EUROPEAN DNA PROFILING GROUP (EDNAP) MEETING

Rome, Italy

8 November 2016

Host: Vince Pascali
Chairman: Niels Morling

A list of participants is attached.

Welcome
Vince Pascali welcomed members to Rome.

Presentation
What is inside a mixture? Vince Pascali
Vince Pascali presented research on biostatistics analysis of mixtures of DNA from two or more individuals. The data will be published elsewhere.

Update on exercises
A SNaPshot based method targeting 18 common mtDNA mutations Arnoud Kal
The manuscript is in press (presentation attached).

Second exercise on methylated DNA and age 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 Cordula Haas
Cordula Haas gave an update of the NGS based study of discrimination between various tissues and body fluids (presentation attached).

Updates from other groups

High quality DNA sequence database - STRidER Ingo Bastisch
Ingo Bastisch informed about the update of the advice on formulas on the website, http://strider.online. Colleagues are invited to submit data to the database. In the near future, STRidER will be used as a screening tool and repository for population genetic information that is sent to Forensic Science International: Genetics.

EUROFORGEN-NoE – General update Peter Schneider
Peter Schneider gave an update concerning the project (presentation attached).

EDNAP website update (www.isfg.org/EDNAP) Peter Schneider
Members are encouraged to visit the website. Suggestions are welcome.
Future activities
Niels Morling
At the next EDNAP meeting, Cordula Haas will suggest a follow-up exercise on mRNA typing with NGS.

Next meeting
Niels Morling
The next EDNAP meeting will be held 25 April 2017 in Vilnius, Lithuania in connection with the meetings of CODIS users and the DNA Working Group of ENFSI. The meetings will be organised by Gintautas Šinkūnas (gintautas.sinkunas@vrm.lt).

If you are willing to host the EDNAP meeting in the autumn of 2017, please contact Niels Morling.

Any other business
Niels Morling
There was no other business.

Closing of the meeting
The meeting closed with sincere thanks to Vince Pascal, Francesca Brisighelli 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
  - Arnoud Kal: Report on mtDNA SNP typing
  - David Ballard: Report on methylated DNA and age determination
  - Cordula Haas: Report on mRNA NGS
  - Peter Schneider: Report on EUROFORGEN-NoE.
AGENDA FOR THE EDNAP MEETING
ROME – 8 NOVEMBER 2016
DRAFT

Expected duration: 09.00 - 17.00

Coffee: 10.15 – Lunch: 12.30-13.30 – Coffee: 15.15

Host: Vince Pascali
Chairman: Niels Morling

Welcome

What is inside a mixture?          Vince Pascali
Validation of software – ENFSI – draft  Peter Gill
Education, competence, certification, accreditation - ENFSI  Niels Morling

Update on activities concerning
  mtDNA SNP screening – two PCRs, 18 SNPs  Arnoud Kal
  Methylated DNA and age exercise  David Ballard
  Exercise on mRNA typing with MPS  Cordula Haas

Updates from other groups
  High quality DNA sequence database  Walther Parson
  EUROFORGEN-NoE  Peter Schneider

Future activities
  EDNAP meeting 25 April 2017 in Vilnius, Lithuania  Niels Morling
  EDNAP meeting in the fall of 2017 – where? Please suggest

Any other business  Niels Morling
Dr. Ricky Ansell  
National Laboratory of Forensic Science  
S-58194 Linköping  
Sweden  
Tel: +46 1056 28119  
Fax: +46 13 14 57 15  
E-mail: ricky.ansell@polisen.se

Dr. David Ballard  
Forensic and Analytical Science  
King's College London  
Franklin Wilkins Building  
Waterloo  
SE1 9NH London  
UK  
Tel:  
Fax:  
E-mail: david.ballard@kcl.ac.uk

Dr. Regine Banemann  
KT31  
Bundeskriminalamt  
Thaerstrasse 11  
D-65193 Wiesbaden  
Germany  
Tel: +49 61155 16053  
Fax: +49 611 5545 089  
E-mail: regine.banemann@bka.bund.de

Ms. Ilaria Boschi  
Laboratoria Genetica Forense  
Largo Francesco Vito 1  
I-00168 Roma  
Italy  
Tel:  
Fax:  
E-mail: ilaria.boschi@policlinicogemelli.it

Dr. Francesca Brisighelli  
Laboratoria Genetica Forense  
Largo Francesco Vito 1  
I-00168 Roma  
Italy  
Tel: +39 6 3550 7031  
Fax: +39 6 3550 7033  
E-mail: francesca.brisighelli@unicatt.it

Ms. Alessandra Caglia  
Laboratoria Genetica Forense  
Largo Francesco Vito 1

Dr. Ingo Bastisch  
KT31  
Bundeskriminalamt  
Thaerstrasse 11  
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: +44 121 200 3830
Fax:
E-mail: alessandracaglia@interno.it

Dr. Denise Syndercombe Court
Forensic and Analytical Science
King's College London
Franklin Wilkins Building
Waterloo
SE1 9NH London
UK
Tel: +44 20 7848 4155
Fax: +44 20 7848 4129
E-mail: Denise.syndercombe-court@kcl.ac.uk

