40th ENFSI DNA WG Meeting
Warsaw, Poland
27-29th April 2016

ENFSI DNA Working Group - Delegates Action List

1. **All members** – are encouraged to mail on interest on the present vacant positions as QA liason (replacing Tom H), R&D contact (replacing Ingo) and E&T contact (new position). For any active member an additional attendance by the same laboratory is allowed for: Mail Sander; Lívia or Ricky if interested. **[Item 2]**

2. **All members and participants -** Are encouraged to reply on the questionnaire that will be sent out by Walther regarding needs and use of STRbase/STRidER. **[Item 5]**

3. **The QA-subgroup** to activate the revision of the Best Practice Manual for DNA Pattern Recognition and comparison. **[Item 6]**

4. The QA subgroup to send out a new draft version of the "Contamination prevention guidelines" taking into account all comments given during the meeting. **[Item 8]**

5. **Peter G** to, a) update the mixture circulation made in 2013 to discover if there have been any changes in the interim (new ENFSI labs will be invited as well), b) draft ENFSI guidelines for labs wishing to carry out internal validation of complex mixture software. **[Item 9]**

6. **All members -** Are encouraged to create login for the (temporary) ENFSI intranet webpages for access to meeting presentations and other documents. Information on how to proceed is attached to the minutes. Also Noel F can be contacted. **[Item 23]**

7. **All members -** Are encouraged to contribute with ideas regarding the future activities of the working group, to WG chair, subgroup chairs or secretaries.

8. **All members** - Are also encouraged to contribute with actions, queries etc., for the steer committee meeting for this autumn (in November).

ENFSI DNA Working Group – Steer Committee

Steering group composition:

The composition of the DNA WG steering group is as follows:

Chair:	Sander Kneppers
Vice Chair:	Lívia Zatkalikova
Secretary:	Ricky Ansell
Co-Secretary:	Astrid van der Ham Quak
WG treasurer:	Ingo Bastisch
Subgroup chairs:	See below!
Web master:	Fabrice Noel
ENFSI Standing Committee contact for QA, R&D, E&T:	QA - Vacant R&D - Vacant E&T - Vacant
EDNAP representatives:	Niels Morling Peter Schneider

Hosts of present, previous and coming meeting are invited to attend SC meetings.

Subgroups:

Subgroup A: QA subgroup	Co-chairs: Annick Delaire and Tom Heylen
Subgroup B: Methods, Analysis & Interpretation	Co-chairs: Peter Gill and Walter Parson
Subgroup C: DNA-database & Legislation	Chair: Vanessa Vanvooren Co-chair: Dyan Daly
Subgroup D: Automation & LIMS	Chair: Johannes Hedman Co-chair: Shazia Khan
Subgroup E: Casework/Forensic biology	Co-chairs: Rainer Wenzel and Ricky Ansell (from next meeting Arnoud Kal replaces Rainer)

ENFSI DNA Working Group – Meeting Minutes

The presentations are to be found on the temporary ENFSI intranet website (intranet.enfsiweb.eu/user/login?current=user/register). For website(s) access see attached documentation.

For photographs from the meeting see the following link:
https://www.dropbox.com/s/qlkpky9783yqto6/ENFSIDNA2016_Warsaw.zip?dl=0
(Does not seem to work for all - If you have issues with the link, please contact Magda!)

Item 1: Welcoming address

Director Waldemar Krywczyk of the Central Forensic Laboratory of the Polish Police welcomed the working group to Warsaw. He wished the group a fruitful meeting and to enjoy the stay in Warsaw.

Item 2: Organizational issues (Sander Kneppers)

Sander directed a warm gratitude and thanks to the organizers, especially Jakub Mondzelewski Magdalena Jab•o•ska, for their efforts in preparing for the meeting.
A new associate member from Kosovo represented by Fatmir Ademi was welcomed to the group.

The meeting has some 108 attendees with 88 participants and 18 company representatives from 11 companies. 30 countries are presented and almost 50 speakers have been registered.

There are three vacancies that need to be filled: QA representative (replacing Tom H), R&D representative (replacing Ingo), and E&T representative (new position, no standing ENFSI committee active).

Role in quality Assurance:
WG representative on QA issues within the WG.
Attend and give input about DNA activities in the QCLG yearly meetings.
Be the contact person for ENFSI QCC.
Give feedback of interesting topics/information going on in the ENFSI QCC group to the WG.
Develop ideas and support organization of WG proficiency tests.
Liaison for inter-WG QA issues.
Produce input to Chair on QA projects for yearly reports/plans and for Joint meeting.
Support members in their QC work, accreditation, etc.
Initiate the development and maintain the quality of BPMs for the WG.

Role in Research and development:
WG representative on R&D issues within the WG.
Liaison for inter-WG R&D issues.
Produce input to Chair on R&D projects for yearly reports/plans and for Joint meeting.
Where relevant to keep contact to subgroups and their activities in R&D.

Role in Education and Training:
WG representative on E&T issues.
Liaison for inter-WG E&T issues.
Produce input to Chair on E&T projects for yearly reports/plans and for Joint meeting.
Collect and identify training needs within the WG.

