

## National DNA Intelligence Databases in Europe – Report on the Current Situation

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DNA databases for offender identification are a modern intelligence tool for criminal investigations. The methods used for the processing of the samples derived from those established for routine casework DNA analysis. All currently existing European DNA databases are working on the basis of Short Tandem Repeat (STR) markers, taking advantage of the sensitivity of these systems and the ability to co-amplify them in multiplex reaction assays.

In order to exchange DNA profiling results between the member states of the European Union, a set of four core loci has been suggested by the DNA Working Group of the European Network of Forensic Science Institutes (ENFSI) and Interpol including the STR loci TH01, vWA, FGA, D21S11. These loci have initially been recommended by the European DNA Profiling Group (EDNAP), based on a series of collaborative exercises (1-3).

The first European DNA database for offender identification was established in the United Kingdom in 1995. In 1997, DNA databases have been introduced in the Netherlands and Austria. Germany followed in 1998 (4). Eight more countries (Belgium, Denmark, Finland, France, Norway, Spain, Sweden and Switzerland) are planning their database projects at different levels of preparation and currently only three countries (Ireland, Greece and Portugal) do not plan to introduce a database in the near future (5).

**Thus, there is no general agreed model of a DNA database at the European level. However, a principal model can be defined, demonstrating three organizational features of a national DNA database:**

- 1) The laboratory unit is processing anonymous reference samples and sends the profiles onto the database. In some countries (U.K., Netherlands and Austria) this laboratory also performs the DNA analysis of the casework samples.
- 2) The DNA database itself is storing the profiles, which are linked to personal records by identification tags used to anonymize the DNA samples. The personal record database generally has no direct access to the physical DNA sample.

- 3) The executive force is collecting and sometimes also typing casework samples that enter the DNA database.

There is significant heterogeneity within the existing DNA databases in terms of (see also 4)

- entry and storage criteria of database samples
- anonymization requirements
- removal of entries from the database
- number of entries and
- DNA systems used.

The U.K. and Austria enter and store DNA profiles and reference samples from suspects, convicted offenders and unknown samples, whereas in the Netherlands DNA profiles only have been stored from convicted offenders and unknown samples for serious crimes with a minimum imprisonment penalty of two years after court order. In Germany, DNA typing results obtained from routine casework analysis, which has to be ordered in every case by a judge, is entered automatically into the database. In cases of serious crime where no DNA analysis was performed, the DNA profile of a suspect or a convicted offender can be obtained separately and entered into the database after a judge's decision, which has to be based on a prognosis about the risk of future criminal activities of the offender. In the U.K. any recordable offense is entered into the database in contrast to the other 3 existing databases, where only serious crimes are included (e.g. crimes against life and health, sexual abuse, robbery, theft, arson, blackmail, drug-related and organized crimes...). In the U.K., the Netherlands and Austria the personal data of the suspects are stored anonymously in a separate register. In Germany, the DNA profiles are stored openly together with the personal records in a central offender database of the police, whereas personal as well as crime scene samples are being processed anonymously in the laboratories. Reference DNA and/or blood samples from suspects and offenders are kept permanently on the Austrian and UK database, but not in Germany or the Netherlands, where these samples have to be destroyed by law after the case has been closed or the final court decision has been reached. The total number of database entries is 360.000 reference profiles and 40.000 casework profiles in the U.K. database, 1.000 and 800 in the Netherlands, 8.000 and 1.000 in the Austrian, and

about 500 profiles in the German database, respectively. All database projects apply the 4 European core loci, the U.K., the Netherlands and Austria use the SGM (FSS, Birmingham, 6,7) and Germany is using ACTBP2 (SE33).

### SCHEME OF THE AUSTRIAN DNA INTELLIGENCE DATABASING PROJECT

The Austrian DNA database project initiated October 1<sup>st</sup>, 1997. The two components are the executive branch which is located at the Ministry of the Interior in Vienna, and the laboratory unit situated at the Institute of Legal Medicine, University of Innsbruck. Within the last year, this laboratory has processed 8.000 reference samples and 1.000 crime scene samples.

### LOGISTICS

The laboratory is producing kits, which are sent out to the police personnel for collecting buccal cells. These sets contain sterile buccal scrapes, bar-coded reaction tubes and a blank form, all identified by the same barcode. When a buccal scrape is taken by a police officer, it is sent to the laboratory anonymously. The personal data of the suspect is administrated at the Ministry of the Interior. Each reaction tube containing a buccal scrape is unambiguously characterized by its barcode. This barcode information is the only link between the personal data and the obtained DNA profile of the suspected person. Throughout the entire laboratory operation, a sample is addressed by its barcode. This is achieved by a LIMS program (Laboratory Information Management System), which has been designed for databasing purposes.

The sample is directed through the typing process by the LIMS program. The status of a sample (extraction, PCR setup, amplification, detection, and analysis) can be constantly reported to reconstruct the history of the sample in the laboratory.