Dr. Theresa Gross
Institute of Legal Medicine
University of Cologne
Melatenguertel 60-62
D-50823 Cologne
Germany
Tel: +49 221 478 89447
Fax:
E-mail: theresa.gross@uk-koeln.de

Dr. June Guiness
Home Office
Forensic Science Regulator Unit
5 St. Philips Place, Colmore Row
B3 2PW Birmingham
UK
Tel: +31 708 886 729
Fax: -
E-mail: a.kal@nfi.minvenj.nl

Dr. Eirik Hanssen
Department of Forensic Biology
National Institute of Public Health
PO Box 4404
Nydalen
N-0403 Oslo
Norway
Tel: +44 20 7848 4155
Fax: +44 20 7848 4129
E-mail: eiha@fhi.no

Dr. Cordula Haas
Institut für Rechtsmedizin Zurich
Winterthurerstr. 190
CH-8057 Zurich
Switzerland
Tel: +41 44 635 5656
Fax: +41 44 635 6858
E-mail: cordula.haas@irm.uzh.ch

Dr. Arnoud Kal
Department of Human Biological Traces
Netherlands Forensic Institute
Laan van Ypenburg 6
24 97 GB The Haque
The Netherlands
Tel: +31 708 886 729
Fax: -
E-mail: a.kal@nfi.minvenj.nl
Dr. Alexander Kneppers
Department of Human Biological Traces
Netherlands Forensic Institute
Laan van Ypenburg 6
24 97 GB The Hague
The Netherlands
Tel: 
Fax: 
E-mail: s.kneppers@nfi.minvenj.nl

Dr. Francois-Xavier Laurent
Institut National Police Scientifique Lyon
31, avenue Franklin Roosevelt
69134 Ecully
France
Tel: 
Fax: 
E-mail: francoisxavier.laurent@interieur.gouv.fr

Ms. Alessandra Marucci
Laboratoria Genetica Forense
Instituto di Sanita Publica
Universita Cattolica
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: 
Fax: 
E-mail: ale.marrucci@gmail.com

Dr. Helle Smidt Mogensen
Section of Forensic Genetics
Department of Forensic Medicine
Faculty of Health Sciences
University of Copenhagen
Frederik V’s Vej 11
DK-2100 Copenhagen
Denmark
Tel: +45 3532 6212
Fax: +45 3532 6270
E-mail: helle.smidt@sund.ku.dk

Professor, dr.med. Niels Morling
Section of Forensic Genetics
Department of Forensic Medicine
Faculty of Health Sciences
University of Copenhagen
Frederik V’s Vej 11
DK-2100 Copenhagen
Denmark
Tel: +45 3532 6115
Fax: +45 3532 6270
E-mail: niels.morling@sund.ku.dk

Dr. Fabrice Noël
National Institute of Forensic Science
98-100 Chaussée de Vilvorde
B-1120 Bruxelles
Belgium
Tel: +32 2243 4604
Fax: +32 2240 0501
E-mail: fabrice.noel@just.fgov.be

Mr. Giovanni Battista Paliani
Laboratoria Genetica Forense
Instituto di Sanita Publica
Universita Cattolica
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: +351 239 854230
Fax: +351 239 826132
E-mail: gbpaliani@gmail.com

Dr. Vince Pascali
Instituto di Sanita Publica
Universita Cattolica
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: +39 6 3550 7031
Fax: +39 6 3550 7033
E-mail: vincenzolorenzo.pascali@unicatt.it

Instituto di Sanita Publica Chris Phillips
Forensic Genetic Unit
Department of Legal Medicine
University of Santiago de Compostela
San Francisco, s/n
E-15705 Santiago de Compostela
Spain
Tel: +34 98158 2327
Fax: +34 98158 0336
E-mail: c.phillips@mac.com

Instituto de Medicina Legal
Laboratoria Genetica Forense
Instituto di Sanita Publica
Universita Cattolica
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: +351 239 854230
Fax: +351 239 826132
E-mail: gbpaliani@gmail.com

Dr. Francesca Scarnicci
Laboratoria Genetica Forense
Instituto di Sanita Publica
Universita Cattolica
Largo Francesco Vito 1
I-00168 Roma
Italy
Tel: +39 6 3550 7031
Fax: +39 6 3550 7033
E-mail: fscarnicci@libero.it

Prof. Dr. Peter M. Schneider
Institute of Legal Medicine
University of Cologne
Melatenguertel 60-62
D-50823 Cologne
Germany
Tel: +49 221 4788 8345
Fax: +49 221 4788 8370
E-mail: peter.schneider@uk-koeln.de

Dr. Astrid v d Ham-Quak
Department of Human Biological Traces
Netherlands Forensic Institute
Laan van Ypenburg 6
24 97 GB The Haque
The Netherlands
Tel:
Fax:
E-mail: a.quak@nfi.minvenj.nl

