Differences in DNA Preservation Between Adult and Subadult Human Skeletal Remains As Evidenced by Individuals From Two 19th Century Cemeteries

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To explore differences in DNA preservation between adult and subadult remains and to determine if enough DNA was present to permit determination of familial relatedness, the skeletal remains of eleven adults and seven subadults from two 19th century cemeteries from Indianapolis, Indiana were tested via DNA analysis. Eleven 1 g bone samples and six 0.4 g samples were taken from adult long bones, and seven 0.4 g subadult bone samples were taken under sterile conditions. To obtain DNA, samples were processed via decalcification, solubilization, organic extraction, and concentration. The processed samples were tested via yield gel analysis, demonstrating total DNA yield of the extract, and by slot blot hybridization, using human-specific DNA probes, revealing the amount of human DNA in the extract. The samples were combined with lambda DNA and subjected to Polymerase Chain Reaction (PCR) using lambda DNA primers to test for the presence of PCR inhibitors within the extracts. The DNA samples were subjected to PCR using primers for amelogenin, which provide sex information, and with primers for two Short Tandem Repeats (STR), TPOX and FES/FPS, which can provide data for familial relationships. The results of this study conclude that biological age does not strongly influence the quantity of human DNA obtained (slot blot bands, if present, were between 0.4 and 10 pg for both age groups) or the quality of lower molecular weight DNA sequences (e.g., ability to amplify amelogenin and TPOX). However, biological age did have an influence on the ability to amplify high molecular weight sequences, such as those tested with the FES/FPS primers. The amount of bone sample used appears to influence the success rate for the amplification of DNA products. Greater success was obtained using 1 g samples than the 0.4 g samples in some tests, whereas the 0.4 g samples performed better in others. The DNA present in these samples was not preserved well enough to permit familial testing. Future studies, using larger amounts of bone and employing smaller STR's, may allow one to successfully determine familial relatedness in 19th century assemblages.

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