Therefore extraction lists, parameters for PCR setup, sample sheets and injection lists for electrophoresis as well as analysis parameters are provided by the LIMS. Samples failing to amplify or producing unexpected results are designated to separate lists according to the problem which occurred during the process and wait to be repeated. The program also takes care of quality control, mission of results to the Ministry of the Interior via a high-security mailing system and storage of the physical DNA after the typing process.

### METHODOLOGY

When a buccal scrape sample is returned to the laboratory, its barcode undergoes validation. Since the barcode has been produced at the laboratory, a sample can be recognized as valid. Remarks to the sample can be added interactively using dialog windows, again being linked to the barcode data. Subsequently, the sample is added to the extraction list and goes into the DNA laboratory. DNA from the epithelial buccal cells from the scrapes is extracted performing Chelex (8).

The reference samples are typed on the basis of highly polymorphic STR loci using the SGM Multiplex (6,7). Amplification products are detected fluorescently on automated capillary electrophoresis devices (ABI CE 310) and analyzed using GeneScan<sup>®</sup> software (PE/ABD). Analyzed data are then imported into Genotyper<sup>®</sup> software (PE/ABD) for macro-automated allele designation. Analysis and manual inspection of the data is performed twice and independently by two experienced analysts. The obtained results are then compared by LIMS and sent to a transfer list, which contains the results to be sent onto the DNA database at the Ministry of the Interior.

### AUTOMATED FEATURES

The Austrian National DNA Database project was implemented into an existing forensic DNA laboratory performing routine casework analysis. Thus, a new sample management has been developed to increase the sample through-put, not only by expansion of manpower, but above all, by simplifying the typing process of reference samples. The reproducible nature of a buccal scrape sample compared to more complex casework stains offered the application of standardized protocols and the implementation of appropriate robotic devices. The processing of the reference samples involves four generations of reaction tubes, which are all – except of the first - loaded by robots to avoid mixing-up of samples.

*First generation.* Buccal swabs are returned to the laboratory in 1.5 ml reaction tubes, which are barcode labeled. In these tubes Chelex extraction is performed after decantation of the transport medium.

*Second generation.* An aliquot of the extracted DNA is transferred into another 1.5 ml vial. These vials serve as both source tube of DNA for amplification set-up as well as storage medium for the extracted DNA after analysis.

*Third generation.* The PCR is set up in 0.2 ml MicroAmp<sup>™</sup> reaction tubes changing into the 96 well microtiterplate. Chelex extraction and PCR-setup are

performed automatically by a 4 channel robotic microplate processor (3002 Rosys/Anthos). Amplification is performed in 9600 GeneAmp™ thermocyclers (PE), located in the *Amplified DNA* working area

*Fourth generation.* Aliquots of the amplification products are transferred into another 96 well format tray, combined with deionized formamide and internal lane standard (GeneScan® 500 Tamra, PE/ABD) using an ASYS HiTech™ (Asys) robotic device, which is again located in the amplification area. The amplification tray is then loaded on the CE 310 (ABD). After analysis, the amplification products are discarded. Extracted DNA is stored at –20°C.

### ANALYSIS OF THE STR PROFILES

Analysis and allele calling of the STR fragments is a process which involves automated routines applying macros on commercially available software (Genotyper® 2.0) and subsequent manual inspection by two experienced analysts. Analyzed data from GeneScan® 2.1 software are imported into a Genotyper® file including categories for the true allele size ranges and macros of commands to perform the labeling of the peaks. First, the internal lane standard of each injection (up to 105 per run) is controlled by inspection in the plot window.

Subsequent runs on a capillary may deviate from each other. To eliminate run-to-run variability of fragment size values in categories, the offset for each ladder fragment is calculated according to the actual size Allelic ladders are injected every 20 to 25 samples. The offset values determined by one of the ladder injections are subsequently compared to control the performance of the entire run. Fragment lengths are labeled according to the ISFH nomenclature (9), with respect to a ±0.5 bp window. A filtering option deletes labels from peaks known to contain no valid information for the profile (e.g. stutter bands, background noise, peaks missing the non-template base addition). After manual inspection, the peak labels are imported into LIMS, where the two independent analyses are compared automatically.

The LIMS program registers extraction and amplification negative controls and logs these data. The values for the positive control are checked by the program. They have to meet the expected values, in order to load the entire run. Differences between the independent analyses are reported as well as rare alleles and failed STR loci. Affected samples can be directed to the repetition lists for further investigation. Finally, the results identified by the corresponding barcode are sent on

to the DNA database to the Ministry of the Interior for matching purposes.

### MATCH STATISTICS OF THE AUSTRIAN DNA DATABASE

Since the beginning of the project the laboratory typed more than 8.000 reference samples with a very high success rate in obtaining a full profile at first attempt (>94%). This success is attributed to the fact that the logistics of the kit and the setup of the laboratory process were appropriate. The casework section processed more than 1.100 casework stains in the same time frame. Until October 1998, 180 matches were observed within the database. 104 reference profiles matched 124 offenses, including 16 crimes against health and life (3 murder cases), 99 thefts and some other crimes. Additionally, 76 matches between crime samples were observed rising from 32 different crime scenes.

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