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A report of the 2000 and 2001 Paternity Testing Workshops of the English Speaking Working Group of the International Society for Forensic Genetics

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Abstract

During the last 10 years, the English Speaking Working Group (ESWG) of the International Society for Forensic Genetics (ISFG) has once a year arranged a Paternity Testing Workshop in which blood samples as well as a questionnaire concerning laboratory strategies were distributed to the participating laboratories. In 2000 and 2001, paper challenges were included in the workshops. Here, we present the results of the 2000 and 2001 Paternity Testing Workshops. The numbers of participating laboratories were 33 (2000) and 36 (2001). A total of 36% (2000) and 31% (2001) of the laboratories submitted typing results of variable number of tandem repeats (VNTRs) investigated with restriction fragment length polymorphism (RFLP) and single locus probes (SLPs). A total of 91% (2000) and 86% (2001) submitted typing results of polymerase chain reaction (PCR) based systems. Typing errors occurred in 0.3% of the submitted PCR-based results in 2000 and in 0.1% in 2001. The results of the paper challenges showed a high degree of variation in the formulas used for calculation of the weight of evidence of rare events such as inconsistencies or possible silent alleles. The majority of the laboratories used the same formulas for calculations of frequently occurring events. © 2002 Published by Elsevier Science Ireland Ltd.

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

1. Introduction

The English Speaking Working Group (ESWG) of the International Society for Forensic Genetics (ISFG) offers once a year a Paternity Testing Workshop involving genetic analysis in a paternity case [1–3]. The purpose of the exercise is to compare typing results as well as laboratory strategies among the participating laboratories. As the laboratories do the analyses and statistical calculations using there own methods and frequency data, it is not possible to compare statistical calculations. In order to investigate how the laboratories do statistics, a paper challenge has been included in the Paternity Testing Workshop since the year 2000. The paper challenges were designed to include both routine combinations and rare events such as inconsistencies, possible silent alleles and rare alleles.

When performing paternity testing, there is a need for obtaining knowledge about mutation rates for the systems used. As the information obtained in each laboratory is often limited, the laboratories were encouraged to provide information about inconsistencies observed in their own laboratory.

Here, we present the results of the Paternity Testing Workshops 2000 and 2001 including evaluation of laboratory strategies and typing results. Also presented are the results of the paper challenges and the calculated mutation rates based on the information given by the participating laboratories.

2. Materials and methods

Blood samples were sent to the participating laboratories together with a questionnaire and a paper challenge. The

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numbers of participating laboratories were 33 (2000) and 36 (2001). A list of participating laboratories is shown in Appendix A.

In 2000, the blood samples were drawn from three children and their biological mother. The issue in question was whether child 3 was child of the same non-investigated man as children 1 and 2.

In 2001, the blood samples were drawn from two children and an alleged father. The children were known to be children of the same non-investigated mother and the issue in question was whether the children were children of the alleged father.

Laboratories that do immigration cases were encouraged to treat the cases as they would do in immigration cases in addition to the paternity cases.

The collated results were presented and discussed by the members of the ESWG at meetings held in 2000 (Söderköping, Sweden) and in 2001 (Münster, Germany).

3. Results

3.1. Methods used for genetic investigations

Table 1 shows methods available for genetic investigations in the participating laboratories. A total of 94% of the laboratories used polymerase chain reaction (PCR) based systems for paternity testing. The numbers of laboratories offering typing of variable number of tandem repeats (VNTRs) with restriction fragment length polymorphism (RFLP) and single locus probes (SLPs) decreased from 2000 to 2001. In 2001, less than 50% of the laboratories had SLPs available for paternity testing. The percentage of laboratories using conventional systems decreased from 18% in 2000 to 11% in 2001. There was an increase in the number of laboratories having mitochondrial DNA (mtDNA) and/or Y-chromosomal short tandem repeats (Y-STRs) available for typing. In 2001, these systems were available in a larger number of laboratories (44%) than the SLPs (42%).

Table 2 shows methods used in all cases, methods used in addition when necessary and methods available for use in very special cases. Only 3% (2000) or 0% (2001) of the laboratories used mtDNA and/or Y-STRs for typing in all cases whereas 12% (2000) to 14% (2001) used these systems additionally when necessary, and 24% (2000) to 33% (2001) had mtDNA and/or Y-STRs available for very special cases.

