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A report of the 1997, 1998 and 1999 Paternity Testing Workshops of the English Speaking Working Group of the International Society for Forensic Genetics

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Abstract

We present the results of the 1997, 1998 and 1999 Paternity Testing Workshops of the English Speaking Working Group of the International Society for Forensic Genetics. The numbers of participating laboratories were 24 (1997), 31 (1998) and 32 (1999). In 1997, all laboratories drew the correct conclusion that the alleged father was the biological father of the child. In 1998, the alleged father was the biological brother of the child and all laboratories excluded him. The scenario in 1999 was a deficiency case consisting of mother, child and the parents of the alleged father and all but one laboratory drew the correct conclusion.

The percentage of laboratories routinely performing variable number of tandem repeat (VNTR) investigations using single locus probes (SLPs) and restriction fragment length polymorphism (RFLP) decreased from 83% in 1997 to 66% in 1999. In the three workshops, more than 90% of the laboratories used polymerase chain reaction (PCR) based systems. In 1999, 80% of the laboratories performing PCR, used commercially available short tandem repeat (STR) kits. Other commonly used systems were HLA and PolyMarker investigated with PCR. Conventional systems and RFLP investigations of VNTRs with multi loci probes (MLPs) were used routinely by approximately 20% of the participating laboratories.

All laboratories submitting results in the three workshops used RFLP-based VNTRs or/and PCR based VNTRs/STRs. Inter-laboratory comparisons of the results showed a very high concordance. The overall coefficients of variation between the laboratories of the results of RFLP typing of the commonly used VNTRs D2S44, D7S21, D7S22 and D12S11 were 1.2–1.3%. Consistent results were obtained in the great majority of the systems investigated by PCR and typing errors counted for less than 0.3% of the PCR based results.

Keywords: Paternity testing; DNA profiling; Collaborative exercise; STR; VNTR; Single locus probes; PCR; RFLP

1. Introduction

Since 1991, the English Speaking Working Group (ESWG) of the International Society for Forensic Genetics (ISFG) (formerly International Society for Forensic Haemogenetics (ISFH)) has, once a year, offered an exercise involving genetic analysis in a paternity case [1,2]. The exercises enable the participating laboratories to compare their typing results, laboratory protocols and strategies with those of other laboratories. Today, the participation in such comparative exercises is an essential part of the quality programme in many laboratories.

During the last 10 years, the DNA Commission of the ISFG has worked toward standardisation of

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nomenclature and methods for investigation of DNA profiling systems investigated by restriction fragment length polymorphism (RFLP) [3] and polymerase chain reaction (PCR) [4–6].

The weight of evidence in favour of paternity varied between the laboratories primarily depending on the number of genetic systems investigated. In previous paternity testing workshops of the ESWG, the reported weight of the evidence for a non-excluded man varied from paternity indices (PI) of 100 to more than 1,000,000 corresponding to *W*-values of 99% to more than 99.9999% [2].

Here, we present the answers to questionnaires concerning laboratory protocols and the results obtained by the laboratories participating in the 1997, 1998 and 1999 paternity testing workshops of the ESWG.

2. Materials and methods

Blood samples (1997 and 1998) or DNA samples (1999) and questionnaires were sent to the participating laboratories listed in the Appendix A. The numbers of participating laboratories were 24 (1997), 31 (1998) and 32 (1999). The laboratories were asked to perform paternity testing according to their usual strategies and methods. In 1998, the laboratories were encouraged also to treat the case as an immigration case. In total, typing results have been reported from 18 variable number of tandem repeat (VNTR) loci investigated with RFLP and single locus probe (SLP) technique and three multi locus probes (MLPs). Typing results of 52 VNTRs and short tandem repeats (STRs) investigated by PCR and of 28 conventional systems were reported. The collated results were presented and discussed by the members of the ESWG at meetings held in 1997 (Oslo, Norway), in 1998 (Heathrow, UK) and in 1999 (San Francisco, USA).

