International Congress Series 1261 (2004) 476–478

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Effect on paternity index of substituting the biological father by his brother—preliminary report

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Abstract. *Background*: In cases of analysis of trios with the biological father, inconsistencies never appear (barring the possibility of a mutation occurring). The paternity index (PI) calculated for such trios always has a value greater than zero. If in such a trio the biological father is substituted by his brother, it can cause a change in PI if the brother's genotype is different from the genotype of the biological father. The purpose of this study was to determine what the effect on PI for a trio would be if the biological father in the trio was replaced by his brother. In the study, a computer simulation was used of all theoretically possible trios with the biological father and his brother. For all the simulated trios, PIs were calculated and compared. The calculations were based on SGM Plus systems. It was determined that PI calculated for the trio with the biological father's brother can only have one of four possible relations to PI for the trio with the biological father. Most often, there was no change in the PI—this occurred in over half the cases (53.7%, SD = 0.9%). Significantly less frequent was the situation in which the result of the substitution was an inconsistency (32.3%, SD = 3.8%). The remaining two possibilities—twice greater or lesser PI resulting from substituting the father in the trio—were very rare and appeared with medium frequency of only a few percent (4.7%, SD = 1.0% and 5.3%, SD = 2.0%, respectively). Substituting, for the biological father in a trio, his brother, in so far as no inconsistency appears as a result, does not cause any change in PI in the majority of cases. Thus, distinguishing the biological father from his brother can occur practically only by means of excluding the brother.

Keywords: Paternity index; Avuncular index; Relatives; SGM Plus; Population data

1. Introduction

The rare cases where even DNA testing does not resolve the question of paternity are almost always those in which the true and alleged fathers are related [1]. Older publications remark only that in this situation the analysis is more difficult, since the results may provide little information [2]. In 1988, Morris et al. [3] defined the Avuncular Index (AI), which brought certain possibilities of a more analytical approach to the problem. The aim of this study was to determine how the substitution, for the true father in a trio, of a brother affects paternity index (PI) for the trio.

2. Materials and methods

In the study, a computer simulation was run on all theoretically possible trios with a true father and his brother. The analysis was based on 10 DNA systems from SGM Plus

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doi:10.1016/S0531-5131(03)01452-3

Table 1
Population genetics of SGM Plus multiplex—population sample of 100 unrelated persons (200 alleles) from central Poland

Allele	D3S1358	VWA	D16S539	D2S1338	D8S1179	D21S11	D18S51	D19S433	TH01	FGA
6									0.260	
7									0.145	
8			0.005		0.015				0.120	
9			0.100		0.010				0.215	
9.3									0.250	
10			0.035		0.070		0.010		0.010	
11			0.290		0.065		0.010	0.005		
12			0.325		0.200		0.060	0.065		
13	0.005		0.220		0.290		0.100	0.210		
13.2								0.020		
14	0.140	0.150	0.025		0.215		0.175	0.340		
14.2								0.035		
15	0.220	0.070		0.010	0.095		0.190	0.145		
15.2								0.060		
16	0.220	0.165		0.075	0.030		0.135	0.075		
16.2								0.035		
17	0.265	0.300		0.235	0.010		0.150			
17.2								0.005		
18	0.145	0.225		0.065			0.080			
18.2								0.005		
19	0.005	0.080		0.075			0.050			0.095
20		0.010		0.115			0.020			0.120
21				0.055		0.005	0.015			0.190
22				0.025						0.205
22.2										0.030
23				0.105						0.135
23.2										0.005
24				0.120			0.005			0.135
25				0.105		0.005				0.055
26				0.015						0.020
27						0.060				0.010
28						0.200				
29						0.185				
30						0.220				
30.2						0.035				
31						0.050				
31.2						0.085				
32.2						0.105				
33.2						0.040				
34.2						0.010				

multiplex. Allele frequencies came from the authors' own population from central Poland of 100 non-related persons (200 alleles) and are shown in Table 1.

In the systems studied for all theoretically possible combinations of genotypes, the PI for the true father and his brother, and the frequency of each combination of genotype in the population were calculated. Then, on that basis was calculated the frequency of change in PI values in the population F_{PI} between trios with the true father and the true father's brother, i.e., how often the quotient: PI of true father's brother over PI of true father had the values: 0, 0.5, 1 or 2, since only these values are possible, and where: 0 means exclusion of the brother; 0.5 means that the brother's PI is two times lower than the father's PI; 1 means that the brother's PI is equal to the father's PI; and 2 means that the brother's PI is two times greater than the father's PI. The F_{PI} values thus obtained and corresponding minimal, maximal and average values, along with the standard deviation, were arranged in Table 2.

3. Results

Table 2
Results of F_{PI} calculations for the 10 microsatellite systems from SGM Plus multiplex (for symbols see Materials and methods)

System	$F_{\mathrm{PI}}(0)$	$F_{\mathrm{PI}}(0.5)$	$F_{\mathrm{PI}}(1)$	$F_{\mathrm{PI}}(2)$
D3S1358	0.293007	0.109571	0.542637	0.054785
VWA	0.302522	0.104207	0.541167	0.052104
D16S539	0.260491	0.124407	0.552899	0.062203
D2S1338	0.376388	0.065232	0.525764	0.032616
D8S1179	0.315245	0.097600	0.538354	0.048801
D21S11	0.350989	0.078971	0.530554	0.039486
D18S51	0.368379	0.069603	0.527217	0.034801
D19S433	0.314204	0.097511	0.539529	0.048756
TH01	0.289647	0.111212	0.543535	0.055606
FGA	0.356737	0.075863	0.529468	0.037932
Average	0.322761	0.093418	0.537112	0.046709
S.D.	0.038452	0.019908	0.008647	0.009954
Minimum	0.260491	0.065232	0.525764	0.032616
Maximum	0.376388	0.124407	0.552899	0.062203

4. Discussion

The study has shown that in the case of replacing the true father with his brother, most often, there was no change in the PI. For the SGM Plus systems, this occurred in over half the cases (0.537112, SD = 0.008647). Significantly less frequent was the situation in which the result of the substitution was an inconsistency (0.322761, SD = 0.038452). The remaining two possibilities—twice greater or lower PI values—were very rare and appeared with medium frequency of only a few percent (0.046709, SD = 0.009954 and 0.053418, SD = 0.019908, respectively). Furthermore, it is worth emphasizing that—as was noted by Presciuttini et al. [4]—the results of an analysis are easily carried over to other systems or STR system sets, and therefore also permit generalizations which go beyond the loci sets chosen for this study.

5. Conclusion

Substituting, for the true father in a trio, his brother, in so far as no inconsistency appears as a result, does not cause any change in PI values in the majority of cases. Thus, distinguishing the biological father from his brother can occur practically only by means of excluding the brother.

Acknowledgements

This project was supported by the Medical University of Lodz grant no. 502-11-785(35).

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