EUROPEAN DNA PROFILING GROUP (EDNAP) MEETING

Athens, Greece

25 October 2017

Host: Maria Vouropoulou

Chairman: Peter Schneider

A list of participants is attached.

Welcome

Penelope Miniati welcomed members to Athens on behalf of the Hellenic Police.
Peter Schneider forwarded greetings to all participants from Niels Morling who is unfortunately unable to attend the meeting.

Presentation of the Hellenic Police Laboratory Katerina Kondili

Katerina Kondili gave an overview on the structure and workflow of the DNA laboratory of the Hellenic police forensic science division (presentation attached).

Update on exercises

Second exercise on methylated DNA and age prediction David Ballard

David Ballard presented the results of the second collaborative EDNAP exercise on age estimation by means of measurements of methylation of selected DNA positions (presentation attached).

Exercise on mRNA typing with NGS, part 2 CordulaHaas

Cordula Haas presented the results of the second collaborative EDNAP exercise on NGS based study of discrimination between various body fluids, including the sequence analysis of coding SNPs (presentation attached).

mtDNA quantification collaborative exercise ArnoudKal

Arnoud Kal presented an update on the preparation of a new exercise on mtDNA quantification by real time PCR. An invitation to participate will be sent out after the meeting, the results will be presented at the next meeting in April 2018 (presentation attached).

Updates from other groups

Forensic science and humanitarian identification - DNA analysis and centralized DNA database PenelopeMiniati

Penelope Miniati presented the current situation of migrants entering Greece via the Aegean Sea and the problems with the identification of deceased refugees, as well as the reunification of separated families (presentation attached).

High quality DNA sequence database - STRidER Walther Parson

Walther Parson informed about the update of the website, https://strider.online. Colleagues are invited to submit population genetic data to the database. STRidER will be used as a quality control tool and data repository for population genetic studies to Forensic Science International: Genetics. The website will be ready very soon to provide instructions about the submission format and procedure (presentation attached).

EMPOP update Walther Parson

Walther Parson gave a short update about new analytical tools (SAM2) for mitochondrial DNA data alignment. The new software will be implemented into the EMPOP website in Q1 of 2018 (presentation attached).

ISFG report Walther Parson

Walther Parson gave an update of the activities of the ISFG and the outcome of the recent congress in Seoul (presentation attached). Two new calls for short term fellowships are planned for March and October 2018.

The EU-funded project 'VISAGE' WaltherParson

The project has started on 1st May 2017 and will run for 4 years. Analytical tools using SNP and methylation markers to predict appearance, age and ancestry by using MPS technology will be developed and validated by extensive user testing. In this context, there may also be a role for EDNAP at a later stage (presentation attached).

EUROFORGEN-NoE – Final outcome and activities Peter Schneider

Peter Schneider gave a final update on the project that is now associated with the ISFG. There will be a Forensic Genetics Summer School in the years between the international congresses. The first Summer School will take place in September 2018 in Southern Italy in connection with the Italian speaking DNA working group meeting (Ge.F.I.) and will have a format similar to the pre-congress workshops at the ISFG congresses (presentation attached).

Plans in Germany to introduce forensic DNA phenotyping Peter Schneider

Peter Schneider gave an overview on the origin and current situation to introduce legislation allowing the application of forensic DNA phenotyping using ancestry, pigmentation markers and age prediction in criminal investigations. It can be expected that the legislative process will be resumed next year, after the new German government has been formed (presentation attached).

ENFSI Update SanderKneppers

Sander Kneppers gave a presentation on the structure of ENFSI and the recent and future activities of the EDNAP DNA Working Group (presentation attached).

Other activities

Verbal scale discussions PeterGill

Peter Gill gave a presentation on the use of verbal scales to express the strength of evicence following likelihood ratio calculations. We participates in a SWGDAM commission representing ENFSI which is addressing this issue for the forensic DNA community in the US (presentation attached).

Database searches revisited. PeterGill

Peter Gill gave a presentation addressing the biostatistical treatment of hits following DNA database searches. He points out that different propositions have to be considered within an ongoing criminal investigation compared to the courtroom scenario (presentation attached).

Future activities Peter Schneider

No other collaborative exercises are planned in addition to the exercise on mtDNA quantification in preparation by the NFI (Arnoud Kal, see above).

Next meetings Peter Schneider

At the ENFSI Steering Group meeting, the colleagues from Rome informed the group that they are planning the EDNAP/CODIS/ENFSI meeting in 2018 during the week 16–20 April 2018.

For the second meeting in 2018 an invitation was extended by Walther Parson to come to Innsbruck. The planned dates will be October 30th for the ENFSI Steering Group meeting and October 31st for the EDNAP meeting. At this occasion, the 30th birthday of the EDNAP group will be celebrated.

Any other business Peter Schneider

There was no other business.

Closing of the meeting

The meeting closed with sincere thanks to Maria Vouropoulou and all other colleagues, who helped to organise the meeting.

Attachments are found at the EDNAP website http://www.isfg.org/EDNAP/Meetings:

- Agenda
- List of participants
- Presentations
  - Katerina Kondili: Presentation of the Hellenic Police Forensic Science Division
  - David Ballard: Report on methylated DNA and age determination
  - Cordula Haas: Results from the second collaborative exercise on mRNA by NGS
  - Arnoud Kal: Update on the collaborative exercise on mtDNA quantification
  - Penelope Miniati: Forensic DNA analysis and humanitarian identification in Greece
  - Walther Parson: STRidER report
  - Walther Parson: EMPOP report
  - Walther Parson: ISFG report
  - Walther Parson: VISAGE update
  - Peter Schneider: Report on EUROFORGEN-NoE
  - Peter Schneider: Plans for FDP legislation in Germany
  - Sander Kneppers: ENFSI Update
  - Peter Gill: Verbal scale discussions
  - Peter Gill: Database searches

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FORENSIC SCIENCES DIVISION

Subdivision of Biological and Biochemical Examinations and Analyses

Aikaterini Kondili PhD
Police Colonel-Biochemist

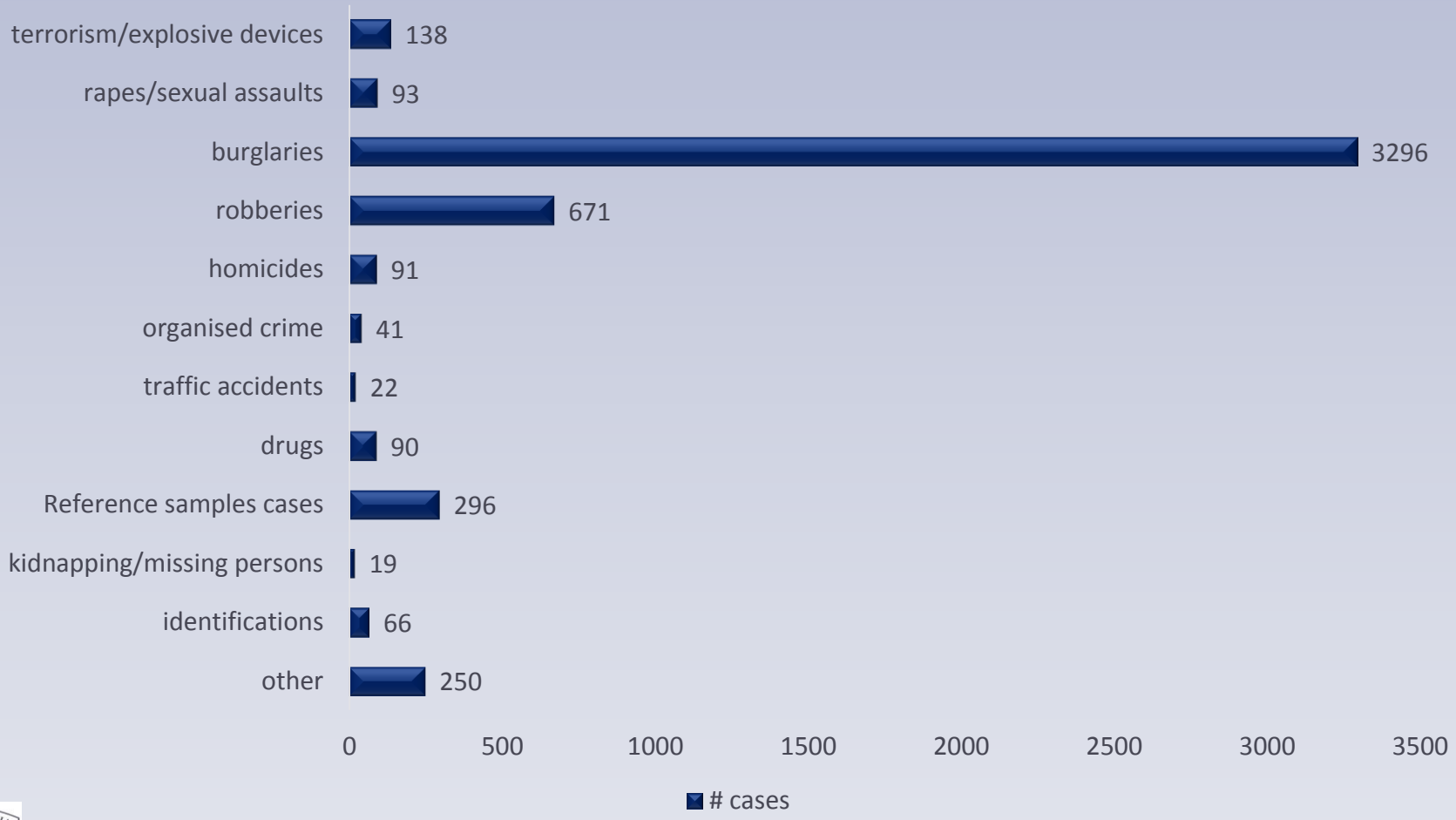
Subdivision of Biological and Biochemical Examinations and Analyses

- Administration Section
- Biological Materials Analysis Section
- National DNA Database Section
- Scientific Support Section

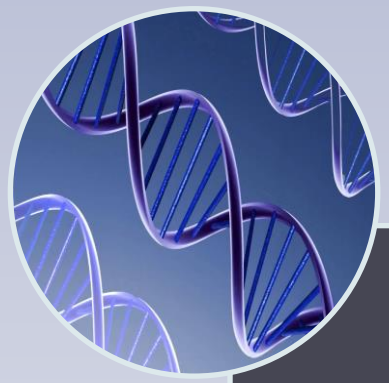
INCOMING CASES
2007-2017

*2017: JAN - SEP

type of cases
2017 (JAN-SEP)



Outgoing cases 2017



61 people personnel

- 26 DNA experts
  - 15 hold PhD
- 16 technicians
- 19 Police officers

Training programme

- ENFSI DNA WG / Quality Assurance Programme, -------
- ENFSI DNA WG / Concept training document, Nov. 2010

Continuous training

EUROFORGEN Network of Excellence

CEPOL

trainers

- Police academy and forces
- Public servants
- CEPOL webinars, on line modules

performance per year

- 20.000 pieces of evidence
- 30.000 PCR
- 3.000 reports
- 5.000 profiles searched
- 600 matches

equipment

- 2 AB 3500xl Genetic Analyzers
- 3 Qiagen Biorobot Universal
- 3 9700 GeneAmp PCR
- 3 AB Veriti 96 PCR
- 1 AB 7500 RT-PCR

Where we want to go :

- Fully automated lab for DNA typing of reference samples
- LIM system
- One fully automated line for DNA typing in the casework lab
- Massively Parallel Sequencing technology in the Subdivision

Where we are :

- Fully automated line for DNA typing of reference samples

Internal validation on BRU platforms using the Globalfiler express PCR amplification kit for the direct amplification of reference samples

Where we are :

- **LIM system**

To be installed in the 1st Section by the end of October

- **One fully automated line for DNA typing in the casework lab**

- **Massively Parallel Sequencing technology in the Subdivision**

Submission to Ministry of Interior a Proposal for funding from the European Internal Security Program

Thank you

Methylated DNA & Age Exercise

David Ballard

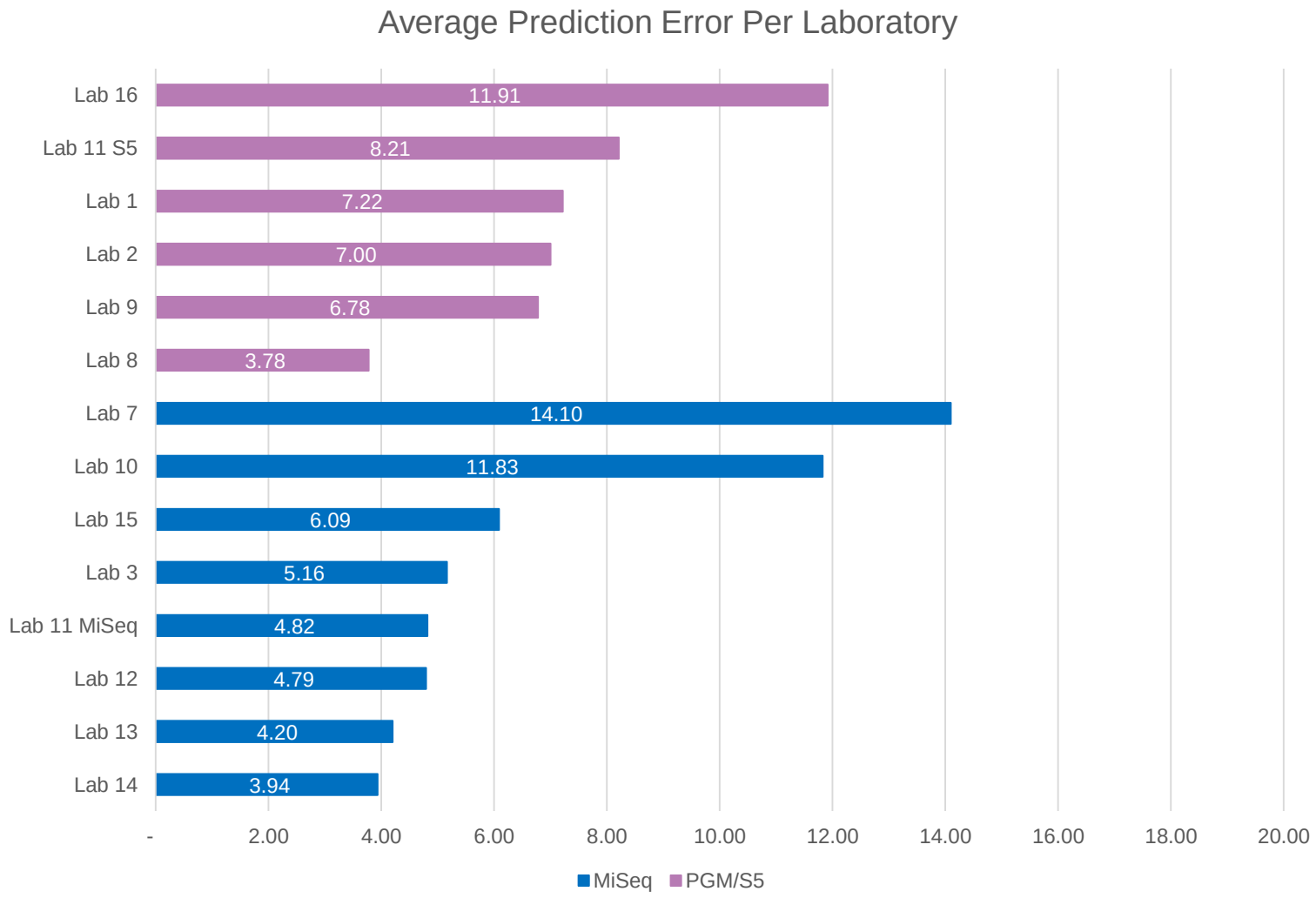
EDNAP, Athens 2017

KING'S College LONDON

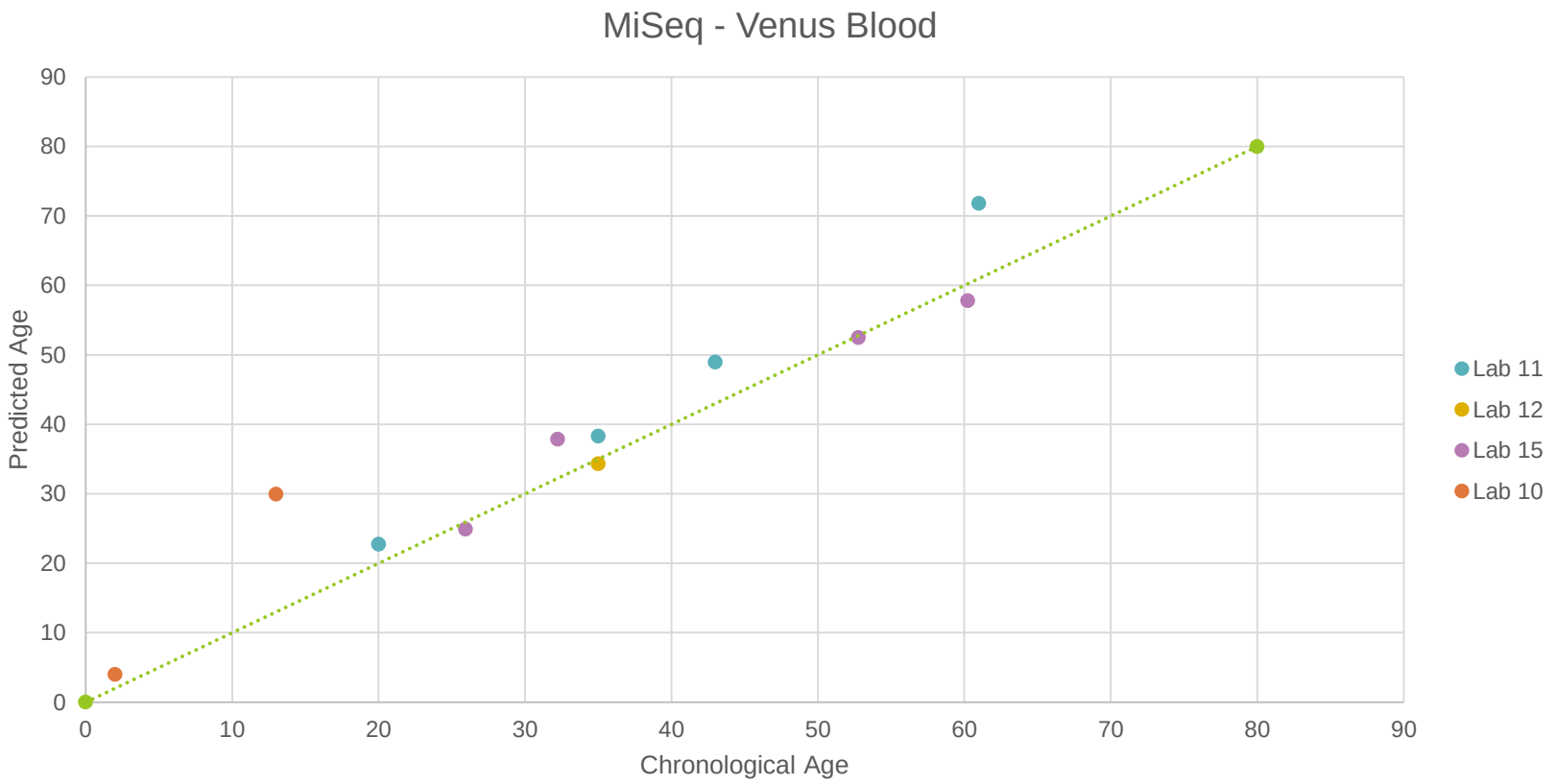
EDNAP Exercise

- 15 laboratories participated
  - 8 MiSeq only
  - 5 PGM only
  - 2 MiSeq and PGM/S5
- Part 1 - 7 Methylation standards between 0-100% sent out to all labs
- Part 2 – 7 blood stains sent out to laboratories to test. Also optional submission of extra blood samples. Age prediction by ANN from methylation values at 12 markers.

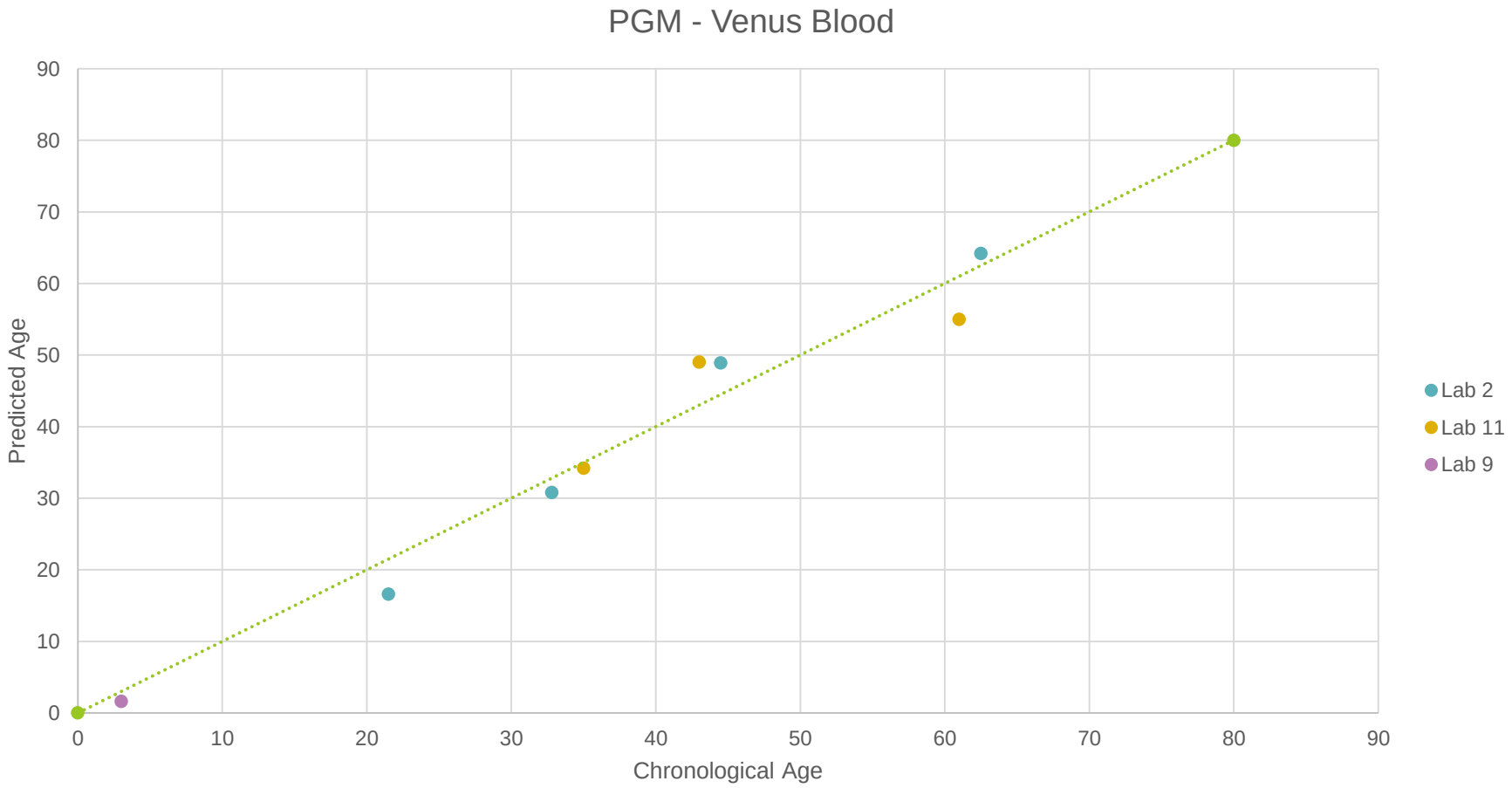
Combined prediction results from EDNAP labs for samples A-G



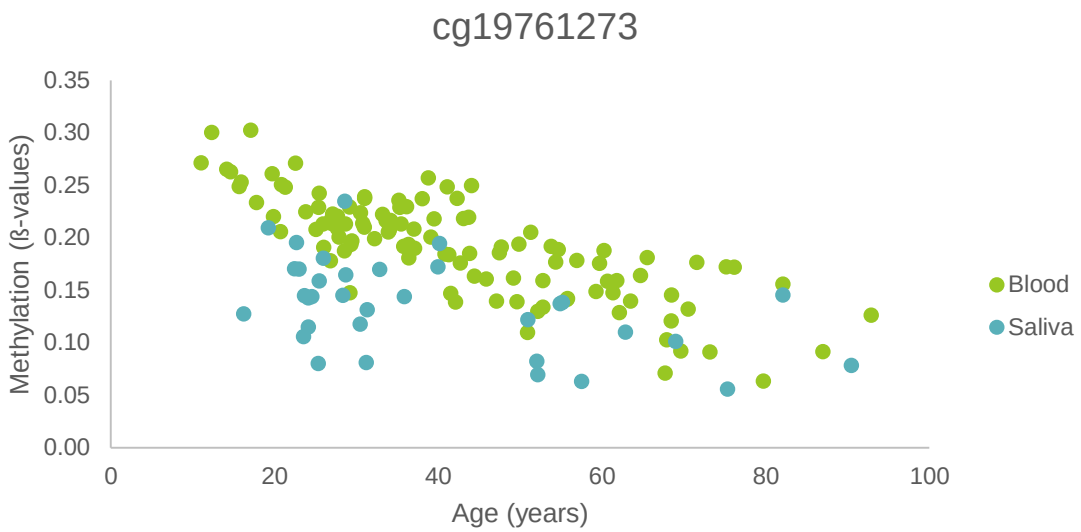
Blind age predictions of extra MiSeq results