3. Results

3.1. Methods used for genetic investigations

Table 1 shows methods available in the participating laboratories. The most frequently used methods were PCR and RFLP. The use of RFLP investigated with SLPs and HLA serology decreased from 1998 to 1999 whereas the use of other available methods was fairly constant. However, most laboratories would not use all methods in a normal case. Table 2 shows methods used in all cases, methods used additionally if necessary, and methods available for very special cases. The percentage of laboratories that used PCR in all cases increased from 33% in 1997 to 80% in 1999. The percentage of laboratories that used HLA serology decreased from 8 to 3% and the use of SLPs decreased from 75 to 45%. Methods used additionally when necessary was fairly constant although VNTRs investigated with RFLP and MLPs as well as systems like Y-STR and mt-DNA-polymorphism were used increasingly.

3.2. RFLP typing

Typing results of VNTR systems investigated by RFLP were reported by 21 laboratories in the

Table 1
Methods available for genetic investigations in paternity testing

Methods	1997 ($N = 24$) (%)	1998 ($N = 30$)[a] (%)	1999 ($N = 32$) (%)
PCR based analysis	92	97	94
VNTR/STR systems (PCR)	92	97	94
SLP systems	83	87	66
HLA systems (PCR)	46	37	34
PolyMarker (PCR)	29	27	28
MLP systems	17	17	22
Conventional systems	21	20	19
Other (mt-DNA, Y-STR etc.)	8	10	19
HLA serology	13	13	6

[a] In 1998, 31 laboratories participated. However, one laboratory did not offer paternity testing at that time.

Table 2
Methods used always, additional if necessary, and available for special cases

Methods	1997 ($N = 24$)	1998 ($N = 30$)[a]	1999 ($N = 32$)
Always (%)			
PCR-VNTR/STR	33	53	80
SLP	75	67	45
Conventional	21	20	19
MLP	13	7	13
HLA (PCR)	0	7	6
HLA serology	8	3	3
PolyMarker (PCR)	4	3	3
Other (mt-DNA, Y-STR, etc.)	0	0	0
Additional (%)			
PCR-VNTR/STR	71	73	74
SLP	58	63	55
HLA (PCR)	33	30	26
PolyMarker (PCR)	25	27	23
Conventional	13	7	13
MLP	0	10	10
Other (mt-DNA, Y-STR, etc.)	0	3	6
HLA serology	4	7	3
Available (%)			
PCR-VNTR/STR	33	20	19
Other (mt-DNA, Y-STR, etc.)	8	13	16
SLP	8	3	13
HLA (PCR)	13	7	10
Conventional	0	7	10
MLP	4	3	6
HLA serology	0	3	3
PolyMarker (PCR)	0	0	3

[a] In 1998, 31 laboratories participated. However, one laboratory did not offer paternity testing at that time.

workshops in 1997 and 1998 and by 15 laboratories in 1999.

Table 3 shows the most frequently used VNTR systems in routine testing. A total of 17 systems were used routinely by the participating laboratories. D2S44, D12S11 and D7S21 were used by more than 75% of the laboratories.

Almost all the laboratories used the restriction enzyme *Hin*fI whereas the enzymes *Taq*I, *Alu*I or *Hae*III were used by only three laboratories (in 1997, 1998) or four (in 1999).

The MLPs GTG5, 33.6, 33.15 and MZ1.3 were used routinely in four laboratories.

Table 4 shows a summary of methods used for RFLP typing. More than half of the laboratories used non-organic methods for DNA purification. Non-radioactive labelling was used by approximately 75% of the laboratories.

From 1997 to 1999 there was a slight decrease in the number of laboratories using the NICE DNA analysis ladder from Gibco-BRL as reference for estimation of the molecular weight. This decrease was matched by an increasing number of laboratories using the MW100 ladder. More than half of the laboratories used DNA from the commercially available cell line K562 as positive control. However, the numbers of laboratories that used in house controls — either alone or in addition to K562 — increased.