For any active member an additional attendance by same laboratory for DNA working group meetings is allowed for. Commitment to attend meetings including steering group meetings (small travel budget available). If you are interested contact Livia, Ricky or Sander at meeting or send an email. Decision made by the steering group **[Action 1].**

Item 3: Update from NDIS, FBI and SWGDAM (Dough Hares)

NDIS:
779.781 convicted offender profiles and 91.588 arrestee profiles were contributed to NDIS over the past year. Also some 73.112 forensic profiles were contributed. As summarised some 43.025 investigations were aided over the past year. Offender profiles in NDIS by March 31st totals 14.546.159 individuals and 690.789 forensic profiles (58.139 mixtures, 87.642 partial profiles). The vision is that the elapsed time from taking a reference sample until reply from a database search should be achieved within 4 hours.

SWGDAM:
There are as usual a lot of ongoing activities in the different committees of SWGDAM, for example guidelines for validation of NGS, Interpretation guidelines for NGS, Autosomal STR interpretation guideline (binary models), Plans for implementation of Rapid DNA.

SWGDAM consists of the following committees and groups: Autosomal STR Interpretation; CODIS; Enhanced Detection Methods and Interpretation (EDMI); Next Generation Sequencing Working Group; Rapid DNA; Sexual Assault Kit Evidence Processing Working Group (New 2015); Quality Assurance; Y-STR; SAFER SAK Working Group; Committee of Detail.

See the presentation for more details! Even more useful information including reports and other valuable documents are available on the website: www.swgdam.org

Item 4: STRbase/STRidER update (Walther Parson)

STRbase historically started in 2001 and has been open for us all since 2004. In the near future it will transform into STRidER. All data in the database have been thoroughly controlled. And a tool for quality control will be part of the database. There are no true genotypes available in the database; the profiles present are "shuffled" (combinations made from the genotypes present in the raw data). This shuffling has been made for privacy reasons. All allele frequencies in STRidER can easily be exported from the database in xml-format.

Concern has been raised on formulae used today in the ENFSI STRbase. The database is not intended to solve statistical problems in forensic genetics but to provide allele frequencies needed for the community. STRidER should contain formulae for corrections. One option could

be not to have any kind of formulae in the database, rather links to open software. All members of the WG are asked to give response to which methods are used in each laboratory and what are the wishes to have on the database **[Action 2].** Decision will be taken on the next meeting following a suggested solution.

Item 5: The DNASeqEx Project: Exploring STR sequencing and global exchange (Antonio Alonso)

"There is a pressing need to produce a standardized framework for describing complex sequences that enable comparison with currently used repeat allele nomenclature derived from conventional CE systems." Parson et al., Massive parallel sequencing of forensic STRs: Considerations of the DNA commission of the International society of Forensic genetics (ISFG) on minimal nomenclature requirements. FSI Genetics 2016 (22) 54-63.

Objectives of DNASEQEX project on global exchange of MPS-STR data:

- To promote standardized nomenclature including backward compatibility with "traditional" CE alleles.
- The development of expert analysis software (managing "Coverage" instead of "Height", "Strings" instead of "Repeat number", "Libraries" instead of "Ladders", but also generating when possible "CE-compatible allele calls".
- The development of MPS-STR information exchange formats and tools (CODIS and PRÜM exchange).
- To promote a selection process on new STR markers based on forensic validation data.
- To assess the impact on National DNA Databases searches.

Item 6: BPM on DNA Pattern Recognition and Comparison, and eDNA software (Ulrich Neuhaus-Steinmetz)

The Best practice manual ("Best Practice Manual for DNA Pattern Recognition and Comparison", ENFSI-BPM-DNA-01, version 01, November 2015) was not really discussed as such. The time was mainly spent as a live demo to go through some of the features of the eDNA software. The graphical user interface makes the software easy to handle, which is aided further by the use of different colours in for instance representation of matches in mixtures.

A short publication on eDNA is available: Haldemann et al., eDNA – An expert software system for comparison and evaluation of DNA profiles in forensic casework. FSI Genetics Suppl Ser 2015 (5) e400-402.

A one day workshop of the eDNA software have previously been announced, to be held in Berlin June 9th. This is also the release date of the software.

Regarding the BPM, the Steer Committee have decided that the document should undergo revision also taking into consideration parts of the forensic DNA analyses that are not covered by the present version (such as search/recovery, wet lab, genotyping and reporting). This will

assumingly be a task for the QA subgroup with an expected engaged input from everyone in the WG **[Action 3].**

Item 7: Company presentations

Eleven companies were present at the meeting, ten had booths and gave presentations. Their presentations are as indicated to be found on the ENFSI website along with the other presentations.

GE Healthcare (Igor Olewiecki):
GE Healthcare Update EDNAP, CODIS Users & ENFSI DNA Working Group Meetings.

Promega Corporation (Martina Vokurková Chocová):
What's Up and Coming from Promega?

Foster & Freeman Ltd (Owen Lang):
Improving the quality of Forensic Evidence.