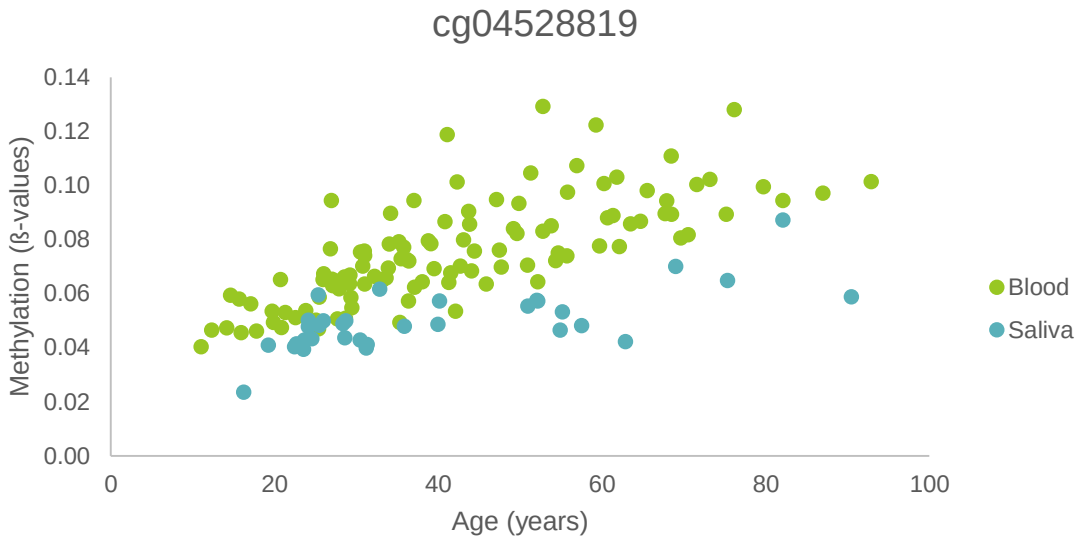


Blind age predictions of extra PGMresults

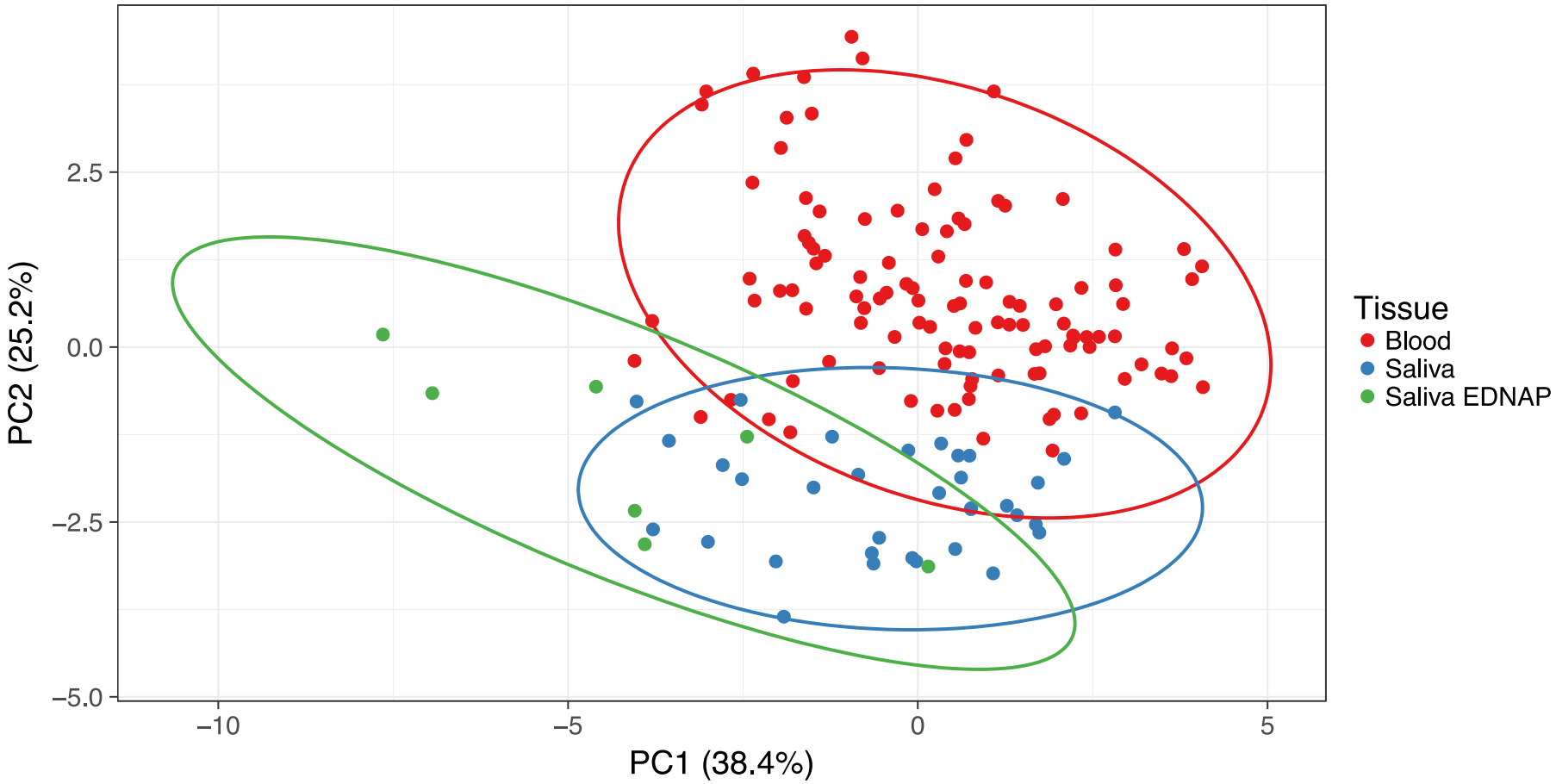


Blood/saliva samples

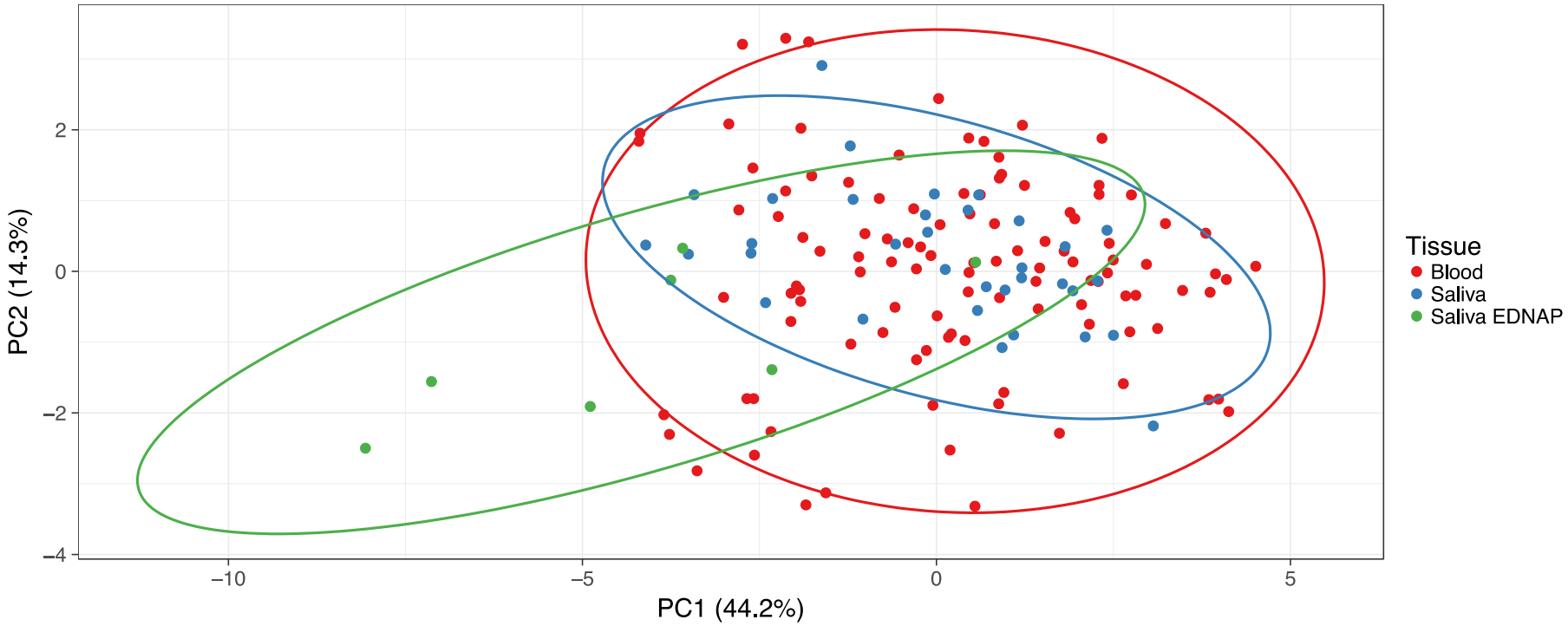




Blood/saliva samples



Saliva samples normalised to blood data

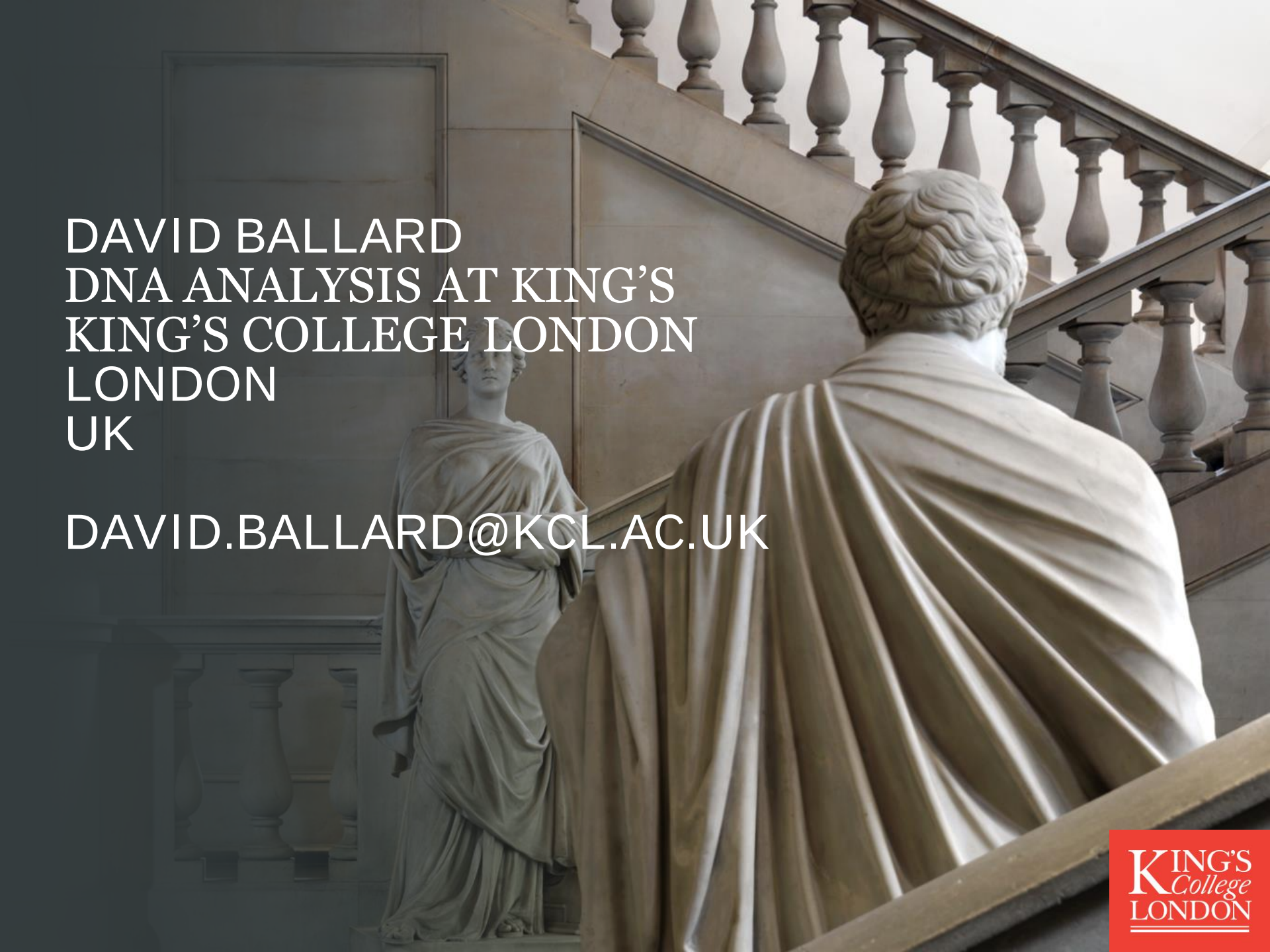


Next steps

- Paper is being written up, will be circulated when ready.

Acknowledgments

- Anastasia Aliferi
- Athina Vidaki
- Leon Barron
- Denise Syndercombe Court



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EUROFORGEN / EDNAP mRNA NGS exercise 2

Assay for body fluid/tissue identification and assignment to donor(s)

Cordula Haas / Sabrina Ingold / Guro Dørum
Erin Hanson / Jack Ballantyne

25. October 2017, Athens

Collaborative exercise mRNA NGS part 1

targeted mRNA NGS approach for the identification of blood, saliva, semen, vaginal secretion, menstrual blood, skin

- 14/17 labs successfully implemented the mRNA NGS approach
- MiSeq-assay satisfying, PGM-assay needs some optimization
- PGM protocol is more lab-work
- manual RNA-extraction!
- Manuscript under review

Body fluid identification using a targeted mRNA massively parallel sequencing approach – results of a EUROFORGEN / EDNAP collaborative exercise

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EUROFORGEN-NoE is funded by the European Commission within the 7th Framework Programme

Collaborative exercise mRNA NGS part 2

- only **MiSeq** laboratories (1/2 library kit left from exercise 1)
- targeted **mRNA** NGS approach for the identification of blood, saliva, semen, vaginal secretion, menstrual blood, skin and **cSNPs** assay to associate specific mRNA transcripts to an individual (separate assays)
- RNA extraction (manual or kit), DNase treatment, quantification
- Protocols and primerpools were provided
- Laboratories analyzed 12 samples provided by UZH
- Results (FASTQ files) were collected and evaluated by UZH

EUROFORGEN-NoE is funded by the European Commission within the 7th Framework Programme

Targeted mRNA NGS approach for body fluid/tissue identification and assignment to donor(s)

Body fluid/tissue	Gene	mRNA 33plex	cSNPs 35plex
Blood	ALAS2		
	ANK1		4
	SPTB		
	CD3G		
	CD93		3
	AMICA1		2
Semen	PRM1		
	PRM2		
	TGM4		4
	SEMG1		
	SEMG2		2
	KLK3		
Saliva	HTN3		
	HTN1		
	STATH		
	PRB3		
	PRB4		
	PRH2		
	MUC7		2
Vaginal	CYP2B7P1		
	DKK4		
	FAM83D		
	CYP2A6		
	CYP2A7		2
Menstrual	MMP10		2
	LEFTY2		
	MMP7		
	MMP11		
	SFRP4		
Skin	LCE1C		2
	CCL27		
	IL37		
	SERPINA12		
	KRT77		2
	COL17A1		3

Provided stains

stain number	composition			primer pool 1 (mRNA)	primer pool 2 (cSNPs)
1	50 µL blood on swab			x	x
2	50 µL semen on swab			x	x
3	50 µL saliva on swab			x	x
4	1/4 vaginal secretion swab			x	x
5	1/4 menstrual blood swab			x	x
6	skin swab			x	x
7	25 µL blood	25 µL semen		x	x
8	25 µL saliva	25 µL semen		x	x
9	12.5 µL saliva	1/4 vaginal swab		x	
10	12.5 µL saliva	1/4 mens. swab		x	
11	7 µL blood	7 µL saliva	1/4 vaginal swab	x	
12	25 µL semen	25 µL saliva	skin swab	x	
13	25 µL blood	25 µL blood			x
14	25 µL blood	25 µL saliva			x
15	12.5 µL blood	1/4 vaginal swab			x
16	12.5 µL blood	1/4 mens. swab			x

Participating laboratories

Copenhagen, Denmark

Innsbruck, Austria

London, UK*

Lyon, France

NFI, Netherlands*

NIST, USA

Orlando, Florida, USA

Rome, Italy

Rotterdam, Netherlands*

Zurich, Switzerland

* no data yet

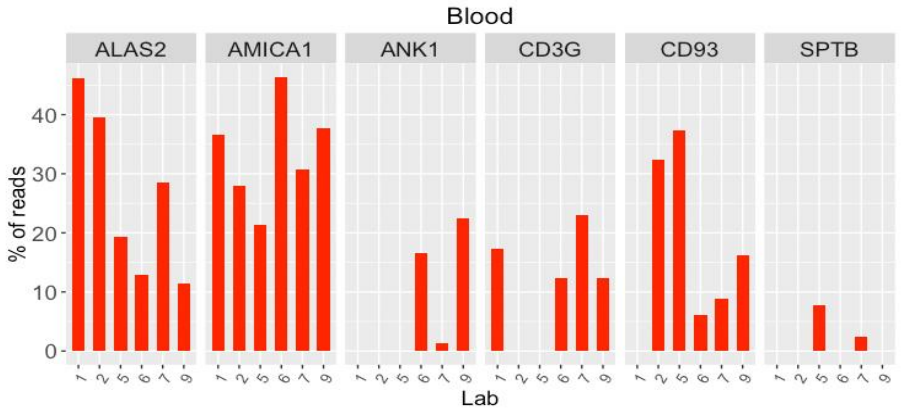
Summary Questionnaire

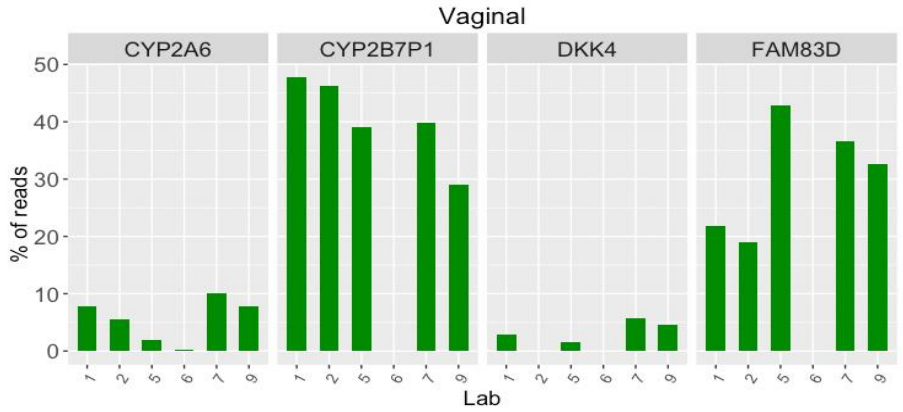
- Delivery time Fedex (samples+primers): all labs within 1-2 days
- 2x manual RNA extraction, 6x RNA extraction kit (RNeasy, mirVana)
- 5x RNA quantification (Qubit, RiboGreen, Quantus), 2x no quant
- RT: 8x ProtoScript II Reverse Transcriptase

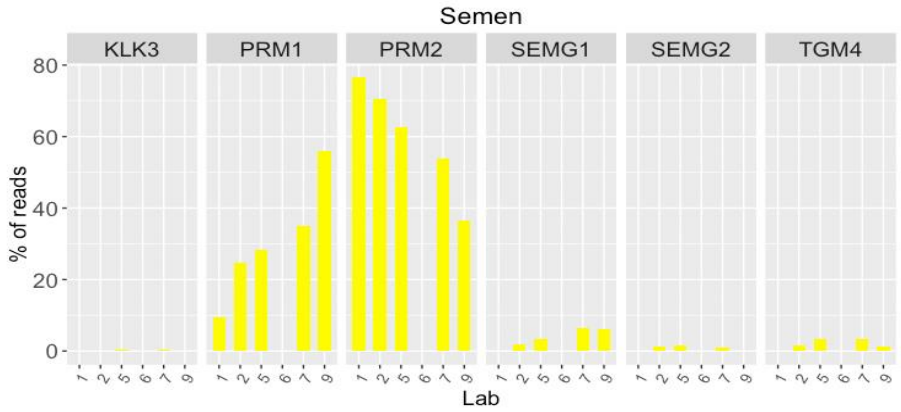
RNA-Quantification

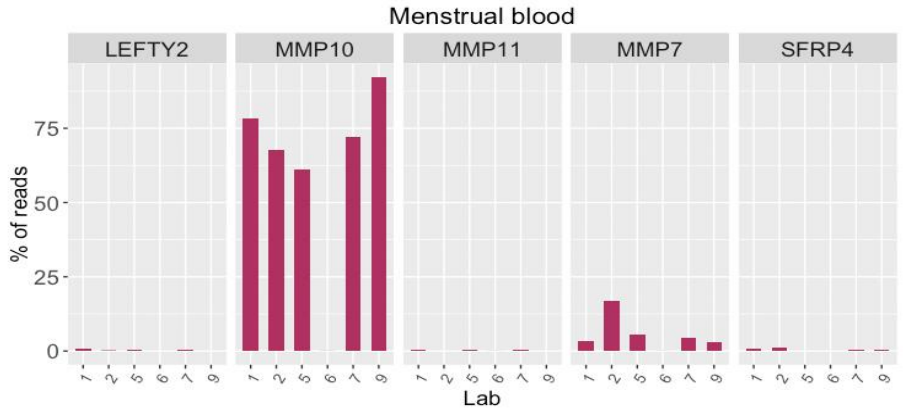
[ng/µL]	extraction method	quantification method	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
Lab_1	Rneasy Mini	Qubit	undet	undet	undet	292	62	undet	undet	undet	90.4	25.6	49.8	7.2	undet	4.4	122	15.7
Lab_2	Rneasy Mini	Qubit	undet	undet	undet	>	38	undet	undet	undet	55	29	31	undet	undet	undet	8.67	undet
Lab_3	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
Lab_4	Rneasy Mini	no quant	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Lab_5	Rneasy Mini	Qubit	undet	undet	2.4	85	7.9	undet	undet	undet	58	34.4	25.7	2.1	undet	undet	87	10.7
Lab_6	manual	Quantus	22	21	18	270.5	131.5	0.97	22	8.8	251	89.85	566.5	35.75	18	11	242	68.75
Lab_7	manual	Quant-iT RiboGreen	5.4	19.7	5.8	202.5	42.8	undet	14	1	205.7	129.1	210.9	11.1	8	2.6	168	139
Lab_8	mirVana	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?
Lab_9	Rneasy Mini	no quant	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Lab_15	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?	?

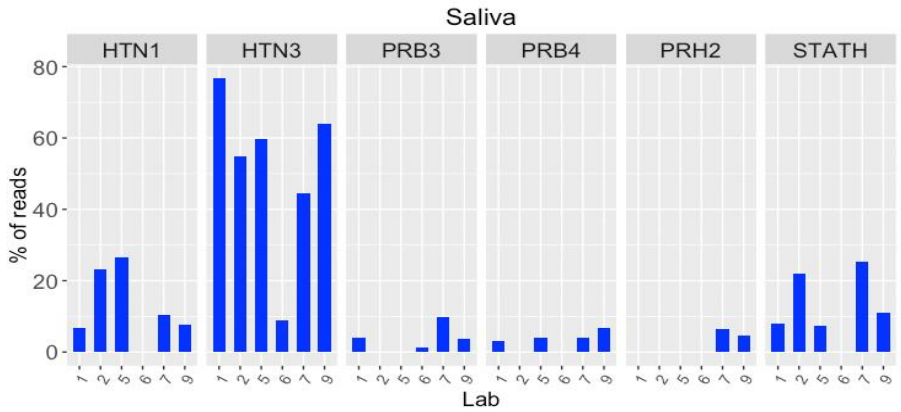
Comparison among laboratories (mRNA assay, single stains)

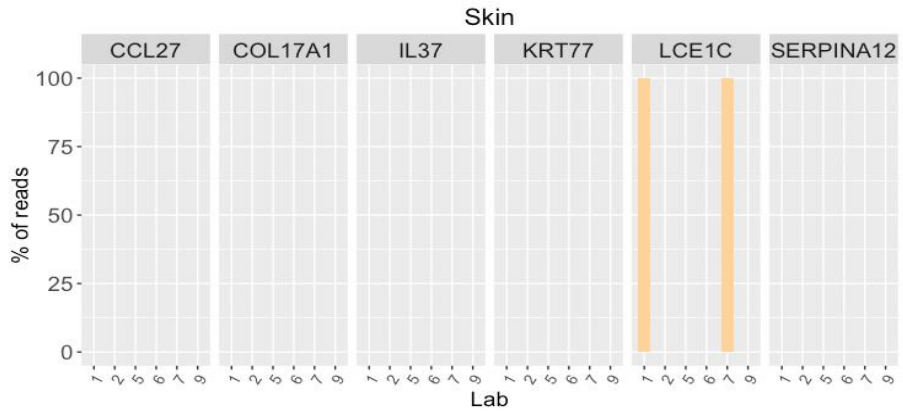




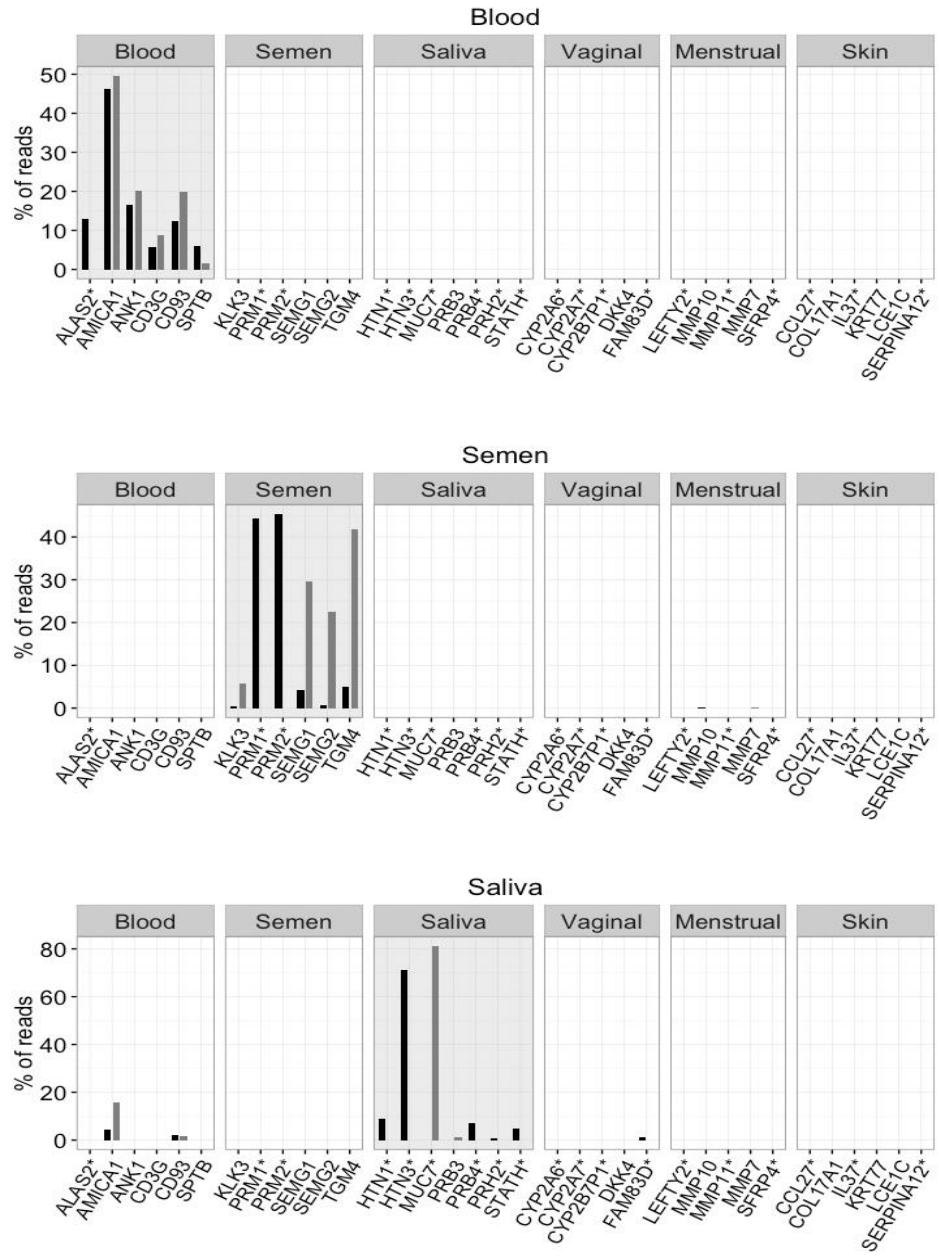


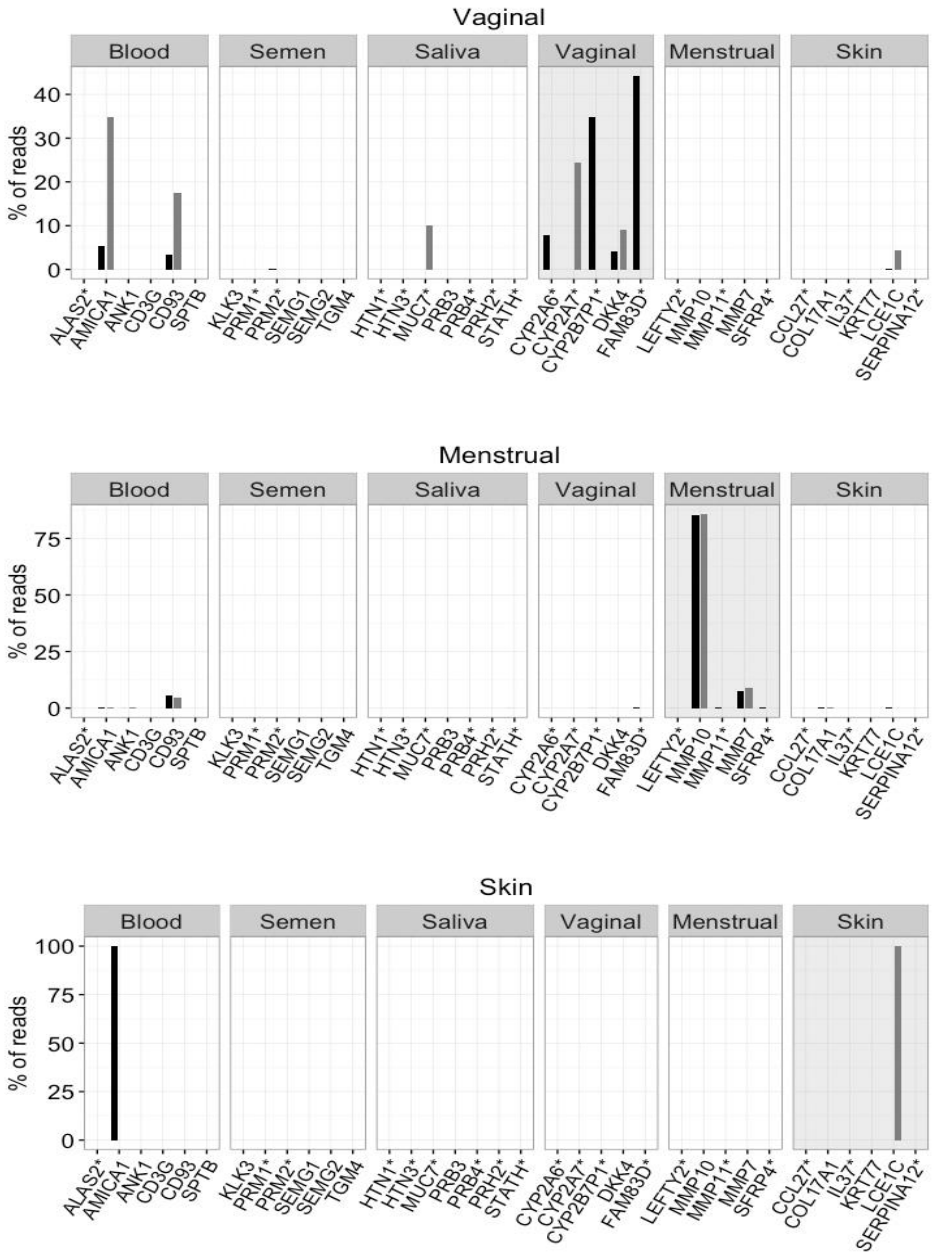


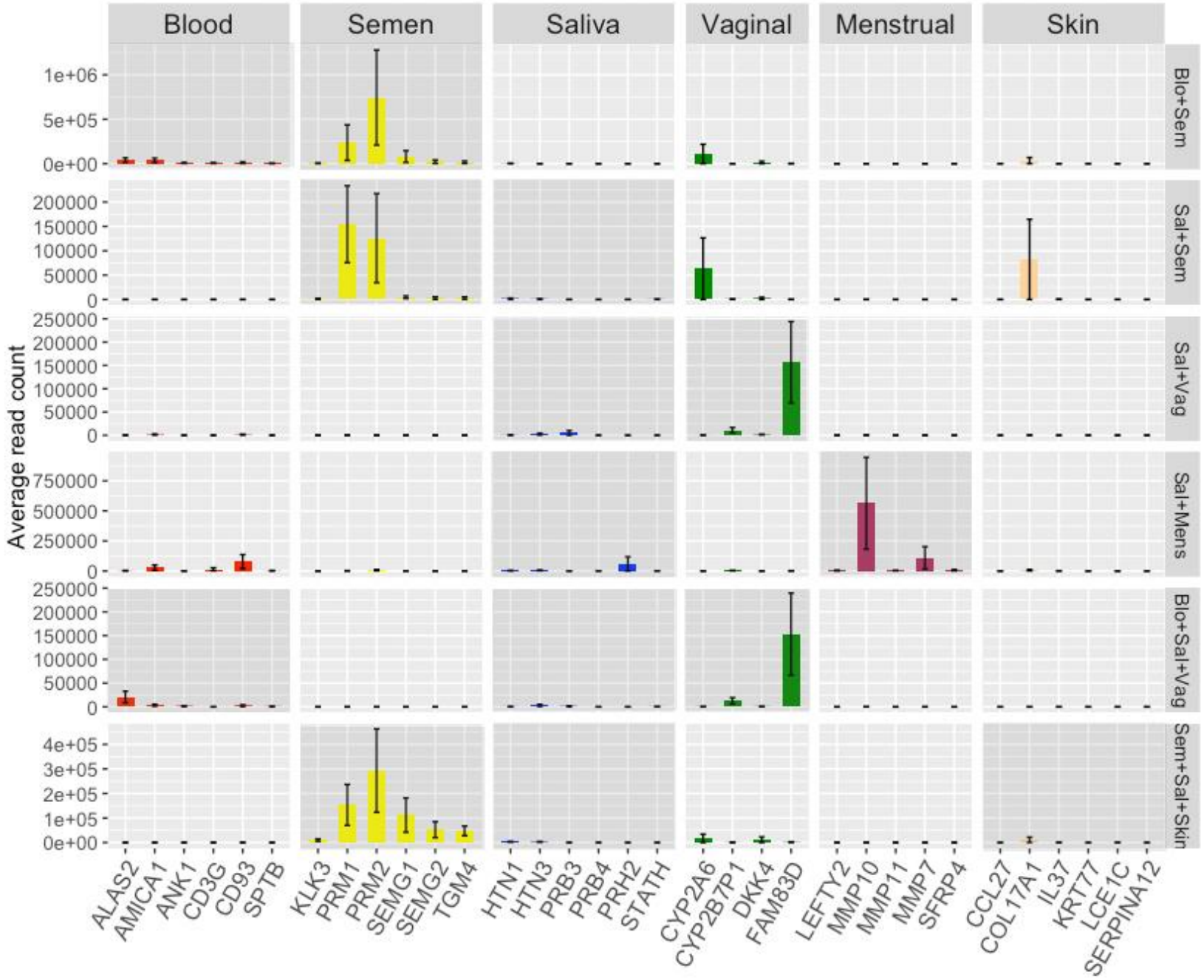




Comparison mRNA-cSNP assays






Blood
Semen
Saliva
Vaginal
Menstrual
Skin
Blo+Sem
Sal+Sem
Sal+Vag
Sal+Mens
Blo+Sal+Vag
Sem+Sal+Skin
Average read count
ALAS2
AMICA1
ANK1
CD3G
CD93
SPTB
KLK3
PRM1
PRM2
SEMG1
SEMG2
TGM4
HTN1
HTN3
PRB3
PRB4
PRH2
STATH
CYP2A6
CYP2B7P1
DKK4
FAM83D
LEFTY2
MMP10
MMP11
MMP7
SFRP4
CCL27
COL17A1
IL37
KRT77
LCE1C
SERPINA12

Results of mixed stains

Stain number 8: saliva (♂) – semen mixture (saliva 2 SNPs, semen 6 SNPs, remaining 1 saliva and 2 semen SNPs not discriminatory for this example)

