

COMPARISON OF STR PROFILES AFTER WHOLE GENOME AMPLIFICATION FOR MODERN DNA AND DESTROYED DNA SAMPLES

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In forensic cases, samples that are obtained often have DNA of poor quality and/or quantity. This can lead to incomplete STR profiles with a low number of allele calls. Furthermore, traditional methods of PCR amplification target a limited number of STR loci. Whole genome amplification (WGA) is a method of replicating the complete genome prior to subsequent downstream genotyping applications. In this study, DNA samples from body fluids and known DNA standards were destroyed using two different methods, via restriction endonucleases and sonication. The samples were subjected to whole genome amplification using the Repli-G kit or the Ampli1 WGA kit. The STR profiles before and after the destructive treatments were obtained using the Qiagen Investigator 24plex QS and the ForenSeq DNA Signature Prep Kit. The profiles of the destroyed samples obtained after WGA showed an increase in the number of alleles called when compared to samples that did not undergo WGA. This showed that more complete profiles can be obtained from intact and destroyed DNA samples after whole genome amplification. The data also showed that next generation sequencing can produce more complete STR profiles and obtain more information than capillary electrophoresis.