Professor Livia Zatkalikova
Institute of Forensic Science
Slovenská L’upca
Priboj 560
976 13
Slovak Republic
Professor Livia Zatkalikova
Institute of Forensic Science
Slovenská L’upca
Priboj 560
976 13
Slovak Republic
Final Update
Exercise mtDNA
SNaPshot

8 November 2016, Rome
A control region-based mtDNA SNaPshot selection tool, integrated into a mini amplicon sequencing method

- Targets 18 SNPs in HVS I - II – III

- Degenerate bases in 3’ part primer to cover SNPs at primer binding site positions

- Two SNaPshot multiplexes for PCR products of mini amplicon mtDNA multiplexes (Eichmann et al 2008)

<table>
<thead>
<tr>
<th>SNP</th>
<th>Base change</th>
<th>Frequency</th>
<th>Haplogroup</th>
</tr>
</thead>
<tbody>
<tr>
<td>73</td>
<td>A&gt;G</td>
<td>0.5551</td>
<td>HV / H / V</td>
</tr>
<tr>
<td>146</td>
<td>T&gt;C - T&gt;a</td>
<td>0.0933 - 0.0001</td>
<td></td>
</tr>
<tr>
<td>150</td>
<td>C&gt;T - C&gt;g</td>
<td>0.1028 - 0.0001</td>
<td></td>
</tr>
<tr>
<td>152</td>
<td>T&gt;C</td>
<td>0.2007</td>
<td></td>
</tr>
<tr>
<td>182</td>
<td>C&gt;T</td>
<td>0.0088</td>
<td></td>
</tr>
<tr>
<td>185</td>
<td>G&gt;A - G&gt;t - G&gt;c</td>
<td>0.0541 - 0.0031 - 0.0004</td>
<td></td>
</tr>
<tr>
<td>195</td>
<td>T&gt;C - T&gt;a</td>
<td>0.1986 - 0.0002</td>
<td></td>
</tr>
<tr>
<td>489</td>
<td>T&gt;C</td>
<td>0.1351</td>
<td>M / J</td>
</tr>
<tr>
<td>497</td>
<td>C&gt;T</td>
<td>0.0419</td>
<td>K</td>
</tr>
<tr>
<td>16126</td>
<td>T&gt;C</td>
<td>0.1799</td>
<td></td>
</tr>
<tr>
<td>16129</td>
<td>G&gt;A - G&gt;c</td>
<td>0.0689 - 0.0111</td>
<td></td>
</tr>
<tr>
<td>16223</td>
<td>C&gt;T</td>
<td>0.1405</td>
<td></td>
</tr>
<tr>
<td>16270</td>
<td>C&gt;T</td>
<td>0.0876</td>
<td></td>
</tr>
<tr>
<td>16278</td>
<td>C&gt;T</td>
<td>0.0646</td>
<td></td>
</tr>
<tr>
<td>16294</td>
<td>C&gt;T - C&gt;a - C&gt;g</td>
<td>0.1071 - 0.0003 - 0.0002</td>
<td></td>
</tr>
<tr>
<td>16311</td>
<td>T&gt;C</td>
<td>0.1676</td>
<td></td>
</tr>
<tr>
<td>16362</td>
<td>T&gt;C</td>
<td>0.0743</td>
<td></td>
</tr>
<tr>
<td>16519</td>
<td>T&gt;C</td>
<td>0.6642</td>
<td></td>
</tr>
</tbody>
</table>
Same PCR product for sequencing and SNaPshot

**Mini-mtDNA**
- DNA (5µl)
- Two 5-plex PCRs (50µl)
- Purification
- Sequencing
- Purification
- CE

**SNaPshot**
- Purification
- Single base extension (SBE) PCR
- a SNaPshot multiplex for each PCR multiplex
- Purification
- CE
- Selection of mtDNA samples

**Example:**
*Case with 30 hairs → 600 sequencing reactions*
*SNaPshot: Selection of 3 hair samples → 60 sequencing reactions*
Optimised SNaPshot assay

- SNP number preceded by ‘r’: reverse primer
- Allele call followed by ‘-’: rCRS allele
EDNAP Exercise: 3 parts – 14 labs (excl NFI)

① SNaPshot assays on 13 samples for which PCR products are provided

② Paper challenge: compare results 1 to list of 8 references given in standard nomenclature

③ Optional: NGS full mtDNA analysis of 2 samples
   » Commercial control DNA sample (cell line)
   » Sample with heteroplasmy
Warsaw meeting april 2016

Draft manuscript almost finished
A collaborative EDNAP exercise on SNaPshot™-based mtDNA control region typing