Table 1
Methods available for genetic investigations in paternity testing

Methods	2000 ($N = 33$) (%)	2001 ($N = 36$) (%)
VNTR/STR systems (PCR)	94	94
mtDNA, Y-STR	39	44
SLP systems	58	42
HLA systems	33	25
MLP systems	15	14
PolyMarker (PCR)	18	11
Conventional systems	18	11

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

Methods	2000 ($N = 33$)	2001 ($N = 36$)
Always (%)		
STR (PCR)	76	86
SLP	33	22
Conventional	15	11
VNTR (PCR)	6	6
MLP	6	6
HLA	3	6
PolyMarker (PCR)	0	3
mtDNA, Y-STR	3	0
Additional (%)		
STR (PCR)	76	78
SLP	45	36
HLA	24	14
mtDNA, Y-STR	12	14
VNTR (PCR)	6	8
MLP	6	8
Conventional	6	3
PolyMarker (PCR)	12	0
Available (%)		
mtDNA, Y-STR	24	33
STR (PCR)	15	14
HLA	18	11
PolyMarker (PCR)	6	8
SLP	9	6
Conventional	6	3
MLP	6	3
VNTR (PCR)	6	3

3.2. Inter-laboratory comparisons of RFLP typing with SLPs

Typing results of systems investigated with RFLP were submitted by 12 laboratories in 2000 and by 11 laboratories in 2001. Typing results from 14 SLPs were reported in 2000 and of these, results from nine systems were reported by more than one laboratory. In 2001, typing results from 10 SLPs were reported and of these, results from nine systems were reported by more than one laboratory. In 2001, all laboratories used *Hin*fI as a restriction enzyme. Table 3 shows the most commonly used systems in 2000 and 2001. The mean coefficient of inter-laboratory variation of DNA-fragment sizes of the VNTR systems D2S44, D7S21, D7S22 and D12S11 was 1.03% in 2000 and 1.38% in 2001.

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

VNTR systems	Probe	2000 ($N = 19$) (%)	2001 ($N = 15$) (%)
D2S44	YNH24	89	93
D12S11	MS43a	84	93
D7S21	MS31	84	87
D5S110	MS621	68	80
D7S22	g3	53	73
D16S309	MS205	68	53
D1S7	MS1	37	47
D5S43	MS8	37	47
D4S139	pH30	26	33

Table 4
Frequently used STR-kits for PCR-based typing in paternity testing in 2000 and 2001

Kits	2000 ($N = 27$[a]) (%)	2001 ($N = 31$[a]) (%)
SGM Plus (Applied Biosystems)	56	68
Profiler Plus (Applied Biosystems)	59	48
PowerPlex 16 (Promega)	–	45
Profiler (Applied Biosystems)	30	19
FFFL (Promega)	22	19
Cofiler (Applied Biosystems)	22	13
Polymarker (Applied Biosystems)	19	13

[a] Number of laboratories using commercially available STR-kits for DNA-typing.

3.3. PCR typing

In 2000, a total of 31 participating laboratories performed STR analysis. Of these, 27 laboratories used commercially available kits. In 2001, a total of 34 participating laboratories performed STR analysis and of these, 31 laboratories used commercially available kits. Table 4 shows the most commonly used kits for STR analysis. The use of allelic ladders for assigning the alleles increased from 74% in 2000 to 94% in 2001 (data not shown). Repeat units as nomenclature for the alleles was used, either alone or in combination with other kinds of nomenclature, by approximately 80–90% of the laboratories (Table 5). Among the PCR-based typing results submitted in the paternity testing exercises in 2000 and 2001, inconsistent nomenclature was only reported in the two systems DYS389 and D19S253.

3.4. Inter-laboratory comparisons of results of PCR typing

Typing results from a total of 64 (2000) and 58 (2001) PCR-based systems were submitted in the paternity testing exercises. Results from 43 (2000) and from 36 (2001) systems were reported by more than one laboratory.

Inter-laboratory comparisons of the results showed typing errors that was not caused by inconsistent nomenclature or by reporting errors with frequencies of 0.3% in 2000 and 0.1% in 2001. In 2000, no reporting errors were observed. In 2001, reporting errors counted for 0.1% of the submitted results.

3.5. Mutation rates

The participating laboratories were encouraged to submit information about genetic inconsistencies observed in their own laboratory (Tables 6 and 7). In general, the paternal mutation rates were higher than the maternal mutation rates and the overall mutation rates were higher for the VNTR systems than for the STR systems. For the VNTR systems, paternal mutation rates higher than 1% were seen in the systems D1S7, D4S139 and D7S21. For all STR systems, the mutation rates were below 0.5%.