For sizing of DNA fragments, scanners have replaced the video cameras (Table 5). For evaluation of a match, almost half of the laboratories used a fixed match criterion. The numbers of laboratories that used visual match of DNA fragments on the same gel has increased. An increasing number of laboratories used

Table 3
The most frequently used VNTR systems for RFLP typing with SLPs in paternity cases

VNTR-systems	Probe	1997 ($N = 21$) (%)	1998 ($N = 26$) (%)	1999 ($N = 21$) (%)
D2S44	YNH24	86	81	86
D12S11	MS43a	81	77	86
D7S21	MS31	76	77	86
D16S309	MS205	71	65	71
D7S22	g3	62	50	57
D5S110	MS621	52	54	62
D1S7	MS1	43	31	33
D5S43	MS8	33	38	29
D4S139	pH30	10	23	29

Table 4
Methods used for purification of DNA, labelling of probes, ladder and controls for RFLP typing

	1997 ($N = 21$) (%)	1998 ($N = 26$) (%)	1999 ($N = 21$) (%)
DNA purification			
Non-organic	48	50	52
Organic	48	46	48
No information	5	4	0
Labelling of probes			
Non-radioactive	76	77	81
Radioactive	10	12	14
Non-radioactive and radioactive	14	8	5
No information	0	4	0
Ladder			
NICE DNA analysis ladder (BRL)	62	73	43
NICE + MW100 probe	14	0	10
MW100	10	15	24
Other	10	12	19
None	5	0	5
Positive control			
K562 only	67	58	38
In house only	14	31	29
K562 and in house	5	8	14
Other	10	4	5
None/no information	5	0	14

Table 5
Methods used for measurements of the sizes of RFLP fragments, match criteria, and frequency windows

	1997 ($N = 21$) (%)	1998 ($N = 26$) (%)	1999 ($N = 21$) (%)
Method of sizing			
Video-camera	67	54	43
Digitizer	19	19	24
Scanner	0	4	19
Manual	10	19	10
Video-camera and scanner	0	4	0
None/no information	5	0	5
Match criteria — same gel			
Fixed	48	46	48
Visual	29	35	43
Fixed and visual	14	15	5
Not applied/no information	10	4	5
Match criteria — different gels			
Fixed	33	54	52
Visual	10	8	10
Fixed and visual	0	0	0
Not applied/no information	57	38	38
Frequency window			
Match criterion = window size	29	42	43
Match criterion < window size	14	4	5
Not comparable	48	38	33
Not applied/no information	10	16	19

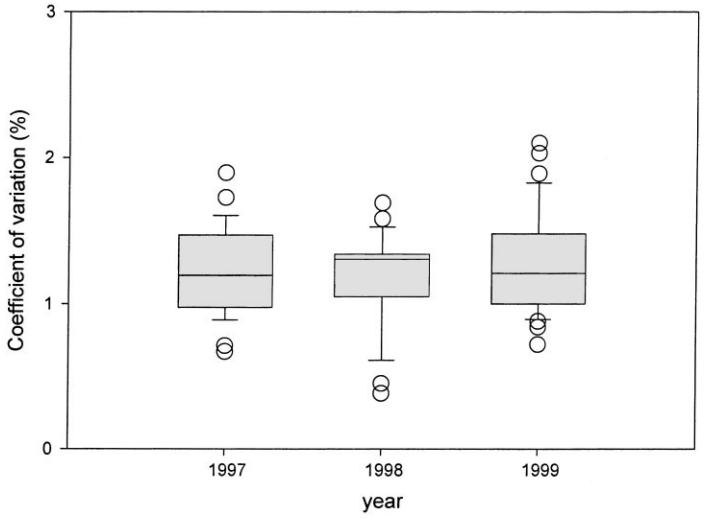

Fig. 1. The overall coefficients of variation of the measurements of the lengths of DNA fragments of the VNTR systems D2S44, D7S21, D7S22 and D12S11.

a match criterion that equals the window size for frequency calculations.

3.3. Inter-laboratory comparisons of results of RFLP-typing with SLPs

Fig. 1 shows the coefficients of variation of the DNA fragment lengths obtained by RFLP typing of four of the most frequently used VNTR systems: D2S44; D7S21; D7S22; and D12S11. The coefficients of variation were very similar during the 3 years, 1.20% in 1997, 1.18% in 1998 and 1.28% in 1999.

