown in Table 2. In all but D16S539 loci the value of PD exceeded 0.9.

Conclusions

- The distribution of allele frequencies of 10 autosomal STR loci in the examined population sample from southern Poland is found to be in agreement with Hardy-Weinberg equilibrium.
- Statistical parameters for 10 autosomal loci can be used for forensic purposes.
- Analytical costs are rather low, which is quite important in case of screening examinations involving many samples.