Sample/ Marker	MUC7_1	MUC7_2	SEMG1	SEMG2_1	SEMG2_2	TGM4_1	TGM4_3	TGM4_4
Donor 1 (♂) (DNA)	CC	CC	TT	CC	AA	TT	GC	AA
Donor 2 (DNA)	CT	CG	TA	CA	AG	GG	GG	GG
saliva-semen mix (RNA)	CC C: 50’613 T: 59	CC C: 69’115 G: 14	TA T: 48’537 A: 35’771	CA C: 25’139 A: 11’172	AG A: 3625 G: 9056	GG G: 39’208 T: 5	GG G: 20’696 C: 1	GG G: 63’476 A: 100

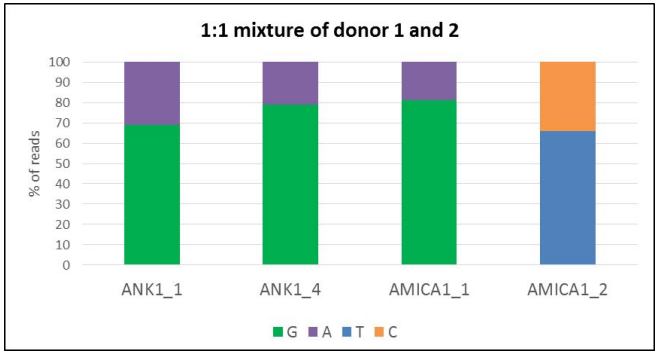
Results of mixed stains

Stain number 13: blood – blood mixture

(4 SNPs, remaining 7 SNPs not discriminatory for this example)

Sample/ Marker	ANK1_1	ANK1_4	AMICA1_1	AMICA1_2
Donor 1 (DNA)	GG	GA	GA	TT
Donor 2 (DNA)	GA	GG	GG	TC
blood-blood mix (RNA)	GA G: 32’825 A: 15’081	GA G: 20’650 A: 5613	GA G: 29’210 A: 6737	TC T: 93’229 C: 47’364

Sample/Marker	ANK1_1		ANK1_4		AMICA1_1		AMICA1_2	
Donor 1 (DNA)	G	G	G	A	G	A	T	T
Donor 2 (DNA)	G	A	G	G	G	G	T	C



Results of mixed stains

Stain number 14: blood – saliva mixture
(blood 4 SNPs, saliva 0 SNPs, remaining 7 blood not discriminatory for this example, 2 saliva SNPs no coverage, 1 saliva SNP not discriminatory)

→ Blood can be assigned to donor 1

→ 98% of reads align to blood amplicons

→ More saliva SNPs needed

Sample/ Marker	AMICA1_1	AMICA1_2	ANK1_1	ANK1_4
Donor 1 (DNA)	GG	TC	GA	GG
Donor 2 (DNA)	AG	TT	GG	GA
blood-saliva mix (RNA)	GG G: 16'532 A: 18	TC T: 24'984 C: 39'451	GA G: 9996 A: 8861	GG G: 17'007 A: 5613

Gene Name	Stain number 14
AMICA1	16562
AMICA1	62972
ANK1	6714
ANK1	18835
ANK1	17033
ANK1	2433
CD3G	3508
CD93	6398
CD93	4489
CD93	5742
SPTB	3322
KLK3	0
SEMG1	0
SEMG2	0
SEMG2	0
TGM4	0
TGM4	0
TGM4	0
TGM4	0
PRB3	0
MUC7	0
MUC7	1506
CYP2A7	0
CYP2A7	0
DKK4	0
MMP10	2
MMP10	4
MMP7	0
KRT77	0
KRT77	0
LCE1C	2
LCE1C	4
COL17A1	0
COL17A1	0
COL17A1	0

Results of mixed stains

Stain number 15: blood (♀) – vaginal secretion mixture
(blood 1 SNP, vaginal secretion 1 SNPs,
remaining 10 blood SNPs not enough coverage,
remaining 2 vaginal secretion SNPs not discriminatory for this example)

→ Inconclusive result

→ More vaginal secretion SNPs needed

→ Skin marker LCE1C supports assignment of vaginal secretion to donor 2

Sample/ Marker	AMICA1_1	CYP2A7_1	LCE1C_1
Donor 1 (♀) (DNA)	AG	CC	AA
Donor 2 (DNA)	GG	AC	GG
blood - vag mix (RNA)	GG? G: 1131 A: 0	AC A: 402 C: 1993	GG G: 1011 A: 1

Gene Name	Stain number 15
AMICA1	1133
AMICA1	79
ANK1	638
ANK1	21
ANK1	3
ANK1	4
CD3G	5
CD93	4
CD93	4
CD93	1
SPTB	5
KLK3	2
SEMG1	29
SEMG2	10
SEMG2	8
TGM4	0
TGM4	2
TGM4	8
TGM4	7
PRB3	0
MUC7	0
MUC7	0
CYP2A7	2097
CYP2A7	2462
DKK4	2437
MMP10	0
MMP10	3
MMP7	0
KRT77	0
KRT77	1
LCE1C	1025
LCE1C	0
COL17A1	0
COL17A1	0
COL17A1	0

Results of mixed stains

Stain number 16: blood (♀) – menstrual blood mixture
(blood 5 SNP, menstrual blood 0 SNPs,
remaining 2 blood SNPs not discriminatory / 4 SNP not enough coverage,
remaining 3 menstrual blood SNPs not discriminatory for this example)

→ More menstrual blood SNPs needed

→ 3 of 5 blood SNPs show alleles from blood and menstrual blood

→ 2 of 3 vaginal secretion SNPs discriminatory → assignment of menstrual blood still possible

Sample/ Marker	ANK1_1	ANK1_4	CD93_1	CD93_2	CD93_3	CYP2A7_1	CYP2A7_2
Donor 1 (♀) (DNA)	GA	GG	AG	TT	GA	AA	TC
Donor 2 (DNA)	GG	GA	GG	CC	AA	CC	TT
blood – mb mix (RNA)	GA G: 2526 A: 3450	GG G: 1153 A: 1	(A)G A: 273 G: 3024	CT T: 1629 C: 1352	AA G: 20 A: 5832	CC C: 905 A: 0	TT T: 1750 C: 1

Thanks for participating!

Netherlands Forensic Institute
Ministry of Justice

EDNAP mini-Exercise proposal mtDNA quant

24 October 2017, Athens

Kris van der Gaag
Arnoud Kal

Benefits of a good mtDNA quantification

- Establish if sufficient mtDNA is present in the sample

- Optimize the input for your favourite typing method
  - Sanger (mini-mito)
  - MPS (equalize input for multiple samples in one run)

  Note: mtDNA copy number varies for cell types, individuals

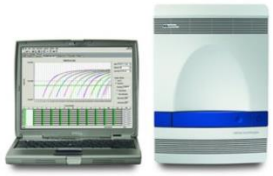
Strategy

Real time multiplex PCR assay:

- 40 cycles
- total & male based on Nicklas and Buel 2006
- Buffer system: TaqPath Multiplex Master Mix
- NEW: short mtDNA amplicon

DNA	Probe	Bp	Dye	Sensitivity
Total DNA	Alu Ya5	127 bp	VIC	0,5 pg/µl
Y DNA	DYZ5	137 bp	FAM	4 pg/µl
mtDNA	16533-180	217 bp	JUN	?
mtDNA	2502-2571	70 bp	ABY	?

! Need a 7500 !



Current status @NFI

Primers and probes total/Y/mt1	✓
Primers and probes mt2	in progress
PCR protocol	✓
Optimizing primer concentrations	in progress
Standard reference material	in progress

Are you interested?

NFI provides:

- Primers and probes
- Challenging samples
- Protocols

You provide:

- Your own favourite sample
- Your own total/Y/mtDNA quantification method

We will send you an invitation via email soon!

Forensic Science and Humanitarian Identification

DNA Analysis & Centralized DNA Database

Athens, 25 October 2017

Dr. Penelope Miniati, Ph.D.

HELLENIC POLICE –
FORENSIC SCIENCE DIVISION

HELLENIC POLICE –
FORENSIC SCIENCE DIVISION

FORENSIC SCIENCE DIVISION (F.S.D.)

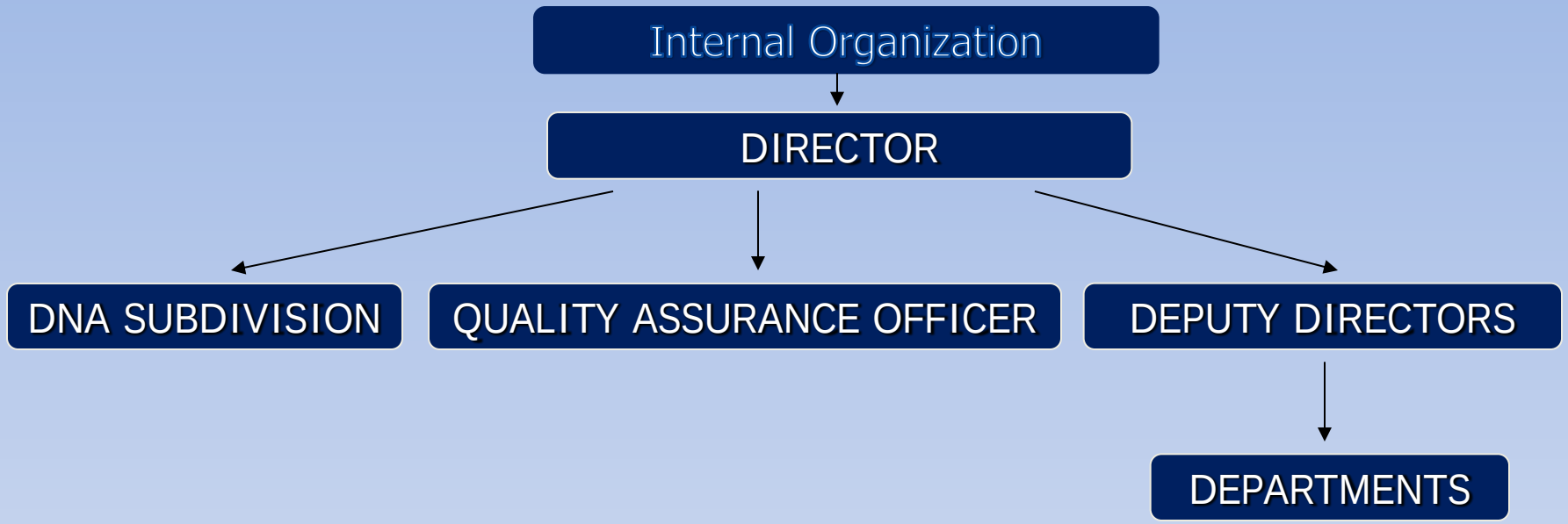
is:

- ✓ the National Forensic Service of Greece
- ✓ One of the five Central Divisions of the Hellenic Police, that reports directly to the Chief of the Hellenic Police Forces

Accreditations

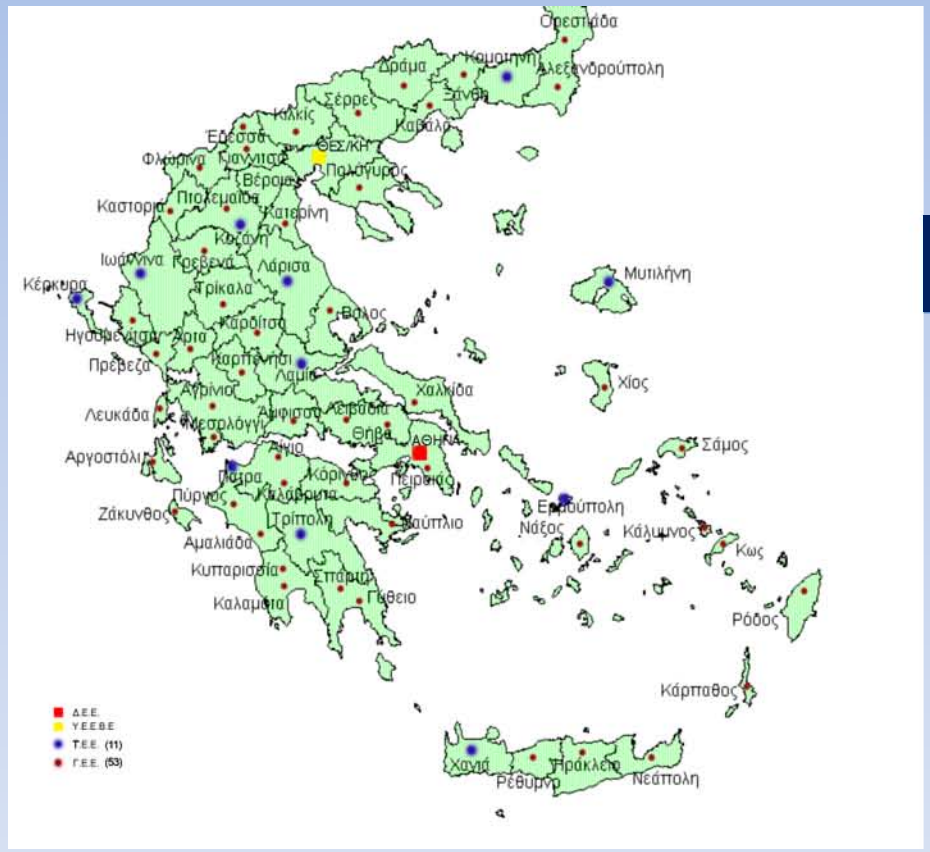
- Certification: ISO 9001
- Accreditation : ELOT-EN ISO/IEC 17025 / 17020

Forensic Science Division



1. Administration
2. Fingerprints
3. Crime Scene Investigations
4. Ballistics and Tool Mark Examinations
5. Document Examination & Forgery
6. Chemical and Physical Examinations
7. Digital Examinations
8. Photography / Voice & Video Analysis
9. Statistical Data
10. Archives

Furthermore the F.S.D. supervises the Forensic Science Subdivision of Northern Greece (F.S.S.N.G.), as well as 11 Forensic Science Sections (F.S.S.) and 53 Forensic Science Offices (F.S.O.)



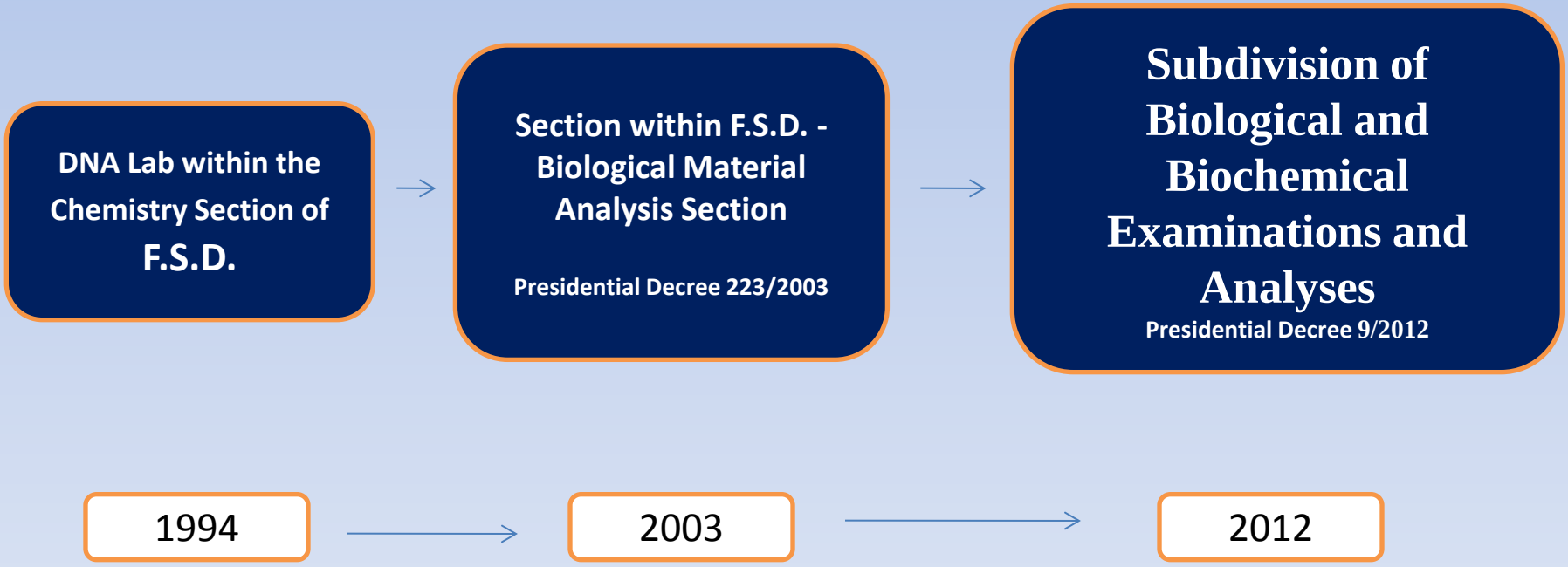
F.S.D.

F.S.S.N.G.

53 F.S.O.

11 F.S.S.

DNA in Hellenic Police



Greece has been a popular transit route for migrants and refugees many decades now – Meeting point of two/ three continents

DNA analysis for identification purposes has been used in Greece since the mid ’90s

Evros borders

- *Large influx of non paper migrants / refugees*

Evros Fence

- *12.5 km barbed-wire fence along the land border with Turkey succeeded in blocking one of the most popular transit routes for migrants and refugees seeking to make their way to the West*

Aegean islands borders

The sharp drop in undocumented migrants/ refugees entering Greece through Evros has been accompanied by a tremendous increase in the influx via the islands of the Aegean Sea.

During 2015 – 2016 more than one million people have travelled through Greece to different European countries


ΑΓΝΟ ΤΟ ΜΙΚΡΟ
ΝΟΣΤΗ
30-9-15


www.lesvosnews.net
No 14 .5
-1-2015

“HELIOS” Airplane Crash

"HELIOS" Airplane Crash

92 DNA Identifications

Extensive Fires in Peloponnese

53 victims identified through DNA

The impressive speed and accuracy in the identification of victims at the foretold Mass Disasters (Helios Airplane Crash, Large Fires in the Peloponnese)

proved that DNA was a very "useful method" for the identification of deceased - Disaster Victim Identification.

Identification needs - DNA analysis

❖ ***Identification of Deceased Migrants / Refugees***

❖ ***Family reunification***

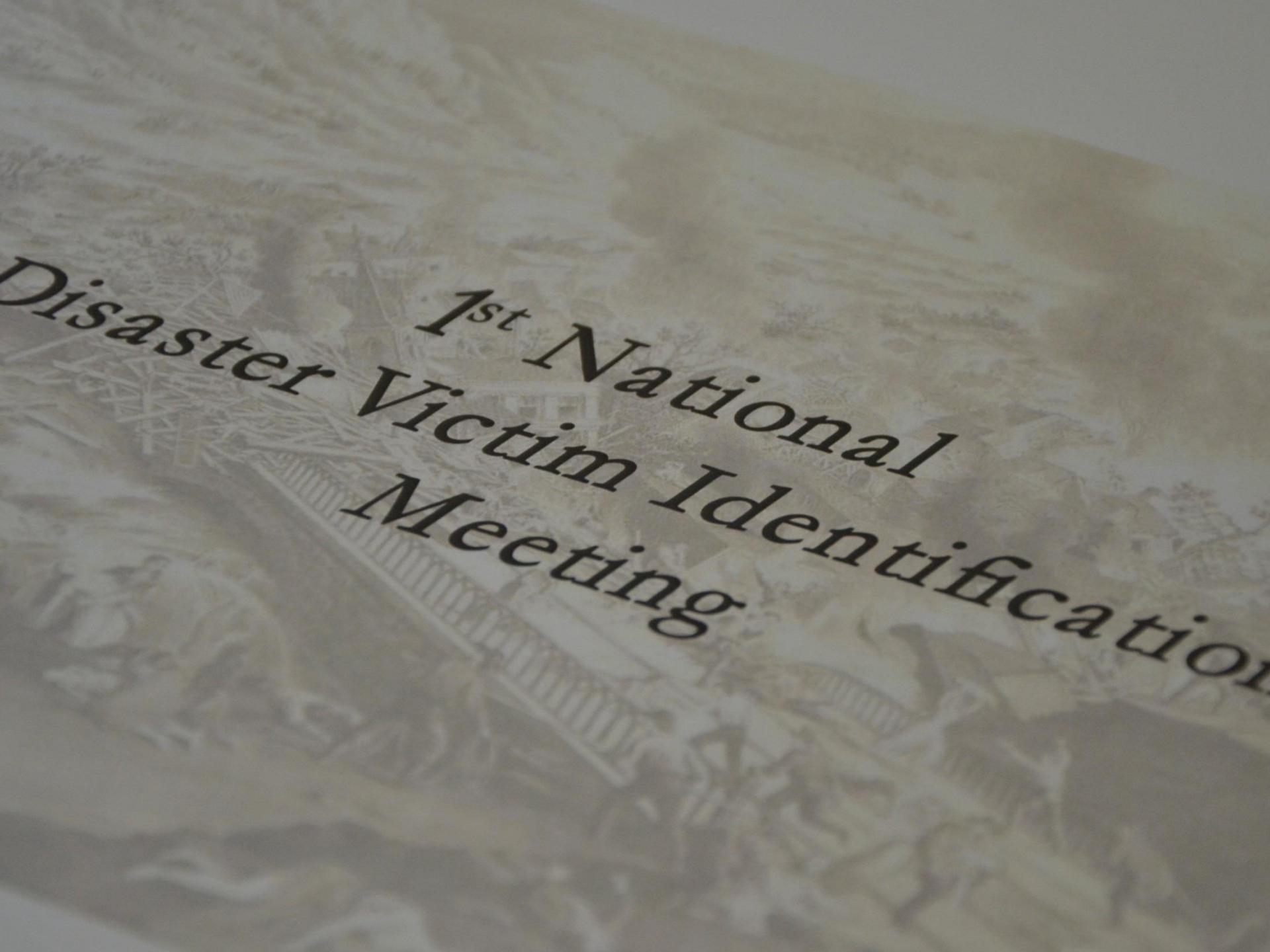
- ***Non-accompanied Children - Determination of Familial Relationships:***

- A case of a 14-year old refugee

<u>a future challenge</u>

“Unidentified deceased refugees / migrants abroad”

Interpol/Europol Requests → **DNA Database Search** → **Interpol/Europol**


1st National
Disaster Victim Identification
Meeting

President of Interpol's DVI Steering Committee Carlos Eduardo Palmares Machado


1st National DVI meeting

ICRC

Ημερίδα με θέμα:

Ορθές πρακτικές ταυτοποίησης νεκρών αγνώστων στοιχείων, με έμφαση στη διαχείριση δεδομένων

Roundtable on

best practices for the identification of unidentified bodies, with emphasis on data management

Αθήνα Athens 4 Οκτωβρίου October 2016

Best Practices in Human Identification with emphasis data collection – Organized by ICRC and FSD Athens, 4 October, 2016

These Meetings resulted

- High Officials such as the Attorney General, the General Secretary of the Ministry of Interior, the Chief of Police etc. in supporting the cause
- High Officials from all Ministries involved and from the Data Protection Agency working together not only to solve every day problems but also to standardize the procedures.

UNHCR
The UN Refugee Agency

Athens DNA lab helps trace those lost at sea on Aegean crossing

Mediterranean crisis sees DNA lab in Athens go from dealing with about 30 cases a year on average to as many as 70 in two days.

By: Maria Petrakis, eds: Andrew Dobbie/Jonathan Clayton | 5 April 2016

| Français | عربي

TOP NEWS

Wed Aug 17, 2016 | 4:46 PM EDT

Naming the nameless: experts struggle to identify drowned migrants

Aug 17, 2016 | 01:23

Forensic teams in Greece struggle to identify drowned migrants

●●●○○ COSMOTE 4G 3:53 μ.μ. 74%

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euronews.

ΔΙΕΘΝΗ ΝΕΑ 19/08/2016

Η δύσκολη δουλειά της ταυτοποίησης των μεταναστών που πνίγονται στο Αιγαίο

The use of Centralized Databases

The example of centralized DNA Database

National DNA Database

National DNA Database

According to the **Greek Law** (recently modified):

- There is a **centralized data base**.
- "…All the state and institutional laboratories, performing DNA analyses following orders of judicial or investigate authorities, submit the analyses results to the National DNA Database…"

Hellenic DNA Database includes

- 700 DNA profiles from Unidentified Human Remains (UHR) – the majority of them refer to refugees / immigrants
- 250 reference samples
- 186 pedigrees

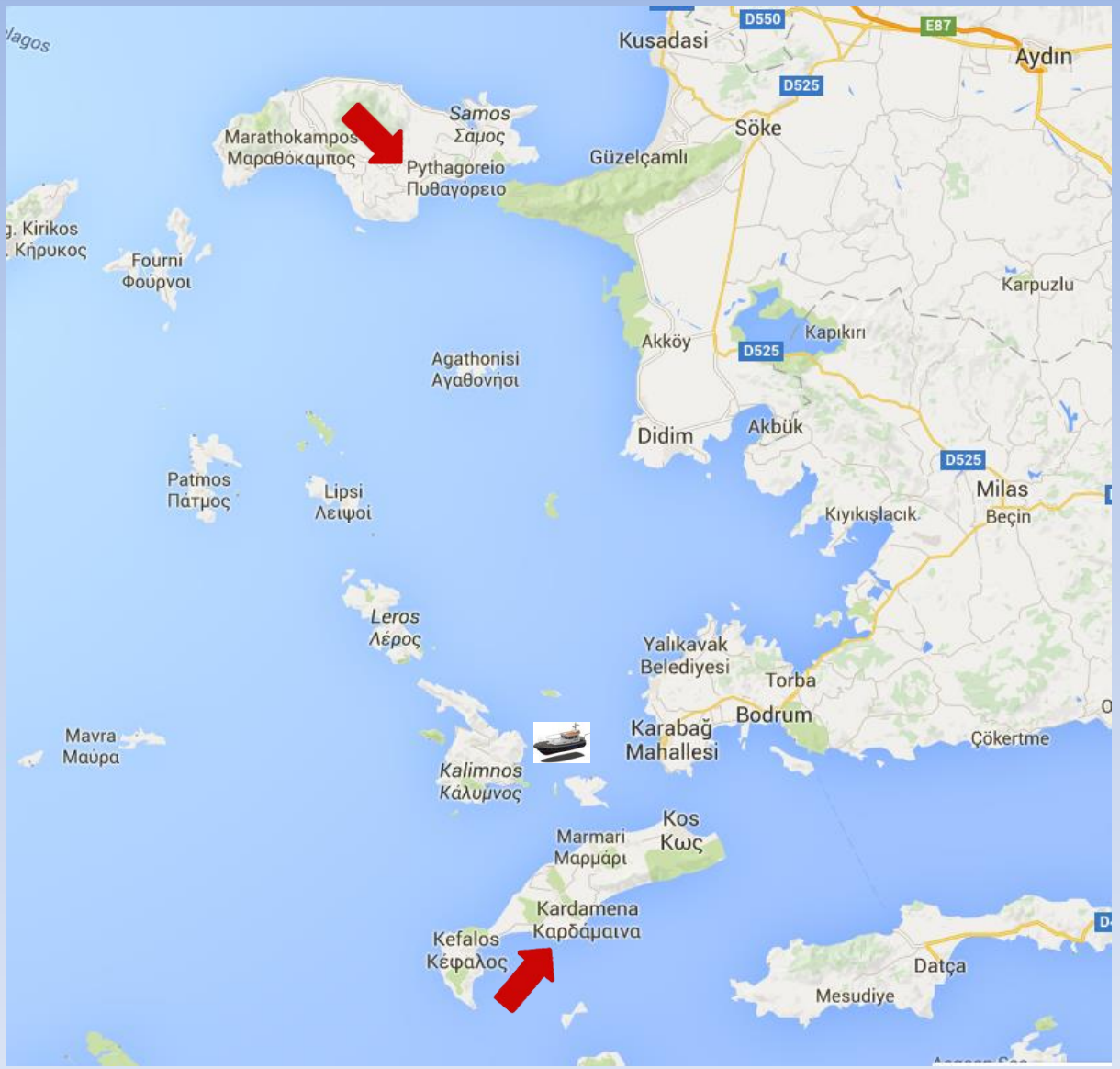
Reference Material cannot be accepted by non-governmental agencies or individuals

- Police and Coast Guard (Judicial Order)
- Embassies
- Interpol Offices

All ante-mortem information are important for identification purposes and non-governmental agencies play a crucial mediator role between the families that are searching for their loved ones and the governmental agencies

Shipwreck between the islands of Kalymnos and Kalolimnos (29-10-2015, 02:50)

- 160 people on board
- 139 people saved
- 19 people drowned
- 2 people were missing

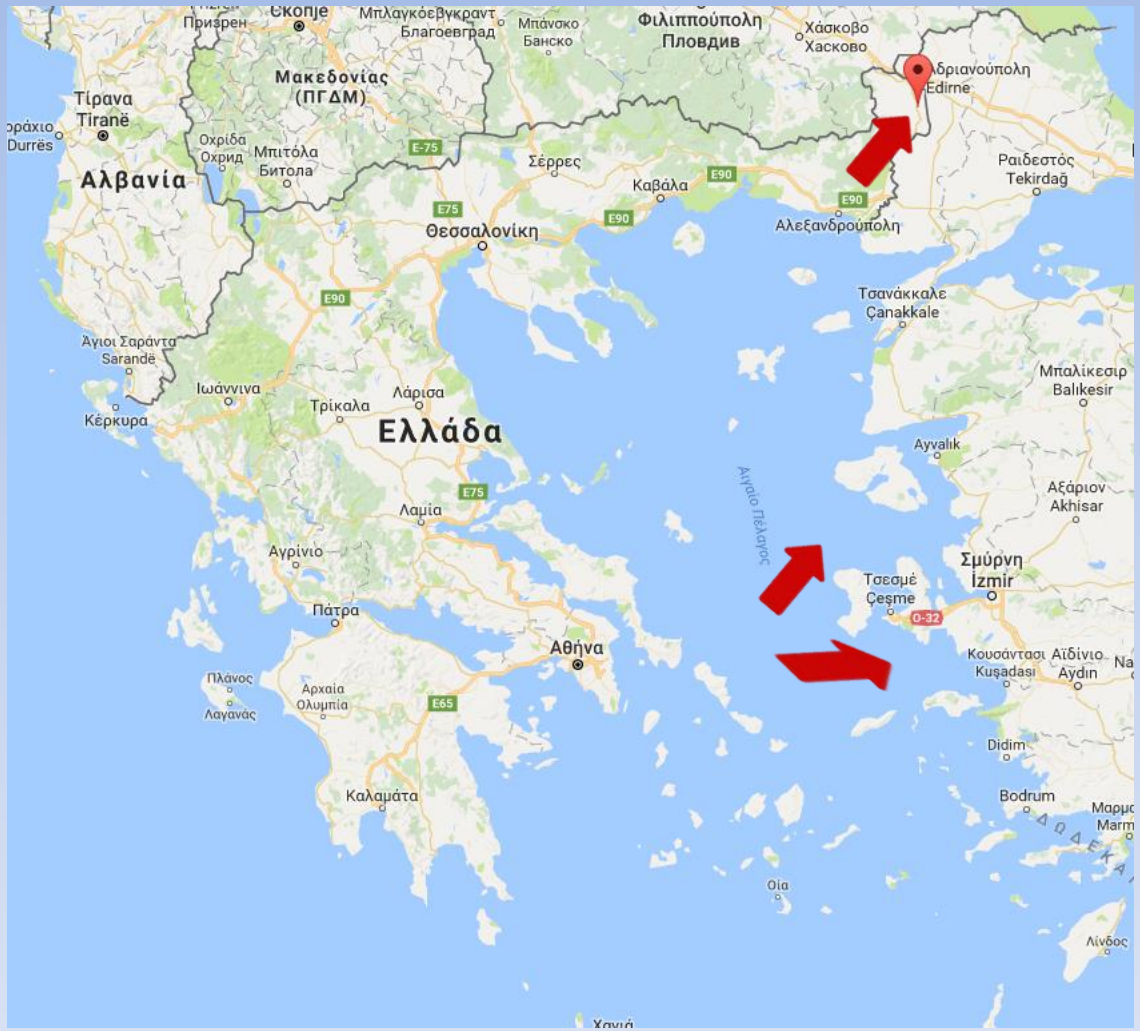

Kusadasi
D550
E87
Aydın
D525
Söke
Güzelçamlı
Samos
Σάμος
Marathokampos
Μαραθόκαμπος
Pythagoreio
Πυθαγόρειο
Fourni
Φούρνοι
Karpuzlu
Akköy
Kapıkırı
D525
Agathonisi
Αγαθονήσι
Didim
Akbük
D525
Milas
Beçin
Kıyıkışlacık
Patmos
Πάτμος
Lipsi
Λειψοί
Leros
Λέρος
Yalıkavak
Belediyesi
Torba
Bodrum
Karabağ
Mahallesi
Çökertme
Mavra
Μαύρα
Kalimnos
Κάλυμνος
Kos
Κως
Marmari
Μαρμάρι
Kardamena
Καρδάμαινα
Kefalos
Κέφαλος
Datça
Mesudiye