N.E.C. Weiler\textsuperscript{a}, K. Baca\textsuperscript{b}, D. Ballard\textsuperscript{c}, F. Balsa\textsuperscript{d}, M. Bogus\textsuperscript{e}, C. Børsting\textsuperscript{f}, F. Brisighelli\textsuperscript{g}, J. Červenáková\textsuperscript{h}, L. Chaitanya\textsuperscript{i}, M. Coble\textsuperscript{j}, V. Decroy\textsuperscript{k}, S. Desmyter\textsuperscript{k}, K.J. van der Gaag\textsuperscript{a}, K. Gettings\textsuperscript{j}, C. Haas\textsuperscript{l}, J. Heinrich\textsuperscript{m}, M. João Porto\textsuperscript{d}, A.J. Kal\textsuperscript{a}, M. Kayser\textsuperscript{i}, A. Kúdelová\textsuperscript{h}, N. Morling\textsuperscript{f}, A. Mosquera-Miguel\textsuperscript{n}, F. Noel\textsuperscript{k}, W. Parson\textsuperscript{m,p}, V. Pereira\textsuperscript{f}, C. Phillips\textsuperscript{n}, P.M. Schneider\textsuperscript{e}, D. Syndercombe Court\textsuperscript{c}, M. Turanska\textsuperscript{o}, A. Vidaki\textsuperscript{c}, P. Woliński\textsuperscript{b}, L. Zatkalíková\textsuperscript{o}, T. Sijen\textsuperscript{a,*}
MPS data in Supplemental Materials

In summary, four laboratories submitted two samples to MPS using two different platforms. Some differences were reported, but these were observed to be calling errors when the data were re-analysed through the same software. Although the average read coverage varied markedly between the four laboratories, the ratio between the two bases at a heteroplasmic position was similar for all four laboratories. MPS appeared to generate reliable mtDNA typing results.
Big THANK YOU ALL!!
Methylated DNA & Age Exercise

David Ballard
EDNAP, Rome 2016
EDNAP EXERCISE

Part 1
Part 1

- Results now received from 15 laboratories
  - 8 MiSeq only
  - 5 PGM only
  - 2 MiSeq and PGM
- 7 Methylation standards between 0-100% sent out to all labs
CpG 5

Observed Methylation Fraction

Expected Methylation Fraction

CpG 6

Observed Methylation Fraction

Expected Methylation Fraction

CpG 7

Observed Methylation Fraction

Expected Methylation Fraction

CpG 8

Observed Methylation Fraction

Expected Methylation Fraction

MiSeq  PGM
EDNAP EXERCISE

Part 2
Part 2

• Results now received from 12/15 laboratories

• Samples sent:
  o 7 blood stains
  o 2 methylation standards

• Also possible to analyse 3-6 samples unique to the laboratory
Methylation Age Predictions

ANN Based Prediction Model

Predicted Age vs. Chronological Age

- **Training**
- **Validation**
- **Test**

The graph shows a scatter plot of predicted age against chronological age, with points representing training, validation, and test sets. The trend line indicates a positive correlation between the two variables.
Stain D

• Actual age 47
  o Prediction KCL – 48.8
  o MiSeq Lab 13 - 50.6
  o MiSeq Lab 14 - 49.55
  o MiSeq Lab 3 - 48.3
  o MiSeq Lab 10 - 47.5
  o MiSeq Lab 12 - 44.35
Lower read numbers lead to less accurate predictions
Stain D

- Actual age 47
  - Prediction KCL – 48.8
  - MiSeq Lab 13 - 50.6
  - MiSeq Lab 14 - 49.55
  - MiSeq Lab 3 - 48.3
  - MiSeq Lab 10 - 47.5
  - MiSeq Lab 12 - 44.35
  - MiSeq Lab 11 - 42.2
Stain D

- Actual age 47
  - Prediction KCL – 48.8
  - PGM Lab 9 - 46.9 (48.6)
Normalisation of PGM values to MiSeq values

**CpG 9**

- Observed Methylation Fraction
- Expected Methylation Fraction

**CpG 6**

- Observed Methylation Fraction
- Expected Methylation Fraction

**CpG 8**

- Observed Methylation Fraction
- Expected Methylation Fraction
Stain D

- Actual age 47
  - Prediction KCL – 48.8
  - PGM Lab 9 - 46.9 (48.6)
  - PGM Lab 8 - 66.4 (47.6)
  - PGM Lab 16 - 55.35 (42.8)
  - PGM Lab 11 - 57.65 (33.8)
  - PGM Lab 2 - 50.15 (27.4)

Predictions for Stain D – lower coverage leads to less accuracy
Blind age predictions of extra MiSeq results

MiSeq - Venus Blood

Predicted Age vs. Chronological Age

- Lab 11
- Lab 12
- Lab 15
- Lab 10
Blind age predictions of extra PGM results
Acknowledgments

• Anastasia Aliferi
• Athina Vidaki
• Denise Syndercome Court
• Leon Barron
DAVID BALLARD
DNA ANALYSIS AT KING’S
KING’S COLLEGE LONDON
LONDON
UK

DAVID.BALLARD@KCL.AC.UK
EUROFORGEN / EDNAP
mRNA NGS exercise 1
Assay for body fluid/tissue identification

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

8. November 2016, Rome
Association of a Body Fluid with a DNA Profile by Targeted RNA/DNA Deep Sequencing

Cordula Haas*, Sabrina Ingold*, Erin Hanson°, Jack Ballantyne°
*University of Zurich, °University of Central Florida
Objectives

1. set up a targeted mRNA/miRNA NGS approach for body fluid/tissue identification
   → establish a probabilistic approach to call/predict the presence of a body fluid