3.4. Typing by PCR

Typing results of systems investigated with PCR were submitted by 22 laboratories in 1997, by 25 laboratories in 1998 and by 28 laboratories in 1999. The overall number of systems reported increased from 35 in 1997 to 52 in 1999.

In 1999, 24 laboratories routinely used commercially available STR kits. In Table 6, the most frequently used systems in 1999 are compared with the systems used in 1997 and 1998. HumTH01 and HumvWA31/A were the two most popular systems. HumFES was the third most frequently used system in 1997, but in 1999, the use of HumFES was exceeded by 12 other STR systems (data not shown).

Table 7 shows the methods used for PCR. The percentage of laboratories using non-organic methods for DNA purification increased from 50% in 1997 to 73% in 1999. In 1999, approximately half of the laboratories measured the DNA amount before performing PCR.

The percentage of laboratories using DNA sequencers for gel electrophoresis increased from 64% in 1997 to 83% in 1999. Among those who used DNA sequencers, the percentage of laboratories using an allelic ladder as reference increased from 29% in 1997 to 72% in 1999 (Table 8).

Table 6
The most frequently used DNA systems for PCR based typing in paternity cases in 1999 compared with results of 1997 and 1998

Systems[a]	1997 ($N = 22$) (%)	1998 ($N = 29$) (%)	1999 ($N = 30$) (%)
HumTH01	91	90	93
HumVWA31A	82	86	93
HumCSF1PO	14	66	73
D18S51	32	41	70
D21S11	32	45	70
TPOX	9	59	70
D13S317	0	31	67
HumFibra/FGA	50	59	67
D5S818	0	31	63
D7S820	0	31	63

[a] All systems are STRs.

Table 7
DNA purification, quantitation and electrophoresis for PCR analysis

	1997 ($N = 22$) (%)	1998 ($N = 29$) (%)	1999 ($N = 30$) (%)
DNA purification			
Non-organic	50	66	73
Organic	41	34	27
No information	9	0	0
DNA quantitation			
Spectrophotometry	27	34	30
Blotting	23	24	20
Electrophoresis	9	7	3
Different techniques	–	10	3
Not measured	27	21	43
No information	14	3	0
Electrophoresis			
Manual	68	48	33
DNA sequencer	64	76	83

3.5. Inter-laboratory comparisons of results of PCR typing

An increasing number of laboratories use the number of repeat units as allele nomenclature in PCR based typing (Table 9), and consistent nomenclature was submitted by the laboratories in the majority of the PCR based systems. Inconsistent nomenclature was submitted in the following systems: D18S51 (1997); D21S11 (1997, 1998, and 1999); ApoB (1997, 1998); TPO (1997); ACTBP2/SE33 (1998); Col2A1 (1998); D19S253 (1998, 1999).

In STR systems, rare variant alleles of intermediary length exist, and some laboratories did not distinguish between such variants and the closest alleles of full repeats. In HumTH01, the alleles 9.3 and 10 were submitted as 9.3/10 by several laboratories. In HumF13A01, the allele 3.2 was submitted as 4 or 3.2/4 by a few laboratories. Typing errors that were not caused by discrepancies in nomenclature were observed in 0.28% of the results in 1997, 0% in 1998 and 0.24% in 1999. None of the errors gave rise to wrong conclusions.

3.6. Database and statistics

Most laboratories use statistics when reporting results of paternity testing with positive evidence for paternity. Statistical calculations require knowledge about allele frequencies. During the last 3 years, the use of own data for estimating VNTR allele frequencies has become more common (Table 10)

Table 8
Ladders and markers used for analysis with DNA sequencers

Ladder	1997 ($N = 14$) (%)	1998 ($N = 22$) (%)	1999 ($N = 25$) (%)
Allelic ladder	29	55	72
GS500	7	32	36
GS350	29	32	20
CXR400	0	0	12
GS2500	14	9	0
GS400HD	0	5	8
Marker for ALF	7	5	8
Other	0	9	8
Not specified/no information	21	14	4