Thermo Fischer Scientific (Paola Concio):
Applied BiosystemsTM Precision ID NGS System, and Forensic-Grade products manufacturing (ISO18385).

Qiagen GmbH (Laurent Moncomble):
Innovative Solutions.

Illumina (Nicola Oldroyd Clark):
Illumina NGS Solutions for Forensic Genomics: ENFSI DNA Working Group Update.

Hamilton Robotics AG & AQUA AG (Willem van Loon):
Next Generation Forensic solutions.

STRmix (Adam McCarthy):
Resolve More DNA Mixtures.

Qualitype GmbH (Frank Götz):
Your partner for forensic software solutions.

Alpha Helix (Mikael Havsjö):
ForenSafe – a concept on handling trace (LCN) DNA samples from crime scenes.

IntegenX (Laura Bimbashi):
No presentation.

Item 8: Report from subgroup A: QA subgroup

(Co-chairs; Tom Heylen & Annick Delaire)

No subgroup activities at this meeting. It has been decided that due to the developments made in the QA field with most labs now being accredited etc, this subgroup will be active on an "ad hoc" basis as things arises, and use meeting time in plenary for sharing relevant information rather than having separate workshops.

A draft new version of the "Contamination prevention guidelines", which has been sent round for commenting, was discussed in plenary. Several important changes have been suggested and was approved for. Further comments to the document were given at the session and a new draft version will be sent out for commenting **[Action 4].**

Item 9: Report from subgroup B: Methods, analysis and interpretation

(Co-chairs; Peter Gill & Walter Parson)

A number of interesting topics were discussed:

1) Tacha Hicks provided an update on the 'Evaluation of Evidence' following on from the publication of the 'ENFSI guideline for evaluative reporting in forensic science'. She discussed reporting at the 'activity level' using probability logic. A real example was provided of a wrongful conviction originally based on non DNA evidence. Later it was shown that DNA found on evidential material did not match the defendant and analysis at the 'activity level' always generates a likelihood ratio that favours the defence hypothesis, demonstrating that absence of evidence is not necessarily evidence of absence.

2) Walther Parson provided an update on STRider, a platform to collate STR frequency databases, which supersedes STRbase. STRider will be expanded to accept NGS data. There are also some options to apply formulae used to correct probabilities for sampling error and Fst. A questionnaire will be circulated to determine current laboratory practice. An option is to 'do nothing' since corrections could be accommodated by external software such as LRmix Studio.

3) Walther Parson provided an EMPOP update. He showed that there is more than one way to align sequences and this leads to different nomenclatures. The alignment of mtDNA sequences in EMPOP follows a phylogenetic approach (Bandelt and Parson 2008 IJLM). Although the approach is relatively simple to follow, it is difficult to perform for the average forensic practitioner as cognizance of the mitochondrial phylogeny is required. The problem is now solved by using a String Alignment Method (SAM), where the sequences text strings are compared using unaligned searches. This is a 'natural' method that is dependant only upon the DNA sequence and does not depend upon an artificial nomenclature. Consequently reporting is disentangled from database searching and it is guaranteed that sequences are not missed in a search due to different alignment. The SAM approach also provides an important extension to STRs (which will also be subject to the nomenclature dilemma). However, some labs have a requirement to report standardized alignments. An extension of SAM is currently being developed to assist the EMPOP user.

4) Peter Gill provided feedback of a short survey to discover how labs were reporting mixtures. In total there were 23 responses, revealing a wide diversity of methods being used by labs.

5) Peter Gill discussed validation of complex probabilistic models and introduced EuroForMix (EFM) a continuous open-source model supported by the Euroforgen-NOE project that takes account of peak heights, stutters, degradation, allele dropout, allele drop in. It supports analysis of multiple contributors with a practical limit of 4 unknowns, replicated samples, Fst. Training in the new software will begin immediately, in parallel with LRmix Studio.

6) Peter Gill discussed recent court experiences. In the UK, R v Fazal, the prosecution and defence used different methods to analyse a complex mixture, resulting in different LRs. Under UK law, experts from the different sides can collaborate to write a single joint report. This was carried out. We agreed that there was no preferred method. Both methods were valid. The verbal scale was used to assist the jury to provide a 'range' of results. In relation to the use of commercial software by the prosecution, in R v Hamlen, the defence argued that they needed access to the software to carry out a proper evaluation. The judge decided that the trial timeframe was insufficient to allow this to happen and disallowed the evidence. 'Equality of arms' is becoming a significant issue in relation to the restricted access of commercial software.

7) There are two actions agreed by Peter Gill to carry out **[Action 5]:**

a. In 2013, two mixtures were circulated to labs and they asked to report and describe the method used. We will revisit to discover if there have been any changes in the interim. New ENFSI labs will be invited to collaborate.

b. Peter Gill to draft ENFSI guidelines for labs wishing to carry out internal validation of complex mixture software (note that Mike Coble, NIST, is drafting general guidelines as a ISFG DNA commission exercise. This will report soon and it makes sense to base the ENFSI guidelines on this document).