2. select a set of SNPs for each body fluid/tissue, that discriminates individuals the most
   → assign a body fluid to a specific individual

3. combine the RNA analysis with gDNA STR sequencing, allowing simultaneous human individual identification and forensic tissue identification
1A. targeted mRNA NGS approach for body fluid/tissue identification (MiSeq)

- Illumina DesignStudio
- TruSeq Targeted RNA Custom Panel
- TruSeq Targeted RNA Index Kit
- Illumina MiSeq
- Bioinformatics pipeline

- 66 mRNA biomarkers evaluated
- TOP6: 33 biomarkers
- blood, semen, saliva, vaginal secretions, menstrual blood, skin

<table>
<thead>
<tr>
<th>Body fluid/tissue</th>
<th>Gene Name</th>
<th>TOP1</th>
<th>TOP2</th>
<th>TOP3</th>
<th>TOP4</th>
<th>TOP5</th>
<th>TOP6</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood</td>
<td>BD1</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD2</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD3</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD5</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD6</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD7</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>BD2 - cSNP</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

| Semen             | SE1       |      |      |      |      |      |      |
|                   | SE2       |      |      |      |      |      |      |
|                   | SE3       |      |      |      |      |      |      |
|                   | SE4       |      |      |      |      |      |      |
|                   | SE5       |      |      |      |      |      |      |
|                   | SE6       |      |      |      |      |      |      |
|                   | SE7       |      |      |      |      |      |      |
|                   | SE7 - cSNP|      |      |      |      |      |      |

| Saliva            | SA1       |      |      |      |      |      |      |
|                   | SA2       |      |      |      |      |      |      |
|                   | SA3       |      |      |      |      |      |      |
|                   | SA4       |      |      |      |      |      |      |
|                   | SA5       |      |      |      |      |      |      |
|                   | SA6       |      |      |      |      |      |      |
|                   | SA7       |      |      |      |      |      |      |
|                   | SA8       |      |      |      |      |      |      |
|                   | SA9       |      |      |      |      |      |      |
|                   | SA10      |      |      |      |      |      |      |
|                   | SA11      |      |      |      |      |      |      |
|                   | SA12      |      |      |      |      |      |      |
|                   | SA13      |      |      |      |      |      |      |
|                   | SA14      |      |      |      |      |      |      |
|                   | SA15      |      |      |      |      |      |      |
|                   | SA16      |      |      |      |      |      |      |
|                   | SA17      |      |      |      |      |      |      |
|                   | SA18      |      |      |      |      |      |      |
|                   | SA19      |      |      |      |      |      |      |
|                   | SA20      |      |      |      |      |      |      |

| Vaginal           | VS1       |      |      |      |      |      |      |
|                   | VS2       |      |      |      |      |      |      |
|                   | VS3       |      |      |      |      |      |      |
|                   | VS4       |      |      |      |      |      |      |
|                   | VS5       |      |      |      |      |      |      |
|                   | VS6       |      |      |      |      |      |      |
|                   | VS7       |      |      |      |      |      |      |
|                   | VS8       |      |      |      |      |      |      |
|                   | VS9       |      |      |      |      |      |      |
|                   | VS10      |      |      |      |      |      |      |

| Menstrual         | MB1       |      |      |      |      |      |      |
|                   | MB2       |      |      |      |      |      |      |
|                   | MB3       |      |      |      |      |      |      |
|                   | MB4       |      |      |      |      |      |      |
|                   | MB5       |      |      |      |      |      |      |
|                   | MB6       |      |      |      |      |      |      |
|                   | MB7       |      |      |      |      |      |      |
|                   | MB8       |      |      |      |      |      |      |

| Skin              | SK1       |      |      |      |      |      |      |
|                   | SK2       |      |      |      |      |      |      |
|                   | SK3       |      |      |      |      |      |      |
|                   | SK4       |      |      |      |      |      |      |
|                   | SK5       |      |      |      |      |      |      |
|                   | SK6       |      |      |      |      |      |      |
|                   | SK7       |      |      |      |      |      |      |
|                   | SK8       |      |      |      |      |      |      |
|                   | SK9       |      |      |      |      |      |      |
|                   | SK10      |      |      |      |      |      |      |
|                   | SK11      |      |      |      |      |      |      |
|                   | SK12      |      |      |      |      |      |      |
|                   | SK13      |      |      |      |      |      |      |
|                   | SK14      |      |      |      |      |      |      |

| Housekeeping      | HKG1      |      |      |      |      |      |      |
|                   | HKG2      |      |      |      |      |      |      |
|                   | HKG3      |      |      |      |      |      |      |
1B. targeted mRNA NGS approach for body fluid/tissue identification (PGM)

- Ion AmpliSeq Designer
- AmpliSeq RNA library preparation kits
- IonTorrent PGM
- Bioinformatics pipeline

