International Congress Series 1261 (2004) 463-464





Databases: the real importance in paternity testing

A.T. Fernandes*, R. Gonçalves, A. Brehm

Department of Biology, Madeira University, Campus da Panteada, Funchal 9000-390, Portugal

Abstract. Five databases with 15 short tandem repeats (STRs) from populations belonging to Madeira Islands, Açores, Cabo Verde and Guiné-Bissau were separately employed to calculate paternity indexes in thirty case studies from Madeira. The five populations show significant differences among them. For all cases, the results of paternity probability showed no differences when each of the five databases was employed. Due to the high number of loci surveyed and the resolution achieved, the results suggest that there is no need to use databases from specific populations when the goal is to determine the probability of paternity. The results are even more striking if we take into account that two of the databases are of African populations and were employed against cases from a European genetic background. © 2003 Published by Elsevier B.V.

Keywords: Paternity test; Database; Short tandem repeat (STR)

1. Introduction

Databases are important for population studies but are not all-important for paternity analysis. Five databases with 15 short tandem repeats (STRs) of different populations were used, with some populations showing significant differences among them, like the two Cabo Verde populations and the one in Guiné [1,2], and those with the Madeira and Açores [3,4]. There are significant differences between Madeira and Açores and also between the two groups of Cabo Verde islands.

We used 30 paternity cases, from which 20 have data on father, mother and child, in which paternity was confirmed. Two of the cases show a single exclusion (we considered a mutation and used the 10^{-4} value to the mutation rate). In two cases, in the absence of the father, data from paternal grandparents was used. In six cases, we had only the father/son pair, and in three of these paternity was confirmed and in three others excluded.

2. Material and methods

We used the Powerplex 16 from Promega to type all the 15 STRs for the databases. The results were done by ABI Prism 310. The paternity probability was calculated according to statistics group of GEP-ISFG.

^{*} Corresponding author. Tel.: +351-96-7040332; fax: +351-291-705399.

E-mail address: atgf@uma.pt (A.T. Fernandes).

3. Results

In all cases, the differences between the results with the five databases are not statistically significant. In the positive cases, we had a result higher than 99.99% equivalent to "Paternity practically proved" and in cases of exclusion values almost zero. In one case, we had a single exclusion and used more STRs to increase the paternity probability. It will be necessary to do the same when we used the other databases.

References

- A.T. Fernandes, R. Velosa, J. Jesus, A. Carracedo, A. Brehm, Genetic differentiation of the Cabo Verde Archipelago population analysed by STR polymorphisms, Annals of Human Genetics (in press).
- [2] R. Gonçalves, J. Jesus, A.T. Fernandes, A. Brehm, Genetic profile of a multi-ethnic population from Guine-Bissau (west African Coast) using the new Powerplex16 system kit, Forensic Science International 129 (2002) 78–80.
- [3] A.T. Fernandes, A. Brehm, C. Alves, L. Gusmão, A. Amorim, Genetic profile of the Madeira Archipelago population using the new Powerplex16 System Kit, Forensic Science International 125 (2002) 281–283.
- [4] R. Velosa, A.T. Fernandes, A. Brehm, Genetic profile of the Açores Archipelago population using the new Powerplex16 System Kit, Forensic Science International 129 (2002) 68-70.