Item 10: Report from subgroup C: DNA-database & legislation

(Chair; Vanessa Vanvooren, Co-chair; Dyan Daly)

During the meeting of this subgroup the following issues were presented and/or discussed:

Update from each country (15 countries were represented):

Some MS must integrate all the locus analysed, others not.
Some Countries need legislation to be implemented before they can use the new ESS.
Rapid DNA: 300 euros/sample, some countries use for urgent reference profiles or stains.
Elimination database: Mandatory or not, some are limited and others contain more categories.
Many database legislations authorise samples from arrestees/ suspects.

Legislative update:

54 countries have a DNA database with convicted persons (total of 70 millions).
Whole population database: Kuwait and Oman.
Asia: increasing numbers of databased profiles.
US: A low % of rape kits actually get tested (same in some European countries).
Spain is facing a legal problem with their databases that has caused a significant reduction in the amount of samples they can collect.

Short summary of the European CODIS meeting:

New development in CODIS; Timing for new versions; Helpdesk gives feed-back.

Update on the implementation of the EU Prüm Council Decisions:

22 countries are operational, but only 30% of all the connections are done.

Update on the ENFSI Monopoly SmartRank project:
A likelihood ratio software for searching national DNA databases with complex/partial DNA profiles. Based on LR mix studio and is easy to use. Holds possibility to find candidates when Drop in/ Drop out. Software is available as free and open source. Validation and testing with partners is in progress. Educational workshop is to be held 22-23 September 2016 in the Netherlands.

Fighting the issue of false positive DNA hits:
Problem: Large number of hits that turn out to be false after laboratory validation.
The validation is time consuming. Question & context: Can we find a rule that allow us to reduce the efforts made? Solution: Likelihood Ratio, Simulations and Acceptance criteria: Accepted – Warning – Reject.

NGS in the DNA Database:
Not for today (at least 2 years); Nomenclature still has to be fixed; Comparison with the old data has to be possible.

New Irish DNA Database:
Started the 20-11-2015 and used CODIS. It consists of two divisions: The Investigation division with stains and persons, and the Identification division with MP and relatives. More stains have been received since the start of the database. Match rate so far is 7%.

The Italian National DNA database:
Legislation 30-06-2009, decree 7-04-2016 and uses CODIS. Not yet operational, but will hold profiles from stains, persons, missing persons and relatives.

Further discussion on the semi-annual DNA database:
Update is done twice every year.
To start adding Prüm stains and Prüm persons.
International matches are not included in the document.
Statistics available in an EU document.

Certification of the Belgian DNA database by compliance with ISO 9001:
Submission to the accreditation board this summer. Map the process flow, do risk analysis, description of the tasks in methods and validation of the tools (CODIS, homemade).

Certification of the Dutch DNA database by compliance with the Dutch Data protection Law:
DNA-profiles are regarded as personal data. The processing of personal data is regulated by the Dutch Data Protection Law which is derived from the European Data Protection Directive: 95/46. Compliance with the Dutch Data Protection Law can be verified by privacy audit. Certification is for one year.
Scope of the Privacy Audit (Examples: Registration, Quality Control, Process control):
- If regular internal audits are performed.
- If information is properly stored and only accessible to authorized persons.
- If new systems and adjustments to existing information processing systems are properly tested and validated.
- If all employees are properly trained, have signed a secrecy agreement and have a proof of good conduct.

PIES final results:
BE is operational since July 2014, exchange with NL (> 2000 hits), FR (> 5000 hits) and DE (> 2500 hits). 15 % of BE clusters (~ 1000 persons) would not be identified without Prüm.
What pictures of transnational offending can we get?
Research made in BE, FR, NL, UK: Cross border effects.
Beyond hit statistics, what is their usefulness? Research made in BE, FR, NL concluding Prüm is useful but a small percentage of hits are acted further on.

Next meeting 2017:
Survey to be done: Integration of CODIS with other databases.
Information gathered on Elimination DNA database as to retention of profiles and categories of persons.
Follow-up on NGS
Pedigree and DNA database searching

Item 11: Report from subgroup D: Automation and LIMS workshop, ENFSI DNA WG

(Chair; Johannes Hedman)

The main focus of this meeting was the progress of automated workflows for NGS analysis, specifically library preparation. Three companies (Qiagen, Thermo Fisher Scientific and Hamilton) as well as the University of Copenhagen presented their solutions for streamlined NGS analysis. Apart from NGS, presentations were also directed towards the development of Rapid DNA analysis instruments, general laboratory automation and LIMS. At each Automation and LIMS subgroup meeting, specific companies are invited to give presentations on the main topic(s) of the meeting. Also, all attending companies are invited to give a short talk on a chosen topic relating to laboratory automation. In total, 16 ENFSI DNA WG delegates (members, associate members and guests) as well as 10 company representatives participated. The last hour of the workshop was closed for the companies.

