CHARACTERIZING A SIMPLE SAMPLE PROCESSING METHOD FOR DNA ISOLATION FROM FORENSIC BONE SPECIMENS

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Forensic scientists are called upon to identify human remains in criminal cases. A number of methods are used to identify human remains. The most common of these methods includes identification of facial characteristics; recognition of individualizing scars, marks, or other special features; the comparison of dentition with premortem dental records; and fingerprint comparison. In many situations, these methods cannot be used because of extensive putrefaction and decomposition of the remains. Human remains undergo a series of changes during decomposition. The rate of degradation of human remains varies greatly with environmental conditions (such as climate, bacterial growth, and insect and animal scavengers). After a period of time, soft tissues may be lost, while bone tissue may remain stable. In this type of case, DNA typing is a useful tool for identifying human remains.

Thus, bone tissue is often used to recover DNA samples for the purpose of human identification. However, bones are challenging biological samples for DNA isolation since bone samples are difficult to process. Due to the potential of having co-mingled remains, contamination by physical contact, environment-born inhibitors, and bacterial contamination that interferes with forensic DNA analysis, the outer surface of a bone fragment must be cleaned using a current method, such as sanding. This initial cleaning of the bone is a labor-intensive and time-consuming step. Moreover, it is difficult to adapt the current method for automation. To address these issues, an alternative processing method for bone samples was developed in this study. Trypsin, secreted in the digestive system, is a proteolytic enzyme that breaks down proteins through a process referred to as proteolysis. Trypsin was chosen due to its ability to degrade various types of proteins. Trypsin also has been utilized in enzymatic maceration methods for processing bone samples in anthropological laboratories. In this study, the trypsin-based maceration technique was adapted to the sample processing method prior to DNA isolation from bone samples. By incubating samples with a trypsin solution, the outer surface of the bone fragment samples was removed. The trypsin-processed bone fragment or a portion of the fragment can then be used for DNA isolation.

Our data suggest that this method can be used in the initial sample preparation for cleaning the outer surface of human bone samples prior to DNA isolation. This method potentially has a low risk of cross-contamination between samples and diminishes safety concerns generated by laboratory analysts' exposure to bone powder. This method can potentially be adapted for automated DNA isolation for human identification of bone samples, namely, from mass fatality incidents.

The application of trypsin on DNA isolation of bone will be presented. In particular, the yield of DNA isolated will be evaluated and the quality of the DNA will be assessed.