3.6. Conclusions of the Paternity Testing Workshop and statistics used in general

In 2000, 94% of the laboratories correctly concluded that the biological father of children 1 and 2 was excluded from

Table 5
Nomenclature used for PCR-based systems

Nomenclature	2000		2001	
	Manual electrophoresis ($N = 9$) (%)	DNA sequencer ($N = 27$) (%)	Manual electrophoresis ($N = 9$) (%)	DNA sequencer ($N = 33$) (%)
Repeat units	67	78	56	73
Bp	0	4	0	6
'Types'	11	0	11	6
Repeat units and 'types'	0	4	0	3
Repeat units and bp	11	11	11	3
Repeat units and bp and 'types'	11	0	11	0
No information	0	4	11	9
Sum	100	101	100	100

Table 6
Mutation rates for VNTR systems

VNTR system	Probe	Paternal			Maternal		
		Meioses N	Mutation rate (%)	No. of labs	Meioses N	Mutation rate (%)	No. of labs
D1S7	MS1	1157	4.24	4	1448	3.80	4
D1S80	–	1522	0.26	2	1507	0.13	2
D2S44	YNH24	9843	0.23	5	10319	0.17	6
D4S139	pH30	2245	1.25	3	2671	0.15	3
D5S110	MS621	1833	1.71	3	2106	0.52	3
D7S21	MS31	10704	1.47	7	11293	0.06	7
D7S22	g3	2604	0.77	4	3071	0.10	4
D12S11	MS43a	10270	0.10	6	10780	0.01	6
D16S309	MS205	2452	0.82	4	2804	0.36	4

Table 7
Mutation rates for STR systems

STR system	Paternal			Maternal			Inconsistency between woman and child or man and child (*N*)
	Meioses N	Mutation rate (%)	No. of labs	Meioses N	Mutation rate (%)	No. of labs	
Amelogenin	5753	0.05	3	5418	0.02	2	‘0’
CSF1PO	4596	0.13	4	5038	0.02	3	‘0’
D2S1338	1755	0.23	5	2295	0.09	7	‘0’
D3S1358	5762	0.21	5	6837	0.04	7	2
D5S818	5113	0.16	5	5634	0.07	4	‘0’
D7S820	5031	0.10	5	5933	0.03	6	‘0’
D8S1179	2613	0.34	5	3295	0.03	7	‘0’
D13S317	5545	0.20	6	5603	0.04	4	‘0’
D16S539	1544	0.19	3	2088	0.05	4	‘0’
D18S51	3346	0.30	5	3043	0.03	6	‘0’
D19S433	2582	0.12	4	2167	0.09	6	1
D21S11	4200	0.19	6	4029	0.15	8	1
F13A01	723	0.14	2	760	‘0’	2	‘0’
FIBRA (FGA)	6926	0.46	7	7504	0.01	7	1
Penta D	233	‘0’	2	325	‘0’	2	‘0’
Penta E	415	0.24	2	384	‘0’	2	‘0’
TH01	6242	0.02	3	7112	‘0’	5	‘0’
TPOX	4579	0.04	3	5098	‘0’	3	‘0’
vWA	17717	0.30	9	19116	0.02	10	3

paternity of child 3. A total of 3% of the laboratories concluded that the results were inconclusive and 3% did not submit a conclusion. In 2001, all laboratories correctly concluded that the alleged father could be the biological father of both investigated children.

The probability of paternity (*W*) and/or the paternity index (PI) for calculating the weight of evidence in routine paternity cases were used by 73% (2000) and 78% (2001) of the laboratories (Table 8). Only 6% (2000) and 3% (2001) did not use statistics when evaluating the results in routine paternity cases.

The requirements for issuing a report with positive weight for paternity varied among the laboratories. In general, the requirements increased from 2000 to 2001 and in 2001, 33% of the laboratories required a paternity index of 10,000 or more for issuing a report (Table 9).

4. Paper challenge

4.1. The paper challenge

As laboratories used different systems for typing as well as different frequencies in calculations, comparison of calculated PI-values in the performed paternity testing was not possible. In order to compare calculations and to compare

Table 8
Statistics used in reporting results of paternity testing

Statistics	2000 ($N = 33$) (%)	2001 ($N = 36$) (%)
W (probability of paternity)	73	78
PI (paternity index)	73	78
EM value	18	14
Probability of exclusion /exclusion chance	15	11
Other	9	3
No statistics	6	3
No information	–	3

how laboratories deal with inconsistencies, possible silent alleles as well as rare alleles, a paper challenge was included in the exercise.