Automated workflows for NGS
Library preparation is generally work-intensive and would benefit from automation both in terms of improved working environment (less manual pipetting) and elevated quality of results. Qiagen presented how their robots Qiagility and Qiacube can be applied for target enrichment and library preparation. Through their work together with CLC Bio, Qiagen also provide bioinformatics solutions. Thermo Scientific presented their set-up with Ion Chef, Ion S5 and Converge software, complementing CE analysis. Ion Chef enables automation of library preparation, template preparation and chip loading. The University of Copenhagen presented their automation of library preparation with BioMek 3000. This work required 230 pipettings for ten samples in the manual set-up. Applying the Thermo Scientific HID 124 SNP panel, it was not possible to automate library purification with the Ion Chef, therefore they prepared their own scripts for the BioMek 3000. University of Copenhagen use Ion Chef for template preparation. Hamilton is collaborating with Illumina to automate library preparation with the ForenSeq kit.

Rapid DNA analysis
GE (DNAscan) and IntegenX (RapidHIT 200) presented their latest developments. DNAscan is the first NDIS approved Rapid DNA instrument, meaning that profiles generated from reference

buccal swabs by the instrument applying specified kits and software, in an accredited laboratory, can be loaded into CODIS in the US. IntegenX has released RapidHIT ID which is a one-sample per run instrument. RapidHIT is considered a Modified Rapid DNA analysis system, as manual review of electropherograms is required prior to loading profiles into CODIS in the US.

In the US and UK, the goal is to apply Rapid DNA instruments in booking suites, to analyse samples from arrestees. The Metropolitan Police has initiated a project to use Rapid DNA instruments in the London area, and intend to roll these devices out within all custody suites (pending the decision and implementation of appropriate accreditation for these devices). In the US, work is performed to enable quicker DNA data transfer, so that the DNA profile of an arrestee can be generated through Rapid DNA analysis, searched against the national DNA database, and information on hits sent back to police within 4 hours.

Laboratory automation
NBI, Finland, has automated the washing of sperms as part of differential lysis DNA extraction. Qiacube performs at least as good as the manual method, with only 15 minutes of manual labour per batch. The laboratory now has two Qiacube systems to increase throughput, and analyse about 1500 differential lysis samples per year.

NFC, Sweden, has recently automated normalization prior to STR PCR set-up, saving about 5% of manual pipettings. They have also developed and implemented a manual direct lysis protocol for tapes, going from 20 to five pipettings per sample. Their strategy is to simplify and automate the process one module at a time.

Automation, LIMS and kit inventory list
The Automation, LIMS and kit inventory list has been updated and now contains:

- Information about automation from 43 laboratories, and a total of 178 robotic systems
- Information on LIMS from 32 laboratories, of which 17 have LIMS in place
- Information on analysis kits from 17 laboratories, including kits from three vendors plus home-brew qPCR assays.

The list is continuously updated and put on enfsi.eu. Send new information to johannes.hedman@tmb.lth.se.

New co-chair
Shazia Khan, Metropolitan Police, is the new co-chair of the subgroup.

Below follows a list of the talks. The presentations can be found on enfsi.eu:

Automated workflows for NGS, company presentations
QIAGEN new automated solutions for high throughput sample preparation and assay set-up using QIAGEN chemistry and QIAGEN NGS Portfolio in Forensics, Mirella Reimer, Qiagen.

Automated NGS workflow, Thomas Simon, Thermo Fisher Scientific.

Automating NGS Library Prep by Hamilton, Willem van Loon, Hamilton Robotics AG & AQUA LAB.

Automated workflows for NGS, user presentation
Automation of library preparation for PGM, Helle Smidt Mogensen, Department of Forensic Medicine, Copenhagen University, Denmark.

Rapid DNA analysis, company presentations
GE Healthcare update, Matthias Lindner, GE Healthcare.

Latest developments on RapidHIT and RapidHIT ID Systems, Laura Bimbashi, IntegenX.

Laboratory automation, user presentations
Automated differential lysis and current status of automation, Markus Pirttimaa, NBI, Finland.

Strategies for high-throughput STR analysis, Johannes Hedman, NFC, Sweden.

General company presentations
Safe and easy – new generation PCR pipetting robots, Mikael Havsjö, AlphaHelix.

SMART Police – SMART Lab, Frank Götz, Qualitype.

Feedback from subgroup meeting
Feedback, Automation and LIMS workshop, Johannes Hedman, NFC.

Item 12: Report from subgroup E: Casework/Biology

(Co-chairs; Rainer Wenzel & Ricky Ansell)
The Workshop focused on the following items:

- ENFSI Stain Test Survey
- Study on Case and Resource Management
- DNA evidence in court (Presentation of Harald Schneider, see the minutes)
- Project on identification of missing persons by skeletal remains analysis in Poland (Presentation of Magdalena, see the minutes)
- Interaction of swabs with tests (Presentation of Fabrice Noel, see the minutes)
- Study on transfer of trace DNA (primary/secondary transfer) (Presentation of Regine Banemann, see the minutes)
- Election of a new chair
- Way forward

ENFSI Stain Test Survey
It was decided to summarize the results in a recommendation document format: The document shall serve as general approach in daily routine work (no complex stains or rare events).
Furthermore, the chair will contact GEDNAP for setting up an additional module for stain characterization (optional, no complex scenarios, designed for stain characterization in routine work).

