

3. Single cells from samples contaminated by blood or other cell types;
4. Single cells from archived cases.

The forensic analysis of difficult samples, such as single cells, can also be undertaken using SNPs (single nucleotide polymorphisms) and mitochondrial analysis.

The application of these analysis techniques for counter-terrorist purposes such as document security and anti-counterfeiting will also be discussed.

#### References:

1. Findlay I., Frazier R., Taylor A., Quirke P., Urquhart A. Single cell DNA fingerprinting for forensic applications. *Nature* 389, 555-556.

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#### IP-3

##### STR PROFILING STRATEGY AND THE DEVELOPMENT OF NATIONAL DNA DATABASES IN EUROPE – A SUCCESS STORY

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The introduction of multiplex PCR systems has greatly facilitated the rapid typing of samples and computer-based storage of results in large DNA profile databases. Since 1995, more and more European countries have introduced national DNA databases for storing DNA profiles from unsolved crimes and known offenders.

The existing databases have been created within the framework of the respective national legal systems. Therefore, an obvious heterogeneity exists among the European DNA database systems regarding the catalogue of offenses leading to a database entry of an offender's DNA profile, and the criteria for a removal of an entry, the procedure for obtaining reference samples, the possibility of long-term storage of these samples, as well as the criteria for database searches. Fortunately, significant progress has been made regarding the harmonization of typing systems within Europe. The European DNA Profiling (EDNAP) Group has initiated a series of scientific collaborative exercises for the evaluation of new DNA typing methods and systems. As a result, a number of loci were recommended suitable as common European systems. To coordinate and standardize operational processes of DNA typing in casework within the police laboratories as well as in the laboratories providing this service for the police, the DNA Working Group of the European Network of Forensic Science Institutes (ENFSI) has been founded four years ago. Based on the initial EDNAP exercises, and on recommendations by ENFSI, seven systems have been defined as the European standard set of loci – THO1, VWA, D21S11, FGA, D3S1358, D8S1179 and D18S51 (ESS loci). Furthermore, the Interpol DNA Monitoring Expert Group has adopted these loci as Interpol Standard Set of Loci (ISSOL). These loci now form the core of all existing criminal DNA databases in Europe, and will serve as a "common language" to facilitate the exchange of DNA profiles across national borders. The growing number of database records has led to a steadily increasing number of database hits helping to solve crime cases. From existing databases it becomes evident that the number of hits strongly depends on the rules for entering offender profiles. This has led to recent changes in database legislation in some European countries.

#### IP-4

##### THE FALLIBLE MTDNA DATABASES

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Under certain circumstances mitochondrial DNA may be the molecule of choice for forensic purposes. The key questions concerning a mtDNA sample taken from a victim or suspect are that of identity and geographic or ethnic affiliation. In order to be able to provide answers in the form of match probabilities, mtDNA databases of numerous populations are required for comparison. However, sampling and sequencing strategies, sample handling, and the sequencing process itself were notoriously poor and flawed, as testified by numerous publications in leading forensic journals. Databases typically refer to either "race" (e.g. "Hispanic", "Caucasian" etc.) or nationality, neither of which is meaningful or relevant for the origin of matriline. Often "random" sampling is alluded to, which in reality means that sampling was performed in ignorance of recent immigration history (and resulting social stratification) and regional differences of (former) ethnic groups. Sample sizes are rather small (<250) and sequencing barely goes beyond the popular first and second hypervariable segments of the control region.

There is no reason to keep forensic databases separate from those in the fields of human genetics and molecular anthropology. Any claim of "high quality" of forensic databases in contrast to other databases should be received with much scepticism. The analysis of complete mtDNA sequences has now revealed that one cannot guarantee that mtDNA databases are error free. Although the latter should be the goal, "it is not practical, and it is probably not technically feasible" – as Corinna Herrnstadt and her colleagues have recently stated. It would thus be helpful for workers to be open to the possibility of error and to maintain database errata for their work. When forensic databases are not publicly accessible sequence by sequence for critically examination, then we have to count with errors that are simply hidden away. There are various ways to examine the quality of a data set a posteriori, which are based on phylogenetic analysis, the knowledge about the positional mutation rate spectrum, and an increasing amount of published mtDNA information, the ultimate reference being the emerging worldwide phylogenetic tree of complete mtDNA sequences. Thus, in the analysis of mtDNA in a forensic case, one is confronted with data sets for comparison that greatly differ in quality and information content. Consequently, providing a single match probability is inadequate in view of this complex fuzzy context.

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#### IP-5

##### SNP TYPING FOR FORENSIC APPLICATIONS

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The SNPs represent the most abundant form of genomic sequence variation (one SNP every 200-300 bp), they have low mutation rates, and are suitable for analysis using high throughput technologies. All these characteristics make these markers very useful for a variety of different applications such as forensic genetics, anthropology, clinical genetics, and pharmacogenomics and pharmacogenetics. Approximately 50-70 autosomal SNPs are needed to give a discrimination power that is equivalent to short tandem repeat multiplexes that are currently in use for forensic applications. Whether SNPs will replace STRs as the primary method of choice is a matter of conjecture at present but they have some promising charac-