Syrian citizen declared to the Police Authorities of Orestiada that her husband went missing, after embarking on a boat heading from the Turkish coast to the island of Lesvos (28-10-2015)

The couple's two children ptovided DNA samples to the Police Authorities in Orestiada (20-12-2016)

HIT to the database with the DNA profile of a deceased person found in the sea region between the islands of Lesvos and Samos in 2015

(DNA profile submitted by the DNA lab of the Forensic Medical Service of Athens 16-05-2016)

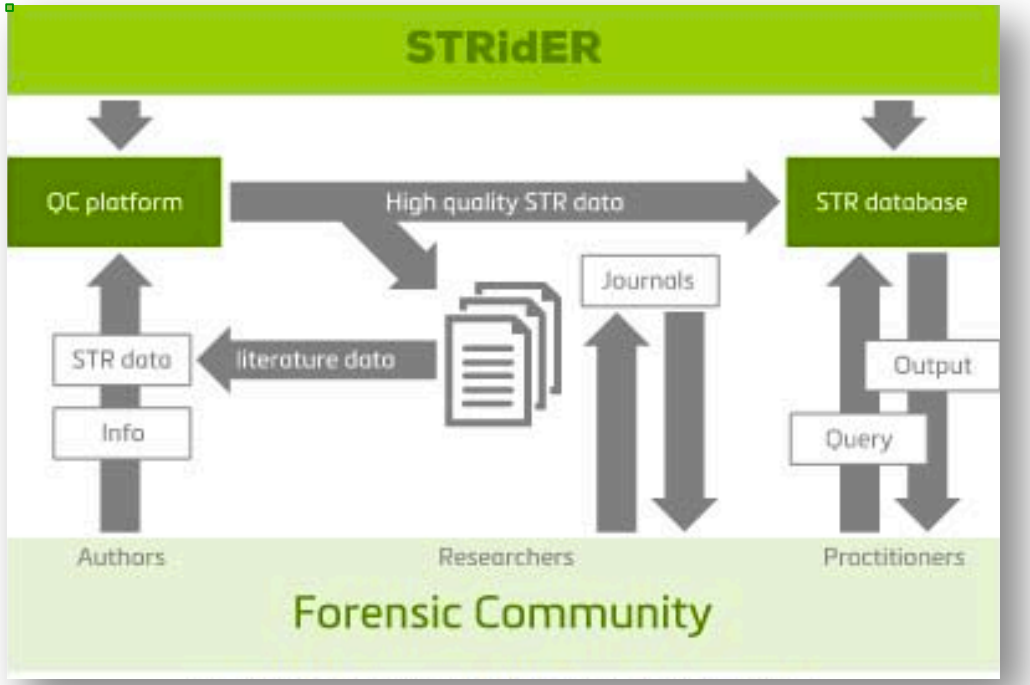

Призрен
Скопје
Μπλαγκόεβγκραντ
Благоевград
Μπάνσκο
Банско
Φιλιππούπολη
Пловдив
Χάσκοβο
Хасково
Αδριανούπολη
Edirne
Μακεδονίας
(ΠΓΔΜ)
Τίρανα
Tiranë
Durrës
Αλβανία
Охрид
Μπιτόλα
Битола
E-75
Σέρρες
Καβάλα
E90
Ραιδεστός
Tekirdağ
E75
Θεσσαλονίκη
Αλεξανδρούπολη
Τσανάκκαλε
Çanakkale
Άγιοι Σαράντα
Sarandë
Ιωάννινα
Τρίκαλα
Λάρισα
Μπαλίκεσιρ
Balıkesir
Κέρκυρα
Ελλάδα
Ayvalık
Αξάριον
Akhisar
Λαμία
Αιγαίο Πέλαγος
Αγρίνιο
Σμύρνη
İzmir
Τσεσμέ
Çeşme
Πάτρα
Αθήνα
Κουσάντασι
Kuşadası
Αϊδίνιο
Aydın
Πλάνος
Λαγανάς
Αρχαία
Ολυμπία
E65
Didim
Καλαμάτα
Bodrum
Μαρμ
Marm
Οία
Λίνδος
Χανιά

- *It is proven once more that the use of centralized DNA Databases is not limited only in providing valuable information to the law enforcement, but also providing valuable information to families that have lost their loved ones, so the grieving process will start for them.*

HELLENIC POLICE
FORENSIC SCIENCE DIVISION

e-mail: p.miniati@hellenicpolice.gr

Thank you!!!



D8S1179

Allele	AUSTRIA	BELGIUM	BOSNIA AND HERZEGOWINA	CZECH REPUBLIC	DENMARK	FINLAND	FRANCE	GERMA
	222	206	171	200	200	230	208	
8	1.8018e-2	7.2816e-3	5.8480e-3	7.5000e-3	1.5000e-2	1.7391e-2	2.4039e-2	1.2840
9	1.8018e-2	1.2136e-2	8.7719e-3	5.0000e-3	1.0000e-2	8.6956e-3	9.6154e-3	1.2840
10	9.4595e-2	8.7379e-2	5.8479e-2	5.5000e-2	9.7500e-2	8.2609e-2	8.4135e-2	8.7613
11	1.0135e-1	9.7087e-2	3.2164e-2	1.0000e-1	8.0000e-2	1.3261e-1	8.8942e-2	7.7795
12	1.6216e-1	1.5049e-1	1.8713e-1	1.5250e-1	1.3000e-1	1.3261e-1	1.3462e-1	1.4199
13	2.9054e-1	3.1311e-1	3.4210e-1	3.5000e-1	3.4500e-1	3.5217e-1	3.1490e-1	3.1269
14	1.9144e-1	1.6990e-1	2.1637e-1	2.1250e-1	2.0750e-1	1.8478e-1	2.0433e-1	1.9864
15	1.0360e-1	1.2379e-1	1.1403e-1	9.7500e-2	8.5000e-2	5.6522e-2	1.0336e-1	1.1933
16	1.8018e-2	3.3981e-2	3.2164e-2	2.0000e-2	2.0000e-2	1.5217e-2	3.6058e-2	3.0211
17	2.2522e-3	4.8544e-3	2.9240e-3		5.0000e-3	1.0870e-2		6.0423

ΣΤΡιδΕΡ Ὑπδατε

Δρ. Ωάλθερ Παρσον
άσσοχ. Προφ. Ἰνστιτυτε ὀφ Λεγαλ Μεδιχινε, Μεδιχαλ Ὑνιψερσιτυ ὀφ Ἰννσβρυχκ, Αὐστρια
αδθ. Προφ. Φορενσιχ Σχιενχε Προγραμ, Πενν Στατε Ὑνιψερσιτυ, ΠΑ, ΥΣΑ
walther.parson@i-med.ac.at

STRidER

STRidER STRs for Identity ENFSI Reference database, v2

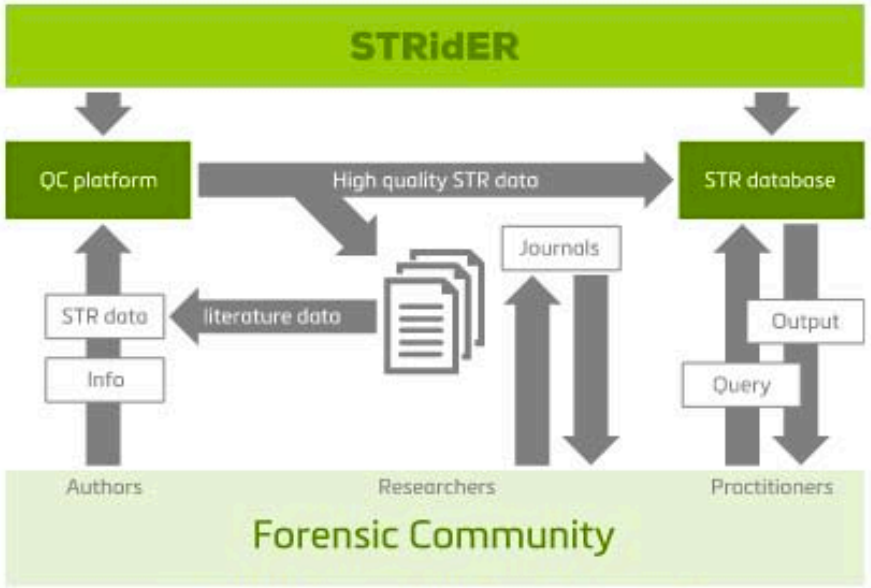
HOME | QUERY | BATCH QUERY | ABOUT | FREQUENCIES | FORMULAE | STR SEQUENCE NOMENCLATURE | CONTACT | TERMS OF USE

Welcome to STRidER!

STRidER (**STR**s for **I**dentity **E**NFSI **R**eference Database) is the expanded and enhanced version of the ENFSI STRbASE (2004-2016). This curated online high quality STR allele frequency population database enables scientifically reliable **STR genotype probability estimates** and provides **quality control** of autosomal STR data. A suite of software tools has been developed at the Institute of Legal Medicine, Medical University of Innsbruck (LINK: https://gerichtsmedizin.at/) to scrutinize STR population data and thus increase the quality of datasets to ensure reliable allele frequency estimates. STRidER acts as **frequency database and software platform** for the development of novel tools for STR data QC and other forensic analyses.

STRidER serves the STR community in forensics and beyond in inter-related ways:

- The high-quality autosomal STR allele frequency database can be directly queried
- Allele frequency tables of STR loci from diverse populations can be downloaded and used for third party software
- Centralized STR data quality control is offered prior to publication
- Accepted datasets will become rapidly available online and receive a unique and traceable STRidER accession number
- Allele frequencies and forensic/population genetic parameters are calculated from datasets
- Individual STR genotypes are not accessible on STRidER to comply with privacy regulations



STRidER in the field of forensic STR typing (from Bodner et al. 2016)

The **concept of STRidER** has been developed together with the DNA Commission of the ISFG) and is outlined in *Bodner M, Bastisch I, Butler JM, Fimmers R, Gill P, Gusmão L, Morling N, Phillips C, Prinz M, Schneider PM, Parson W (2016) Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER): Forensic Sci Int Gen 24:97-102.*

The STRidER online platform is work in progress. Additional datasets and features will continuously become available. To receive periodic news and stay updated about STRidER, register here for the STRidER newsletter.

Please consider **citing STRidER** [https://www.isfg.org/Publication;Bodner2016] when using it with your research.

new URL
https://strider.online/

Forensic Science International: Genetics 24 (2016) 97–102

Contents lists available at ScienceDirect

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journal homepage: www.elsevier.com/locate/fsig

Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER)

Martin Bodner[a], Ingo Bastisch[b], John M. Butler[c], Rolf Fimmers[d], Peter Gill[e,f], Leonor Gusmão[g,h,i], Niels Morling[j], Christopher Phillips[k], Mechthild Prinz[l], Peter M. Schneider[m], Walther Parson[a,n,*]

STRidER newsletter

Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER)

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Content

I) Positioning STRidER relative to other existing databases (STRbase, ALFRED, pop STR, popAffiliator, ALLST*R); **important element of QC**

II) Rationale, concept and workflow of **QC** via STRidER

III) Benefits to forensic and other scientific community

IV) Transparency, traceability and protection of data

V) Outloook: **STR sequence data** in STRidER (MPS)

STRidER
STRs for identity ENFSI Reference database, v2
HOME QUERY BATCH QUERY ABOUT FREQUENCIES FORMULAE QUALITY CONTROL STR SEQ NOMENCLATURE

Quality Control

STRidER provides quality control of autosomal STR data. A suite of software tools has been developed to scrutinize STR population data and thus increase the quality of datasets to ensure reliable allele frequency estimates. The board of the International Society of Forensic Genetics (ISFG) and the editors of Forensic Science International: Genetics invited STRidER to logistically organize and perform quality control (QC) of autosomal STR population data in the course of manuscript preparations for the journal [1]. Before STR population papers are put forward to the editors for review, the authors are requested to submit the data to STRidER. After positive evaluation, the authors will be contacted with the respective STRidER accession numbers that serve as indicator of successful QC for the editors and reviewers. The necessary steps for submission of STR data to STRidER are outlined below.

Step 1

Prepare your **STR data file** as shown in the example file that can be downloaded and used as template. It is a tab delimited text file that can be created using standard text software or MS Excel (then, save file under .txt format). The minimum requirements for population datasets are 16 autosomal STR loci typed in 500 samples (for exceptional populations, the latter number can be smaller, please contact STRidER before submission).

The initial lines (identified using the "#" symbol) specify details of the dataset and origin of the samples. Line 1 must contain a description of population(s) reported (e.g., the title of the study), number of samples, geographic origin, and the number of STR loci. Line 2 must indicate the contact author's name with email address. Further text lines marked with "#" can be included for comments or description of the detailed geographic background and the appropriate metapopulation affiliation of the genotypes. Lines below these text lines list the original STR genotypes. Allele nomenclature criteria are applied as described in the "About" tab of this website. The order of loci does not matter. Alleles for the same locus have to be reported in adjacent columns. Loci names must not contain spaces. Report both alleles for homozygous loci. Use "." instead of "," for incomplete alleles, e.g. "9.3" not "9,3". Note that only complete genotypes are accepted. It is imperative that STR genotypes are reported individually and unshuffled using a unique identifier for each genotype in the dataset. The names are necessary for correspondence.

Also prepare an **accompanying STR information file** per population containing additional information on the dataset as outlined in the example information file. This information might be necessary for evaluation of the dataset. Keep raw data files available for any later inquiries.

Step 2

Submit your files to STRidER by email (see contact). The genotype data should be submitted as a file containing the following notation: Author_country_number of samples.txt (e.g. Parson_AUT_573.txt), the accompanying file should be named Author_country_number of samples_Info.xls or .xlsx (e.g. Parson_AUT_573_Info.xls). The data will be quality checked as outlined in [2] using in-house software.

Step 3

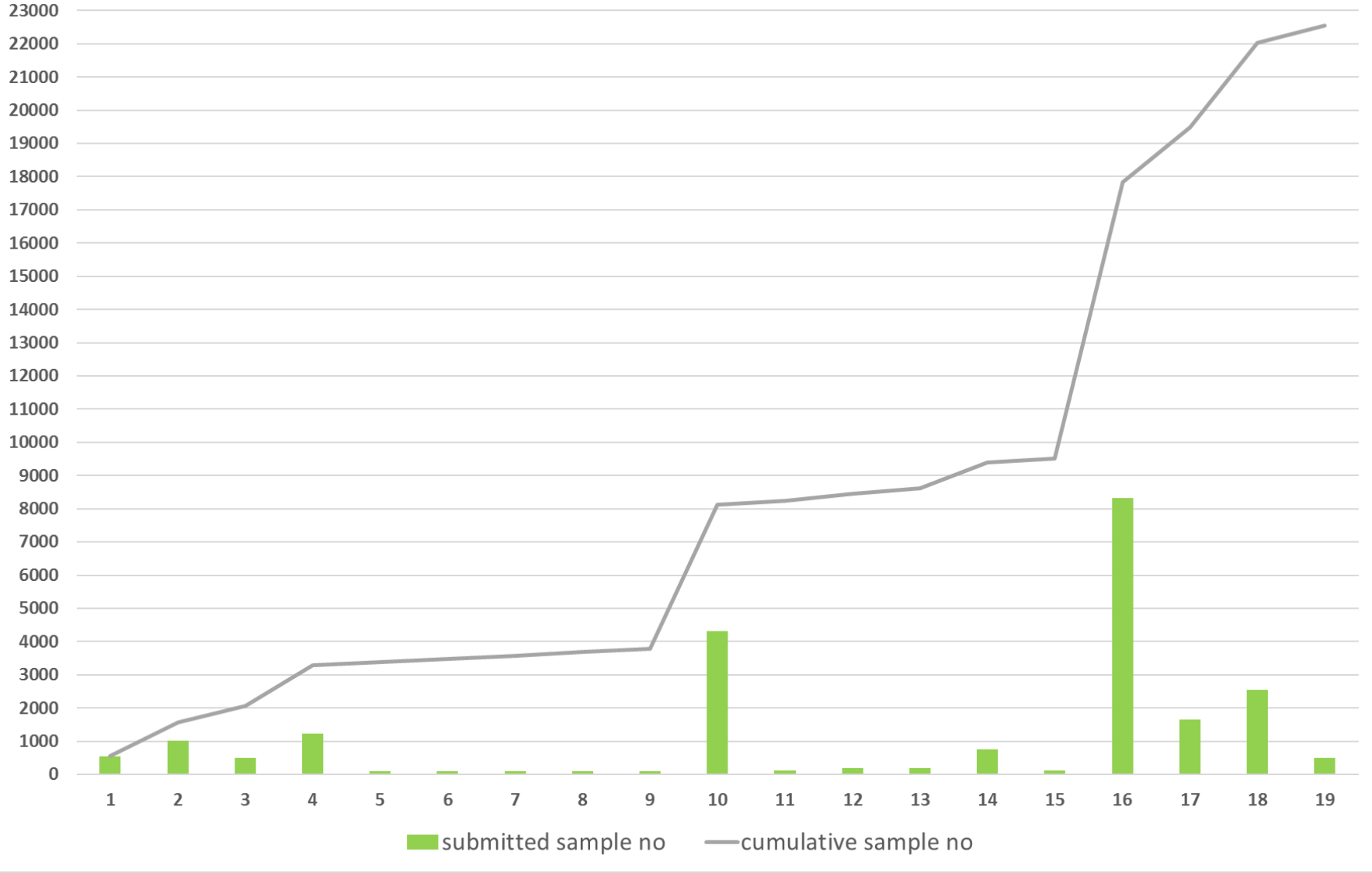
After STRidER evaluation, communication with respect to individual genotypes may follow. Once your data passed QC you will receive the STRidER accession number(s) for your data together with allele frequencies and forensic/population genetic parameters calculated from the dataset(s). Please provide accession number(s) to the journal editor and cite STRidER [2] in your manuscript.

STRidER STRs for identity ENFSI Reference database, v2

HOME | QUERY | BATCH QUERY | ABOUT | FREQUENCIES | FORMULAE | QUALITY CONTROL | STR SEQ NOMENCLATURE | CONTACT

CE datasets submitted to STRidER for QC since 8/2017

MPS	1
submitted sample no	50
sample no cumulative	50



Errors found during STRidER QC

	1	2	3	4	5	6	7	8	9
submitted sample no	550	1008	504	1220	100	100	101	102	102
sample no cumulative	550	1558	2062	3282	3382	3482	3583	3685	3787

QC finished

Note: QC is in progress

80 definitive errors in 3787 samples

2.1% of dataset profiles contained errors

doublets

single alleles

incomplete profiles

wrong alleles (raw data inspection)

non ascending alleles

nomenclature errors

wrong locus names

Note: statistics include errors found in datasets that were retracted - possible more errors, but QC was stopped

NCBI BioProject—STRseq

Mission: To provide high-confidence STR allele sequence records with uniform annotation, facilitating exchange of information across forensic laboratories.

- Collaborators with large datasets "seed" the BioProject
- NIST evaluates raw sequence data with agnostic bioinformatic pipeline
- GenBank record for **all unique sequences**
- BioProject searchable by string (BLAST), locus, allele…

```
LOCUS          AF123456       196 bp  DNA     linear  PRI     19-Jan-2017
DEFINITION     Homo sapien microsatellite D21S11 sequence
ACCESSION      AF123456
VERSION        AF123456.1
DBLINK         BioProject:    PRJNA12345
ORGANISM       Homo sapien
REFERENCE      1 (bases 1 to 196)
AUTHORS        Gettings, K.B., Kiesler, K.M., Steffen, C.R., Borsuk, L.A., and P.M. Vallone.
TITLE          U.S. Population Sequence Data for 27 Autosomal STR Loci, 24 YSTR Loci and 7 XSTR Loci
JOURNAL        Forensic Science International: Genetics
COMMENT        Annotation ("bracketing") of the repeat region is consistent with the guidance of the ISFG (International Society for Forensic
               Genetics), PMID: 26844919. Lower case letters in the bracketed repeat region below (rpt_unit_seq) denote uncounted bases.
               The given length-based allele value was determined using the designated length-based technology. Variation in the length-based
               allele between individuals or assays can result from indels in flanking regions.
               This information is provided as part of the STR Sequencing Project (STRseq), a collaborative effort of the international
               forensic DNA community. The mission of this Project is to provide high-confidence STR allele sequence data and uniform
               characterization, facilitating exchange of information across forensic laboratories and compatibility with preceding
               technology. For questions or feedback, please contact strseq@nist.gov. Allele frequency data can be accessed in the
               strider.online database.

##humanSTR-START##
Sample source          ::     Genomic DNA
Sequencing technology  ::     MiSeq ForenSeq
Coverage               ::     >30X
Length-based allele    ::     28
Length-based tech.     ::     ABI3500xl GlobalFiler
STR locus name         ::     D21S11
STR locus alt. name    ::
Chromosomal location   ::     21q21.1
GRCh38 coordinates     ::     CHR21:19181953-19182149
GRCh38 repeat_region   ::     CHR21:19181973-19182099
##humanSTR-END##

FEATURES       Location/Qualifiers
variation              10..10
                       /db_xref="dbSNP:rs123456"
                       /note="SNP A/C"
repeat_region  21..144
                       rpt_type="tandem"
                       rpt_unit_seq=  "[TCTA]4 [TCTG]6 [TCTA]3 ta [TCTA]3 tca [TCTA]2 tccata [TCTA]10"
                       satellitemicrosatellite="D21S11"
variation              182..182
                       /db_xref="dbSNP:rs12345"
                       /note="SNP C/T"
ORIGIN
1      ATTCCCCAAG TGAATTGCCT TCTATCTATC TATCTATCTG TCTGTCTGTC TGTCTGTCTG
61     TCTATCTATC TATATCTATC TATCTATCAT CTATCTATCC ATATCTATCT ATCTATCTAT
121    CTATCTATCT ATCTATCTAT CTATCGTCTA TCTATCCAGT CTATCTACCT CCTATTAGTC
181    TGTCTCTGGA GAACA
//
```

NCBI BioProject STRseq

- Publication containing sequence
- Description of STRseq
- Metadata
- Annotation
- Sequence String

```
LOCUS          AF123456       196 bp  DNA     linear  PRI     19-Jan-2017
DEFINITION     Homo sapien microsatellite D21S11 sequence
ACCESSION      AF123456
VERSION        AF123456.1
DBLINK         BioProject:    PRJNA12345
ORGANISM       Homo sapien
REFERENCE      1 (bases 1 to 196)
AUTHORS        Gettings, K.B., Kiesler, K.M., Steffen, C.R., Borsuk, L.A., and P.M. Vallone.
TITLE          U.S. Population Sequence Data for 27 Autosomal STR Loci, 24 YSTR Loci and 7 XSTR Loci
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               Genetics), PMID: 26844919. Lower case letters in the bracketed repeat region below (rpt_unit_seq) denote uncounted bases.
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               This information is provided as part of the STR Sequencing Project (STRseq), a collaborative effort of the international
               forensic DNA community. The mission of this Project is to provide high-confidence STR allele sequence data and uniform
               characterization, facilitating exchange of information across forensic laboratories and compatibility with preceding
               technology. For questions or feedback, please contact strseq@nist.gov. Allele frequency data can be accessed in the
               strider.online database.

##humanSTR-START##
Sample source          ::      Genomic DNA
Sequencing technology  ::      MiSeq ForenSeq
Coverage               ::      >30X
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Length-based tech.     ::      ABI3500xl GlobalFiler
STR locus name         ::      D21S11
STR locus alt. name    ::
Chromosomal location   ::      21q21.1
GRCh38 coordinates     ::      CHR21:19181953-19182149
GRCh38 repeat_region   ::      CHR21:19181973-19182099
##humanSTR-END##

FEATURES       Location/Qualifiers
variation              10..10
                       /db_xref="dbSNP:rs123456"
                       /note="SNP A/C"
repeat_region  21..144
                       rpt_type="tandem"
                       rpt_unit_seq=  "[TCTA]4 [TCTG]6 [TCTA]3 ta [TCTA]3 tca [TCTA]2 tccata [TCTA]10"
                       satellitemicrosatellite="D21S11"
variation              182..182
                       /db_xref="dbSNP:rs12345"
                       /note="SNP C/T"
ORIGIN
1       ATTCCCCAAG TGAATTGCCT TCTATCTATC TATCTATCTG TCTGTCTGTC TGTCTGTCTG
61      TCTATCTATC TATATCTATC TATCTATCAT CTATCTATCC ATATCTATCT ATCTATCTAT
121     CTATCTATCT ATCTATCTAT CTATCGTCTA TCTATCCAGT CTATCTACCT CCTATTAGTC
181     TGTCTCTGGA GAACA
//
```

Kit / Instrument / Quality

Length-based allele

Location on reference genome

SNPs or InDels

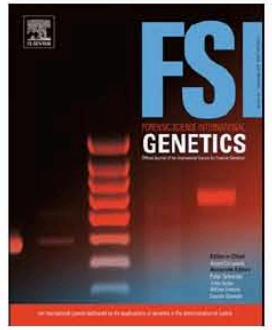
Bracketed Sequence

Forensic Science International: Genetics 31 (2017) 111–117

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsigen



Research paper

STRSeq: A catalog of sequence diversity at human identification Short Tandem Repeat loci

Katherine Butler Gettings[a,*], Lisa A. Borsuk[a], David Ballard[b], Martin Bodner[c], Bruce Budowle[d,e], Laurence Devesse[b], Jonathan King[d], Walther Parson[c,f], Christopher Phillips[g], Peter M. Vallone[a]

NCBI BioProject—STRseq and **STRidER**

Collaboration in QC and exchange of data

STRidER

STRidER STRs for identity ENFSI Reference database, v2

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STR Sequence Nomenclature

The file 'STR Sequence Structure (Supplementary File S1)' is an updated set of forensic STR sequences that accompany the article:

Parson W, Ballard D, Budowle B, Butler JM, Gettings KB, Gill P, Gusmão L, Hares DR, Irwin JA, King JL, de Knijff P, Morling N, Prinz M, Schneider PM, Van Neste C, Willuweit S, Phillips C: **Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements.** Forensic Science International Genetics 2016, 22: 54-63 (doi: 10.1016/j.fsigen.2016.01.009; available at http://www.isfg.org/Publication;Parson2016).

Major changes to this file are currently ongoing. When the review process is finished, a new version of Supplementary File S1 containing updated information will be available for download here. To stay updated about STRidER, register here for the STRidER newsletter.