ENFSI Study on Case and Resource Management
The chair presented the results. Feedback came from 18 labs representing 15 countries. For detailed results see the presentation in the minutes. The study showed that the situation in Europe is very different, there are no general rules for everybody. Despite the wide range, there are quite reasonable estimates for average:

- costs per stain at 36 €
- expert workload (325 cases per year per expert)
- turnaround times (13-42 days depending on case scenario)

No correlation between automation rate and technical staff/turnaround times were found. This may be due to the low number of participating labs and a varying degree of the number of reference sample analysis (databasing).

The purpose of the study was to give some basic information for individual use. Labs are enabled to check their service quality and the study helps to identify possible ways to solve existing problems (capacity, limitations, money, staff).

The SG decided not to perform further studies, but participating labs will be mailed in order to precise their lab capacity (stains vs reference samples).

DNA evidence in court
Harald presented a murder case which served as a good example how contact traces can lead to a false identification of offenders when no additional information is available.

Project on identification of missing persons/unknown bodies in Poland
The presentation of Magdalena focused on the development of an optimized method for the DNA analysis of skeletal remains. The Polish police reveal more than 800 unknown bodies a year and ca. 4400 long-term missing people. The future plan (GeNN project) comprises of the genetic identification of unknown human remains.

Interaction of swabs with tests
Fabrice Noel presented that due to a change in production process, Nylon flocked swabs (FLOQSwabsTM from COPAN) interact with blood tests. The Hexagon OBTI test sensitivity for human blood was greatly reduced when flocked swabs were used. Meanwhile, COPAN has changed its production process and new products are available

Study on transfer of trace DNA
Regine presented a BKA study on primary/secondary transfer of DNA Under test conditions, a significant amount of secondary transfer of DNA is observed. Transfer rate varies from person to person and time to time. After presentation, other examples from the SG were discussed. It turned out that it is extremely difficult up to practically impossible to identify secondary transfer, especially after a long time. Usually, there is no sufficient information to reconstruct evidence history.

Election of a new chair
The SG voted for Arnoud Kal (NFI). He will take over for the next term, co-chaired by Ricky Ansell.

Way forward
Arnoud presented ideas for future topics:

- RNA based body fluid identification – practical aspects for routine labs
- Age of the stain, age of the donor
- Reporting of body fluids
- Evidential value, activity level
- Context information management to reduce bias
- Background, transfer, persistence of DNA
- Limitations, service level agreements

Item 13: Update from ICMP the ENFSI-ICMP DNA exclusion database (Ingo Bastisch)
The ICMP delegate was not present at the meeting, thus Ingo went briefly through the background and history of the database now in function. The decision to establish ICMP as an international organization, as decided in December 2014, turns ICMP to an independent diplomatic entity, makes it even more suitable for hosting the exclusion database.
The first part of database consist of many hundred unsourced contaminant DNA-profiles, including those from the dismounted Forensic Science Service and profiles from Florida Dpt of Law Enforcement (unofficial SWGDAM unsourced contamination database). The second part, the manufacturers' EDB is not yet populated, awaiting participation by manufacturers. The use should largely be self-explanatory, with an easily used online users' manual. Share your unsourced contaminant DNA profiles with the community! Web links of interest:
www.icmp.int
www.ic-mp.org/news/icmp-established-as-international-organization-in-its-own-right/

Item 14: Update from EDNAP (Niels Morling)
Ongoing and finalised activities at EDNAP:

- 6th mRNA collaborative exercise (published: in FSI Genetics 2015 (16) 139-147)
- SNP & Indel typing of AIMs (published in: FSI Genetics 2015 (19) 56-67)
- Exercise mtDNA SNaPshot (to be published)
- Meth-Age exercise part 1 (finalised), part 2 (to be initiated)
- Euroforgen/EDNAP mRNA NGS exercise 1 – Assay for body fluid/tissue identification (ongoing)

Next EDNAP meeting will be held in Rome 8th November.

Item 15: Update on the EUROFORGEN activities (Peter Schneider)
The project is now in its final year.

There is still money for short term fellowships (visits at other laboratories). So far 14 fellowships awarded to 28 colleagues from 10 countries visiting host labs in 11 countries. This third and final

call covers 20 fellowships. Up to 500 Euro for travel support. Completion before end of September is a must. For application details see: http://www.euroforgen.eu/news/short-term-fellowships/

An international dissimination conference to be held in Venice, Italy June 23rd, in collaboration with IALM "Forensic DNA analysis in the light of the new security needs". Sessions included are: "From crime scene to court" (Evidence challenges and advanced interpretation methods, The interpretation debate: miscarriages of justice), "From Genotype to Phenotype" (The next step in forensic genetic intelligence, State-of-the-art and future directions), "Science in Society" (Ethical and legal aspects, the societal dimension of forensic genetics, Security issues in Europe from a DNA perspective). There is a separate session 24th on Forensic Genetics and Genomics, adjunct to the meeting. For registration details: www.ialm2016venice.org

Three CEPOL courses have been successfully arranged in Avila, Spain, with a total of 86 participants. Angel Carracedo is new as WP5-leader (Education, training and career Development) and activities for 2016 includes an extended collaboration with CEPOL, initiation of collaboration with the European Judicial Training Network (EJTN), support for national training workshops, and continuing the development of the virtual Institute website of EuroForGen.

