ASSESSMENT OF DNA DEGRADATION AND THE PREDICTIVE GENOTYPING SUCCESS OF HIGHLY DEGRADED SAMPLES

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Highly degraded biological samples are commonly encountered in the case of mass disasters (eg. tsunamis, earthquakes, terrorist attacks, wars, plane crashes) and some forensic casework. Where conventional methods of victim identification such as fingerprint, visual and dental comparisons are unable to be applied, DNA genotyping of Short Tandem Repeats (STR) becomes the principal means of identification.

As biological tissue degrades DNA becomes progressively more fragmented, resulting in a decreasing ability to obtain a complete STR profile. The successful typing of samples exhibiting very high levels of DNA degradation can be further complicated by presenting in very low quantities. Reduced-length STR multiplexes (mini-STRs), and single nucleotide polymorphisms (SNPs) have proven to be more successful in genotyping degraded samples.

A tool which can simultaneously quantify total human DNA and the extent of DNA degradation in these limited samples would prove valuable in choosing which of the DNA typing systems available will prove to be the most informative. This study presents both a quantitative PCR and capillary electrophoretic method of assessing DNA degradation in highly degraded samples along with their ability to predict the success rate of genotyping such samples using STR, mini-STR and SNP systems.