The updates since the last version are:

-
-
-
-

Updated **STR Sequence Structure file** from ISFG considerations will be available on STRidER

Forensic Science International: Genetics 22 (2016) 54–63

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements

Walther Parson[a,b,*], David Ballard[c], Bruce Budowle[d,e], John M. Butler[f], Katherine B. Gettings[f], Peter Gill[g,h], Leonor Gusmão[i,j,k], Douglas R. Hares[l], Jodi A. Irwin[l], Jonathan L. King[d], Peter de Knijff[m], Niels Morling[n], Mechthild Prinz[o], Peter M. Schneider[p], Christophe Van Neste[q], Sascha Willuweit[r], Christopher Phillips[s]

DNA SeqEx

STR Sequencing & Exchange

INT CIENCIAS FORENSES

CHARITÉ UNIVERSITÄTSMEDIZIN BERLIN

GMI DNA

UNT HEALTH SCIENCE CENTER

Objectives

Promote the implementation of MPS technology for improved STR profiling and international data exchange

Evaluate the impact of STR sequencing on National DNA databases (EU Prüm, CODIS)

Facilitate and standardize forensic STR sequence allele nomenclature

Acknowledgements

R. Scheithauer

Monopoly 2010

Monopoly 2014

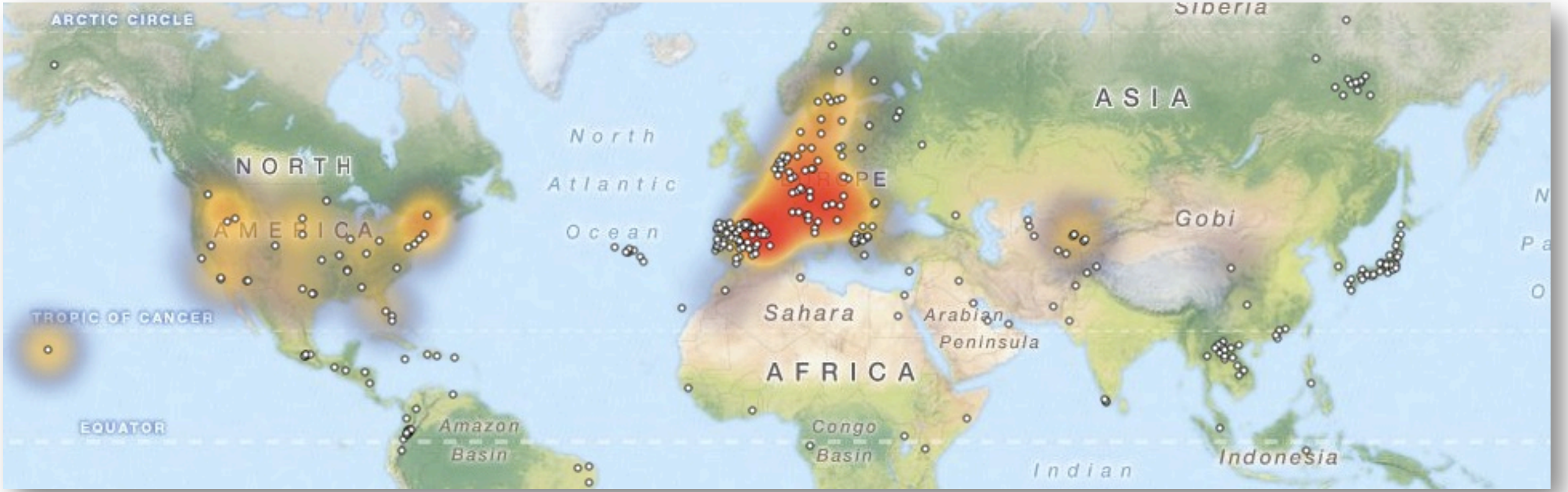
DNA SeqEx
STR Sequencing & Exchange

ISFG Commission on MPS of STRs
ISFG Commission on STRidER

ENFSI laboratories

Peter Gill
Ingo Bastisch
David Ballard
Chris Phillips
Katherine Gettings
Jonathan King
Martin Bodner

STRidER



https://empop.online/

ΕΜΠΟΠ Ὑπδατε

Δρ. Ωἀλθερ Παρσον
ἀσσοχ. Προφ. Ἰνστιτυτε ὀφ Λεγαλ Μεδιχινε, Μεδιχαλ Ὑνιψερσιτυ ὀφ Ἰννσβρυχκ, Αὐστρια
αδθ. Προφ. Φορενσιχ Σχιενχε Προγραμ, Πενν Στατε Ὑνιψερσιτυ, ΠΑ, ΥΣΑ
walther.parson@i-med.ac.at

EDNAP initiative (ISFH 1999)
Create open and freely accessible mtDNA database

EDNAP **M**tDNA **Pop**ulation Database

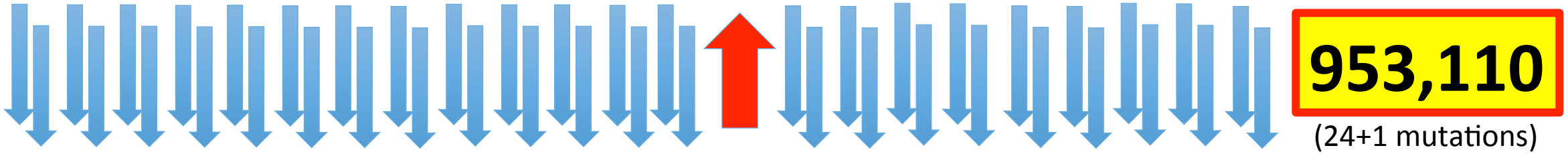
1999

SAM 2

Development of software for automated phylogenetic alignment of mitochondrial DNA sequences

Alignment

16024 TTCTTTCATGGGGAAGCAGATTTGGGTACCACCCAAGTATTGACTCACCCATCAACAACCGCTATGTATTTCGTACATTACTGCCAGCCACCATGAATATTGTACGGTACCATAA
ATACTTGACCACCTGTAGTACATAAAAACCCAATCCACATCAAAACCCCCCCCCCCCATGCTTACAAGCAAGTACAGCAATCAACCCTCAACTATCACACATCAACTGCAACTCCA
AAGCCACCCCTCACCCACTAGGATACCAACAAACCTACCCACCCTTAACAGTACATAGTACATAAAGCCATTTACCGTACATAGCACATTACAGTCAAATCCCCTCTCGCCCCCA
TGGATGACCCCCCTCAGATAGGGGTCCCTTGACCACCATCCTCCGTGAAATCAATATCCCGCACAAGAGTGCTACTCTCCTCGCTCCGGGCCCATAACACTTGGGGGTAGCTA
AAGTGAACTGTATCCGACATCTGGTTCCTACTTCAGGGCCATAAAGCCTAAATAGCCCACACGTTCCCCTTAAATAAGACATCACGATGGATCACAGGTCTATCACCCTATTAAC
CACTCACGGGAGCTCTCCATGCATTTGGTATTTTCGTCTGGGGGGTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCTATGTCGCAGTATCTGTCTTTGATTC
CTGCCTCATCCTATTATTTATCGCACCTACGTTCAATATTACAGGCGAACATACTTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATRATAATAACAATTGAATGTCTGC
ACAGCCGCTTTCCACACAGACATCATAACAAAAAATTTCCACCAAACCCCCCCTCCCCCCGCTTCTGGCCACAGCACTTAAACACATCTCTGCCAAACCCCAAAAACAAAGAACC
CTAACACCAGCCTAACCAGATTTCAAATTTTATCTTTTGGCGGTATGCACTTTTAACAGTCACCCCCCAACTAACACATTATTTTCCCCTCCCACTCCCATACTACTAATCTCATCAA
TACAACCCCCCGCCCATCCTACCCAGCACACACNN--CGCTGCTAACCCCATACCCCGAACCAACCAAACCCCAAAGACACCCCCCCCACA 576



16181C 16182C 16183C 16189C 16213A 16217C 16242T 16261T 16292T 16301T 16519C

61A 62A 73G 183G 263G 309.1C 309.2C 309.3C 315.1C 323N 324N 523Del 524Del

16181C 16182C 16183C 16189C 16213A 16217C 16242T 16261T 16292T 16301T 16519C

61A 62A 73G 183G 263G 308.1C 309.1C 309.2C 315.1C 323N 324N 523Del 524Del

Phylogenetic alignment

Bandelt and Parson (2008)

Consistent treatment of length variants in the human mtDNA control region: a reappraisal

Int J Legal Med 122:1-21

Rule 1. Phylogenetic rule

Rule 2. Anchor 16189 and 310

Rule 3. 3' alignment

adopted by SWGDAM (2013) and ISFG (2014)

Int J Legal Med (2008) 122:11–21
DOI 10.1007/s00414-006-0151-5

ORIGINAL ARTICLE

Consistent treatment of length variants in the human mtDNA control region: a reappraisal

H.-J. Bandelt · W. Parson

Received: 20 March 2006 / Accepted: 13 December 2006 / Published online: 9 March 2007
© Springer-Verlag 2007

Abstract In forensic science, as well as in molecular anthropology and medical genetics, human mitochondrial DNA (mtDNA) variation is being recorded by aligning mtDNA sequences to the revised Cambridge reference sequence (rCRS). This task is straightforward for the vast majority of nucleotide positions but appears to be difficult for some short sequence stretches, namely, in regions displaying length variation. Earlier guidelines for imposing a unique alignment relied on binary alignment to a standard sequence (the rCRS) and used additional priority rules for resolving ambiguities. It turns out, however, that these rules have not been applied rigorously and led to inconsistent nomenclature. There is no way to adopt the priority rules in a reasonable way because binary alignment to a standard sequence is bound to produce artificial alignments that may place sequences separated by a single mutation at mismatch distance larger than 1. To remedy the situation, we propose a phylogenetic approach for multiple alignment and resulting notation.

Keywords Mitochondrial DNA · Haplogroup · Alignment · Phylogeny

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20146 Hamburg, Germany
e-mail: bandelt@math.uni-hamburg.de

W. Parson (✉)
Institute of Legal Medicine, Innsbruck Medical University,
Müllerstrasse 44,
6020 Innsbruck, Austria
e-mail: walther.parson@i-med.ac.at

Introduction

The notation of mitochondrial DNA (mtDNA) variation is reported by reference to the revised Cambridge reference sequence (rCRS; [2]), which is the corrected version of the first fully sequenced mtDNA genome [1]. The forensic community adopted this convention accompanied by guidelines to standardize the mtDNA reporting process [4, 9, 21], in particular by providing general rules for sequence alignment. In a number of cases, however, specifically in the vicinity of the polycytosine stretches of the mtDNA control region, more than one alignment is often conceivable. Therefore, Wilson et al. [24, 25] attempted to standardize nomenclature in length variant regions by introducing formal rules for most parsimonious sequence alignment with respect to the rCRS, which were in principle then applied to the SWGDAM mtDNA database [17].

The increasing body of population data that became available in the past few years improved our understanding of the worldwide mitochondrial phylogeny and revealed that the application of the formal alignment rules could sometimes result in disputable assignments of haplotypes. In this study, we discuss the shortcomings of the Wilson et al. rules and propose a phylogenetic approach to the alignment of mtDNA sequences.

Alignment and nomenclature

In general, the alignment of human mtDNA sequences does not pose serious problems except for the vicinity of polycytosine or dinucleotide tracts that are both prone to considerable length heteroplasmy. Occasionally, however, one faces some real obstacles for unique alignment in some short sequence stretches due to multiple mutations.

Springer

SAM 2

- Manual sequence alignment difficult, ambiguous and error-prone
- We developed new software to perform
  - unbiased sequence searches
  - phylogenetic alignment according to ISFG recommendations
  - haplogrouping of mtDNA haplotypes
- Started external testing in July 2017
- Very positive comments
  - discussing observations/ amending suggested changes
- Publication in preparation
- Change SAM to SAM 2 (Q1 2018)

Query | Result | Details | Neighbors | Alignment | Haplogrouping

Sample ID	
Ranges	16024-576
Profile	16188- 16193.1C 16356C 16519C 263G 315.1C

Query | Result | Details | Neighbors | Alignment

Sample ID	(none specified)
Ranges	16024-576
Profile	16188- 16193.1C 16356C 16519C 263G 315.1C

Entire Database		Frequency	Clopper Pearson CI
	2/26127	7.6549e-5	[9.2706e-6, 2.7649e-4]

Query | Result | Details | Neighbors | Alignment | Haplogrouping

Sample ID

Ranges 16024-576

Profile 16188- 16193.1C 16356C 16519C 263G 315.1C

Query | Result | Details | Neighbors | Alignment | Haplogrouping

Phylogenetic alignment

Input Profile	263G	315.1C	16188-		16193.1C	16356C	16519C
Phylogenetic alignment	263G	315.1C	16188T	16189C		16356C	16519C

Query | Result | Details | Neighbors | Alignment | Haplogrouping

Sample ID

Ranges 16024-576

Profile 16188- 16193.1C 16356C 16519C 263G 315.1C

Query | Result | Details | Neighbors | Alignment | Haplogrouping

Haplogrouping

Rank 1: MRCA: H1b 0.80-0.80

Source	Haplogroup	Cost	Missing Mutations	Private Mutations
PT17		0.80	none	C16188T

SAM 2 schedule

- Expose SamCost to **external testing** (SWGDAM, ISFG WGs,…)
- *Feb 23-24 2017* **mtDNA workshop** at MPI Jena, Germany - presentation to **population genetics**, **anthropology** (W. Haak, M. Richards, A. Torroni, A. Achilli, M. vanOven)
- *Apr 25 2017* **EDNAP**-Meeting - Vilnius, Lithuania
- *Apr 26-28 2017* **ENFSI**-Meeting - Vilnius, Lithuania
- *Jun 06-08 2017* **Human Variome** - Santiago de Compostela, Spain
- *Aug 28-Sep 02 2017* **ISFG** World Conference - Seoul, South Korea
- *May 2018* **Haploid Marker Meeting -** Bydgoszcz, Poland

Acknowledgements

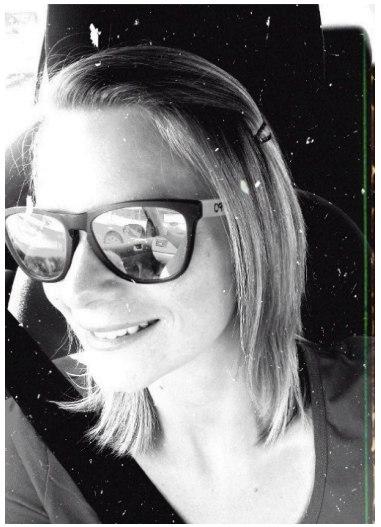
R. Scheithauer

CR and mitogenome

EMPOP database

ISFG Commission on mtDNA
EMPOP collaborators

Arne Dür (Univ. of Innsbruck)
EMPOP Team Innsbruck
IT Team Innsbruck
vxWEB
Nicole Huber



᾽ΙΣΦΓ Υπδατε 2017

President: Walther Parson, Innsbruck • **Vice President**: Mechthild Prinz, New York • **Secretary**: Peter M. Schneider, Cologne
Treasurer: Leonor Gusmão, Rio de Janeiro • **Representative of the Working Parties**: John Butler, Gaithersburg

᾽Αθενς, ᾽Οχτ 25 2017

ISFG Board Meeting in Sept 2016
(held in Minneapolis, MN with ISHI)

27th ISFG World Congress Seoul
Aug 28 - Sep 02 2017

705 participants (excluding local staff and company representatives)

from 68 countries

56 oral presentations

482 poster presentations

11 workshops

27th ISFG Congress Seoul

27th ISFG Congress Seoul

27th ISFG Congress Seoul

27th ISFG Congress Seoul

Status of ISFG Working Groups

https://www.isfg.org/Working%20Groups

Working Group	Working Group Chair (Location)	Recent Activities
German	**Uta-Dorothee Immel** (Halle)	Met June 2016 (Bielefeld), June 2017 (Münster)
English (ESWG-ISFG)	**Andreas Tillmar** (Linköping)	Met Sept 2016 (Budapest), Aug 2017 (Seoul); conducted 2016 and 2017 Relationship Testing Workshops
French	**Vincent Castella** (Lausanne)	Met May 2016 (Predore), May 2017 (Paris)
Italian (Ge.F.I.)	**Susi Pelotti** (Bologna)	Met June 2016 (Rimini)
Spanish & Portuguese (GHEP-ISFG)	**Ulises Toscanini** (Buenos Aires)	Met Sept 2016 (Bayahíbe); published 5 articles since 2015; active proficiency test program
Chinese	**Yiping Hou** (Sichuan)	Met Aug 2017 (Seoul)
Korean	**Soong Deok Lee** (Seoul)	Organized ISFG 2017 (and Asian DNA WG here)
Japanese	--	*Not currently active in ISFG*
DNA Commission	**Peter Gill** (Oslo)	Published 4 articles since 2015
EDNAP	**Niels Morling** (Copenhagen)	Actively meet twice a year; 2 articles since 2015

Proposal for a Polish Working Group

Support expressed from researchers at

1. Jagiellonian University
2. Institute of Forensic Research
3. Pomeranian Medical University
4. Warsaw Medical University
5. Nicolaus Copernicus University
6. Medical University of Gdańsk
7. Wroclaw Medical University
8. Poznan University of Medical Science
9. Medical University of Lublin
10. Central Forensic Laboratory of the Police Biology Department
11. Medical University of Lodz
12. Medical University of Bialystok

Kraków, 18th April 2017

Letter of Intent

Dear President of the International Society for Forensic Genetics
Dear Professor Walther Parson,

By signing this Letter of Intent we hereby declare our intention to initiate a Polish Speaking Working Group within the International Society for Forensic Genetics.

The undersigned institutions collaborate in Poland promoting the exchange of scientific experiences in the field of forensic genetics. The initiative is strongly supported by the local organizers of the 26th ISFG Congress in Krakow and organizers of the successful local meeting – Symposium of Forensic Genetics with the associated workshops co-organized by the EUROFORGEN-NoE consortium. We plan to meet regularly at national level continuing the idea of the Symposium of Forensic Genetics.

We are convinced that formation of the Polish Speaking Working Group will contribute not only to better promotion of forensic genetics in Poland, but also to propagation of standards, sharing best practices and more effective collaboration of Polish forensic DNA laboratories at national and international levels.

Canine DNA Profiling (CaDNAP) Group

Canine DNA profiling group

B. Berger presenting at ISFG 2017

- The **Canine DNA Profiling (CaDNAP) group** was founded in 2003 as collaboration of the **Institute of Legal Medicine Innsbruck** with the **German Federal Criminal Police Office** (Bundeskriminalamt Wiesbaden; BKA).
- In 2008 the **Institute of Veterinary Pathology, Justus-Liebig-University, Giessen** joined the group,
- and in 2015 the **Institute of Forensic Medicine, University of Zurich** joined

- **Objectives:**
- selection, characterization and validation of suitable canine STR markers
- establishment of a harmonized STR nomenclature (based on repeats)
- setting quality standards comparable to human identification (allelic ladders, etc.)
- application in forensic casework

Canine DNA Profiling (CaDNAP) group

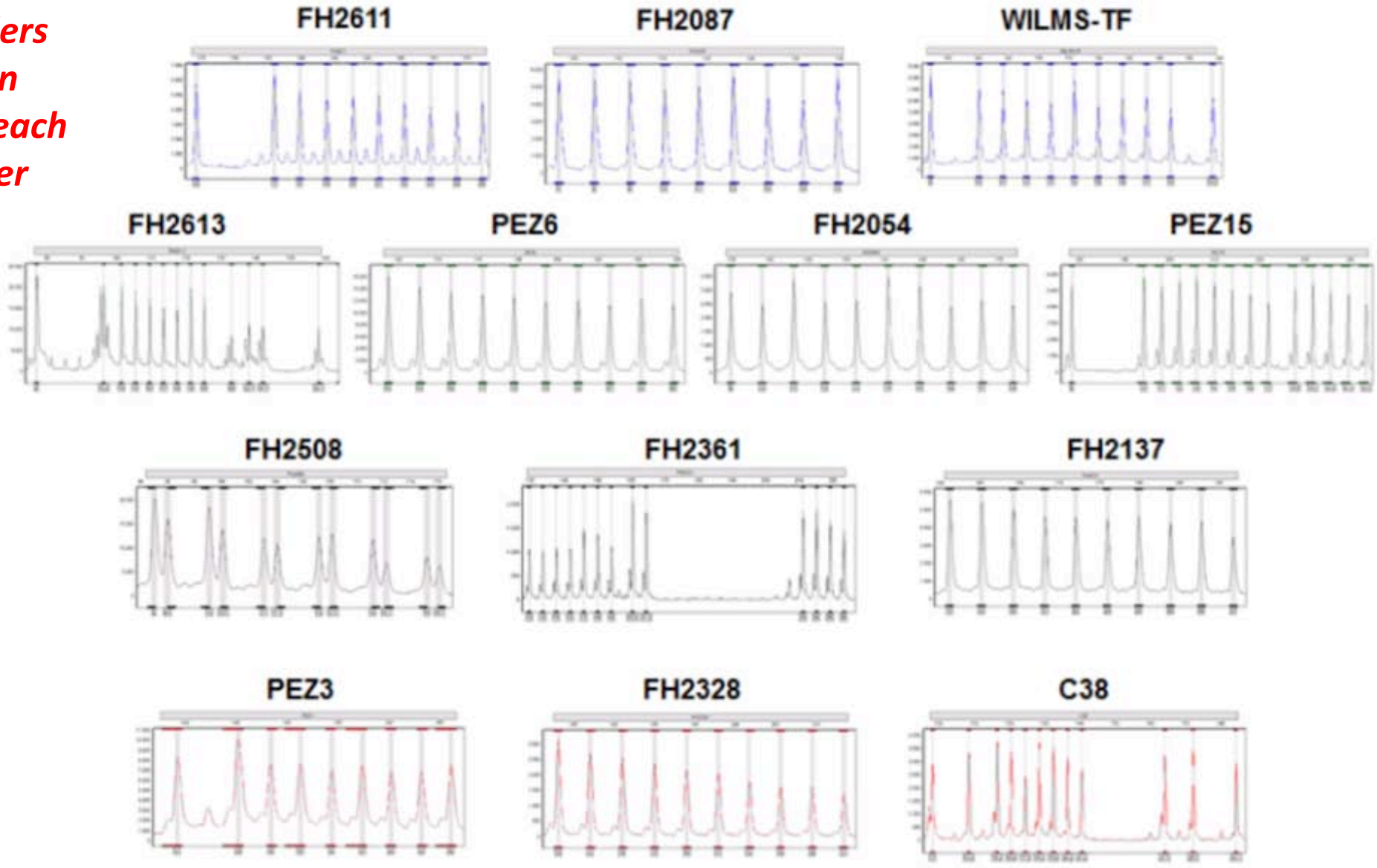
- **„Forensic canine DNA profiling“ Meetings**
  - 12 meetings since 2003
  - alternating organized by the member institutes
  - next meeting: September 2017 in Wiesbaden, Germany, organized by BKA

- **biannual CaDNAP Proficiency Test**
  - first PT: 2014/15 (CaDNAP intern only)
  - second PT: 2016/17 (open to all interested laboratories)

- first papers have been published in 2004
- In 2011 members of the CaDNAP group were invited as co-authors to publish the recommendations of the ISFG regarding the use of non-human (animal) DNA in forensic genetic investigations *[Linacre et al. 2011]*.
- In 2014 the CaDNAP group published protocols for the analysis of dog specific STRs, assembled in two multiplex reactions that were validated according to the above mentioned ISFG guidelines *[Berger et al. 2014]*.

Canine DNA Profiling (CaDNAP) group

Allelic ladders have been created for each STR marker



Canine DNA Profiling (CaDNAP) group

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Canine DNA Profiling (CaDNAP) group

Forensic canine DNA profiling Meeting 2015 in Innsbruck

Forensic Science International: Genetics

Journal Status Report

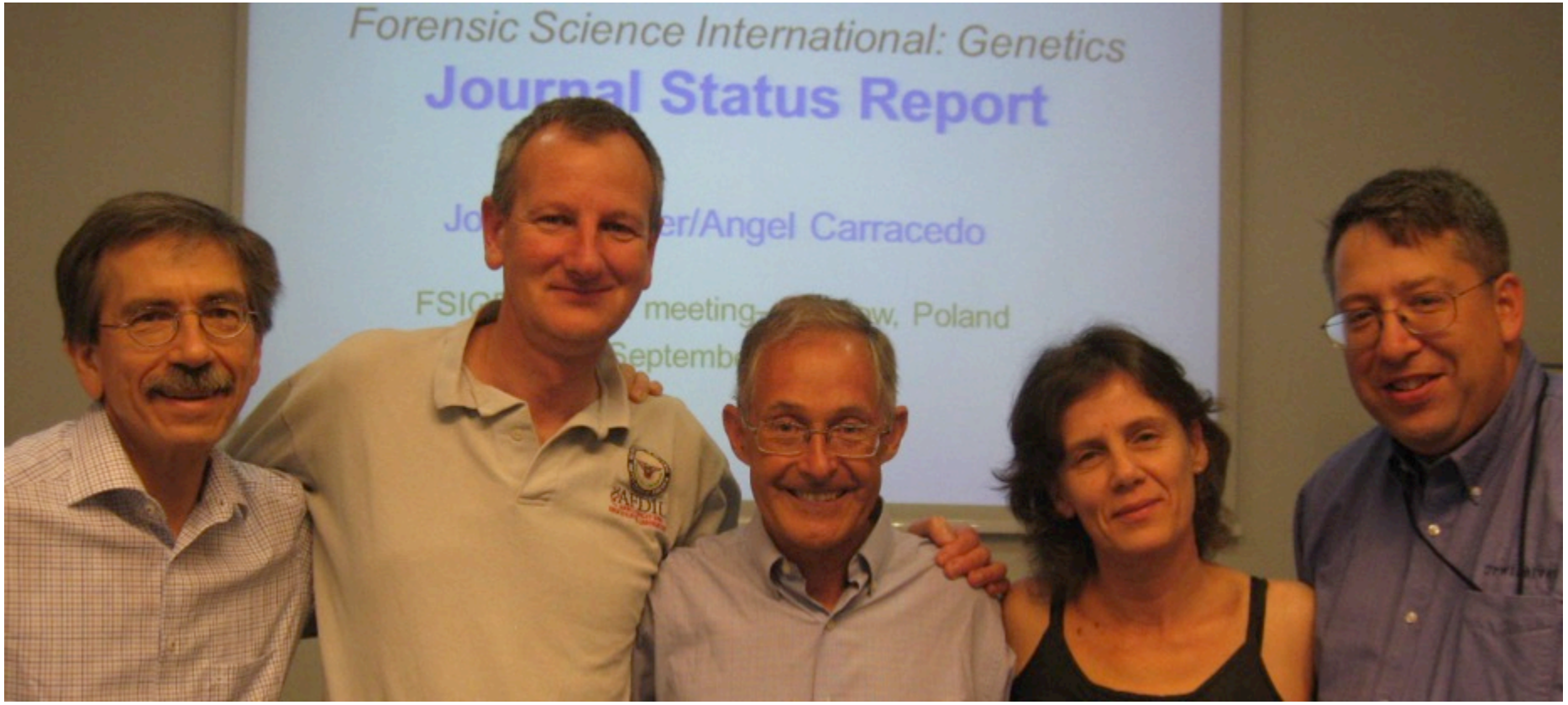
John M. Butler

Associate Editor

ISFG General Assembly – Seoul, South Korea

31 August 2017

Journal Editors



Peter Schneider
(Associate Editor)

Angel Carracedo
(Editor-in-Chief)

John Butler
(Associate Editor)

Adrian Linacre
(Associate Editor)

Leonor Gusmão
(Associate Editor)

Current *FSI Genetics* Editorial Board

Angel Carracedo (Editor-in-Chief)

Peter Schneider (Associate Editor)
John Butler (Associate Editor)
Adrian Linacre (Associate Editor)
Leonor Gusmão (Associate Editor)
Walther Parson (Associate Editor)

8 individuals
were added to the editorial board since 2013

Walther Parson will become an Associate Editor

http://www.fsigenetics.com/edboard

Cintia Alves, Portugal
Charles Brenner, USA
John Buckleton, New Zealand
Bruce Budowle, USA
Michael Coble, USA
Thore Egeland, Norway
Rolf Fimmers, Germany
Peter Gill, UK
Manfred Kayser, The Netherlands
James Lee, Taiwan
Bertrand Ludes, France
Wolfgang Mayr, Austria
Niels Morling, Denmark
Walther Parson, Austria → moving to Associate Editor
Tom Parsons, Bosnia & Herzegovina (now The Netherlands)
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Lutz Roewer, Germany
Antti Sajantila, Finland
Antonio Salas, Spain
Titia Sijen, The Netherlands
Keji Tamaki, Japan
Andreas Tillmar, Sweden
Peter Vallone, USA

Latest *FSI Genetics* Impact Factors

For 2016 (released June 2017)

3.911 based on 3,366 citations

Generally we have experienced an increasing number of citations and a rising impact factor

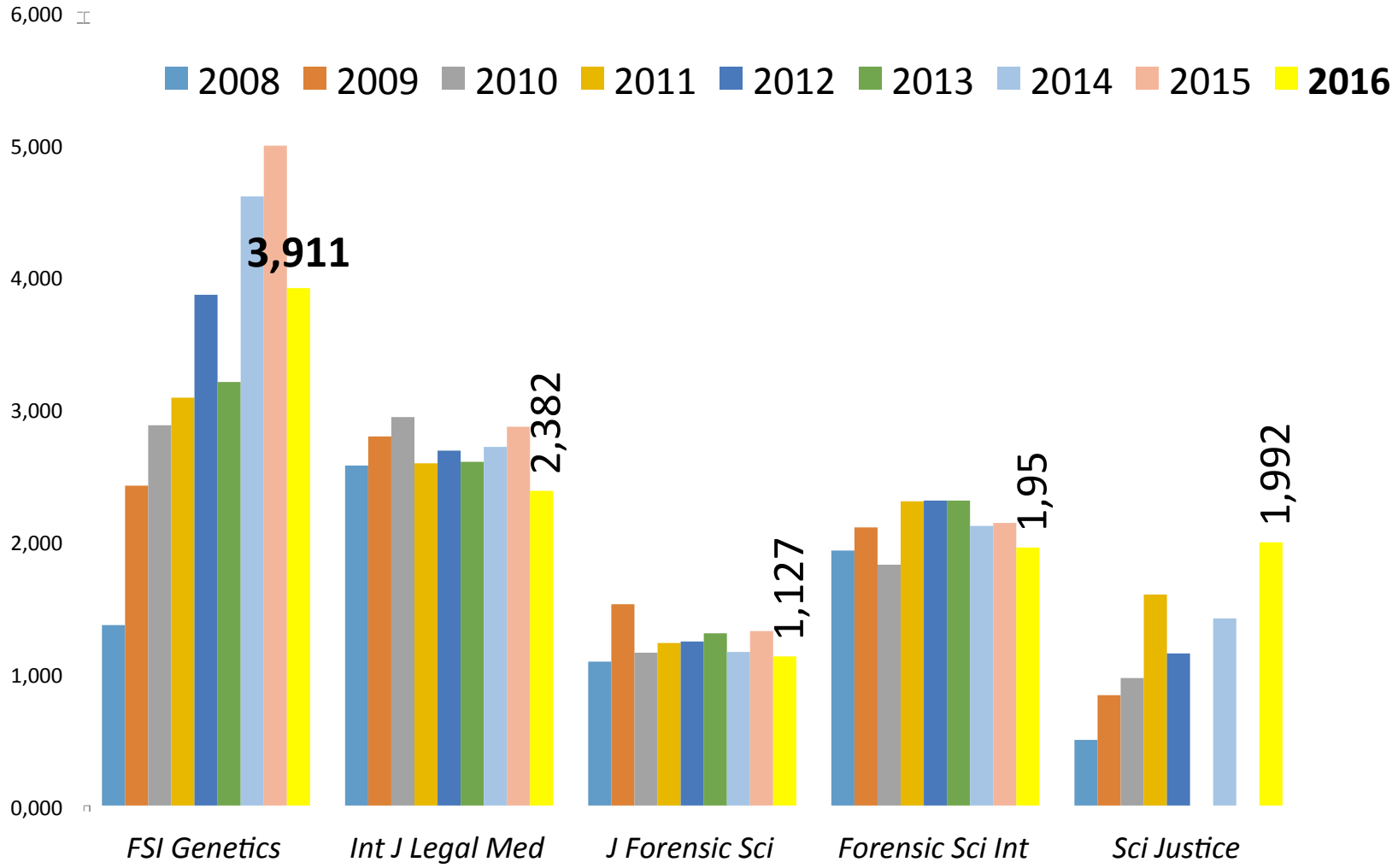
Year	# Citations	Impact Factor
2012	1,461	3.861
2013	1,656	3.202
2014	2,388	4.604
2015	3,424	4.988
2016	**3,366**	**3.911**

FSI Genetics is the #1 Journal

in the Forensic Science & Legal Medicine Category

Rank	Journal	2016 Impact Factor
1	***Forensic Science International: Genetics***	**3.911**
2	*International Journal of Legal Medicine*	2.382
3	*Regulatory Toxicology and Pharmacology*	2.221
4	*Science & Justice*	1.992
5	*Forensic Science International*	1.989
6	*Forensic Science, Medicine, & Pathology*	1.842
7	*Legal Medicine*	1.276
8	*Journal of Law Medicine & Ethics*	1.223
9	*Journal of Forensic and Legal Medicine*	1.135
10	*Journal of Forensic Sciences*	1.127

Impact Factors for Forensic Genetics Journals



2017 Population Data Requirements

Forensic Science International: Genetics 30 (2017) 160–163

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Editorial

Revised guidelines for the publication of genetic population data

- **Introduces a quality check of autosomal STR population data using STRidER**
- **Provides new requirements for MPS generated population data**
- **Provides updates on the minimum number of samples and markers required for autosomal, Y-chromosomal, and X-chromosomal population data**

Updated (2017) Requirements for Population Data Submissions

		Minimum requirements		
		Data[a]	No. samples[c]	Submission to:
Data type	Au-STRs	15 STRs	500	STRidER
	X-STRs	12 STRs	500 (males)	–
	Y-STRs	23 STRs	400	YHRD
	Au-SNPs/ InDels	30 SNPs/InDels	500	–
	X-SNPs/Indels	20 SNPs/InDels	500 (males)	–
	Y-SNPs/Indels	[b]	300	YHRD
	mtDNA_Sanger	Full CR	200	EMPOP
	mtDNA_Sanger	Full mtDNA molecule	100	EMPOP
	mtDNA-SNPs	SNPs in coding region[b]	200	EMPOP
	MPS	MPS–strings	50	–