Item 16: Strengthening quality assurance in forensic laboratories: performance of the accredited GHEP-ISFG proficiency test (Koro Fernández)

Inter-comparison program "Analysis of DNA polymorphisms in blood stains and other biological samples" started in 1992 with 10 participants from 2 countries, formal PT since 1995. Today more than 120 laboratories take part, coming from 18 countries. The tests have developed and expanded in its contents through the years. Today the exercise holds two levels, basic and advanced. The proficiency test was accredited according to ISO/IEC 17043 in 2014 and is open also to non-members of the GHEP-ISFG. More information can be read in Fernández et al., Accreditation of the GHEP-ISFG proficiency test: One step forward to assure and improve quality. FSI Genetics Suppl Ser 2015 (5) e515-517.

Additional information on the GHEP-ISFG can be found at: www.ghep-isfg.org

Item 17: Forensic Science Regulators DNA Anti-Contamination update (June Guiness)

Laboratory:

FSR-G-208 - The control and avoidance of contamination in laboratory activities involving DNA evidence recovery and analysis - available at: https://www.gov.uk/government/publications/laboratory-dna-anti-contamination-guidance

FSR-P-302- The management and use of staff elimination DNA databases - available at: www.gov.uk/government/publications/dna-contamination-detection

ISO 18385 is the standard for DNA consumables used in the DNA process chain, from packaging to analysis, required by the Regulator (This standard only replaces sections 3.2.2/3 and Annex A in PAS 377 Pass/ fail technical requirements for the PAS 377 sections is detailed in sections 8.8.3 – 8.8.5).

Crime Scene:
The latest FSR document "FSR-G-206" is to be published end of summer: The Control and Avoidance of Contamination in Crime Scene Examination involving DNA Evidence Recovery. The consultation of the draft involved also several international responses.

Elimination database (CED):
The outcome of CED will be published by the Regulator, though it is not decided in which format. Letter has been sent to all consumable manufacturers' on the CED.

Forensic Medical Examinations:
The Regulators Medical Forensics Specialist Group (MFSG) is developing a standard for Sexual Assault Referral Centres (SARC's) that aligns to ISO 15189:2012, Medical laboratories – Requirements for quality and competence.

The FSR is conducting an inquiry instigated by a police complaint, caused by the mishandling of materials in a forensic medical facility. When finalized a report will be published by the regulator.

Mixtures:
Work on guidance has initiated now being in a scoping and drafting phase. No deadline presented.

Item 18: Development of a forensically useful age prediction method based on DNA methylation analysis [CFLP] (Zanetta Makowska)

Usefulness of age estimation in forensics: Information about chronological age of an offender chronological age itself can be used to narrow down the number of suspects or minimize of investigating versions. Information about biological age of an offender can be useful to improve Forensic DNA Phenotyping, ageing affects mostly progressive traits like baldness or hair greying.

Candidate markers were selected using a previous study by Hannum et al, "Genome-wide methylation profiles reveal quantitative views of human aging rates." (Mol Cell. 2013 24 49(2) 359-67). 8 of the 71 presented markers was dealt with for further use. More information on the method developed can be read in the following two recent publications:

Zbiéc-Pierska et al., Examination of DNA methylation status of the ELOVL2 marker may be useful for human age prediction in forensic science. FSI Genetics 2015 (14) 161-167.

Zbiéc-Pierska et al., Development of a forensically useful age prediction method based on DNA methylation analysis. FSI Genetics 2015 (17) 173-179.

Item 19: ISFG, incl. ISFG paper NGS considerations (Walther Parson)

Ongoing commissions within the ISFG:

- Recommendations on quality control of autosomal Short Tandem Repeat databasing (STRidER).
- Recommendations on the validation of software programs for statistical interpretation in forensic genetics applications.

- Recommendations on evaluation of evidence.

- Recommendations on the use of X-STRs in forensic genetics.

Walther regarding NGS on STRs: "How to capture this additional information in a convenient format"? The executive board of the ISFG introduced a DNA commission to evaluate initial considerations regarding STR nomenclature. The primary goal is to define minimum criteria for data analyses and database storage. Ultimately, this should facilitate compatibility between MPS STR data generated currently and the data that will inevitably follow with wider adoption, while ensuring backward and parallel compatibility to CE-based STR typing in national DNA databases as well as published population data.

