THE USE OF A SINGLE NUCLEOTIDE POLYMORPHISM (SNP) MARKER PANEL FOR HUMAN IDENTIFICATION FROM COMPROMISED BIOLOGICAL SPECIMENS

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The analysis of DNA samples recovered from compromised biological remains presents some interesting opportunities and challenges for the forensic science community. A panel of single nucleotide polymorphism (SNP) markers, including amelogenin, has been designed to be effective on biological specimens whose DNA has undergone extensive degradation. Our laboratory has developed an assay that utilizes multiplexed PCR in conjunction with SNP-IT™, Orchid's proprietary single base extension technology. This multiplex assay can be run either on an automated, ultra-high throughput system called SNPstream® UHT or using ABI's SNaPshot™ assay for lower test volumes. Our panel consists of 71 identity SNP markers, including amelogenin, whose amplicon sizes are less than 100 base pairs. Using this assay, Orchid completed a pilot study on 1500 tissue samples from a mass disaster, where 42% of the samples gave SNP genotypes on over sixty markers. This test has been shown to be extremely sensitive, generating reproducible results with as little as 80pg of input DNA. Of interest, partial genotype profiles have proven to be helpful in grouping remains from one individual that have been recovered from various sites of a disaster scene. To date, over 6000 samples have been successfully genotyped using this SNP marker panel; and matching profiles demonstrate that the system is greater than 99% accurate.