Gusmao et al. (2017) *Forensic Sci Int Genet* 30: 160-163

Achievements 2015 - 2017

CONGRESS PROCEEDINGS

Freely available

Conference Volumes of the International Society for Forensic Genetics

Progress in Forensic Genetics 16
26th Congress of the International Society for Forensic Genetics,
Kraków, Poland, 2015
Edited by: W. Branicki, T. Kupiec and M. Prinz
Forensic Science International Genetics Supplement Series, Vol. 5, No. 1, 2015

Progress in Forensic Genetics 15
25th Congress of the International Society for Forensic Genetics,
Melbourne, Australia, 2013
Edited by: A. Linacre and N. Morling
Forensic Science International Genetics Supplement Series, Vol. 4, No. 1, 2013

Progress in Forensic Genetics 14
24th Congress of the International Society for Forensic Genetics,
Vienna, Austria, 2011
Edited by: N. Morling
Forensic Science International Genetics Supplement Series, Vol. 3, No. 1, 2011

Achievements 2015 - 2017

Forensic Science International: Genetics 22 (2016) 54–63

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Massively parallel sequencing of forensic STRs: Considerations of the DNA commission of the International Society for Forensic Genetics (ISFG) on minimal nomenclature requirements

Walther Parson[a,b,*], David Ballard[c], Bruce Budowle[d,e], John M. Butler[f], Katherine B. Gettings[f], Peter Gill[g,h], Leonor Gusmão[i,j,k], Douglas R. Hares[l], Jodi A. Irwin[l], Jonathan L. King[d], Peter de Knijff[m], Niels Morling[n], Mechthild Prinz[o], Peter M. Schneider[p], Christophe Van Neste[q], Sascha Willuweit[r], Christopher Phillips[s]

Achievements 2015 - 2017

Forensic Science International: Genetics 24 (2016) 97–102

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Recommendations of the DNA Commission of the International Society for Forensic Genetics (ISFG) on quality control of autosomal Short Tandem Repeat allele frequency databasing (STRidER)

Martin Bodner[a], Ingo Bastisch[b], John M. Butler[c], Rolf Fimmers[d], Peter Gill[e,f], Leonor Gusmão[g,h,i], Niels Morling[j], Christopher Phillips[k], Mechthild Prinz[l], Peter M. Schneider[m], Walther Parson[a,n,*]

Achievements 2015 - 2017

Forensic Science International: Genetics 25 (2016) 191–197

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Research paper

DNA Commission of the International Society for Forensic Genetics: Recommendations on the validation of software programs performing biostatistical calculations for forensic genetics applications

M.D. Coble[a,*], J. Buckleton[b,c], J.M. Butler[d], T. Egeland[e], R. Fimmers[f], P. Gill[g,h], L. Gusmão[i,j,k], B. Guttman[l], M. Krawczak[m], N. Morling[n], W. Parson[o,p], N. Pinto[j,k,q,r], P.M. Schneider[s], S.T. Sherry[t], S. Willuweit[u], M. Prinz[v]

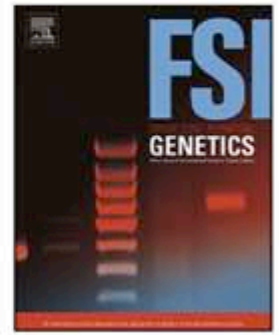
Achievements 2015 - 2017

Forensic Science International: Genetics 29 (2017) 269–275

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig



Research Paper

DNA Commission of the International Society for Forensic Genetics (ISFG): Guidelines on the use of X-STRs in kinship analysis

Andreas O. Tillmar[a,b,*], Daniel Kling[c], John M. Butler[d], Walther Parson[e,f], Mechthild Prinz[g], Peter M. Schneider[h], Thore Egeland[i,1], Leonor Gusmão[j,1]

Member statistics

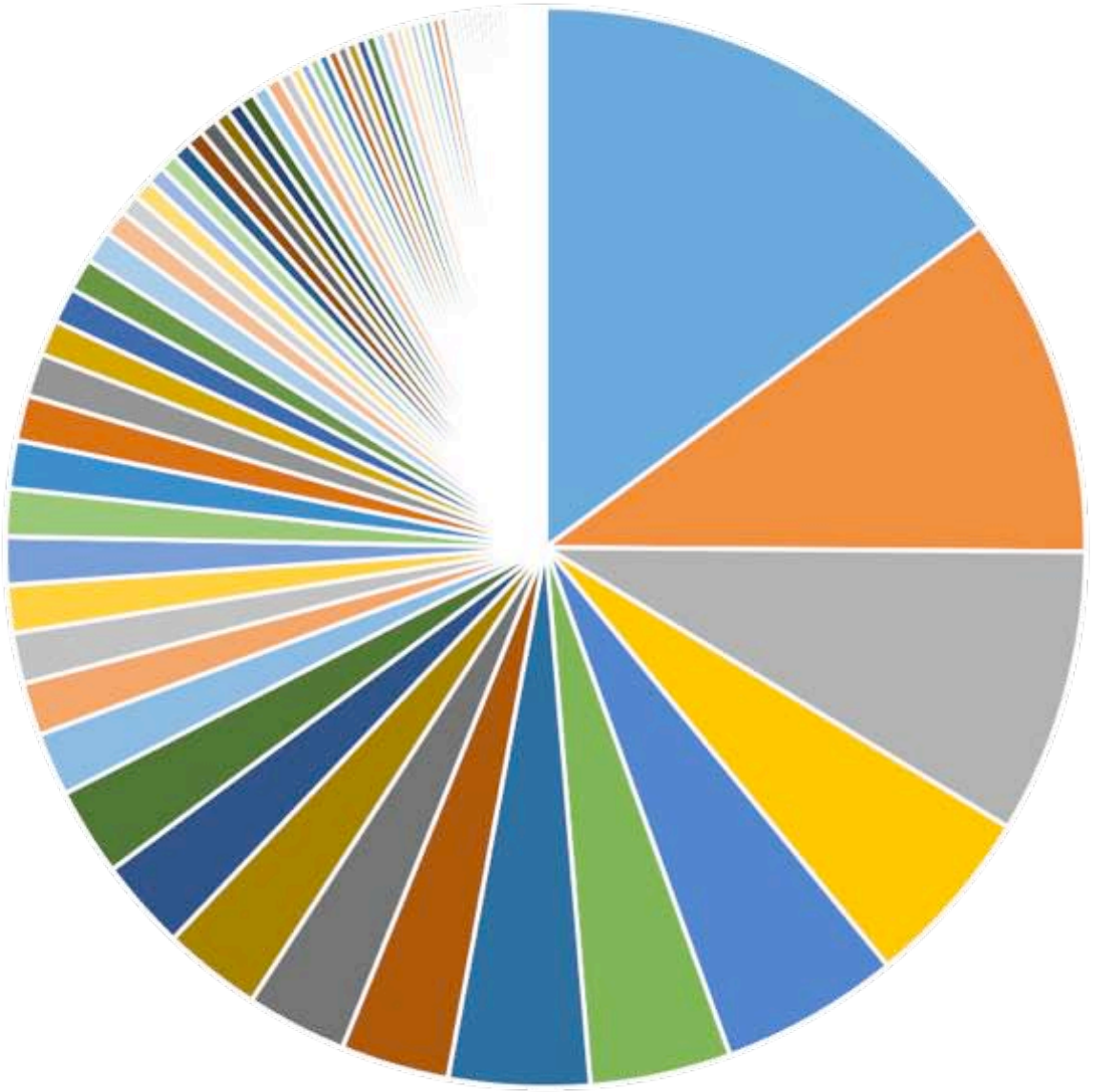
Total number (August 2017):	1325
Countries of origin:	84

Membership has increased by 150 persons since 2015

Changes 2015-2017:

New members accepted:	278
Members removed:	128

Member statistics by country



- United States
- Germany
- Spain
- United Kingdom
- Australia
- Italy
- Korea, Republic of
- Argentina
- Denmark
- Switzerland
- Brazil
- China
- Belgium
- Portugal
- United Arab Emirates
- Austria
- Colombia
- France
- Mexico
- Netherlands
- Poland
- New Zealand
- Norway
- Peru
- Sweden
- Japan

7th ← Korea, Republic of

57

Congress Travel Bursaries

Purpose: To support young scientists presenting at an ISFG congress

- We received 48 applications.
- The initial announcement was for 10 awards. The board reviewed all applicants and spontaneously decided to give out 18 awards.

- This will be made available again for the meeting in Prague 2019.
- For current Terms of Reference, see
  - https://www.isfg.org/files/ISFG_Bursaries_Nov2016.pdf
- We will update this document for the next round.

Travel Bursary Award Winners 2017

Short-term fellowships

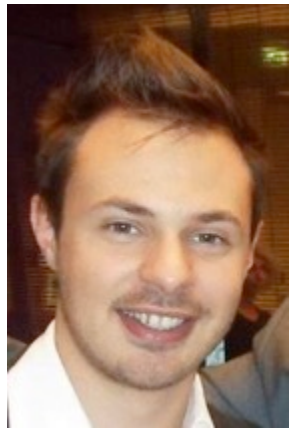
- Purpose: **To support transnational exchange visits between collaborating research groups for specific projects related to forensic genetics**
- For Terms of Reference, see
  - https://www.isfg.org/files/ISFG_Fellowships_Nov2016.pdf
- Announcement was made via the November 2016 ISFG newsletter
- Financial support for travel and accommodations for **up to 1000 euros (within continent)** and **2000 euros (between continents)**
- Applications were received in February and March 2017 with decisions made in April 2017
- Selection committee included the Working Group chairs and was chaired by John Butler from the ISFG Executive Board
- Will be renewed annually depending on available funding

Nine (9) short-term fellowships awarded in 2017

Rui Pereira
Portugal → Brazil

Miriam Ender
Switzerland → Norway

Ana Freire-Aradas
Spain → Poland



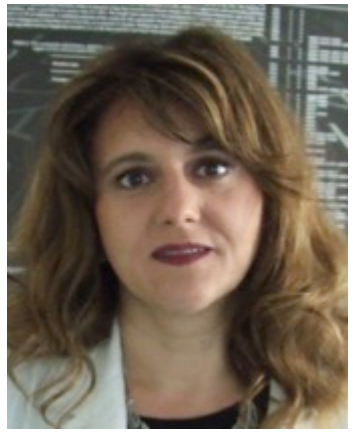
Lode Sibben
Belgium → UK

Runa Daniel
Australia → Spain

Carlo Robino
Italy → Spain

Filipa Simao
Brazil → Austria

Fabio Oldoni
Switzerland → USA



Dragana Zgonjanin
Serbia → United Arab Emirates

Second round of short-term travel fellowships

Second round of short-term fellowships (30 applications)

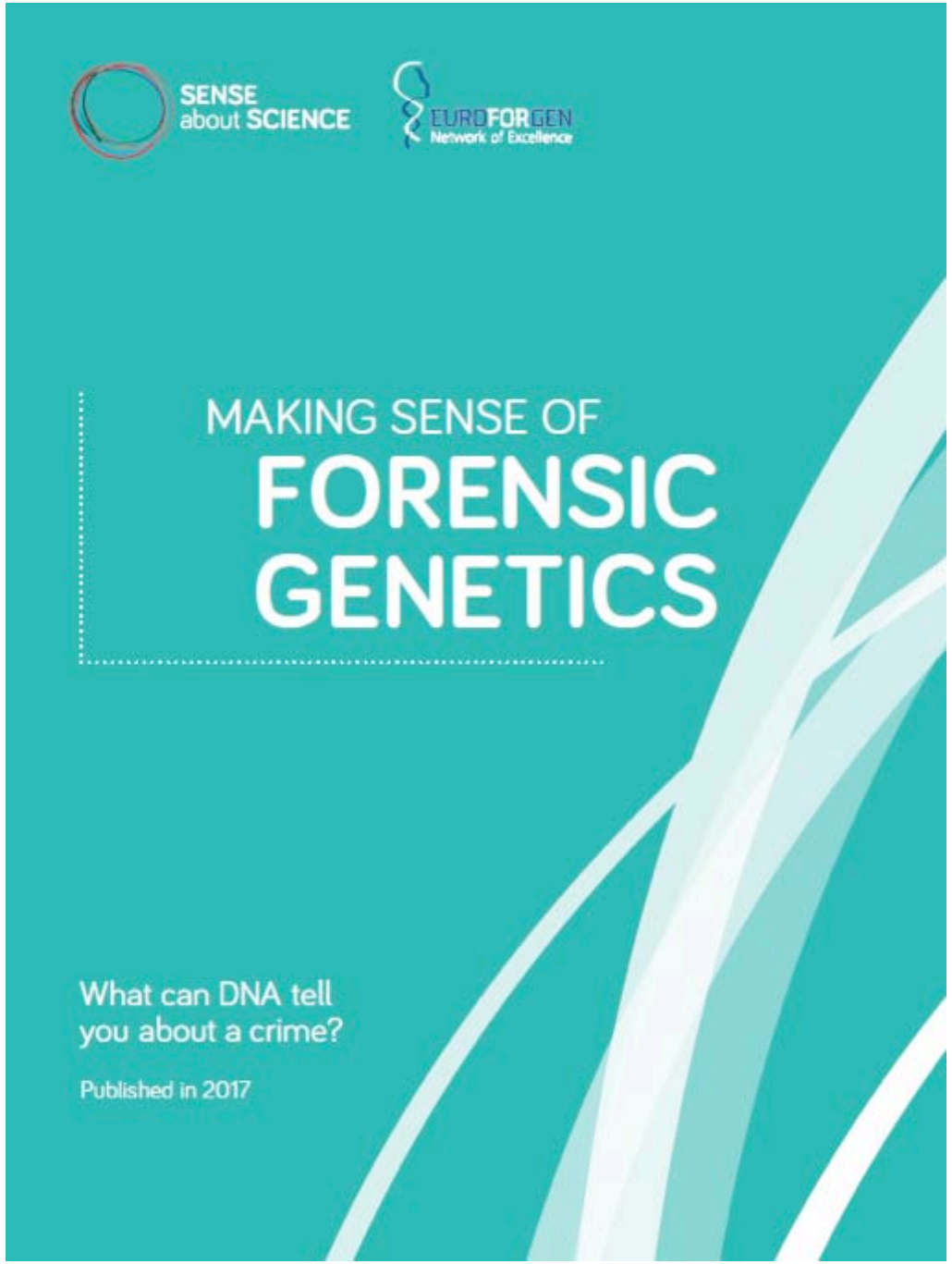
(previous recipients not considered this time)

apply by sending to **fellowships@isfg.org**

first submission deadline October 15th 2017 (open now) for 10 applications

second submission deadline March 1st - April 15th 2018 for 10 applications

third submission deadline September 1st - October 15th 2018 for 10 applications



German

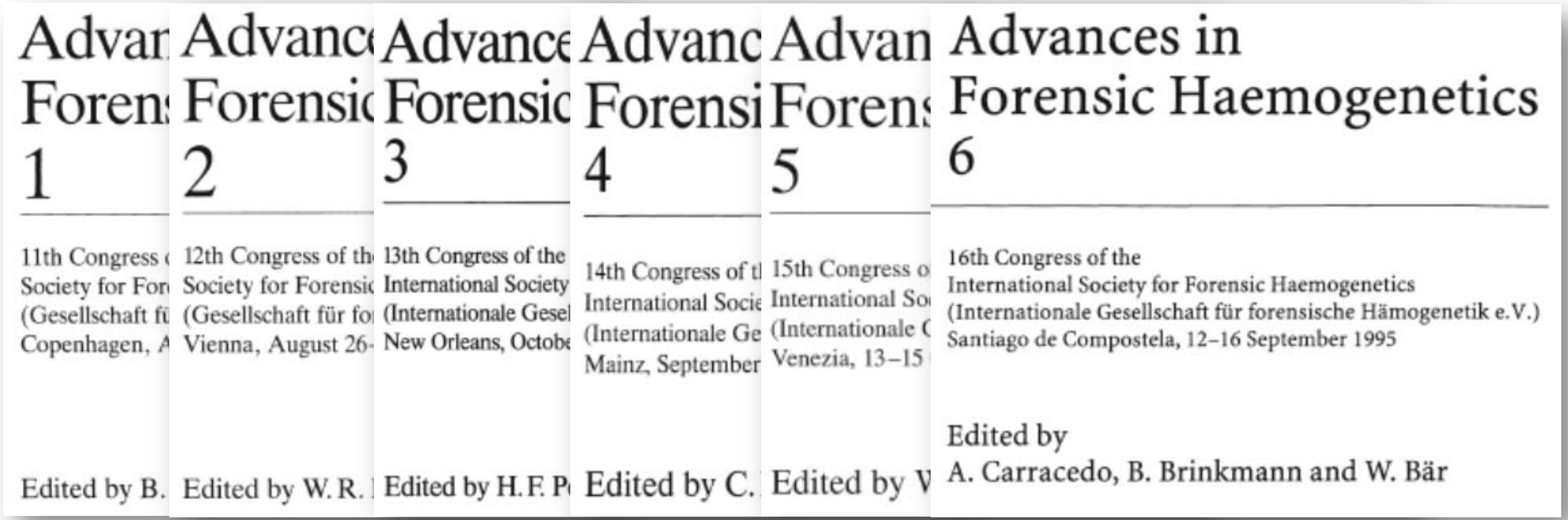
Italian

Spanish

Portuguese

ISFG Website

- Purchase of Springer “Advances in Forensic Haemogenetics” Vol 1-6 (Congress Proceedings 1985 – 1995)
- Will be made available online as a searchable PDF archive



ISFG Newsletter

3 newsletters published 2016-2017

ISFG Scientific Award - Manfred Kayser

Announcements

28th ISFG Congress, Prague

We already started the preparations for the next congress

ISFG
PRAGUE
9–14TH SEPTEMBER 2019
WWW.ISFG2019.ORG

THE 28th CONGRESS OF THE INTERNATIONAL SOCIETY FOR FORENSIC GENETICS

PRAGUE, 9–14TH SEPTEMBER 2019
CZECH REPUBLIC, PRAGUE CONGRESS CENTRE

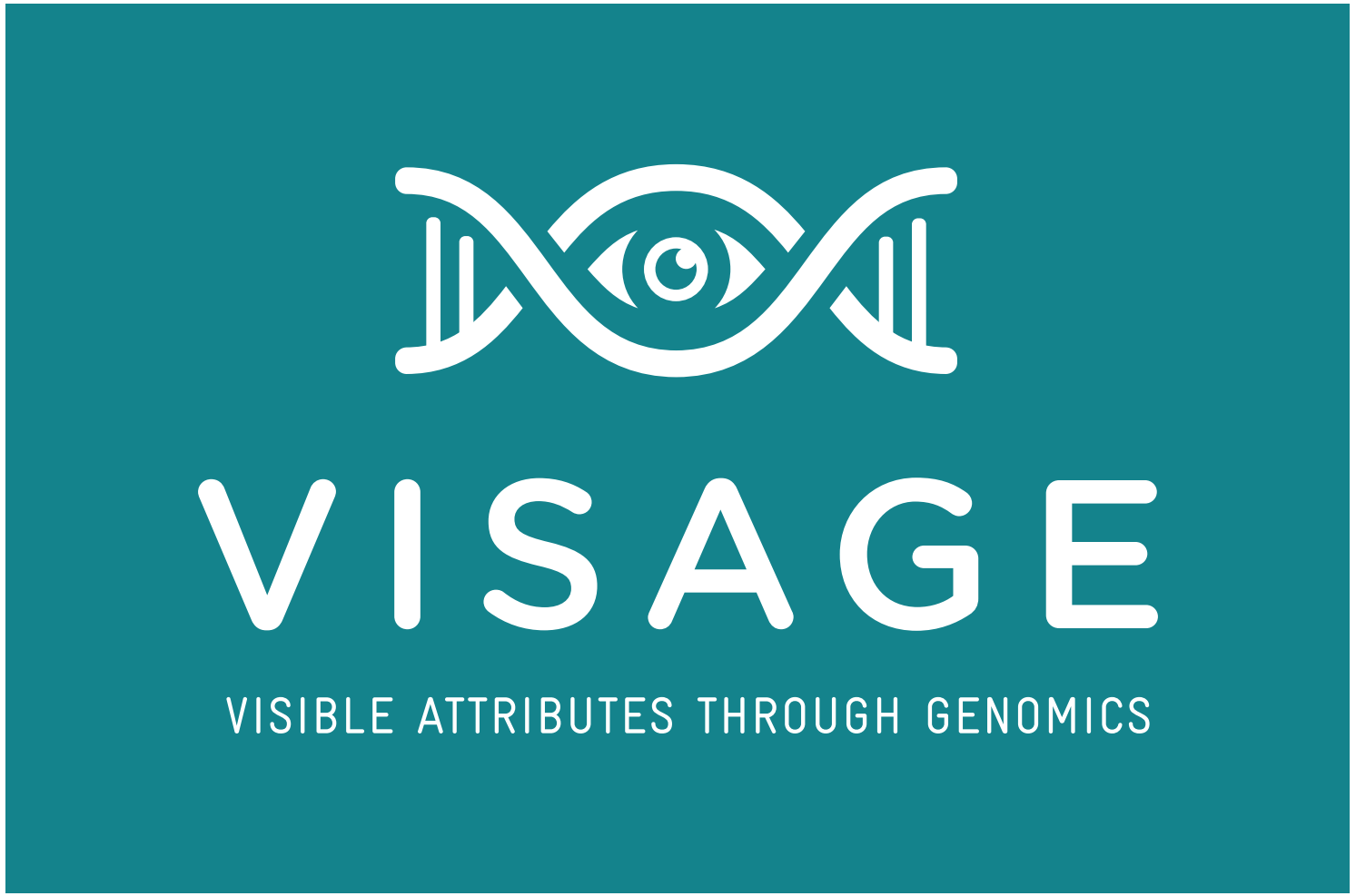
How to become an ISFG member?

- Goto ISFG webpage and click link for membership
- Enter your details
- Nominate 2 reference persons (ISFG members) that support your membership (good to ask them first)
- Have 60 Euro/year ready to spend

Executive committee discusses application

Why should I become a member?

- Because it is cool
- Reduced fee for conferences
- Free access to *Forensic Sciences International Genetics*



ΨΙΣΑΓΕ Ὑπδατε

Δρ. Ωἀλθερ Παρσον
ἀσσοχ. Προφ. Ἰνστιτυτε ὀφ Λεγαλ Μεδιχινε, Μεδιχαλ Ὑνιψερσιτυ ὀφ Ἰννσβρυχκ, Αὐστρια
αδθ. Προφ. Φορενσιχ Σχιενχε Προγραμ, Πενν Στατε Ὑνιψερσιτυ, ΠΑ, Ὑ**ΥΣΑ**
walther.parson@i-med.ac.at

The VISible Attributes Through GEnomics - VISAGE - Consortium will establish new scientific knowledge, develop genotyping and statistical prototype tools, forensically validate and implement them into forensic practice for predicting appearance, age, and ancestry from DNA traces and study its ethical, societal & regulatory dimensions (period: 05/2017-04/2021).

Manfred Kayser (Coordinator) Rotterdam, NED
Wojciech Branicki Krakow, POL
Chris Phillips, Angel Carracedo S. de Compostela, ESP
Walther Parson Innsbruck, AUT
Michael Nothnagel Cologne, GER
Barbara Prainsack Vienna, AUT
Peter M. Schneider Cologne, GER
Ingo Bastisch Wiesbaden, GER
François-Xavier Laurent Lyon, FRA
Titia Sijen The Hague, NED
Johannes Hedmann Linkoping, SWE
Shazia Khan London, UK
Magdalena Spólnicka Warsaw, POL

VISAGE

VISIBLE ATTRIBUTES THROUGH GENOMICS

www.visage-h2020.eu

This project received funding from the European Union's Horizon 2020 Research and Innovation programme under grant agreement No 740580

www.visage-h2020.eu

The VISAGE Consortium

Home

Summary

Objectives

Partners

Scientific Advisory Board

Ethics and Societal Impact Advisory Board

Media

Contact

VISAGE

VISIBLE ATTRIBUTES THROUGH GENOMICS

About the VISAGE Consortium.

The **VIS**ible **A**ttributes Through **GE**nomics - VISAGE - Consortium aims to overcome the general limitation of current forensic DNA analysis by broadening forensic DNA evidence towards constructing composite sketches of unknown perpetrators from as many biological traces and sources and as fast as possible within current legal frameworks and ethical guidelines. The VISAGE Project will establish new scientific knowledge, develop prototype tools for DNA analysis and statistical interpretation, validate and implement these tool in forensic practice,

ResearchGate

Active project | Updates quarterly

VISAGE - Visible Attributes through Genomics

Walther Parson · Manfred Kayser · Christopher P Phillips · Show all 8 collaborators

Goal: Unknown perpetrators of crime cannot be identified with the current forensic use of DNA. The VISAGE Project aims to overcome this major limitation by developing, validating, and implementing in the relevant forensic DNA service environment a set of prototype tools for

Show details

Updates	2	0 new
Recommendations	1	0 new
Followers	40	12 new
Reads	239	76 new

Visage Horizon2020

Walther | Startseite

Visage Horizon2020

@visageh2020

Startseite

Final Report on the European Forensic Genetics Network of Excellence

Prof. Dr. Peter M. Schneider
Institute of Legal Medicine
University Hospital of Cologne

EDNAP Meeting, Athens,
Greece, 25th October 2017

EUROFORGEN-NoE is funded by the European Union
within the 7th Framework Programme

How to wind down a 5-year project

- **The EC requires**
  - Fourth periodic report
  - Final report
  - Financial statement
  - Review meeting
- **The current status**
  - All reports have been accepted after 3 rounds of revisions
  - All financial statements have been accepted (except for some minor expenses for travel and subsistence) by the end of September
  - A major loss due to the bankruptcy of our previous management partner GABO:mi was covered by the EC Guarantee Fund
- **Despite all the painful negotiations, it was worth the effort!**

EUROFORGEN-NoE is funded by the European Union
within the 7th Framework Programme

The Project at CORDIS

- **The final report can be retrieved from the CORDIS server**
  - http://cordis.europa.eu/result/rcn/203192_en.html

EUROFORGEN-NoE is funded by the European Union
within the 7th Framework Programme

The legacy of EUROFORGEN-NoE

- **A European network of forensic DNA labs**
  - connecting >200 members
  - Dissemination via email and social media (Facebook, Twitter)
- **A website with lots of resources such as**
  - Publications & newsletters
  - Videos
  - Education and training resources
- **Integration into the ISFG Working Group activities**
  - Short term fellowship program
  - Summer school educational workshops
  - Support for post graduate curriculum in forensic genetics
- **„Making Sense of Forensic Genetics“**

EUROFORGEN-NoE is funded by the European Union
within the 7th Framework Programme

ISFG Fellowship Program

- The **ISFG** is offering travel fellowships for scientists to support transnational exchange visits between collaborating research groups for projects related to forensic genetics.
- Each fellowship includes financial support for travel and accommodation of up to **EUR 1,000 for visits within the same continent, and EUR 2,000 for visits from continent to continent.**
- Applicants must be ISFG members and have to submit a written application.
- See *https://www.isfg.org/Members+Area/Overview*

EUROFORGEN-NoE is funded by the European Union
within the 7th Framework Programme

ISFG Fellowship Program

- New call with second round of short-term fellowships for 3x 10 applications in 2017-2018
- Apply by sending to fellowships@isfg.org
  - (previous applicants will not be considered again)
- ***First submission deadline October 15th 2017***
- ***Second submission deadline April 15th 2018***
- ***Third submission deadline October 15th 2018***
- All details on ISFG website in Members' Area

International Society for Forensic Genetics

EUROFORGEN-NoE is funded by the European Union within the 7th Framework Programme

Forensic Genetics Summer School

- **The EUROFORGEN – ISFG Summer School will be organized bi-annually**
  - 2 days of educational workshops in locations not visited by ISFG congresses, with topics such as at pre-ISFG congress workshops
  - ISFG will cover expenses for travel and honorarium of faculty, participants pay for local arrangements (hotel, venue, catering)
- **The first Summer School 2018**
  - In connection with the Italian Ge.F.I. meeting in Calabria
  - First half of September 2018
  - 2 full days with 6-9 different topics
  - Details to be published soon!

EUROFORGEN-NoE is funded by the European Union within the 7th Framework Programme

- **Details published in FSI Genetics 28 (2017) e12-e13**

Forensic Science International: Genetics 28 (2017) e12–e13

Contents lists available at ScienceDirect

Forensic Science International: Genetics

journal homepage: www.elsevier.com/locate/fsig

Correspondence

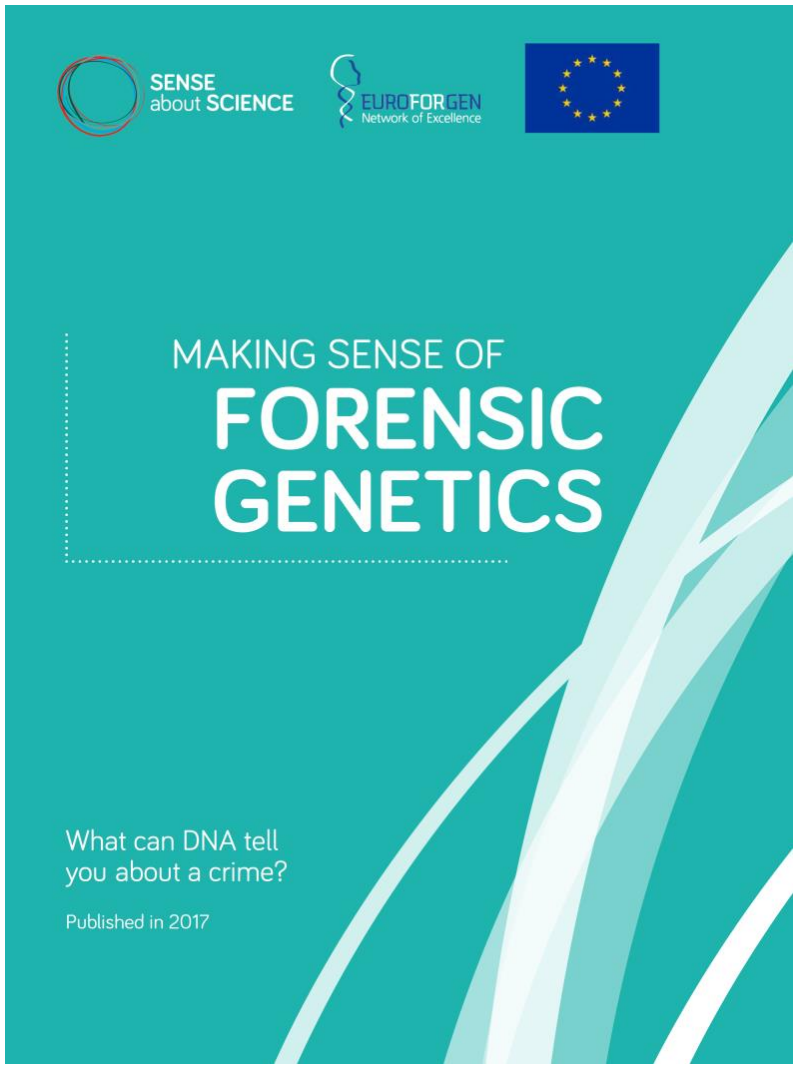
Making progress in education: The EUROFORGEN master degree pilot project in forensic genetics

integration of existing collaborations as well as to establish new interactions in this highly specialized field of security. Therefore, all key players such as scientists, stakeholders and end-users (e.g.