At present, it can be expected that both CE- and MPS-based STR typing methods will continue to coexist. Their application to casework will depend on resources, ease of use, speed of analysis, the value of the increased resolution power, and each technique's relevance to complex and challenging cases. The adoption of sequenced STR alleles in practical forensic work requires considerations at three hierarchical levels: the full sequence (sequence string), the alignment of sequences relative to a reference sequence and the annotation of alleles. A set of eight practical considerations on NGS of STRs (see presentation for details)

Further reading in the recent publication: Massive parallel sequencing of forensic STRs: Considerations of the DNA commission of the International society of Forensic genetics (ISFG) on minimal nomenclature requirements. Parson et al., FSI Genetics 2016 (22) 54-63.
ISFG Membership: If not already a member, do join the ISFG and become a member of a research active forensic genetic community. To become a member all application details are found at: http://www.isfg.org/Apply . The annual fee is 60 euro and entitles: free subscription to FSI Genetics, reduced registration fees for the biannual world conferences and boosts exchange with forensic geneticists all over the world.

Next ISFG congress (27th) will be held in Seoul, South Korea August 28th to September 1st 2017.

Item 20: Feedback from the latest GEDNAP PTs (Karsten Hohoff)

Karsten presented the evaluation of the GEDNAP proficiency tests 50 and 51 and the coming testst 52 and 53. PT50: Reaches 210 participants (43 ENFSI laboratories) from 38 countries, mainly western European countries. PT50 (not mtDNA) was a total of 43506 typing events with 74 errors, thus 99,81% of all typing events were correct. No separate data regarding ENFSI laboratories. Apart from the regular STR's, Y's, mtDNA, biostatistics and presumptive testing included, also extraction efficiency was presented (interesting data for comparison, next round will be with less amounts of DNA).

For additional information visit the GENAP homepages: http://www.gednap.org/

Item 21: Update on the evaluation of evidence (Tacha Hicks)

Following the completion of the project, dissemination and discussion have taken place on several occasions, not only in Europe but also in the states, China and Australia.
Workshops have been held at EuroJust, NFC (Sweden), BKA (Germany), EAFS (Prague), SGRM (Schweiz).

An interesting case example was presented, for which the interested are directed to the presentation on the website!

Some recent publications on the topic:
Champod et al., ENFSI Guideline for evaluative reporting in forensic science: a primer for legal practitioners. Criminal Law & Justice Weekly 2016 180(10) 189-193.

Biedermann et al., The need for reporting standards in forensic science. Law, Probability & Risk 2015 14(2) 169-173.

Coming events:
Two day workshop in the Hague 24-25 November: Beyond the source, beyond the science? For more information visit the following webpage, http://academy.forensicinstitute.nl

Item 22: DNA-database management document - update/approval (Kees van der Beek)

Changes for the 2016 version of the ENFSI DNA WG DNA database document was approved in plenum.

Item 23: Update on DNA WG website (Fabrice Noel)

We still have issues with the web pages, no quick solution is at hands. Old website www.enfsi.eu is still available but only in certain parts, some documents are missing. These pages are not updated.

Interim webpage is available (intranet.enfsiweb.eu/user/login?current=user/register). For website(s) access see attached documentation from Fabrice **[Action 6].**

A long term solution is under discussion (the issue will be discussed further at the November SC meeting). Europol might be a solution for harbouring our webpages.

Item 24: Introduction new associate member laboratory Kosovo (Fatmir Ademi)

Fatmir made a presentation on the forensic DNA facilities in Kosovo: Republic of Kosovo, Ministry Internal Affairs, Kosovo Agency on Forensic (KAF), DNA and Serology Division.

Apparently the DNA and serology division is a small facility with only a few staff members. No case numbers were given, but apart from casework they also perform parental testing and missing person cases. DNA data basing using CODIS started in 2013. DNA and serology came accredited in 2015.

The toolbox holds the following: DNA Extraction (Chelex, Organic, Differential), DNA Quantification (Real-Time 7000 PCR System, Quantifiler), DNA Amplification (GeneAmp PCR System 9700, Identifiler), CE (ABI Prism 310 Genetic Analyser, GeneMapper 3.2).

Ongoing activities: Populations study and development of new methods.

Item 25: Financial matters (Ingo Bastisch)

Membership fees for associate members: The ENFSI board decided in May 2015 for a new option – 20% on top of the meeting fees for associate members and guests (money will go to the board). No (final) official document yet on this decision, but it should be resolved before the next meeting. For the Warsaw meeting the information came too late for the organizers to be able handle it (Note: the official document can be found at the ENFSI website, BRD-FWK-008, Framework for Finances).

Company fees, suggested from the WG SC and voted in favour for during the meeting: 750 euro for company attendance (goes to the WG), 750 euro for a company booth and 250 euro per persons attending on top of normal fee (max 3 persons/company), this money goes to the organizers. When it's possible any surplus of a meeting to benefit the WG.

Item 26: Coming meetings (Lívia Zatkalikova)

Next Steer Committee meeting will be held 7th November in Rome, the day before the EDNAP meeting.

Future WG meetings:

- Spring 2017 Vilnius, Lithuania – decided!

On proposal, (to be decided):

- Spring 2018 Italy
- Spring 2019 Spain
- Spring 2010 France


EDNAP, CODIS users
& ENFSI DNA
Working Group Meetings
WARSAW, Poland • April 26-29
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