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Is SGM Plus™ the sufficient system for paternity testing?

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Abstract. SGM Plus is one of the multiplex systems commonly used in forensic genetics, especially in analyses of biological evidences from crime scenes. In some laboratories SGM Plus is also used to establish fatherhood. One hundred and fifty excluding paternity cases and 150 including ones were analysed to check the validity of this system for paternity testing. The statistical parameters were estimated for standard and motherless cases. Power of exclusion and paternity index were analysed for each of 10 loci as well as for entire SGM Plus set. The results showed that the SGM Plus is not sufficient for paternity testing of standard cases as well as motherless ones. It gives a risk of false paternity inclusion for the cases without mother. © 2005 Elsevier B.V. All rights reserved.

Keywords: SGM Plus; Motherless case; Paternity testing; Statistical evaluation

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1. Introduction

SGM Plus including 10 STR loci is a multiplex system most often used for databasing in Europe. In some laboratories this system is also used to establish fatherhood. The purpose of this study is to compare the usefulness of SGM Plus™ of standard (Trios) and motherless cases (Duos) for paternity testing in Poland.

2. Materials and methods

DNA was extracted from peripheral blood of 900 individuals from Central Poland population (Lodz region), taking part in paternity testing, by means of the salt method by Lahiri and Nurnberger [1] and using Sherlock AX kit (A&A Biotechnology).

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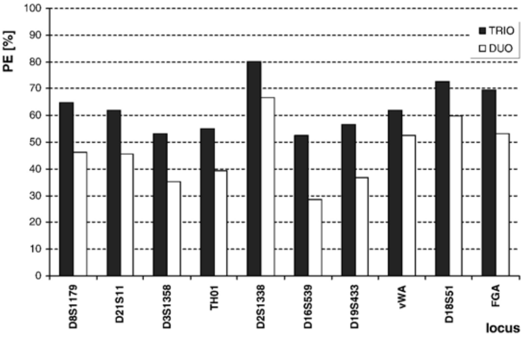

Fig. 1. Power of exclusion values for each locus of SGM Plus computed for 150 standard cases (Trio) and 150 motherless ones (Duo).

The samples were profiled using AmpFlSTR SGM Plus kit. Amplification products were electrophoresed using the ABI Prism 377 Sequencer. Paternity index [PI] by Brenner [2] and probability of paternity [W] by Essen-Möller [3] of 150 including cases were computed on the basis of the population database of Central Poland region [4] and the results were elaborated for standard cases (Trios) and motherless ones (Duos). One hundred and fifty excluding cases were analysed to evaluate the power of exclusion [PE] and the results were also elaborated for Trios and Duos.

3. Results and conclusions

Fig. 1 shows Power of exclusion evaluated for each locus of SGM Plus. The highest PE values were obtained for D2S1338, i.e. 80.27% for Trios and 66.67% for Duos and the lowest PE values were obtained for D16S539, i.e. 52.37% for Trios and 28.57% for Duos (Fig. 1). The minimal number of excluding loci for analyses with using SGM Plus was 2 among Trio cases. Among Duo cases there was an event of false inclusion (Fig. 2), which was revealed after further investigations with additional STR markers.

The minimal value of Paternity Index obtained from analyses of standard cases was 1640.02, which signifies W= 99.93%, while the minimal value of PI obtained from motherless cases analyses was 46.37, which signifies W= 97.89% (Fig. 3). The probability of paternity in almost 60% of Trio

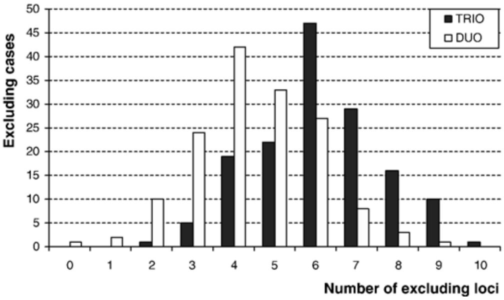

Fig. 2. Comparison of the number of excluding loci of SGM Plus between standard cases (Trio) and motherless ones (Duo).

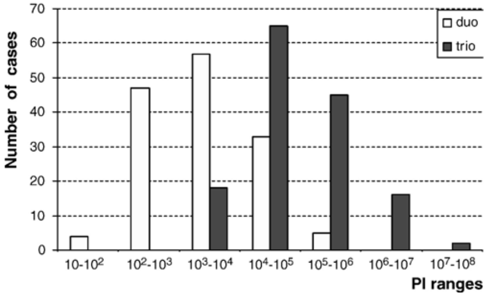

Fig. 3. Comparison of PI values between standard (Trio) and motherless cases (Duo).

cases was 99.99% and lower, which, according to Polish Forensic Genetics Commission, is not sufficient for judging paternity cases. The mean value of probability of paternity in Duo cases was as low as 99.94%. Additionally the number of excluding loci among 27% of Duo cases was 3 and less, which can cause the risk of misjudgement, by the reason of not taking into account mutation events [5,6].

Taking into consideration all the results we concluded that evidence values of paternity cases, both standard and motherless ones, tested with using SGM Plus are not sufficient to submit them in court. This system gives a risk of false inclusion of paternity for the cases, in which mother is not available.

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