- **Supported by more than 8 universities across Europe**
- **Introduced at the University of Roma Tor Vergata**
  - Coordinated and supervised by Prof. Emiliano Giardina and Prof. Giuseppe Novelli
  - Inscription at http://mastergeneticaforense.it/

EUROFORGEN-NoE is funded by the European Union within the 7th Framework Programme

„Making Sense of Forensic Genetics“



German

Italian

Spanish

Portuguese

- other languages are considered

EUROFORGEN-NoE is funded by the European Union within the 7th Framework Programme

Social media presence

Find us on

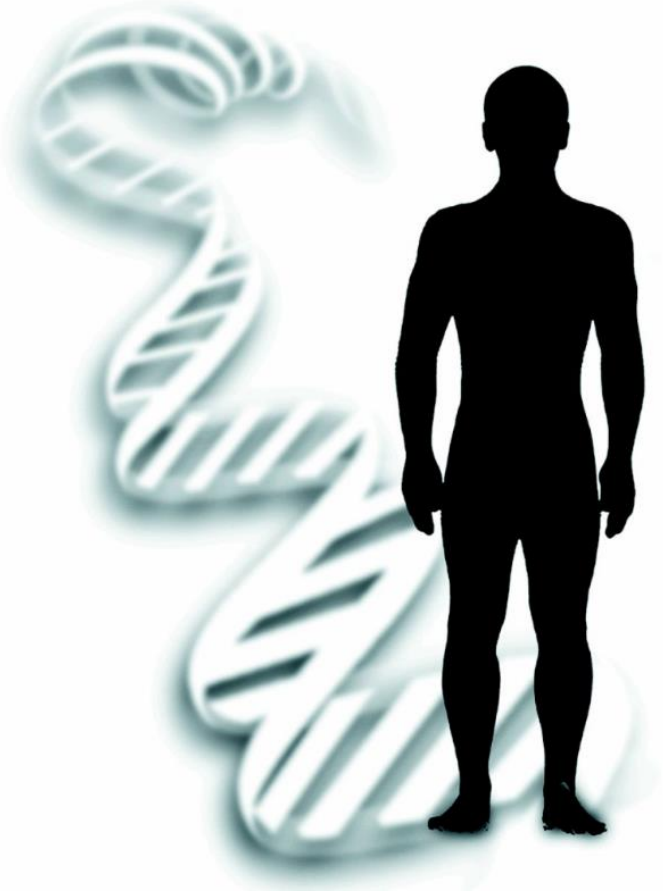
@EUROFORGEN

EUROFORGEN-NoE is funded by the European Union within the 7th Framework Programme

UNIKLINIK KÖLN
Institut für Rechtsmedizin

Plans for the introduction of forensic DNA phenotyping in Germany

Peter M. Schneider



The murder case Maria L.

- A 19-year-old student was raped and killed in Freiburg in October 2016.
- In December 2016, a suspect was arrested. He was identified due due an unusually dyed black-blond hair that could be assigned to him based on CCTV video.
- The suspect was a 18-year-old refugee from Afghanistan who apparently had a previous criminal record from his time in Greece.
- In the context of this case, local police officials as well as the State Minister of Interior called for an amendment of the law to allow DNA-based prediction of hair, eye and skin colour.
- This has started a general debate about „enhanced DNA typing methods“ in Germany.

The public debate

- After these political demands were made public, a group of social scientists from the University of Freiburg published an „open letter“ raising concerns about the reliability and value of DNA phenotyping, as well as the risk of discriminating against ethnic minorities.
  - From these publications and from several newspaper articles it became clear that there is an apparent confusion and lack of knowledge about FDP methods and their scientific background.
- The German Stain Commission published a statement in December to address these issues, and to make clear what can be done, and where limitations exist.
- In March 2017, a public symposium was held in Berlin at the Federal Ministry of Justice to proceed with the debate

The Berlin Symposium (March 2017)

The Berlin Symposium

- **Speakers on March 21st 2017**
- Heiko Maas (Minister of Justice)
- Peter Schneider
- Manfred Kayser
- Ingo Bastisch
- Marion Albers (legal scholar on public law)
- Barbara Praisack (forensic and medical ethics, King‘s College)
- Veronika Lipphardt, Matthias Wienroth (social scientists, Freiburg and Newcastle)

Issues raised against introducing FDP

From: Staubach, Nature (Correspondence) 545: 30, 2017

- The high probabilities for predicting visible traits and … ancestry … do not take into account the prevalence of (observed) traits in the German population.
- Probabilities for rare characteristics can drop to less than 50% when adjusted for prevalence.
- FDP-guided investigations will focus on rare characteristics: a positive test for dark skin … could much more efficiently (even if wrongly) narrow down an investigation than could a positive result for the common trait of light skin.
- Minority groups could therefore become over-represented in police investigations.

Issues raised against introducing FDP

From: Staubach, Nature (Correspondence) 545: 30, 2017

- Biogeographical testing is less reliable for individuals with mixed ancestry or for those from regions that are undersampled in the reference databases.
- Ancestry, ethnicity and appearance are therefore at risk of becoming conflated in policing practice.
- The use of these technologies also requires a balanced framework of governance, including judicial, ethical and regulatory oversight by independent governmental bodies

The current legal basis of forensic DNA analysis in Germany

- The German Code of Criminal Procedures does not allow the investigation of DNA coding regions
- Section 81e:
  - (1) Material *(i.e. reference samples)* may also be subjected to molecular genetic examinations, insofar as such measures are necessary to establish descent or to ascertain whether traces found originate from the accused or the aggrieved person; in so doing the gender of the person may also be determined by examination. … Findings on facts other than those referred to in the first sentence shall not be made; examinations designed to establish such facts shall be inadmissible.
    Examinations admissible pursuant to subsection (1) may also be carried out on trace materials which have been found, secured or seized.

Current proposals to change the code

- Several German Federal States have made proposals in the Federal Council
  - February: Amendment to include only pigmentation markers (eye, hair, skin colour)
  - March: Extension of the amendment to include also biogeographic ancestry and age prediction
- The draft proposal included the need to provide funding of NGS equipment and consumables
- The proposal was rejected to allow further discussions in the parliamentary commissions
- It is expected that the proposal will be resubmitted next year after a new federal government has been formed

Netherlands Forensic Institute
Ministry of Justice

Update ENFSI DNA Expert Working Group activities

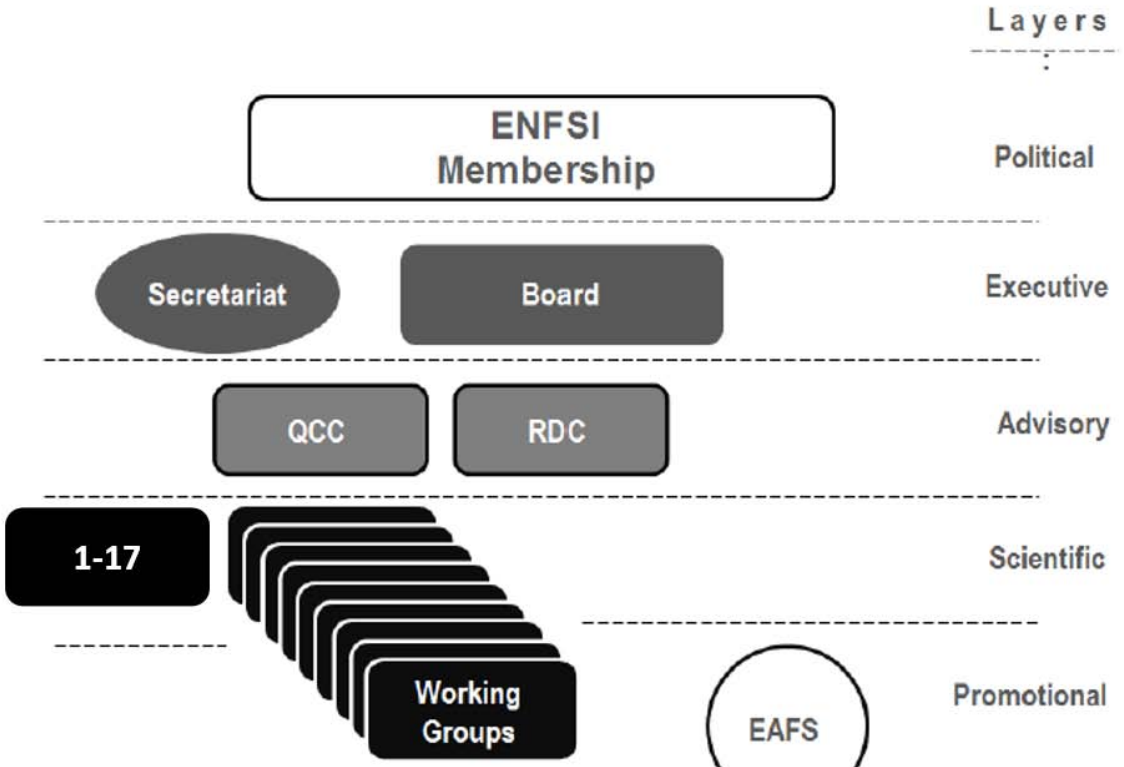
Alexander Kneppers

Chair ENFSI DNA Expert Working Group

NFI Division Biological Traces

SWGDAM meeting Woodbridge July 2017

European Network of Forensic Science Institutes



Blood Pattern Analysis Project Group

Forensic Archeology Project Group

Triennial European Academy of Forensic Science

August 27-31, 2018 Lyon, France

ENFSI member/partner organisations

66 member organisations from 36 countries

67 partner organisations from 27 countries

DNA working group

46 ENFSI member organisations from 35 countries

21 partner organisations from 13 countries

DNA working group

Annual ENFSI board meeting with workgroup chairs

Two steering group meetings DNA working group

Annual meeting of the working group (together with the European CODIS meeting and EDNAP meeting (European DNA Profiling group))

Group A: Quality Assurance

Group B: DNA Analysis Methods & Interpretation

Group C: DNA Database and Legislation

Group D: Automation & LIMS

Group E: Forensic Biology

Documents DNA working group

- DNA database management
- DNA Contamination prevention guidelines
- Minimum validation guidelines in DNA profiling
- Recommendations for the training of DNA staff
- Quality Assurance Programme for DNA Laboratories
- DNA Pattern recognition and comparison (BPM)
- Internal validation of probabilistic software to undertake DNA mixture interpretation (BPM)

Surveys DNA working group

- DNA databases in Europe
- ENFSI Kit, automation and LIMS
- Case management and resources
- Presumptive tests
- Mixture interpretation software
- Rapid DNA

Vilnius 26-28 April 2017
Annual meeting ENFSI DNA Expert Working Group

Host Lithuanian Police Forensic Science Centre

101 persons attending
81 participants
20 company representatives
10 companies
25 countries represented
49 speakers

USA
Singapore
Australia
New Zealand

QA-subgroup

chairs Annick Delaire (France), Tom Heylen (Belgium)

- Contamination prevention guidelines: approval of final version
- Proposal for new contamination survey next year; with questions regarding how labs detect contaminations, which software, only single source stains or not, partial profiles, definition of contamination etc.
- Overarching BPM:
  - Scope to be drafted by February 2018
  - Open for discussion at Spring meeting 2018
  - Different chapters shall be written by the different subgroups according to their expertise

QA-subgroup

chairs Annick Delaire (France), Tom Heylen (Belgium)

- Update document 'Minimum Criteria for the Validation of Various Aspects of theDNA Profiling Process'
- Update Quality Assurance Program for DNA Laboratories
- A survey will be held among the ENFSI laboratories to benchmark contamination rates in different laboratories and to make an inventory of how labs detect contaminations (which software, which kind of profiles (single source, mixtures up to how many persons)

QCLG Meeting

QCC (ENFSI quality control committee)

Quality managers of forensic labs

QCLG liaisons of working groups (June Guiness, FSR, UK)

One day one topic seminar (OOS) on ILAC G19:2014

PT/CT scheme updates

Methods analysis and interpretation sub group

chairs Peter Gill (Norway) and Walther Parson (Austria)

- Training workshop in STR mixture interpretation in conjunction with CEPOL
- EMPOP: Harmonization of mtDNA alignment and notation
  Develop, evaluate and validate software for harmonizing mtDNA alignment and notation across forensic laboratories
- STRidER: Quality control of STR fragment size and sequence data

  Develop, evaluate and validate software for quality control of STR genotypes derived from CE and MPS technologies

DNA database and legislation subgroup

chairs Dyan Daly (Ireland) and Izanda Puncule (Latvia)

European Database:

- Convicted not arrested - Only 11 European Countries (less than 25%) have authorized arrestee testing
- Serious crimes DNA tested, sometimes not all crimes DNA tested
- Very few expansion efforts in last ten years
- Hit rates below 10% except The Netherlands 57% and UK at 60%

DNA database and legislation subgroup

chairs Dyan Daly (Ireland) and Izanda Puncule (Latvia)

- Audit questionnaire: ENFSI DNA Database Management review and Recommendations document contains 34 recommendations > are to be filled in by the persons responsible for the database in their country and returned for compilation. Results presented at Spring meeting 2018

- Subgroup news bulletin on interesting facts for Databases

Update on the implementation of the EU-Prüm Council Decisions

Only 156 connections (33%) have been realized so far

The deadline for the implementation was 26 August 2011 !

The European Commission has written letters to countries that have not yet implemented the Prüm Council Decisions

Automation and LIMS subgroup

Chairs: Christina Forsberg (Sweden) and Shazia Khan (UK)

Exchange knowledge on issues related to laboratory automation, including:

Automated workflows for NGS

Rapid DNA devices

Automation, LIMS and kit inventory list
- Resource for sharing of knowledge

Automation
44 laboratories added information
202 robotic systems listed

LIMS
32 laboratories
17 have LIMS

STR and quantification kits
22 laboratories
STR/qPCR kits from three vendors plus home-brew qPCR

Updated yearly and put on EPE web site

RAPID DNA INSTRUMENT QUESTIONNAIRE

- 11 replies (ENFSI labs and guest)
  - Answers predominantly from labs with interest in the topic
- Send out the questionnaire on rapid DNA again to collect more answers.

Forensic Biology and Casework subgroup

chairs Arnoud Kal (Netherlands) and Ricky Ansell (Sweden)

To address questions from:

- routine casework in and beyond DNA testing
- scene and analytical strategies
- stain characterization
- activity analysis
- case reporting

Two projects still ongoing:

Presumptive test

Study on Case Management and Resources

Updates

- SWGDAM
- ISFG activities
- DNA SEQ EX
- STRbASE>STRidER STR Population Database
- EUROFORGEN Network of Excellence
- GEDNAP > Proficiency testing
- EDNAP > collaborative exercises
- ICMP > Exclusion database

Evaluation of the GEDNAP Proficiency Tests 52 & 53

Carsten Hohoff, Katrin Schnöink & Bernd Brinkmann

Institute of Forensic Genetics, Münster (Germany)

ENFSI DNA WORKING GROUP MEETING:
16:35-17:00, 27 APRIL 2017,
VILNIUS, LITHUANIA

GEDNAP participants

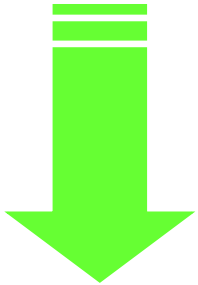
- **230 participants**

  - **university labs: 87**
  - **state labs: 77**
  - **private labs: 66**

44 ENFSI members

GEDNAP 52

39 497 typing events – 33 errors



99.92 % of all analyses are correct

INTERNATIONAL COMMISSION ON MISSING PERSONS

ICMP – EDB

Current statistics

Profiles stored (total 592)

- US collection (Florida): 202
- ICMP collection: 15
- FSS unsourced: 375

Users registered: 39 (last registration 29 Mar 2017)

Searches

- Searches performed: 232
- Matches found: 14

Data storage

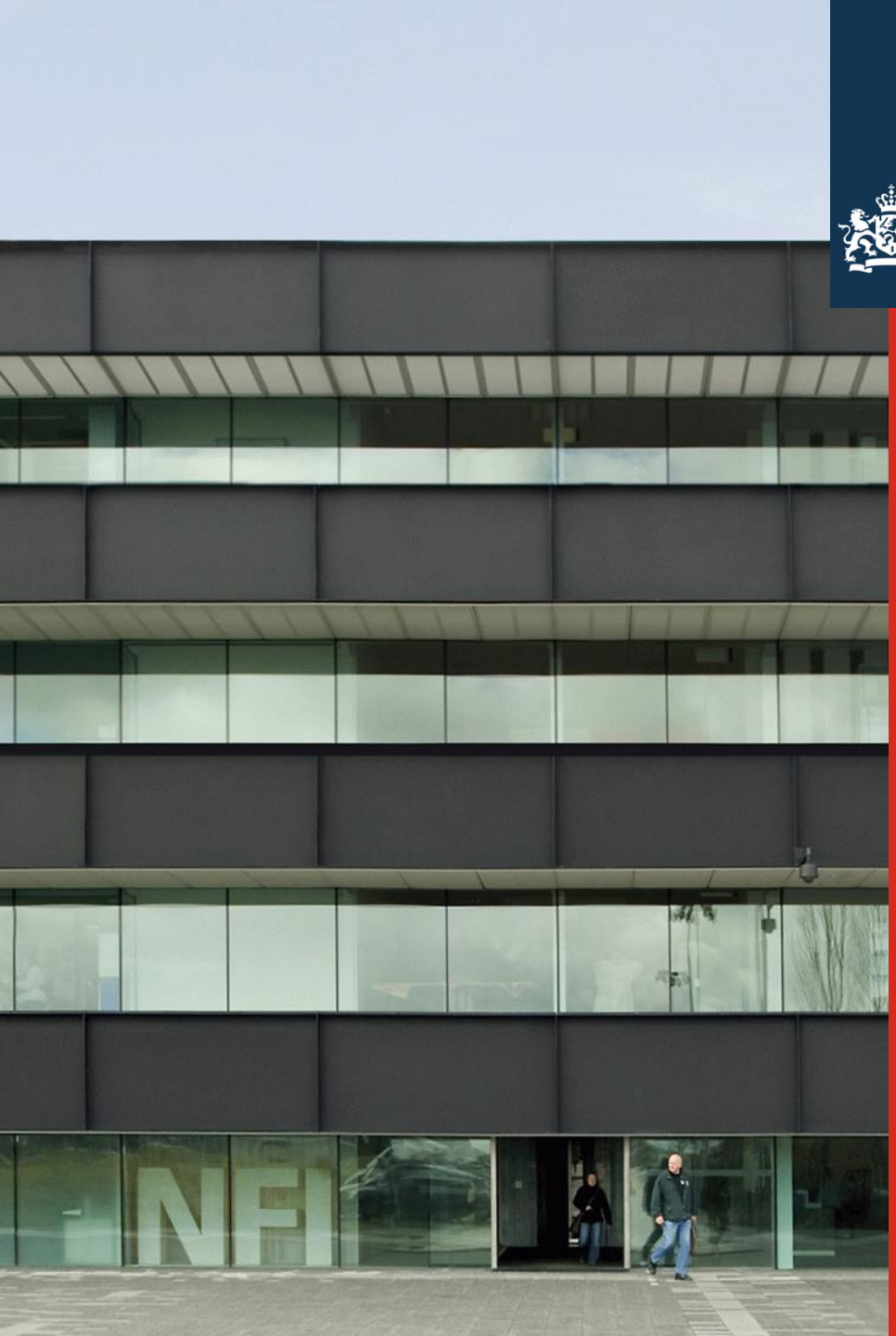
- EDB data are stored at ICMP‘s HQ in The Hague
- ICMP as International Organization can guarantee the inviolability of data processed under ICMP‘s control
- Secured by Host State Agreement (which is an international treaty)

Current situation

- Up to now no profiles from manufacturers or users
- Some users had issues with data stored in BiH (solved), DE will submit profiles
- Manufacturers currently low interest
- ISO 18385 requires process for voluntary samples
- Companies (if following) prefer decentralized solutions

Way forward

- Please request consumables manufactured according to ISO 18385
- Ask for proof of certification for ISO 18385
- Inventory of ‘open issues’ from both manufacturers and laboratories
- Meeting 2018 ICMP/ENFSI/companies in The Hague at ICMP



Netherlands Forensic Institute
Ministry of Justice

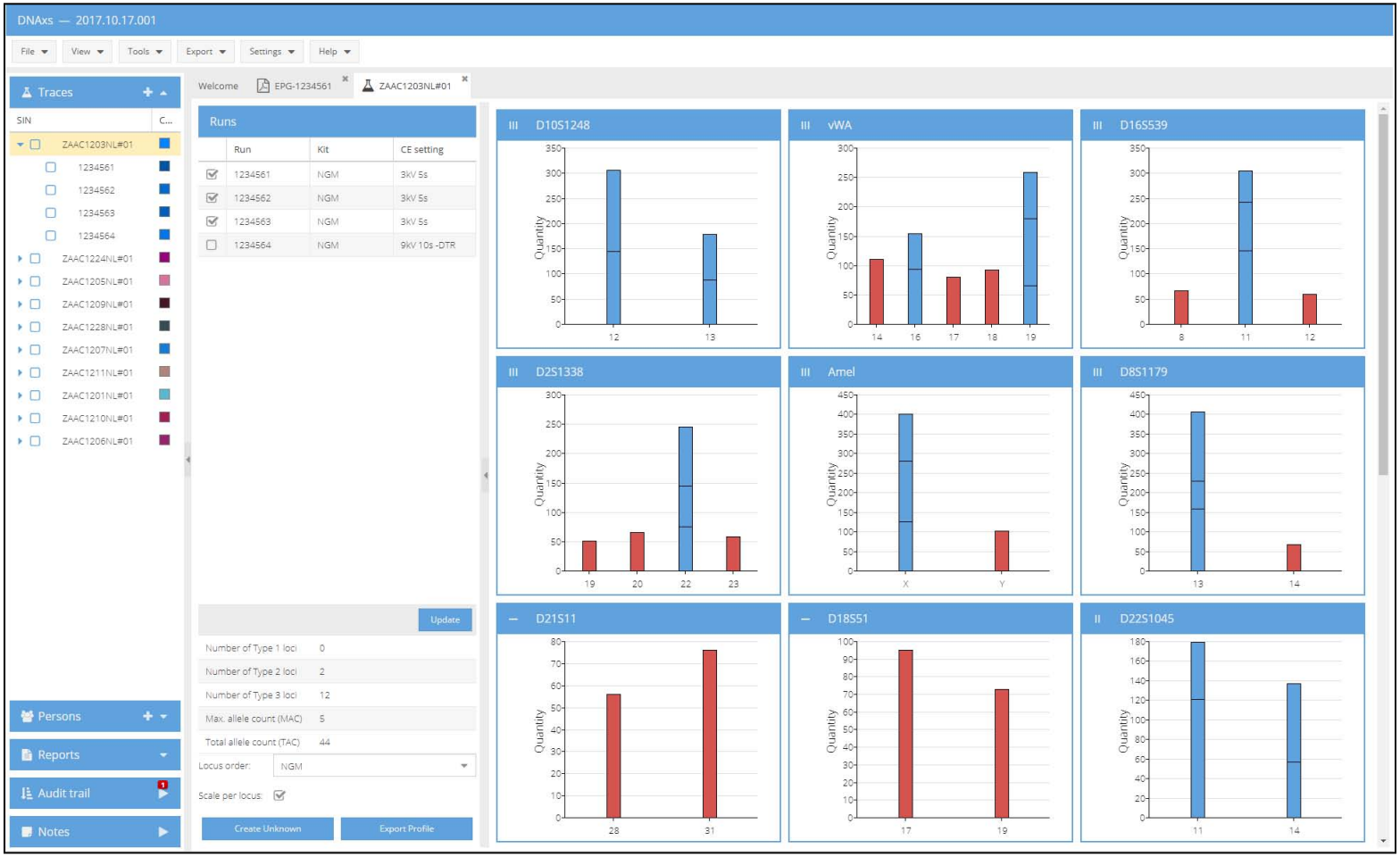
DNAxs
Expert System

DNAxs

- In house built (Java)
- Web application (browser)
- Server based

Functionality

- View profiles
  - Overview of runs and peak heights
  - Link to pdf of EPG
- Match profiles
  - Trace vs person
  - Trace vs trace
- Derive profiles
  - LoCIM inference
  - Consensus
  - Composite
- Match matrix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ZAAC1224NL#01
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1234562 NGM 3kV 5s
1234563 NGM 3kV 5s
1234564 NGM 9kV 10s -DTR
Update
Number of Type 1 loci 0
Number of Type 2 loci 2
Number of Type 3 loci 12
Max. allele count (MAC) 5
Total allele count (TAC) 44
Locus order: NGM
Scale per locus:
Create Unknown
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vWA
D16S539
D2S1338
Amel
D8S1179
D21S11
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D22S1045
Quantity


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Page 6
Allele Report: NFI
Project: C17-3530A REG+CON17202.SGF
Template: LastTemplate
User: Jezwa
Panel: NGM_3500xL
Sample 6 (Group 89): Ref Ladder: A1061781_Ladder_Storstar_F02.hid Run date and time: 07/13/2017 - 12:59:02 -> 07/13/2017 - 13:30:37
Dye: FL - 9 peaks - A1061788_Positieve_controle_isolatie_B12.hid
D10S1248
vWA
D16S539
D2S1338
Dye: JOE - 8 peaks - A1061788_Positieve_controle_isolatie_B12.hid
AMEL
D8S1179
D21S11
D18S51
Dye: TMR-ET - 9 peaks - A1061788_Positieve_controle_isolatie_B12.hid
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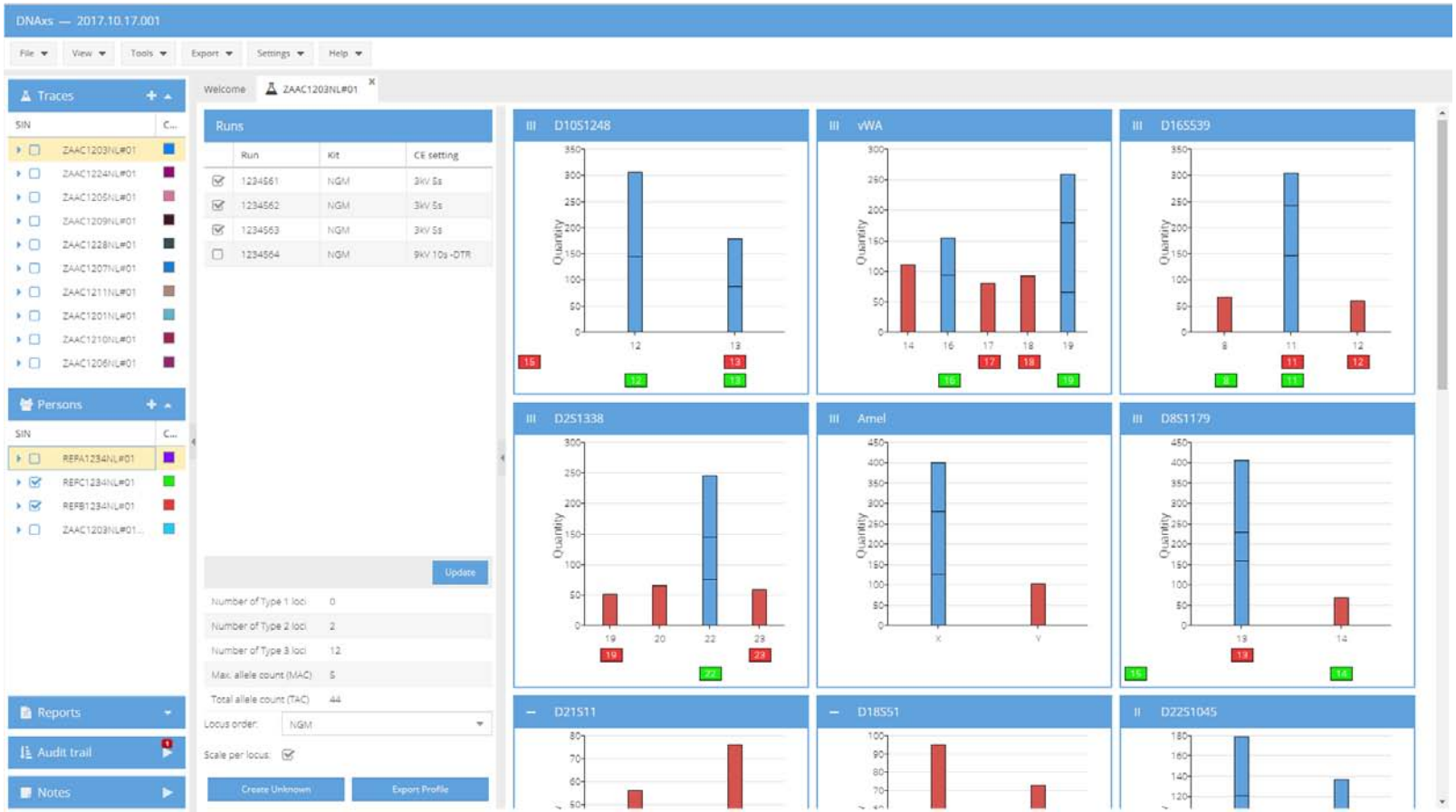
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Update
Number of Type 1 loci 0
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Number of Type 3 loci 12
Max. allele count (MAC) 5
Total allele count (TAC) 44
Locus order: NGM
Scale per locus:
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Export Profile
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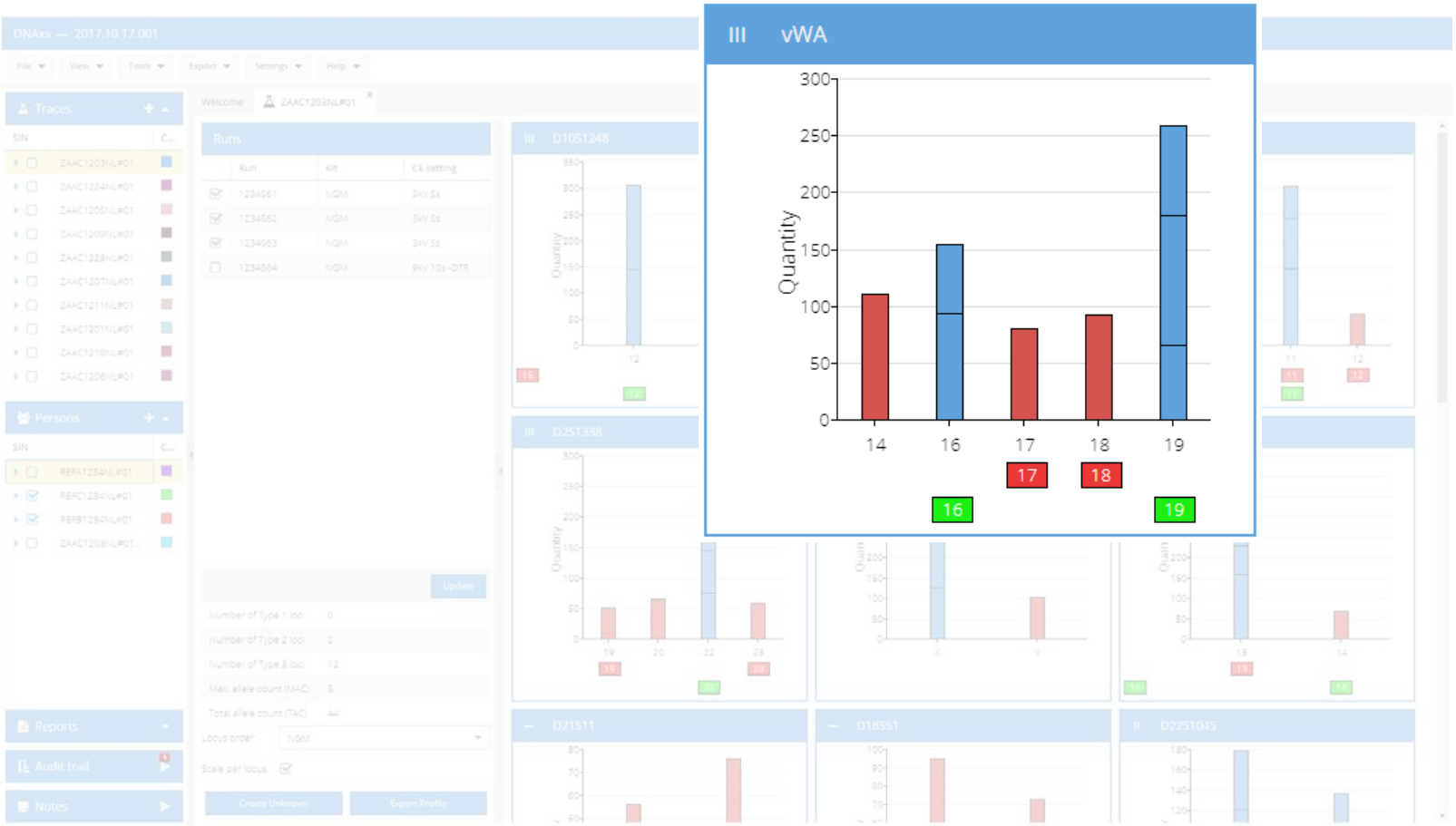
vWA
D16S539
D2S1338
Amel
D8S1179
D21S11
D18S51
D22S1045
Quantity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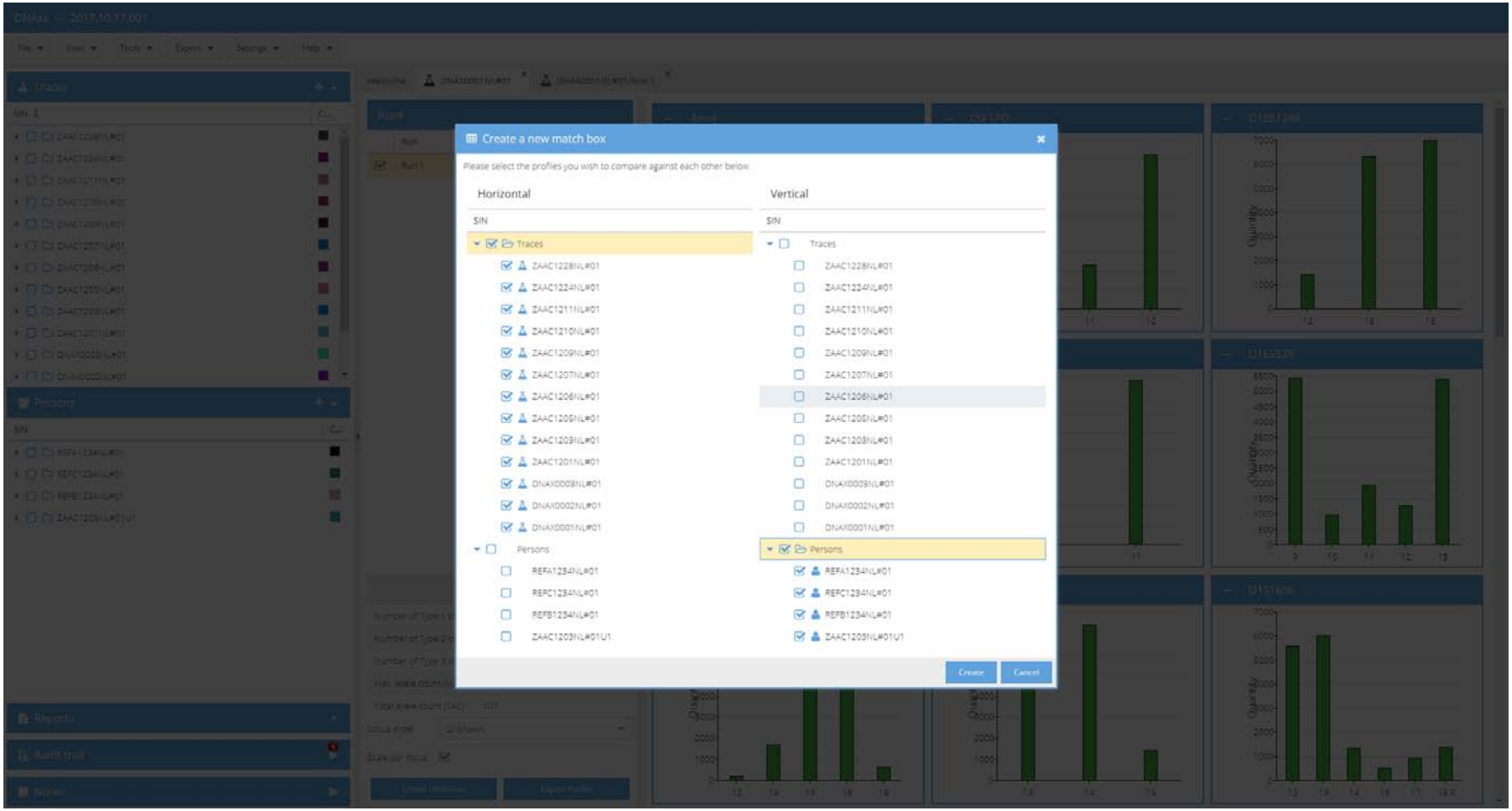
Create a new match box
Please select the profiles you wish to compare against each other below
Horizontal
Vertical
SIN
Traces
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Create
Cancel