- BFP0: same 33 mRNA biomarkers
- BFP3: 29 markers

<table>
<thead>
<tr>
<th>Body fluid</th>
<th>Gene</th>
<th>BFP0 (33plex)</th>
<th>BFP1 (61plex)</th>
<th>BFP2 (37plex)</th>
<th>BFP3 (29plex)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood</td>
<td>B1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>B2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>B3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>B7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>B8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>semen</td>
<td>Sa1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa10</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa12</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa13</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa14</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa15</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa16</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sa17</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Vaginal</td>
<td>V1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V10</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>V11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Menstrual</td>
<td>M1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Blood</td>
<td>M2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>M3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>M4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>M5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>M6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Skin</td>
<td>Sk1</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk2</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk3</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk5</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk6</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk7</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk9</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk10</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk11</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>Sk12</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Collaborative exercise mRNA NGS part 1

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

RNA extraction (manual or kit), DNase treatment, quantification

Protocols for PGM and MiSeq provided by UZH
Primerpools for PGM and MiSeq provided by UZH

Laboratories analysed 8/16 samples provided by UZH and 0/8 own body fluid samples

Results (BAM/FASTQ files) collected and evaluated by UZH
Collaborative exercise mRNA NGS part 1

Participating laboratories:

Cellmark, UK
Coimbra, Portugal
Cologne, Germany
Copenhagen, Denmark
Innsbruck, Austria
Krakow, Poland
London, UK
Lyon, France
NFI, Netherlands
NIPH, Oslo
NIST, USA
Orlando, Florida, USA
Rome, Italy
Rotterdam, Netherlands
Zurich, Switzerland

PGM
S5
PGM
MiSeq
MiSeq
PGM
MiSeq
FGx
FGx
PGM
MiSeq
MiSeq/S5
FGx
PGM
MiSeq/PGM

No data yet

Auckland, New Zealand
Glasgow, Scotland
Münster, Germany
Santiago de Compostela, Spain
Collaborative exercise mRNA NGS part 1

Provided stains:

<table>
<thead>
<tr>
<th>single stains</th>
<th>mixed stains</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Summary Questionnaire

- Delivery time Fedex (samples+primers): 17 labs within 1-4 days (max: 16 days to Italy)
- 2 labs: primers were not immediately stored at -20°C (1-3 weeks at room temp)
- 4x manual RNA extraction (recommended), 11x RNA extraction kit (Rneasy, EZ1 RNA Universal Tissue Kit, mirVana)
- 11x RNA quantification (Qubit, RiboGreen, Nanodrop, Quantus)
- RT (Illumina): 7x ProtoScript II Reverse Transcriptase, 2x others (Retroscript, RT2 First Strand Kit)
RT (PGM): included in library kit
Collaborative exercise mRNA NGS part 1

Results:

RNA quants

| extr method | quant method | s11   | s12   | s13   | s14   | s15   | s16   | s17   | s18   | s19   | s20   | s21   | s 22/23 | s24   | s25   | s26   | s 27/28 |
|-------------|--------------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|         |-------|-------|-------|--------|
| Lab_1       | Kit          | 3.8   | 4     | 2.2   | 2.1   | 30.1  | 130.4 | 15.4  | 3.9   | 62.2  | 86.9  | 39.6  | 2.7    | 127.2 | 10.9  | 30.1  | 7.2     |
| Lab_2       | Kit          | Qubit | undet | undet | undet | 16.5  | 24.6  | 4     | undet | 23.2  | 71    | 29.4  | undet  | 128   | 6.1   | 31.4  | undet   |
| Lab_3       | Kit          | Nanodrop | 3.8   | 4     | 2.2   | 2.1   | 30.1  | 130.4 | 15.4  | 3.9   | 62.2  | 86.9  | 39.6  | 2.7    | 127.2 | 10.9  | 30.1  | 7.2     |
| Lab_4       | Kit          | Qubit | -     | -     | -     | -     | -     | -     | -     | -     | -     | -     | -      | -     | -     | -     | -       |
| Lab_5       | Kit          | Qubit | <0.5  | 0.81  | 1.04  | 0.76  | 4.44  | 15.2  | 2.17  | 1.22  | 9.19  | 44.6  | 9.63  | 0.5    | >60   | 0.69  | 51    | 0.87    |
| Lab_6       | manual       | Quantus | 29.35 | 34.6  | 43.3  | 57.25 | 26.9  | 190   | 24    | 61    | 259.5 | 234.5 | 69.6  | 11     | 377.5 | 74.85 | 212.5 | 36.9    |
| Lab_7       | manual       | Quant-iT RiboGreen | 23    | 25.2  | 64.3  | 79.9  | 18    | 119   | 33.7  | 68.2  | 334.8 | 471.3 | 44.7  | undet  | 525   | 50    | 392.4 | 16.6    |
| Lab_8       | Kit          | no quant | -     | -     | -     | -     | -     | -     | -     | -     | -     | -     | -      | -     | -     | -     | -       |
| Lab_9       | Kit          | Qubit | undet | undet | undet | undet | undet | 10    | 10    | undet | undet | undet | 3.3    | 9.7    | 2.7   | undet | 32    | undet   |
| Lab_10      | Kit          | no quant | -     | -     | -     | -     | -     | -     | -     | -     | -     | -     | -      | -     | -     | -     | -       |
| Lab_11      | Kit          | no quant | -     | -     | -     | -     | -     | -     | -     | -     | -     | -     | -      | -     | -     | -     | -       |
| Lab_12      | Kit          | Qubit/Nanodrop* | 4.8   | 5.5   | 8     | 3.8*  | 11.6  | 4.4   | 4.7*  | 9.6   | -     | -     | -      | -     | -     | -     | -       |
| Lab_13      | Kit          | Qubit | undet | undet | undet | undet | undet | undet | undet | undet | undet | undet | 12.9   | 9.02   | undet | 54.8  | -      | -       |
| Lab_14      | manual       | Qubit | 16.2  | 8.2   | 15.6  | 5.6   | 65    | 39.3  | 2.4   | 129   | -     | -     | -      | -     | -     | -     | -       |
| Lab_15      | manual       | Nanodrop | 117.7 | 223   | 143.7 | 107.7 | 436   | 107.7 | 66.25 | 477.4 | -     | -     | -      | -     | -     | -     | -       |
Results Illumina MiSeq / FGx
Blood (n=4)
Menstrual blood (n=2)
Saliva (n=2)
Semen (n=2)
Skin (n=1)
Vaginal secretion (n=1)
Blood (n=4)