Table 9
Nomenclature used for PCR based typing of VNTR and STR systems

Nomenclature	1997		1998		1999	
	Manual[a] ($N = 15$) (%)	DNA sequencers[b] ($N = 14$) (%)	Manual ($N = 14$) (%)	DNA sequencers ($N = 22$) (%)	Manual ($N = 10$) (%)	DNA sequencers ($N = 25$) (%)
Repeat units	67	57	57	68	70	72
Bp	0	7	21	9	0	4
'Types'	7	7	0	0	10	0
Repeat units and bp	0	0	0	14	0	16
'Types' and bp	7	0	0	0	0	0
Repeat units and 'types'	7	0	14	0	10	4
Repeat units and bp and 'types'	0	0	0	0	10	0
Other/no information	13	29	7	9	0	4

[a] PCR products detected on manually run polyacrylamide or agarose gels.
[b] PCR products detected on polyacrylamide gels on DNA sequencers.

and in 1999, half of the laboratories used their own databases for all systems. For PCR based methods, 50% of the laboratories used only their own database, and in 1999, 30% used data only from other laboratories. Many laboratories referred to the STR databases obtained from the companies supplying the multiplex STR kits.

Table 11 shows statistics used for calculating the weight of evidence. The percentage of laboratories reporting the paternity index (PI) either alone or in addition to other statistical calculations increased from 29% in 1997 to 59% in 1999. Approximately half of the laboratories used the probability of paternity (W).

Table 12 shows statistical values reported in the workshops in 1997 and 1999. The majority of the laboratories reported values in the range of PI = 1,000 to 100,000 ($W = 99.9$ to 99.999%). In 1998, the results strongly argued against paternity.

In 1999, the laboratories were asked for their normal requirements for issuing a report with positive evidence for paternity. For laboratories using statistics, the PI-values required were equally distributed from >100 to >100,000 ($W > 99$ to >99.999%) (Table 13). Almost 20% of the laboratories used inclusions in a certain number of systems investigated as a requirement for issuing a report.

Table 10
Database sources

	1997	1998	1999
	($N = 21$) (%)	($N = 26$) (%)	($N = 21$) (%)
RFLP			
Own	33	42	52
Other	10	12	5
Own and other	24	27	19
No information/not applied	33	19	24
	($N = 22$) (%)	($N = 29$) (%)	($N = 30$) (%)
PCR			
Own	50	48	50
Other	14	10	30
Own and other	18	21	17
No information/not applied	18	21	3

Table 11
Statistics used in reporting results of paternity testing

Statistics	1997 ($N = 24$) (%)	1998 ($N = 31$) (%)	1999 ($N = 32$) (%)
W (Probability of paternity)	54	52	56
PI (Paternity index)	29	45	59
Probability of exclusion/exclusion chance	13	13	13
Other	13	10	16
EM value	8	13	19
No statistics	4	16	6
No information	13	13	3

Table 12
Reported values of paternity indices (PI) and *W*-values in the workshops 1997 and 1999[a]

PI-values	*W*-values	1997 ($N = 24$) (%)	1999 ($N = 32$) (%)
<100	<99%	0	3
100–1000	99–99.9%	13	13
1000–10,000	99.9–99.99%	33	22
10,000–100,000	99.99–99.999%	29	19
100,000–1,000,000	99.999–99.9999%	4	19
>1,000,000	>99.9999	13	6
No statistics/no information		8	19

[a] The a posteori probability of paternity, W_{post}, is calculated based on the a priori probability of paternity, W_{prior}, and the PI which is a true likelihood ratio. $W_{post} = PI \times W_{prior}$. By tradition, the *W*-value is calculated under the assumption that $W_{prior} = 0.5$.

3.7. Analysis of related individuals

During recent years, genetic testing has become more commonly used in immigration cases in many countries. Among the participating laboratories, 40–50% deal with such cases (data not shown). Immigration cases often involve close relatives. To further reveal how the laboratories deal with immigration cases, blood or DNA samples from related individuals were sent out in 1998 and 1999. In 1998, the sample of the alleged father was drawn from the biological brother of the child. All laboratories excluded the alleged father as the biological father of the child. Of 31 laboratories, 16 considered other relationships. Twelve of the laboratories submitted what they considered the most likely hypothesis, and seven laboratories correctly suggested that the alleged father was the biological brother of the child.