DNAxs — 2017.10.17.001
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ZAAC1224NL#01
ZAAC1228NL#01
REFA1234NL#01
REFB1234NL#01
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ZAAC1203NL#01U1
Persons
Reports
Audit trail
Notes
Maximum allowed mismatches:

Future functionality

- Integration of EuroForMix
  - Match mixed profiles using:
    - Maximum Liklihood
    - Deconvolved profiles
- CODIS, Bonaparte export formats
- Trigger based removal of profiles in cases

Time line

Validation finished October 2017

Implementation within NFI November 2017

Present software at next DNA working group meeting April 2018

Contact ENFSI DNA Expert Working Group

Website

www.enfsi.eu

Chair
Sander Kneppers
NFI, the Netherlands, s.kneppers@nfi.minvenj.nl

Vice chair
Livia Zatkalikova
Ministry of Interior, Slovenia, livia.zatkalikova@minv.sk

Secretary
Astrid Quak
NFI, the Netherlands, a.quak@nfi.minvenj.nl

Verbal Scale discussions

Peter Gill

Motivation

- Numerous enquiries about verbal scale.
- Believed that verbal scales may help Juries to better understand evidence.
- However, there is evidence that verbal scales might be misleading
  - Weak evidence effect
  - When evidence is described as weak in favour of the prosecution, it will be interpreted by a juror as favourable to the defence – ie evidence is underated

- Agreed that the number should always be provided.
- The verbal predicator is not compulsory

Universality

- The universal scale provided in the ENFSI guideline is intended to be universal across all evidence types.
- There is discussion about whether we need different scales for DNA, but in general this seems difficult to justify as the likelihood ratio is an absolute expression of strength of evidence – independent of method used

Proposed scale

Table 1. SWGDAM verbal scale for the expression of likelihood ratios

LR for H^p Support and 1/LR for H^d Support	Verbal Expression
1	Uninformative
2 – 99	Limited (or Weak) Support
100 – 9,999	Moderate Support
10,000 – 999,999	Strong Support
≥1,000,000	Very Strong Support

1) Similar to the ENFSI scale
2) A scale that mirrors support for Hp and Hd

A verbal scale to support Hd

- Question of whether it is necessary (or useful) to provide a verbal scale for Hd?
- Or is it sufficient to state that anything below LR=1 is support for the defence proposition of exclusion?

The verbal scale and ‘inconclusive’ calls

- A suggestion to include an ‘inconclusive category’ in the verbal scale e.g. LR<1000 and LR>0.1.
- The range will be based upon experiments carried out with mixtures where the ground truth is known. Inconclusive is defined as a range of LRs where it has been recorded:
  - false positive LRs, i.e false inclusion
  - False negative LRs, i.e. false exclusion

Inconclusive

- Difficulties with defining an inconclusive zone
- It is dependent upon the sample size
- It is dependent upon the method used
- It is dependent upon the kind of sample analysed
- i.e. we would many different inconclusive zones for any method
- The LR is itself an expression of the uncertainty that we have – why is anything else needed?

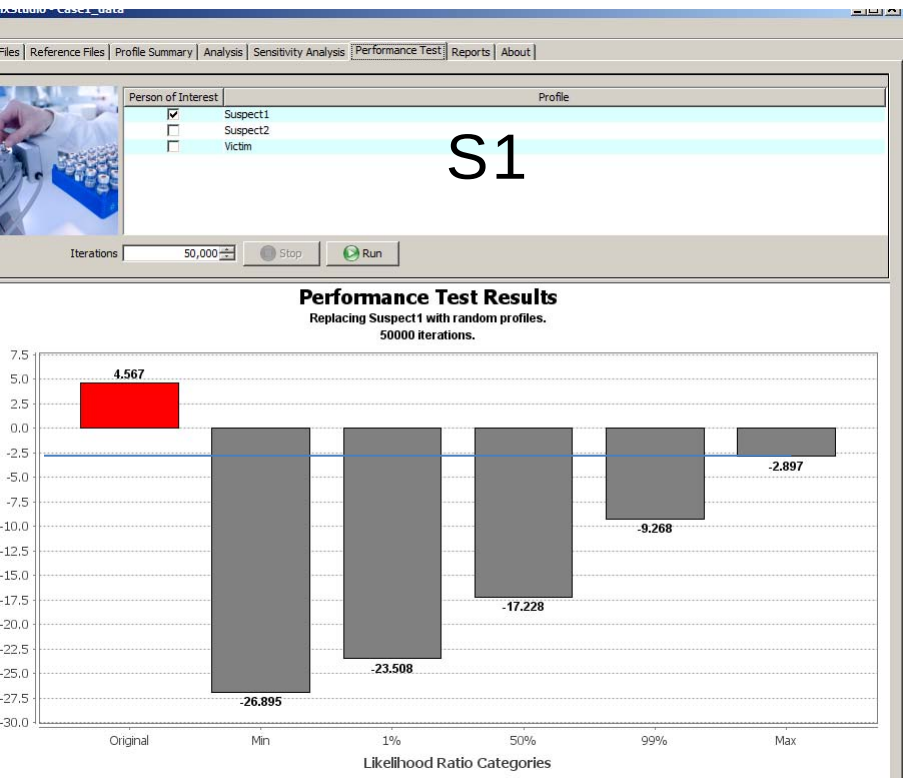
Non-contributor tests

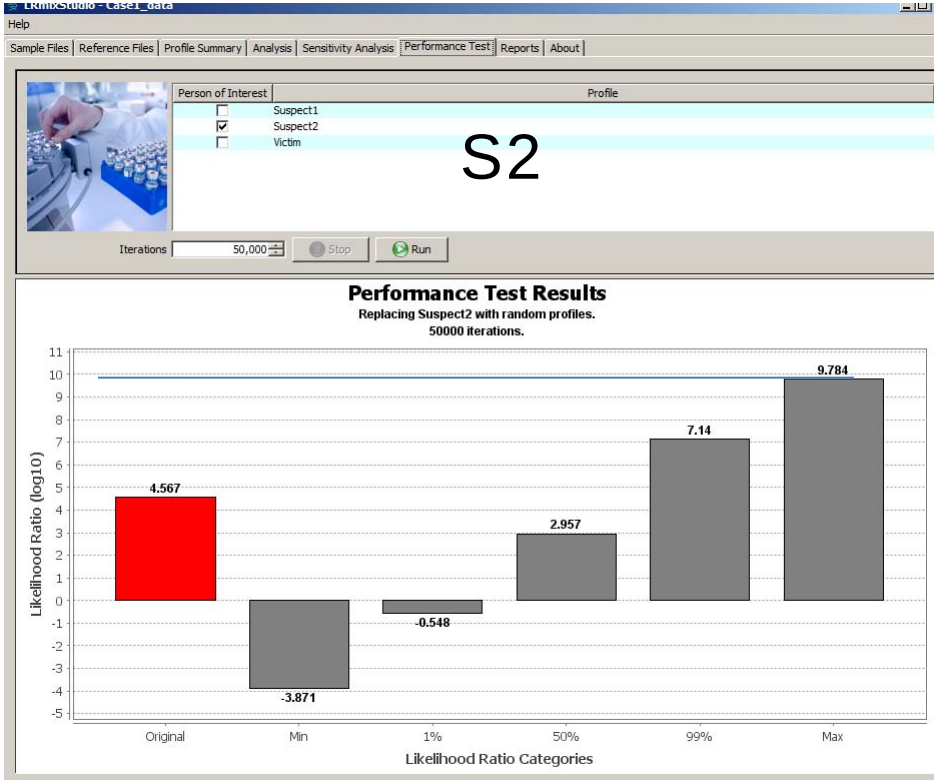
- Advantage as that non-contributor tests can be used on a per sample basis to indicate the distribution of LRs provided by random individuals.
- Non-contributor tests are always compared to the LR actually achieved with the suspect
- The actual LR achieved should be a clear ‘outlier’
- Non-contributor tests can be used to show if a model is not working properly.

Example – two suspect problem

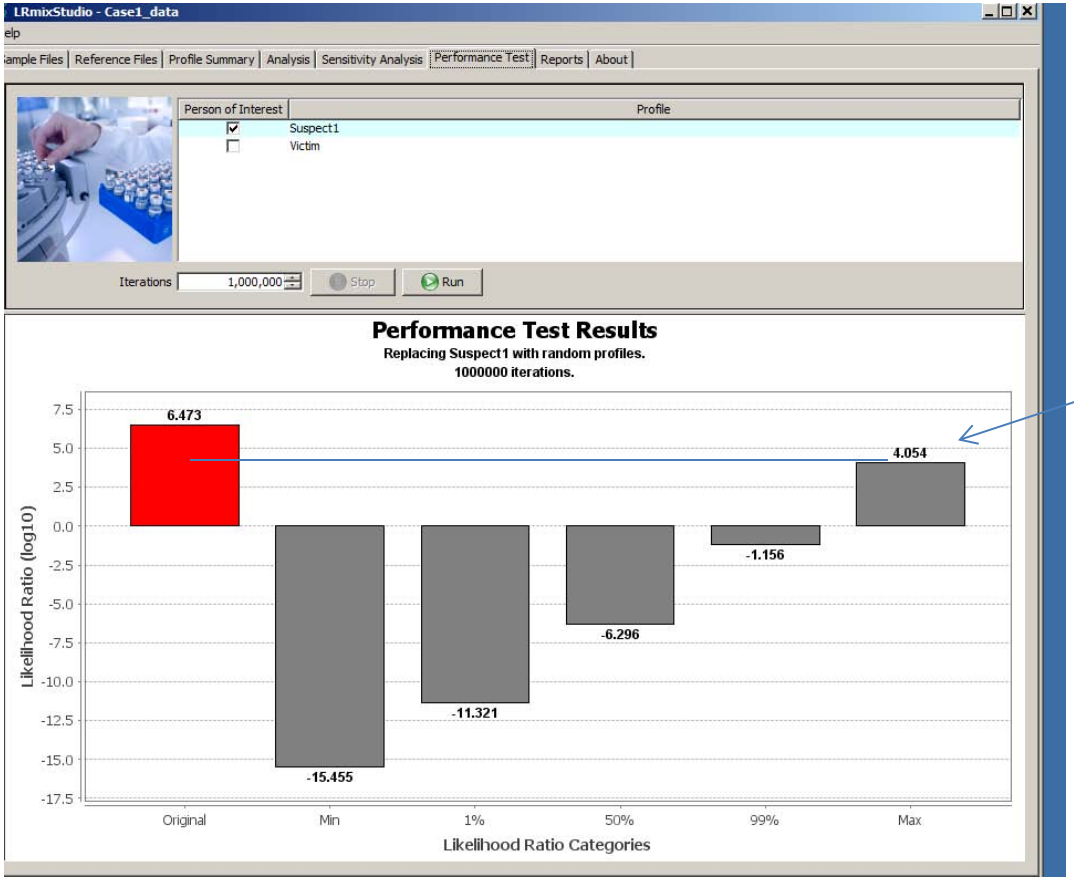
- The crime-stain is from an epithelial swab taken from the female victim
- There are two suspects accused of sexual assault, S_1 and S_2 respectively; both deny the offence.
- This epg is classified as a low template of three or more individuals
- Consequently, the preliminary propositions are formulated as $Hp=V,S_1,S_2$ and $Hd=V,U,U$
- $log_{10}LR=4.56$

Sensitivity plot (evaluate one suspect at a time)





LRmix Studio S1 effect (1 million iterations)



Note this value is less than the LR

Step 6: Non-contributor performance (Np) tests

•*Np* tests can be used to support the conclusion that evidence supporting S_1 is 'inclusionary' whereas evidence supporting S_2 is 'exclusionary'

	Three person mixture			Non-contributor performance
Hp	*Hd*	Random man substituted	$\log_{10}$(LR)	percentiles
S_1,S_2,*V*	*V*,*U*,*U*	S_1	4.5	(-23,-17,-9)
S_1,S_2,*V*	*V*,*U*,*U*	S_2	4.5	(-3,+2.9,+7)
S_1,*V*,*U*	*V*,*U*,*U*	S_1	6.4	(-11,-6,-1)
S_2,*V*,*U*	*V*,*U*,*U*	S_2	-3.8	(-12,-6,-1)

Database searches revisited the effect of database trawls on strength of evidence

Peter Gill

How is the strength of evidence affected by database searches

- Do multiple comparisons with a database diminish the strength of evidence?
- An early NRC report (1996), recommendation 5.1 stated that the match probability in the database search should be calculated as LR=1/Np where n=size of database and p=match probability.
- E.g. LR=1/(5,000,000 x 1/1bn) = 200

Np-rule

- 1/Np rule was proposed by Stockmarr (1999)
- The propositions are:
  - Hp: The donor of the crime stain is in the database
  - Hd: The donor of the crime stain is not in the database
- Note there is nothing wrong with the calculation
- But there was strong criticism – all of which was based on the propositions.

What is the question?

- It was argued by Balding and others, that in fact the strength of evidence is actually increased as a result of a database search.
- Consider Mr X is found as a result of a database search size n.
- Propositions:
  - Hp: Mr X is the donor of the crime stain
  - Hd someone else is the donor of a crime stain

Likelihood ratio as a result of a database search

- The culprit is a member of a population size N and N>n.
- $LR = \frac{1}{p_a}\frac{N-1}{N-n}$
- So if we have N= 30million and n=5million
- Pa=1 billion, for example
- Then LR=(30m/25m)x 1bn
  - Which is slightly greater than 1bn
- So the conclusion was that a database search actually increases the strength of the evidence because it eliminates all but one individual

What are the conditions applied for this logic to be valid?

- From Balding (2002):
  - “1. that, to be convinced of a defendant’s guilt, they must as a matter of logic be simultaneously convinced that every other individual on earth-including each of the defendant’s close relatives-is innocent, and
  - 2. that the scientific evidence must be combined with the nonscientific evidence to come to an overall view on guilt or innocence. “

Other conditions of the formula

- That only one suspect is found
- That all but one member of the database is eliminated
- For mixtures this is not true
  - You can have thousands of matches with LR>1
  - You may miss the donor because his DNA contribution is too low level,

From the jurors perspective

- Is it true that a juror must be convinced to the point that every other individual on earth, including relatives is innocent?
  - Patently this is *not true*
- The benchmark is ‘reasonable doubt’
- Research on juror behaviour shows that they only need to be c. 95% sure of guilt
- DNA evidence tends to be overweighted in the investigator and juror mindset, such that other evidence (that points away from guilt) is underweighted). This is *confirmation bias*.

Classic example described in “sense about science” paper

- The problems are amply demonstrated with the case of Raymond Easton who spent several months in custody on the basis of a DNA ‘match’ resulting from a database search. The evidence was given as *sic*[37-million-to-one].
- This individual was charged with burglary, even though he lived 175 miles away from the crime scene, he was in the advanced stages of Parkinsons disease and was unable to walk more than 10m unaided
- OK – it never went to trial because the defence managed to persuade the police to carry out further tests – but the point is that the *investigators* were subject to confirmation bias
- Other examples, that did go to trial, resulting in conviction include Farah Jamah (Australia)

DNA as sole evidence

- The second Balding condition is:

"that the scientific evidence must be combined with the nonscientific evidence to come to an overall view on guilt or innocence. "

- What if there is none?
- In R v. Tsekiri[3], the defendant was found guilty of burglary. The only evidence was presence of DNA (mixture) on a door handle, and the court acknowledged *" the finding of DNA attributable to a defendant at the scene of a crime was the sole evidence against a defendant*". The jury was provided with a *sic* [match probability 1:1 billion].
- However the conviction was upheld
- In my view the court's reasoning was superficial and misses the point.

How should DNA as sole evidence be reported?

- Clear responsibility of investigators and scientists to make clear the implications of DNA as sole evidence by explaining the effect of priors on the posterior odds
- From Meester R, Sjerps M. 2003

$$Posterior\ odds = \frac{1}{(N-n)p_a}$$

Size of population

Size of database

Example of R v. Tsekiri

- There is no *a priori* reason (evidence) to suggest Mr Tsekeri is guilty
- Let's suppose any male in London is equally likely to have committed the offence and their priors are the same. N=4 million
- A number of these may be eliminated by the national DNA database. We could also eliminate other individuals – too old, too young, infirm etc. Suppose n= 700,000
- So the posterior odds = 1/(4m-700,000) x (1/1bn)
- =303

- The posterior odds of 303 are much lower than the LR of 1 bn.
- With the example of Raymond Easton.
  - LR=37m
  - N-n=30m (based on male population of UK)
  - Posterior odds are neutral

Conclusion

- In a case where the suspect is identified before the DNA test, there is already substantial non-DNA evidence to raise the priors.
  - The jury are in a good position to assess the entirety of the evidence
- When the DNA evidence is sole-plank, then the jury is not in a position to assess the evidence.
  - The fact of the database search is not disclosed so the jury never get to think about population size.
  - The priors (i.e the ‘suspect’ population size is never discussed in court)
  - i.e. the evidence can be misrepresented which invites confirmation bias

Roma 17-20 April 2018

CODIS Meeting – 17 April
EDNAP Meeting – 17 April

ENFSI DNA WG 18-20 April

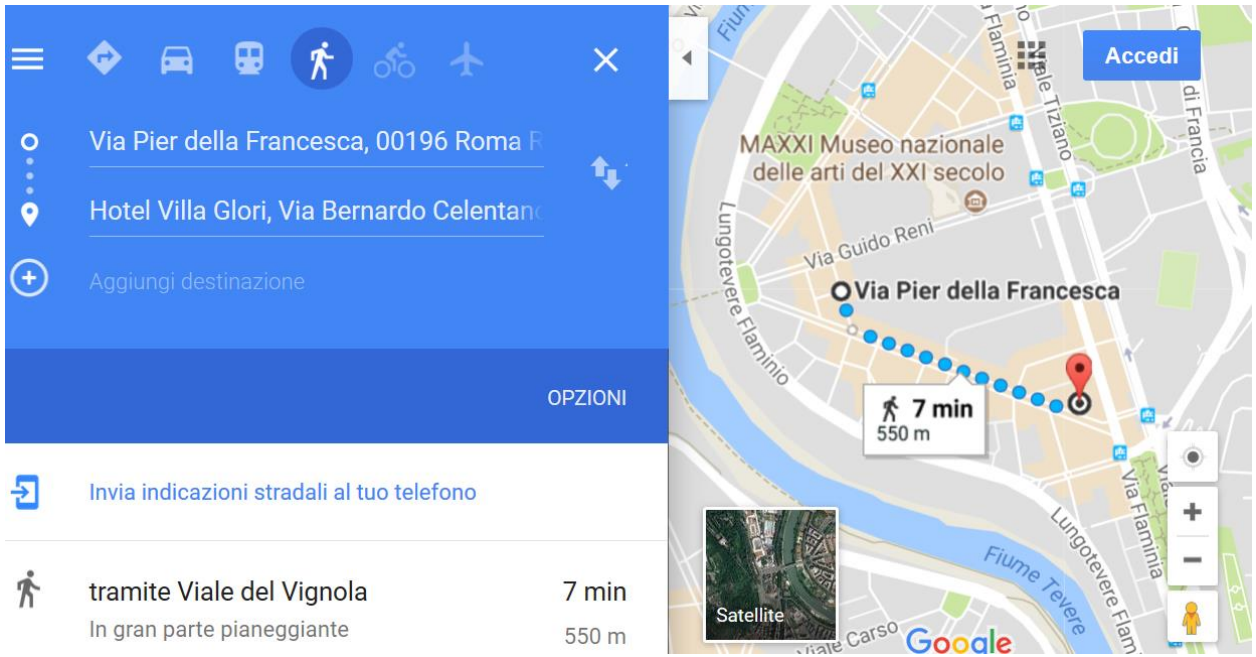
Location

- Scuola Superiore di Polizia

  Address: Via Pier della Francesca, 3

Hotels*

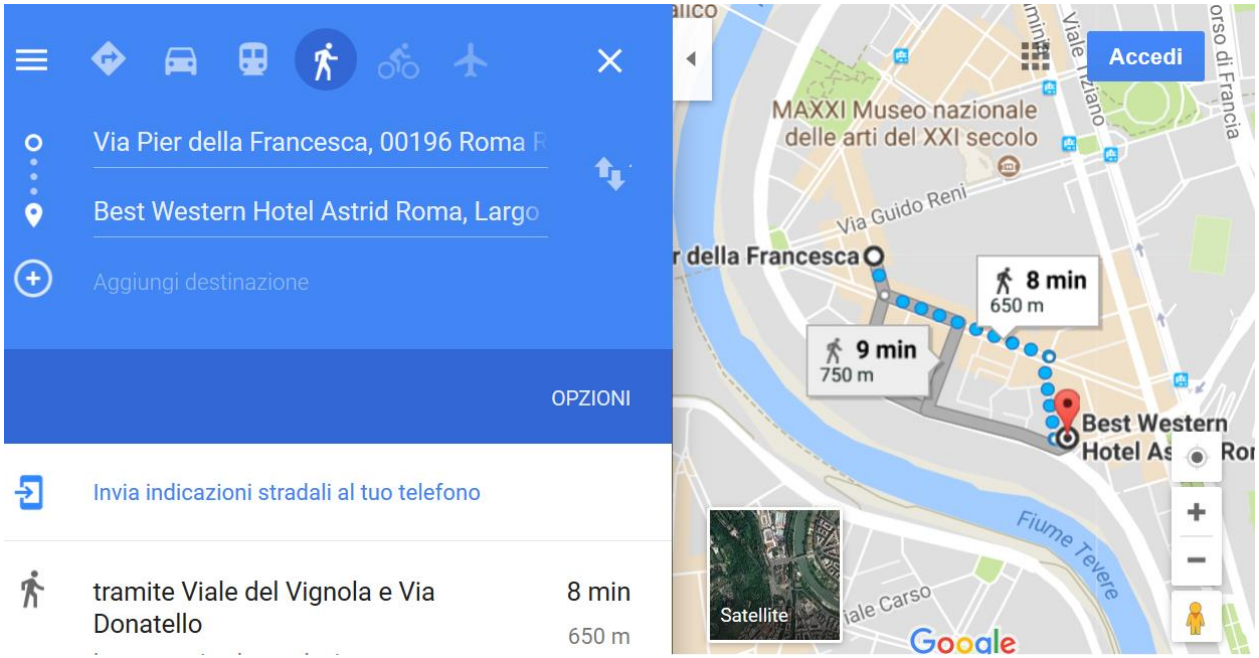
- 40 rooms Hotel Villa Glori **** (500mt from the Meeting Venue) €130 double for single use/€150 double including continental breakfast and free Wi-Fi



*Prices are intended excluding Local Taxes

Hotels*

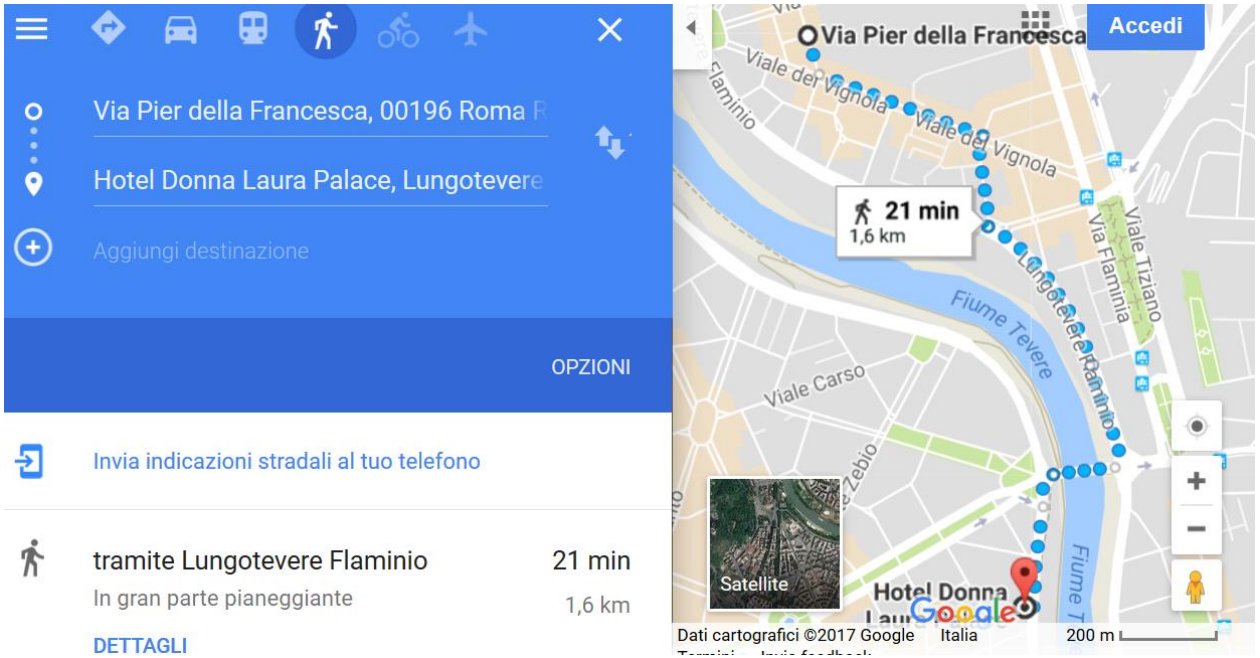
- 20-40 rooms Best Western Hotel Astrid**** (1 Km from the Meeting Venue) €120 double for single use including continental breakfast and free Wi-Fi



*Prices are intended excluding Local Taxes

Hotels*

- 40 rooms Hotel Donna Laura Palace **** (1,5Km from the Meeting Venue) €130 double for single use/€150 double including continental breakfast and free Wi-Fi



*Prices are intended excluding Local Taxes

Web site will be ready in January 2018

- Registration
- Accomodation
- Tourist information
- Information about transfer from/to Airports (Fiumicino and Ciampino) and Railway Station

Registration fees

ENFSI regular participant: 320-350 €

EDNAP and CODIS partecipant: 125-140 €

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Alessandra La Rosa