

# Quality control of paternity investigations in Scandinavia.

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Paternity investigations in Denmark, Norway and Sweden are performed at the Institute of Forensic Medicine in Oslo, the Institute of Forensic Genetics in Copenhagen, and the State Institute of Forensic Serology in Linköping. These three institutes have a joint program to increase the collaboration and to give support in quality improvement. This program is referred to as the Scandinavian Quality Program for Paternity Testing.

The basic concept for the program is that one fictitious paternity case from each of the three institutes should be shipped to and analysed in all three participating laboratories. This should be repeated four times a year. The samples should be analysed according to the local procedures and with the marker systems ordinarily used.

The results are distributed to the participating laboratories. The conclusions and the results of each system are compared and both the intra and the inter laboratory variations are to be focused upon. The results will be the basis for a further discussion to improve the quality of the tests.

## Material and Methods

Samples from six fictitious cases, two from each institute, have been analysed. One case included two putative fathers. The results from this case have been reported as two separate cases thus giving a total of seven cases.

Blood was taken in vacutainer tubes containing EDTA. A set of samples from each case was sent to the laboratories. The samples were included in the routine procedures at each laboratory. The analysis include the systems given in table 1.

Table 1. Marker systems used in routine and extended paternity testing

Laboratories	DNA-systems	Other systems
Denmark	D2S44, D5S43, D7S21, D7S22, D12S11	AB0, Rh, MNSs, HP, GC, PGM <sup>1</sup> , ACP <sup>1</sup> , GPT, ESD, GLO
Norway	D2S44, D7S21, D7S22, D12S11, D14S13	
Sweden	D2S44, D12S11, D14S13	AB0, Rh, MNSs, HP, GC, PI, PGM <sup>1</sup> , ACP <sup>1</sup> , ESD, GLO, F13B

The methods for DNA-typing have been reported elsewhere. The technical procedure is mainly the same in all three laboratories. Different size markers are however used: in Denmark and Sweden Amersham S 5000 and in Norway Gibco/BRL 4401SA. Size estimation is done with different image processing systems. In Denmark and Sweden band matching is obtained by using an interval of tolerance (sliding window) and in Norway by visual comparison.

## Results

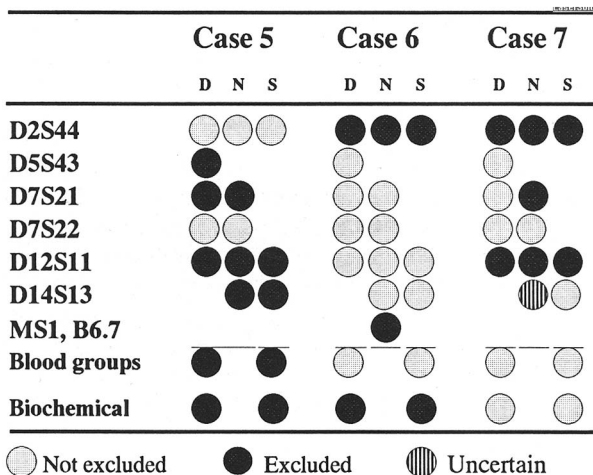
Concordant conclusions were obtained in all cases as shown in table 2. In four cases no exclusions were found. In the conclusions from Denmark and Sweden this was indicated as "No Exclusion". The paternity likelihoods calculated in these cases were greater than 0.9999. These cases were signed with "Paternity Confirmed" in Norway. This conclusion was drawn when no exclusion was found in the five DNA-systems used.

Table 2. The conclusions in the seven cases.

Cases	Denmark	Norway	Sweden
#1	No Exclusion	Paternity Confirmed	No Exclusion
#2	No Exclusion	Paternity Confirmed	No Exclusion
#3	No Exclusion	Paternity Confirmed	No Exclusion
#4	No Exclusion	Paternity Confirmed	No Exclusion
#5	Excluded	Excluded	Excluded
#6	Excluded	Excluded	Excluded
#7	Excluded	Excluded	Excluded

In cases 5, 6 and 7 the putative father was excluded. The exclusions were based on the results obtained in more than one DNA- or conventional marker system.

Figure 1. Exclusions in DNA- and conventional systems.

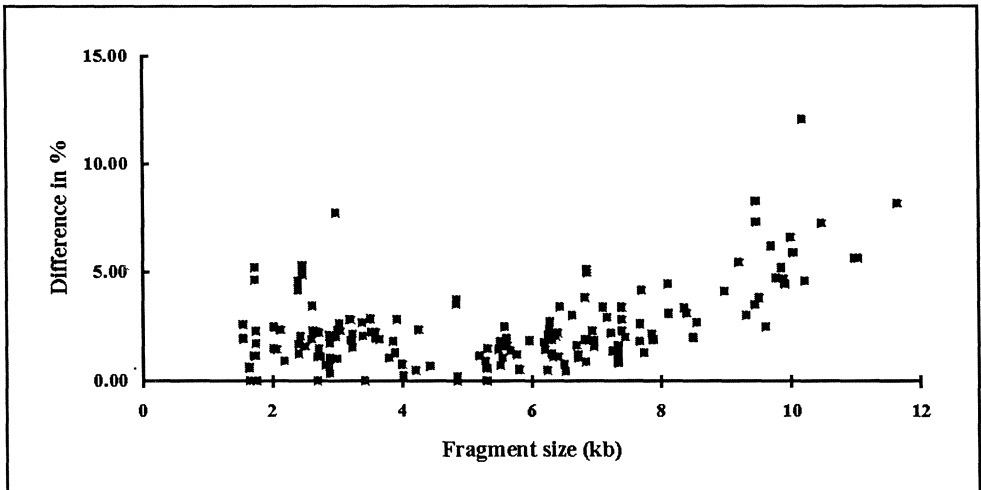


As shown in figure 1 exclusions and no exclusions were in concordance for case 5 and 6. In case 7 two differences were found for the D7S21 and D14S13 systems respectively. These discrepancies were found among a total of 16 excluding combinations.

The reports from Norway included an analysis of close relatives. In case 5, 6 and 7 the mother and the putative father had a common fragment in 4/5, 7/7 and 4/5 systems respectively, which indicates a close relationship between the persons. This was also the case; as for example in case 7 in which the mother and the "putative father" were two sisters.

The differences in fragment size estimation, as shown in figure 2, were below 5 % for most of the fragments up to 10 kb. In 56 out of 80 comparisons the lowest estimated fragment sizes were reported by Norway. This difference in size estimation could be explained by the different size markers used.

Figure 2. Differences in fragment size estimation



### Conclusion

Even with differences in the estimated fragment size and the matching criteria used the final conclusions in each paternity case are in concordance. That is the most important result. However, the discrepancies found in one of the cases indicates that there might be a possibility to increase the sensitivity in the exclusions with a more narrow tolerance interval. This has to be done with great care not to introduce false exclusions. A question that has arisen during this work is also whether a more significant conclusion could be drawn from paternity investigations when no exclusion is found. When is paternity confirmed?