Table 13
Requirements for issuing a report with positive weight for paternity

PI-values	*W*-values	1999 ($N = 32$)	
		N	%
100–1000	99–99.9%	7	22
1000–10,000	99.9–99.99%	7	22
10,000–100,000	99.99–99.999%	6	19
>100,000	>99.999%	1	3
Inclusion by a certain number of systems		6	19
No requirement/other		5	16

In 1999, the alleged father was not presented for testing but samples from the biological parents of the alleged father were analysed. Among the most commonly used RFLP based systems (listed in Table 3), the grandfather could not be excluded as biological father of the child in eight of nine systems. Among the most commonly used PCR based systems (listed in Table 6), the grandfather could not be excluded as biological father of the child in 9 of 10 systems. These results clearly show how difficult it can be to distinguish between close relatives and how important it is to use a sufficient number of genetic systems when investigating cases with close relatives.

3.8. Accreditation

Today, the focus on the quality of genetic investigations in paternity testing is high and the number of laboratories accredited is increasing. In 1998, 19% of the laboratories were either accredited or certified and the percentage increased to 34% in 1999 (data not shown). In 1999, 13% of the participating laboratories were accredited by the EU standard EN 45001, 3% by the ISO 9002 standard and 3% had obtained both the EN 45001 and ISO 9002. A government accreditation appointment was obtained by 9% of the laboratories while 6% were certified by a national scientific organisation.

Among those who had not obtained accreditation/certification in 1999, 13% were in the process of obtaining accreditation/certification and 41% were planning to become accredited/certified.

4. Discussion

The most frequently used methods for genetic investigations in paternity testing were PCR and RFLP. While the percentage of laboratories using VNTR typing with SLPs and RFLP in all cases has decreased from 75 to 45%, the use of VNTR/STR typing with PCR has in the same period increased from 33 to 80%.

During the last three years, there have been only minor changes in the methods used for RFLP typing. More than half of the laboratories still use the K562 cell line as a positive control, but the number of laboratories using in house controls — either alone or in addition to K562 — has increased. Equipment for sizing of DNA fragments is changing and X-rays are scanned in an increasing number of laboratories.

To be able to perform statistical calculations it is necessary to assign the DNA-fragment to a frequency window in a population database. As the allele frequencies deviate between ethnic groups, it is recommended to use local databases [3]. Furthermore, the size of VNTR-alleles determined by RFLP depends on the exact electrophoresis conditions, and most accurate results are obtained when using a database of results from the laboratory. In 1999, 50% of the laboratories used only their own database.

In 1995, 17% of the laboratories used a criterion for matching bands that equals the window size for assessing the frequency of the matching bands [2]. Today, almost half of the laboratories use a criterion of matching bands that equals the window size in accordance with the logical relation between (i) the called match and (ii) a possible match with a random man.

Compared to the RFLP-based methods, there have been greater developments of methods and protocols for PCR. The use of harmless, non-organic methods for purification of DNA used for PCR has greatly increased since 1997. The PCR procedures appear to have become more robust and, in 1999, almost half of the laboratories did not find it necessary to measure the DNA concentration before performing PCR. In 1999, 80% of the laboratories performing PCR used commercial STR kits. Many of these kits require that the PCR products are detected on DNA sequencers and the numbers of laboratories using such equipment has increased. In 1999, 83% of the laboratories detected the STR/VNTR fragments on a DNA sequencer and, of these, 88% used a DNA sequencer from PE Biosystems (data not shown). Among the laboratories using a DNA sequencer, only 72% used an allelic ladder as a reference in spite of the fact that the use of sequenced allelic ladders is recommended by the DNA Commission of the ISFG [5–7], and sequenced allelic ladders are often supplied with the commercial kits.

