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Which tissue to take? - A retrospective study of altered human remains

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Introduction

In forensic medicine, the clarification of the deceased identity is of crucial importance. Various methods can be used to identify a corpse. However, in case of severe alteration or missing reference data, the most reliable method is DNA genotyping [1,2]. A typical DNA profile consists of 16 polymorphic genetic markers, which is then compared to a reference profile, either an ante-mortem sample or an assumed relative. However, factors like heat or decomposition can lead to a fragmentation of the DNA. This degradation varies among tissue types and has an impact on the genotyping success (Fig. 1) [3,4].

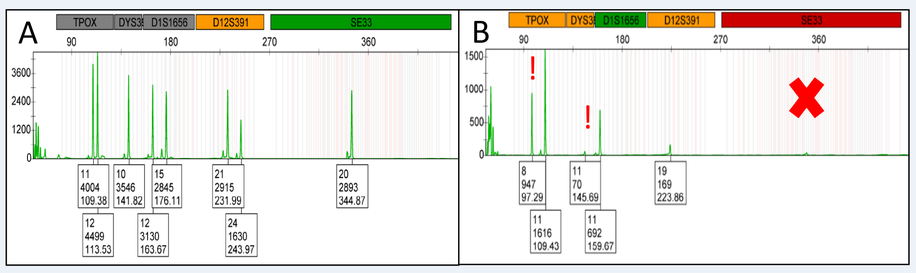


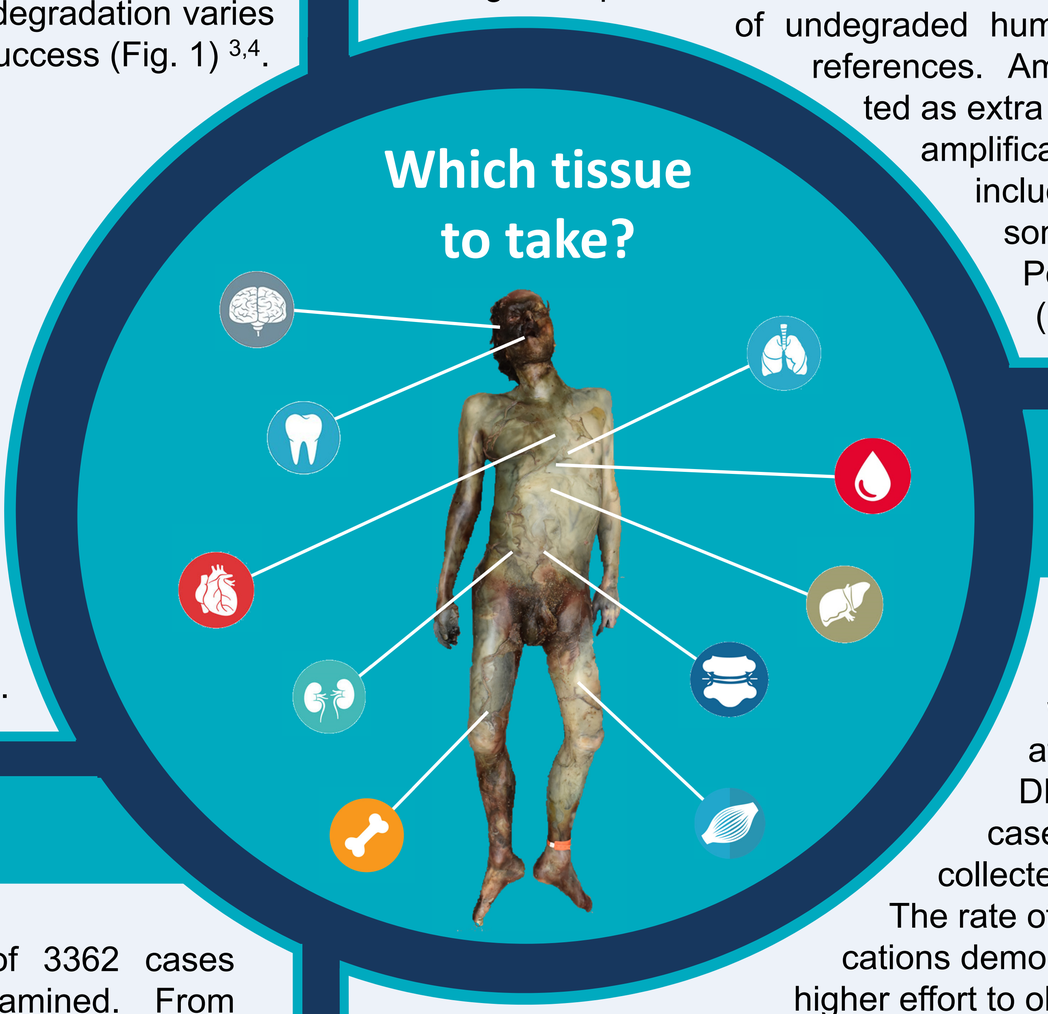
Fig. 1: Sections of DNA profiles generated from unaltered (A) and altered (B) tissue samples of different corpses. Intra- and Inter-imbalances (!) and drop outs (x) are marked

