PATERNITY TESTING WITH FIVE VNTR SYSTEMS IN DANES

Hanna E. Hansen & Niels Morling

Institute of Forensic Genetics, University of Copenhagen,
11 Frederik Den Femtes Vej, DK-2100 Copenhagen Ø, Denmark

INTRODUCTION

This study presents the results of examinations with five VNTR systems in Danish paternity cases. The efficiency of the five systems, the reliability of exclusions, and the mutation rates of the systems have been examined. The linkage relationship between the systems D7S21 and D7S22 has been investigated through family studies.

MATERIAL AND METHODS

The material comprised 174 cases of disputed paternity in which all parties were unrelated Danes, 84 mother-child pairs, and 32 families with 70 children. The techniques used for DNA preparation, electrophoresis, autoradiography, and calculation of kilobase values have been described previously (Morling & Hansen, 1992). The restriction enzyme was *Hin*f1. The systems used were: D7S22 (g3), D5S43 (MS8), D7S21 (MS31), D12S11 (MS43) (Wong et al 1987), and D2S44 (YNH24) (Wyman & White 1980).

RESULTS AND DISCUSSION

No paternity case was evaluated before DNA from all the parties could be run side by side on the same gel. Since migration distances never exceeded 1.25 mm between bands identical by descent in mothers and children (Morling & Hansen 1992), exclusion of paternity was established when the distance between the paternally derived band of the

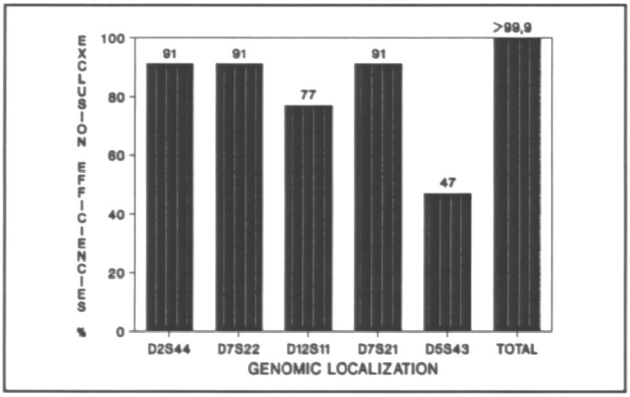

Fig. 1. Exclusion efficiencies of five VNTR systems in 53 Danish paternity cases

Advances in Forensic Haemogenetics 4
Edited by Ch. Rittner and P. M. Schneider

child and the nearest band of the alleged man exceeded 1.25 mm. Examinations with VNTR systems were carried out at the second step of the routine paternity investigations, and consequently a comparatively large number of non-excluded men was found in the present material.

The combined efficiency of the five VNTR systems used exceeded 99.9 % (fig. 1). All 53 alleged men, excluded as the fathers by one or more of 12-15 conventional marker systems, were also excluded by at least two of the VNTR systems used. In another eight cases, the alleged men were excluded only by the VNTR systems. In six other cases, two alleged men were full sibs, and two VNTR systems provided the only exclusions of a brother in four of these cases, while two VNTR systems and the HLA-A,B-system excluded one brother in one case, and only the HLA-system gave guidance in the last case.

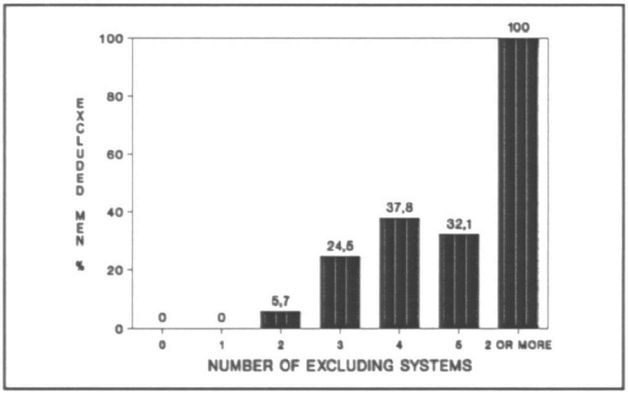

Fig. 2. Exclusion efficiencies of VNTR combinations in 53 Danish paternity cases

The systems D2S44, D7S22, and D7S21 could exclude paternity for 48 (91%) of the 53 men who were excluded by the conventional marker systems. D12S11 and D5S43 were found to be less efficient, excluding 41 (77%) and 25 (47%) men, respectively.

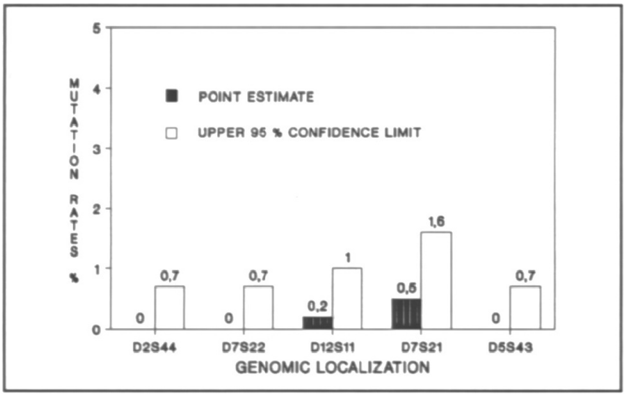

Fig. 3. Mutation rates of five VNTR systems (557 informative meioses)

The presence of parent-child exclusions due to possible mutations was examined in 258 mother-child-pairs and 32 families with 70 children. Presuming that 159 alleged men were the biological fathers since their paternity could not be excluded by any of the 12-15 conventional marker systems or by 2-5 VNTR systems, 557 meioses were obtained. Four cases of exclusions of a parent by only one VNTR system were observed: A mother and a family father, respectively, were excluded by D7S21, and in two paternity cases, the alleged men were excluded by D7S21 (PI = 4740) and by D12S11 (PI = 227), respectively. This leads to observed mutation frequencies of 0.2% for D12S11 and 0.5% for D7S21. No mutations were observed in the D2S44, D7S22, and D5S43 systems (fig. 3).

Table 1. Linkage analysis of D7S21 (MS31)-D7S22 (g3) in 22 families with 2-5 children

	Observed number of:		
Informative haplotypes:		Recombinants:	
Maternal	57	21	(36.8%)
Paternal	51	13	(25.5%)
Total	108	34	(31.5%)*

*) $chi^2 = 7.4$, $p < 0.01$

The linkage relationship between D7S21 (MS31) and D7S22 (g3) was examined in 22 families with 57 children (Table 1). The deviation from the 0.5 ratio was significant ($p < 0.01$). The estimate of the recombination distance between the two loci was about 32 cM.

CONCLUSION

With the five VNTR systems used, a combined exclusion efficiency exceeding 99.9% was found. Because of the chance of mutations exclusion of paternity should not be based on mismatch in only one system.

REFERENCES

Morling N, Hansen HE (1992) Matching criteria for paternity testing with VNTR systems. Advances in Forensic Hemogenetics 4, Springer-Verlag, Berlin Heidelberg, (this issue)

Wong Z, Wilson V, Patel I, Povey S, Jeffreys AJ (1987) Characterization of a Panel of highly variable minisattelites cloned from human DNA. Ann Hum Genet 51:269-88

Wyman AR, White R (1980) A highly polymorphic locus in human DNA. Proc Natl Acad Sci USA 77:6754-6758