In 2000, the paper challenge included a total of eight systems. In one system, a shared silent allele between the man and the child was present. In two systems, inconsistencies were present. It was not possible to decide whether the inconsistencies were between the woman and the child or between the man and the child. A total of 40% of the laboratories that calculated the paper challenge concluded that 'paternity is excluded'. A total of 50% concluded that 'results are inconclusive' and 10% concluded that 'results are in favour of paternity'.

A total of 13 laboratories submitted results of PI-values calculated for each system. Due to the inconsistencies and possible silent alleles, a total of five laboratories did not calculate a cumulative paternity index. All the remaining eight laboratories reported different cumulative PI-values.

In 2001, the paper challenge included nine systems. In one system, an inconsistency between the woman and the child was present. In two systems, the man and the child shared a rare allele and in three systems possible silent alleles were present. A total of 65% of the laboratories concluded that 'results are in favour of paternity' whereas 35% concluded that 'paternity cannot be excluded, additional testing is recommended'.

A total of 22 laboratories submitted results of PI-values calculated for each system. A total of 21 different cumulative PI-values were submitted. The main difference in the reported PI-values were caused by different calculations when possible silent alleles, inconsistencies and rare alleles were present. In the remaining systems, 82–91% of the laboratories reported consistent PI-values.

4.2. Rare alleles

In the 2001 paper challenge, information about the number of observations of the allele in the database and the total number of alleles in the database was provided. Approximately 50% of the laboratories used a minimum frequency for alleles that were in the database with zero or one observation (Table 10). For alleles that were not present in the database, 32% used a frequency of $1/N_{tot}$, where N_{tot} is the total number of alleles in the database. A total of 5% did not calculate a paternity index and a total of 9% used a frequency in which the alleles observed in the present case were added to the database.

If the allele was in the database with only one count, 45% used a frequency of $1/N_{tot}$ whereas 5% used a frequency in which the observed alleles in the present case were added to the database.

4.3. Silent alleles

In the 2000 paper challenge, one system included a possible silent allele shared between the man and the child. A total of 23% of the laboratories did not consider possible silent alleles. In the 2001 paper challenge, three systems included possible silent alleles shared between the man and the child.

Table 11 shows how frequencies of possible silent alleles were calculated. The constellations shown are from the paper challenge in 2001. The percentage of laboratories that did not consider silent alleles as possible alleles varied from 64 to 82% depending on whether silent alleles was present in the database and whether the alternative to a shared silent allele was an inconsistency or not. Among the

Table 9
Requirements for issuing a report with positive weight for paternity

PI-values	*W*-values[a]	2000 ($N = 33$) (%)	2001 ($N = 36$) (%)
100–1000	99%–99.9%	24	19
1000–10000	99.9%–99.99%	33	22
10000–100000	99.99%–99.999%	21	25
>100000	> 99.999%	3	8
Less than a certain number of inconsistencies	9	11	
No requirement/other	9	14	

[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 $W_{prior} = 0.5$.

Table 10
Frequency calculation of rare alleles in the 2001 paper challenge ($N = 22$)

Constellation			No. (x) of observed c-alleles in database	Calculation of the frequency of allele c			
Woman	Child	Man		A minimum frequency[a] (%)	$1/N_{tot}$[b] (%)	$(x + \text{act. obs.})/(N_{tot} + \text{act. obs.})$[c] (%)	x/N_{tot} (%)
ab	bc	cd	0	55	32	9	5
ab	bc	cd	1	50	45x	5	$= 1/N_{tot}$

[a] Among the 11 and 12 laboratories using a minimum frequency for calculation, a total of 10 different frequencies were used. Four of these were reported as formulas ($3/N_{tot}$, $5/N_{tot}$, $5/(2N_{tot})$ and $1 - 0.05^{1/N_{tot}}$) whereas seven were reported as a fixed frequency ranging from 0.003 to 0.015.
[b] N_{tot} is the total number of alleles in the database.
[c] act. obs. is the number of allele c observed in the present case.

Table 11
Frequency calculation and number of formulas used in constellations with silent alleles ($N = 22$)

Constellation			No. (x) of observed 0-alleles in database[a]	Calculation of the frequency of the 0-allele			No. of formulas used for calculation of PI
Woman	Child	Man		0-alleles not considered (%)	x/N_{tot}[b] (%)	Minimum frequency (%)	
ab	b	c	2	64	20	16	12
a	a	a	2	77	9	14	4
ab	a	a	0	82	9	9	5

[a] 0-alleles: silent alleles.
[b] N_{tot}: the total number of alleles in the database.

three systems containing possible silent alleles, a total of 4–12 different formulas were used for calculations.