The aim of this study was to highlight the challenges of identifying altered remains considering the success rate of DNA genotyping. The amount of performed additional DNA amplifications and tissue-specific variances were evaluated.

Methods

The survey addressed autopsied cases from 2014 to 2019 involving the identification of decomposed, burnt and skeletonized deceased as well as bodies found in water.

DNA extraction as well as the amplification methods and the resulting DNA profiles were recorded and compared with the results of undegraded human remains serving as references. Amplifications were counted as extra when the two mandatory amplifications were exceeded, including additional autosomal and gonosomal Polymerase chain reaction (PCR) kits.



Medical results

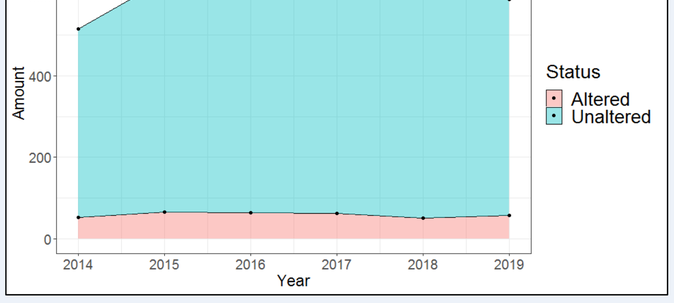


Fig. 2: Distribution of altered and unaltered corpses

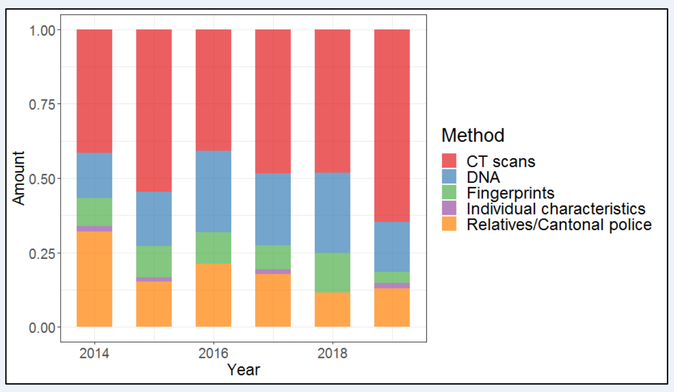


Fig. 3: Distribution of identification methods

A total of 3362 cases were examined. From these, a mean of 9.7 % showed signs of alteration. Each unknown or uncertain deceased was successfully identified (Fig. 2).

Five methods had been applied for identifying the corpses (Fig. 3). With a mean of 49.1 %, comparing ante-mortem and post-mortem CT (computed tomography) scans was the most common method.

Genetic results and discussion

A total of 140 unknown human bodies with or without signs of alteration were identified by DNA genotyping. In most cases a muscle sample was collected from the body (Fig. 4). The rate of additional DNA amplifications demonstrated the significantly higher effort to obtain a DNA profile from the altered deceased. In comparison to unaltered bodies, 86 % of the cases required more than the two amplifications (Fig. 5).

