Identification Strategies for Unknown Victims from Mass Disasters and Unknown Perpetrators from Violent Crime or Terrorist Attacks

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Abstract: Background: The identification of unknown victims from mass disasters, violent crimes, or terrorist attacks is frequently facilitated through information from missing persons lists, portrait photos, old or recent pictures showing unique characteristics of a person such as scars or tattoos, or simply reference samples from blood relatives for DNA analysis. In contrast, the identification or at least the characterization of an unknown perpetrator from criminal or terrorist actions remains challenging, particularly in the absence of material or data for comparison, such as fingerprints, which had been previously stored in criminal records. In scenarios that result in high levels of destruction of the perpetrator's corpse, for instance, blast or fire events, the chance for a positive identification using standard techniques is further impaired. Objectives: This study shows the forensic genetic procedures in the Legal Medicine Service of the German Air Force for the identification of unknown individuals, including such cases in which reference samples are not available. Scenarios requiring such efforts predominantly involve aircraft crash investigations, which are routinely carried out by the German Air Force Centre of Aerospace Medicine as one of the Institution's essential missions. Further, casework by military police or military intelligence is supported based on administrative cooperation. In the talk, data from study projects, as well as examples from real casework, will be demonstrated and discussed with the audience. Methods: Forensic genetic identification in our laboratories involves the analysis of Short Tandem Repeats and Single Nucleotide Polymorphisms in nuclear DNA along with mitochondrial DNA haplotyping. Extended DNA analysis involves phenotypic markers for skin, hair, and eye color together with the investigation of a person's biogeographic ancestry. Assessment of the biological age of an individual employs CpG-island methylation analysis using bisulfite-converted DNA. Forensic Investigative Genealogy assessment allows the detection of an unknown person's blood relatives in reference databases. Technically, end-point-PCR, real-time PCR, capillary electrophoresis, pyrosequencing as well as next generation sequencing using flow-cell-based and chip-based systems are used. Results and Discussion: Optimization of DNA extraction from various sources, including difficult matrixes like formalin-fixed, paraffin-embedded tissues, degraded specimens from decomposed bodies or from decedents exposed to blast or fire events, provides soil for successful PCR amplification and subsequent genetic profiling. For cases with extremely low yields of extracted DNA, whole genome preamplification protocols are successfully used, particularly regarding genetic phenotyping. Improved primer design for CpGmethylation analysis, together with validated sampling strategies for the analyzed substrates from, e.g., lymphocyte-rich organs, allows successful biological age estimation even in bodies with highly degraded tissue material. Conclusions: Successful identification of unknown individuals or at least their phenotypic characterization using pigmentation markers together with age-informative methylation profiles, possibly supplemented by family tree search employing Forensic Investigative Genealogy, can be provided in specialized laboratories. However, standard laboratory procedures must be adapted to work with difficult and highly degraded sample materials.

Keywords: identification, forensic genetics, phenotypic markers, CPG methylation, biological age estimation, forensic investigative genealogy

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