

Paternity index (PI) vs. residual PI in real cases. Inferences about Exclusion Power and real exclusion rates over 11 STR polymorphic systems in Entre Ríos population in Argentina

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Abstract. Eleven polymorphic systems were analysed in 107 trios comprising the alleged father, mother and child. PI, Residual PI (RPI), and the respective distribution descriptive parameters were obtained. In cases in which the exclusion of paternity was determined, the exclusion percentage was evaluated for each system and was compared with the calculated Exclusion Power. Only three PI values were observed to be inside the RPI value curve, although this only occurs for 2.5% of cases. Like other authors regarding other populations, we conclude that in this population, more polymorphic systems must be analyzed when PI values under 1000 are observed. Total Exclusion Power for this polymorphic system was 0.99973 and D13S317 was the system with highest Exclusion Power (0.6183). However, the highest real exclusion rate in this population was observed in the F13A01 system (0.7000), calculated over the number of F13A01 exclusions over the total paternity exclusions observed. © 2005 Published by Elsevier B.V.

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1. Introduction

In forensic genetics laboratories, it is not unusual to encounter paternity studies in which the PI value calculated for cases in which the alleged father cannot be excluded as the child's

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biological father are relatively low in comparison with the international recommendations [1]. This has led many laboratories to increase the number of polymorphic systems to be analysed. Furthermore, there are some cases in which the alleged father is excluded as the biological father and yet the RPI values are remarkably high. The aim of this study was to carry out a comparative statistical analysis of PI and RPI values in 107 paternity cases from the province of Entre Ríos (Argentina), considering 11 polymorphic systems used routinely in our laboratory, with the aim of establishing a cut-off value from which it is considered necessary to analyse a greater number of systems in order to increase the PI to prevent it from being included in the range of RPI values. The EP were calculated for each system [1] and, in order to evaluate how real this estimate was in our population, the EP was compared with the real EP observed. For this purpose, a new forensic genetics parameter had to be defined, which we have called Real Exclusion Power (REP), calculated as the total number of exclusions observed in a polymorphic system over the total number of paternity exclusions observed in the routine work of a specific population.

2. Materials and methods

107 typical trios (alleged father, mother and child) were analysed. DNA was extracted from the blood samples according to the extraction protocol adapted by Corach et al. [2] or using chelating resins according to the method recommended by Walsh et al. [3]. 11 STRs (CSF1PO, TPOX, TH01, F13A01, FES-FPS, vWA, D16S539, D7820, D13S317, F13B and LPL) were investigated, following the manufacturer's recommendations [4]. Exclusion Power (EP), Paternity Index (PI) and Residual Paternity Index (RPI) were calculated using BDGen 1.0 [5]. Real Exclusion Power (REP) was calculated manually as the proportion of exclusions observed in a system throughout the cases in which paternity exclusion was observed. Descriptive statistics were used for the variables PI and residual PI. When both variables were compared, a logarithmic transformation was performed; normality was thus achieved in both groups. All the data were processed using SPSS 9.0.1 Software.

3. Results

107 parentage studies were carried out, 77 paternity exclusions and 30 non-exclusions. EP was compared with REP, calculating the latter as the proportion of exclusions per system over the total exclusions observed (Fig. 1).

The difference between logarithm PI (log PI) and logarithm RPI (log RPI) means was highly significant ($p < 10^{-4}$) when a *t*-test was applied for mean differences between the two distributions.

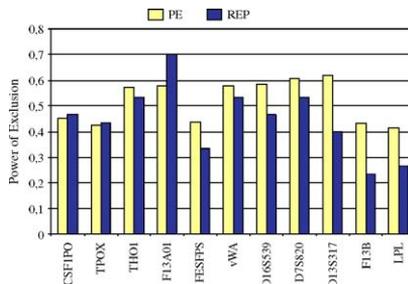


Fig. 1. Exclusion power (EP) vs. real exclusion power (REP) for each STR system.

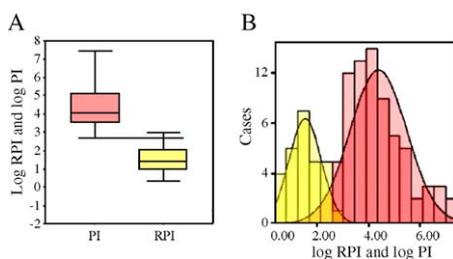


Fig. 2. (A) Box graph in which the logarithmic distributions of RPI and PI can be seen, showing minimum and maximum values, percentiles 25 and 75, and median. (B) Bar graph in which the logarithmic distributions of RPI and PI values are shown in terms of the number of cases analysed.

Fig. 2A shows the box diagrams in which the following values can be analysed: minimum, percentile 25, median, percentile 75 and maximum. The horizontal line shows that only one case in the RPI group has a value above the minimum value observed in the PI group. Following the percentile criterion, both curves (PI and RPI) coincide on the cut-off point applying to value 889 approximately (equivalent to the antilogarithm of 2.9488), in percentile 97.5 for RPI and percentile 2.5 for PI. See value distributions in Fig. 2B.

4. Conclusions

The total Exclusion Power for the 11 systems studied is 0.99973; the highest EP is observed in system D13S317 (0,6183), whereas the greatest REP was obtained in system F13A01 (0,7000). When theoretic REP and EP distributions were compared by means of Chi-squared statistics, the difference was non-significant ($\alpha=0.05$), indicating that the calculation of EP is quite reliable for foretelling the behaviour of polymorphic systems investigated in real cases in the population under study, despite the fact that we worked with a total of only 30 paternity exclusions. When the PI and RPI values were compared, a cut-off value of 889 was found for the population analysed. This value is slightly below the PI of 1.000 that is usually recommended; we could probably come close to this value with a larger sample size. Bearing in mind that there is hardly any difference between the value obtained and the value recommended and maintaining a conservative position, we conclude, as do other authors, that in the absence of exclusions, if PI values below 1.000 in our population and with the STR systems tested, it is advisable to analyse a larger number of polymorphic systems.

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