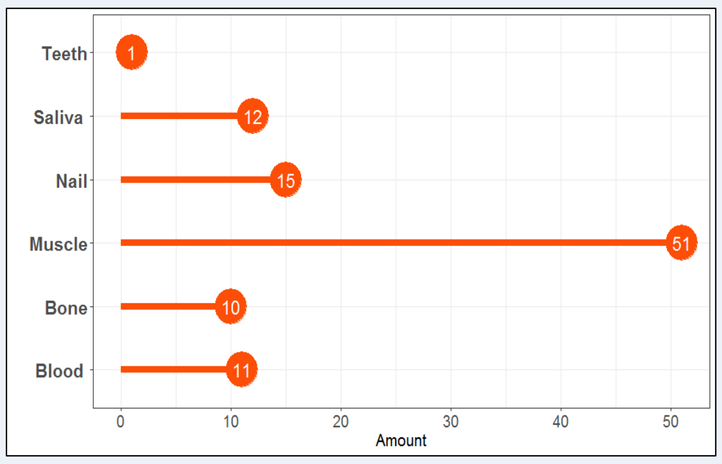


Fig. 4: Tissue samples collected from altered human remains during autopsies and provided for DNA analyses

The additional rate of PCRs also varied between tissue types (Fig. 6). For each tissue, the mean and median of the additional PCRs was lower in bodies without signs of decomposition or burning. Muscle and nail samples in particular revealed a distinct variance. Bone samples were only sampled from fully skeletonized bodies because of the invasiveness of the extraction and the effortful retrieval.

Conclusion

In 86 % of the altered corpses identified by DNA analyses, extra amplifications were conducted, demonstrating a high uncertainty in terms of the DNA profiling success. These retrospective results reflect the necessity for a systematic approach to detect the optimal tissue depending on each corpse type and degradation degrees, a multicenter work which is currently being done in our and cooperating laboratories.

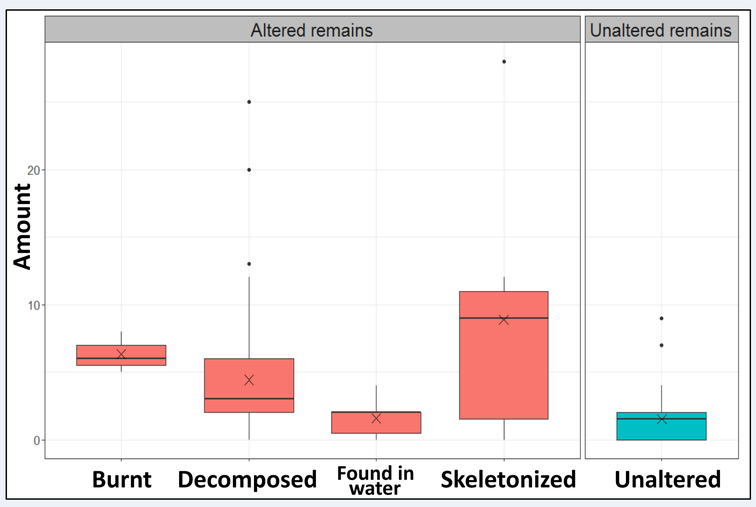


Fig. 5: Amount of additional (parallel or successive) PCRs for altered and unaltered remains

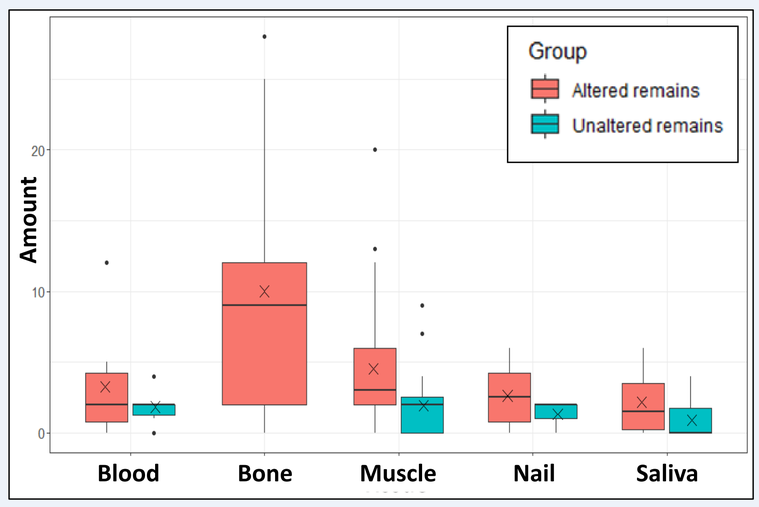


Fig. 6: Amount of additional (parallel or successive) PCRs separated by tissue types

References
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3. Gouveia N, Brito P, Bogas V et al. (2017) Forensic Sci Int Genet. 6 **4.** Brito F, Prata D, Martha S (2015) Forensic Sci Int Genet. 6