COMPARISON OF DNA PROFILES PRODUCED WITH AND WITHOUT WGA FOR MODERN AND HISTORIC BONES

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Historical bones and modern bones will often have highly variable amounts of DNA due to differing environmental conditions as they age. Environmental factors such as temperature, pH, and radiation can speed up the degradation process in bone. Degraded DNA can produce incomplete STR profiles with a limited number of allele calls. These profiles can be obtained using capillary electrophoresis (CE) and next generation sequencing (NGS). In this study, profiles of degraded samples from historic bones have been compared to samples from modern bones. The historic bone samples (~400 yrs old) came from the Calverton site in Calvert County, MD, provided by the laboratory of Dr. Dana Kollmann. The modern bones came from the Anatomy Gifts Registry. The bone DNA samples were extracted, quantitated, amplified with Repli-G whole genome amplification kit, followed by Qiagen Investigator 24-plex QS, and separated by CE. The results were then reviewed to ensure samples were amplified correctly.

Library preparation was then performed on all samples using the Verogen ForenSeq DNA Signature Prep Kit, and the samples were placed on the flow cell of the MiSeq FGx instrument and sequenced.

The NGS results and the CE results were examined to determine the total alleles called per sample and to identify any instances of potential dropout, stutter, and peak height imbalance for each method.The results of both analyses were examined to determine if WGA of historical and contemporary bone samples produced more complete CE and NGS profiles with fewer instances of dropout, stutter, and peak height imbalance. The results of this research showed that more complete profiles were achieved after performing both WGA and NGS when compared to CE without WGA. More complete profiles were also obtained from contemporary bone samples when compared to historic bone samples.