Menstrual blood (n=2)

Saliva (n=2)
Semen (n=2)

Skin (n=1)

Vaginal secretion (n=1)
additional samples from labs:

5x blood
2x mens
7x saliva
4x semen
3x skin
2x vag
1x nasal
2x urine
4x vag/semen
1x vag/blood
1x blood/saliva
Results IonTorrent PGM / S5

→ not analyzed yet...
Blood (n=8)

Semen (n=8)

Saliva (n=8)

Vaginal secretion (n=8)

Menstrual blood (n=8)

Illumina MiSeq
Illumina MiSeq
Skin (n=8)

IonTorrent PGM
Skin (n=2)
Collaborative exercise mRNA NGS part 1

Technical challenges:
- no target region / manifest-files provided
- plan run / sequencing mode

Conclusion:
- 7/9 MiSeq labs successfully implemented the mRNA NGS approach
- MiSeq-assay satisfying, PGM-assay needs some optimization
- PGM protocol is more lab-work
- manual RNA-extraction!
2. Body fluid/tissue specific SNPs

→ associate specific mRNA transcripts to an individual (on mRNA)

- 35 cSNPs
- Illumina MiSeq (and IonTorrent PGM)

→ estimate RNA-SNP allele frequency by testing of population samples (on DNA)

- 35 cSNPs
- Illumina MiSeq (and IonTorrent PGM)
Timeline

11/2016  Presentation of results of Collaborative exercise, part 1 (mRNA)

04/2017  Submission of a manuscript on part 1

04/2017  Suggestion for Collaborative exercise, part 2 (cSNPs)

06/2017  Shipment of samples, primers, protocols

10/2017  Submission of results
Thanks for participating!
EUROFORGEN-NoE Update: EDNAP Meeting Rome 2016

Peter M. Schneider
Institute of Legal Medicine
University of Cologne (Germany)
Overview on recent activities

• Conferences
  – EUROFORGEN Conference in Venice
  – Security Research and Innovation (SRIE) in The Hague

• Dissemination activities
  – A new guide explaining our science

• The Training Academy
  – For online learning

• The end of funding … but not of EUROFORGEN
  – Sustaining the network structures
EUROFORGEN Conference Venice 2016

International Dissemination Conference -
“Forensic DNA analysis in the light of the new
security needs”

The European Forensic Genetics Network of Excellence - EUROFORGEN-NoE
- held its International Dissemination Conference “Forensic DNA analysis in the
light of the new security needs” on 23rd June 2016 in Venice, in connection
with the Intersocietal Symposium of the International Academy of Legal
Medicine (IALM).
Security Research and Innovation Event, The Hague
June 1-2, 2016

• Panel Discussion on Forensics
  – CHAIR: Michele Socco (DG Home, EC)
  – Arie Ijzerman (Chair of the COSI)
    • COSI = Standing Committee on Internal Security
  – Jan de Kinder (Chair of ENFSI)
  – Dominique Saint-Dizier (Head, Institute of Criminalistics, France)
  – Peter M. Schneider (Coordinator EUROFORGEN-NoE)
What are the challenges today and tomorrow?

Challenges exist at several levels:

- the **crime scene** with forensic evidence
- the adequate **interpretation** of evidence
- searching integrated forensic databases (such as DNA)
  - Lack of transnational, powerful interconnected database systems
- acceptance of **new technologies** in society and legislation
- the **diversity** of legal systems across Europe

For the time being, the challenges of today will stay with us until tomorrow, as there is a constant stream of technological innovations suitable for **forensic casework**, searching **missing persons**, and identifying **victims of disaster and war**.
What are the answers?