There has been an increase in the use of the nomenclature of STRs based on repeat units. This nomenclature is recommended by the DNA Commission of the ISFG [6,7] and it is, in general, used by the companies supplying allelic ladders with the kits. The increasing uniformity in the nomenclature of VNTRs/STRs investigated by PCR is reflected by the fact that, in 1997, inconsistent nomenclature was reported in four out of 35 PCR based systems while this number decreased to only two out of 52 systems in 1999, D21S11 and D19S253. Two common ways of designating D21S11 alleles have been suggested [8,9] and in 1999, the repeat based nomenclature recommended by ISFG [6,7] was used by 93% of the laboratories submitting D21S11 data.

While methods and nomenclature have reached a high degree of standardisation, the requirements for issuing a report with positive evidence for paternity vary between laboratories. The two most frequently

used statistics for expressing the weight of evidence is the probability of paternity (W) and the paternity index (PI). While the use of W was constant during the last three years, the use of PI increased greatly. One third of the participating laboratories did not require a certain statistical weight of evidence before issuing a report concerning a non-excluded man. Among the laboratories that required a certain statistical weight of evidence, the required paternity index varied from >100 to >100,000 ($W > 99\%$ to >99.999%).

In conclusion, the overall quality of the investigations including the new PCR based methods in the 1997, 1998 and 1999 Paternity Testing Workshops was high and only very few discrepancies were observed. Most of the discrepancies observed by PCR technique were caused by the use of different nomenclatures while typing errors counted for less than 0.3% of the PCR based results. Furthermore, as an increasing number of laboratories use commercial kits for STR typing, a more concordant nomenclature and an even higher degree of uniformity might be expected in the future.

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Appendix A.

The participating laboratories are given below.

Abteilung für Laboratoriumsmedizin, Berlin (1998, 1999)
Antwerp Blood Transfusion Centre, Edegem (1997, 1998, 1999)
Artz für Laboratoriumsmedizin, Heidelberg (1997, 1998, 1999)
Cellmark Diagnostics-Zeneca, Abingdon (1997, 1998, 1999)
Department of Forensic Genetics, Copenhagen (1997, 1998, 1999)
Department of Haematology, St. Bartholomew's and The Royal London School of Medicine and Dentistry, London (1997, 1998, 1999)
Department of Forensic Medicine, Warsaw (1998, 1999)
Department of Immunogenetics, CLB, Amsterdam (1997, 1998, 1999)
Department of Molecular Biology, Bratislava (1997, 1998, 1999)
Etablissement de Transfusion Sanguine, Lille (1997, 1998)
Forensic Biology Department, Lisbon (1999)
Forensic Science Laboratory, Edinburgh (1998, 1999)
Forensic Science Service, Wetherby (1997, 1998, 1999)
Genedia GmbH, München (1998, 1999)
Institut de Médicine Légale, Strasbourg (1997, 1998, 1999)
Institute of Forensic Genetics, Linköping (1997, 1998, 1999)
Institute of Forensic Medicine, Oslo (1997, 1998, 1999)
Institute of Haematology and Blood Transfusion, Prague (1997, 1998, 1999)
Institut für Blutgruppenforschung, Köln & Düsseldorf (1997, 1998, 1999)
Institut für Blutgruppenserologie und Genetik, Hamburg (1998, 1999)
Institut für Rechtsmedizin, Mainz (1997, 1998, 1999)
Institut für Rechtsmedizin, St. Gallen (1997, 1998, 1999)
Institut für Rechtsmedizin, Zürich (1997, 1998, 1999)
Institut national de Transfusion Sanguine, Paris (1997, 1998, 1999)
Institut Universitaire de Médecine Legale, Genève (1997, 1998, 1999)
Institut Universitaire de Médecine Légale, Lausanne (1997, 1998, 1999)
Laboratoire IDNA, Brussels (1998, 1999)
Laboratory for Tissue Immunology, Cape Town (1998, 1999)
Medical University, Lublin (1999)
Medical Academy of Wroclaw, Wroclaw (1998, 1999)
National Institute of Forensic Science, Brussels (1997, 1998, 1999)
National Public Health Institute, Helsinki (1997, 1998, 1999)
Police Forensic Science Laboratory, Dundee (1997)
University Diagnostics Limited, London (1997, 1998, 1999)

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