4.4. Inconsistencies

In 2000, the paper challenge included two systems with inconsistencies. It was not possible to decide whether the inconsistency was between the woman and the child or between the man and the child. A total of 13 laboratories submitted data for these two systems. Of these, five laboratories did not calculate a paternity index. Among the eight remaining laboratories, four different formulas were used for calculations.

In 2001, a maternal inconsistency was present in a single system. Three laboratories did not calculate a paternity index for that system. Among the remaining laboratories, a total of nine different formulas were used for calculation of PI.

5. Discussion

From 1995 to 2001, the percentage of laboratories using RFLP typing with SLPs decreased from 100 to 42% ([2], Table 1). Inter-laboratory comparison of the results for the systems D2S44, D7S21, D7S22 and D12S11 showed a mean coefficient of variation of 1.03% in 2000 and of 1.38% in 2001. The slightly higher variation in 2001 seemed to be due to a higher variation among laboratories in general.

In 2001, analysis of mtDNA and/or Y-STRs was available in a larger number of laboratories than RFLP-based analysis with SLPs. As mtDNA and Y-STR testing investigate female and male transmission, respectively, these investigations are especially useful in cases with special circumstances. mtDNA and/or Y-STR typing was mainly used when additional systems had to be included in the analysis or when special circumstances were present.

In laboratories using DNA sequencers for STR analysis, allelic ladders were used only by 74% in 2000 but this percentage increased to 94% in 2001. Inclusion of sequenced allelic ladders in STR analyses improves the accuracy of allele designation [4] and has been recommended by the DNA Commission of the ISFG [5–7]. Commercial allelic ladders generally use a nomenclature based on the number of repeat units as recommended by the DNA Commission of the ISFG [6,7]. In 2000 and 2001, almost 80–90% of the laboratories performing STR analysis used a nomenclature based on repeat units.

Inconsistent nomenclature was observed in the systems DYS389 and D19S253. A new nomenclature has been recommended for the system DYS389 (http://www.ystr.charite.de) and the inconsistency here was due to the fact that some laboratories used the old nomenclature.

Reported errors were seen in 0.3% of the typing results investigated by PCR in 2000 and in 0.2% in 2001. In 2000, all errors seemed to be due to errors in typing. In 2001, 0.1% reporting errors were observed and 0.1% seemed to be due to typing errors.

As mutations are rare events, the information that each laboratory is able to collect is limited and the Paternity Testing Workshop cumulated information about mutation rates (Tables 6 and 7). Different laboratories may, however, use different criteria for the definition of a mutation in VNTR systems. The VNTR systems had in general higher mutation rates than the STR systems. Comparison of the mutation rates with those collected by the American Association of Blood Banks (AABB) (http://www.aabb.org/) showed differences mainly in the VNTR systems D1S80, D5S110, D7S21, D7S22, D16S309 and in the STR systems D3S1358, F13A01 and FGA. In the remaining systems there was a good concordance between the mutation rates observed in the AABB surveys and in the ESWG exercises.

In 1999, 55–60% used the PI or/and *W*-value when evaluating the weight of evidence [3]. This percentage has increased and today, almost 80% of the laboratories report the PI or/and the *W*-value. During the last 3 years, the requirements for issuing a report with positive weight for paternity has increased. In 1999, 21% of the laboratories required a PI-value of 10,000 or more [3]. This percentage increased to 33% in 2001 (Table 9).

To analyse how laboratories performed statistical analyses, a paper challenge was included in the workshop. The paper challenge consisted of a fictive paternity case in which constellations included inconsistencies, possible silent alleles and rare alleles.

Some laboratories did not calculate a PI-value if inconsistencies were present. Among the laboratories that did consider mutations, a large number of formulas were used for calculation.

Silent alleles have been described for several systems and occur, e.g. when the allele size is outside the range of the measurement. In PCR-based systems, silent alleles may also be caused, e.g. by mutations in a primer binding site [8].

In the paper challenges, 23–82% of the laboratories did not consider silent alleles. Among the remaining laboratories, silent alleles were treated differently and different formulas were used for calculations.

For rare alleles the frequencies used for calculations varied. Almost half of the laboratories used a fixed minimum frequency when the allele in question was absent or found only once in the database. The minimum frequency differed among the laboratories.