There is a lack of high level scientific and technological research in particular in the field of new forensic genetic applications such as:

- reliable and validated prediction of externally visible characteristics beyond pigmentation, age prediction and ancestry,
- the transition from standard DNA analysis to sequence-based typing using Massively Parallel Sequencing (MPS) for DNA Databasing, Missing Persons and Disaster Victim identification (DVI),
  - highly focused optimization of platforms, DNA targets, and work flow tailored for specific applications,
- the early assessment of direct DNA sequencing using long read single molecule sequencing,
What are the answers?

• transition / extension of National DNA Databases to accept MPS-based DNA data,
• providing suitable training for casework analysts to understand the scope of new technologies and probabilistic genotyping for adequate courtroom presentation,
• ensuring genetic privacy by using smart filtering of the accumulated data
  – due to considerable heterogeneity regarding the acceptance of genotyping in various legal systems across Europe,
  … as a prerequisite for the development and introduction of reliable forensic tests and applications, and for obtaining acceptance of these advanced typing technologies in by legislators, in the courtroom and by society.
What is the role for the EU?

Real progress requires **activities at all levels**, and including all players in the forensic arena:

- **EFSA 2020** serving as framework and reference for all activities
- **Horizon 2020** focusing on funding high level basic and applied research projects aiming to achieve real scientific progress (to avoid falling behind the US NIJ level of funding)
- **ISF** supporting the practical implementation of new forensic technologies at the practical casework level
- **CEPOL, EJTN, Europol, Eurojust** establishing a cross cutting training network involving academic professionals, as well as all stakeholders and end users
- **Other EC funding** providing support for ethical, legal and societal research to understand public concerns and the political processes required for adopting new legislation
What is the role for the EU?

- **EU legislative initiatives**: Priorization of centralized resources and operational systems whenever possible to address current limitations relating to separate national jurisdictions and legal systems.
  - Support and promotion of mechanisms for cross border data exchange anchored in appropriate policies and data protection.
  - Establish policy mechanisms and fund operation of forensic elimination databases.

- **Strengthening human rights applications of forensic investigations** to give visibility and effect to benefits derived from effective workflows safeguarding the rule of law and human rights.
The “wish list”

- Involve relevant advisors from all fields of expertise in forensics for drafting topics for new calls in H2020:
  - academic researchers, police investigators & scientists, technology developers, legal experts, social scientists

- Consider a more prominent role for the ICMP (International Commission of Missing Persons) as a high-profile collaborating international institution based in Europe, to strengthen the expertise in the forensic arena and serve as a protected data repository able to bridge gaps in operational data exchange.
„Making Sense of Forensic Genetics“ Guide

• Collaboration with the non-profit charity „Sense about Science“
• Production of brochure and a series of media and public relation events for launch
• To address public misconceptions and explain the basics

Sense about Science is an independent campaigning charity that challenges the misrepresentation of science and evidence in public life. We advocate openness and honesty about research findings, and work to ensure the public interest in sound science and evidence is recognised in public discussion and policy making.

http://senseaboutscience.org/
The EUROFORGEN Online Training Academy:

- Online lectures on basic and advanced topics in forensic genetics
- WEBEX-based interactive presentations with Q & A session
- Participants need to register and can obtain a certificate for successful participation, after submitting their answers to a web-based questionnaire
- Presentations will be recorded for individual viewing accessible to members of the “Virtual Institute”
- At least 3 lectures this year, more lectures scheduled for 2017
WP5: Education, Training and Career Development

Course

Course title: WEBINAR: Relationship Inference with Familias

Subject: The aim of this webinar is to educate/train DNA experts in statistical methods of relationship testing as well as the new development on the Familias software

Institute: EUROFORGEN-NoE

Country: Online

Timeperiod: 09.11.2016

Month: 4

Email Address: euroforgen-webinars(at)eurtd.com

Homepage address: http://www.euroforgen.eu/webinar-registration/
The Virtual Institute of Research for Forensic Genetics

European Virtual Institute of Research in Forensic Genetics - access query

You are interested in becoming a member of the European Virtual Institute of Research in Forensic Genetics?

If you are a scientist working at a forensic genetics laboratory, or a professional working in an institution of the justice system, you are invited to join the Virtual Institute. Please see our Newsletter 3/2014 for further details.

Please enter your personal contact data, and the data of your institution below. We will verify your request and come back to you in the following days.

One requirement to get access to the EUROFORGEN-NoE Virtual Institute of Research in Forensic Genetics is the participation of your institution by submitting the EUROFORGEN-NoE questionnaire.

Your EUROFORGEN-NoE team.
The end of funding … ?

… but not of our network!

• The EC-funded project will end on Dec 31, 2016
• EUROFORGEN will associate with the ISFG to
  – Maintain the Virtual Institute of Research
  – add more content for the website for training and education
  – Continue the online Training Academy
  – Collaborate with other stakeholders (ENFSI, CEPOL)
• The EUROFORGEN Summer School will be organized to offer high level training with experts colleagues and scientists as teachers
  – The first Summer School is scheduled for July 17-21, 2017, to take place in Santiago de Compostela, Spain
EUROFORGEN-NoE is funded by the European Commission within the 7th Framework Programme.

Please do not forget to join our Facebook group!! … already 362 members!!

Thank you for your attention!!