In conclusion, the results of the Paternity Testing Workshops 2000 and 2001 showed a high degree of concordance concerning techniques, systems and nomenclature used. Typing errors counted for only 0.1–0.3% of the PCR-based systems and inconsistent nomenclature was observed in only two systems. Also calculations of PI-values in constellations with no special events showed a high degree of uniformity. However, when rare events such as inconsistencies and possible silent alleles were present, differences in calculations were observed.

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Appendix A.

A.1. Participating laboratories

- Amtlich benannter Sachverständiger für Abstammungsgutachten, Chefarzt am Zentrallaboratorium, Berlin, Germany (2000, 2001).
- Antwerp Blood Transfusion Center, Edegem, Belgium (2000, 2001).
- Arzt für Laboratoriumsmedizin, Heidelberg, Germany (2000, 2001).
- BJ Diagnostik GmbH, Giessen, Germany (2001).
- Cellmark Diagnostics, Abingdon Business Park, Oxon, UK (2001).
- Codgene, Institut de Médecine Légale, Strasbourg, France (2000, 2001).
- Department of Forensic Genetics, Institute of Forensic Medicine, Copenhagen, Denmark (2000, 2001).
- Department of Forensic Medicine & Science, The University of Glasgow, Glasgow, UK (2001).
- Department of Forensic Medicine, Medical Academy of Lodz, Lodz, Poland (2001).
- Department of Forensic Medicine, Warsaw Medical School, Warsaw, Poland (2000, 2001).
- Department of Haematology, St. Bartholomew's and The Royal, London School of Medicine and Dentistry, London, UK (2000, 2001).
- Department of Immunogenetics, CLB, Amsterdam, The Netherlands (2000, 2001).
- Department of molecular Biology, Comenius University, Bratislava, Slovakia (2000).
- Department of Molecular Genetics, Institute of Haematology and Blood Transfusion, Praha, Czech Republic (2000, 2001).
- DNA-ID Labs, Perth, Western Australia (2001).
- Forensic Science Service, Birmingham, UK (2000, 2001).
- Genedia, Gesellschaft für Molekulargenetische Begutachtung Gmbh, München, Germany (2000).
- Genetica DNA Laboratories INC, Cincinnati, USA (2000).
- Institut für Blutgruppenforschung, Köln, Germany (2000, 2001).
- Institut für Blutgruppenserologie und Genetik, Hamburg, Germany (2000).

- Institut für Rechtsmedizin, Johannes Gutenberg Universität Mainz, Mainz, Germany (2000, 2001).
- Institut für Rechtsmedizin, Kantonsspital St. Gallen, St. Gallen, Switzerland (2000, 2001).
- Institut für Rechtsmedizin, Universität Zürich-Irchel, Zürich, Switzerland (2000, 2001).
- Institut National de Transfusion Sanguin, Paris, France (2000, 2001).
- Institut Universitaire de Médecine légale, Genève, Switzerland (2000, 2001).
- Institute of Forensic Medicine, Budapest, Hungary (2001).
- Instituto de Medicina Legal de Lisboa, Faculdade de Medicina de Lisboa Gabinete de Medicina Legal, Lisboa, Portugal (2000, 2001).
- Laboratoire d'hémogénétique, Institut universitaire de Médecine légale, Lausanne, Switzerland (2000, 2001).
- Laboratoire d'Identification Génétique, INCC/NICC, National Institute of Forensic Science, Bruxelles, Belgium (2000, 2001).
- Laboratoire IDNA, Brussels, Belgium (2000, 2001).
- Laboratory for Forensic Genetics and Molecular Archaeology, Center for Human Genetics, Leuven, Belgium (2000, 2001).
- Laboratory for Tissue Immunology, Cape Town, South Africa (2000, 2001).
- Laboratory of Molecular Genetics, National Institute of Chemical Physics and Biophysics, Tallinn, Estonia (2000, 2001).
- Laboratory of Paternity Testing, Medical Academy of Wroclaw, Wroclaw, Poland (2000, 2001).
- Medical University, Lublin, Poland (2000, 2001).
- The Netherlands Forensic Institute, The Netherlands Ministry of Justice, Rijswijk, The Netherlands (2001).
- Paternity Laboratory, Department of Human Molecular Genetics, National Public Health Institute, Helsinki, Finland (2000, 2001).
- Rättsgenetiska Instituttet, Rättsmedicinalverket, Linköping, Sweden (2000, 2001).
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