



B45 Validation of the AmpF[®]STR[®] MiniFiler[™] PCR Amplification Kit and its Application to Identify Human Remains From a 1992 Helicopter Crash at the San Diego Police Department Crime Laboratory

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After attending this presentation, attendees will become more informed about the MiniFiler kit in order to better evaluate its success in recovering complete DNA profiles from challenged samples often encountered in forensic casework. In addition, DNA typing of human remains exposed to the elements of the high desert will highlight MiniFiler's ability to obtain robust and reliable DNA profiles from highly degraded and inhibited samples.

This presentation will impact the forensic community by providing the basis of the eight validation studies conducted according to SWGDAM and ISO 17005 guidelines, five of which will be discussed: sensitivity, stochastic, peak height ratio, concordance, mock casework, and challenged samples that include the DNA typing of bone samples discovered at the site of a 1992 helicopter crash in the high desert of Baja California.

The study established that complete, reliable, and artifact-free DNA profiles can be obtained using between 0.2-0.6 ng of DNA, with the optimum template amount being approximately 0.3 ng. Homozygote genotypes can be reliably interpreted using a homozygote threshold of 450rfu, for both of the Applied Biosystems 310 and 3130 genetic analyzers, as the majority of instances of allelic dropout were observed to occur below this level. The peak height ratio between the two heterozygous peaks averaged approximately 78%. However, imbalance of as much as 36% was observed at all peak height pairs between 500 and 4000rfu. Caution should be exercised in relying on peak height ratios when attempting to elucidate component genotypes in a mixture.

Of the 20 known samples used in this study, concordance was found between the DNA typing results obtained from the MiniFiler and Identifiler kits for all except one sample in which a microvariant allele at the D21S11 locus was observed. This microvariant allele is detected by Identifiler, but fails to be detected by MiniFiler. The insertion/deletion causing this microvariant allele is suspected to occur within the MiniFiler primer binding site for this locus.

The Mock Casework and Challenged Samples demonstrated that for many of the loci in which no alleles were detected using Identifiler, results were obtained using MiniFiler. Therefore, the chance of obtaining complete profile information is greater when MiniFiler is used in conjunction with Identifiler, as opposed to the use of Identifiler alone on degraded or inhibited DNA samples.

For the victim of the 1992 helicopter crash, an incomplete genetic profile was achieved with the use of Identifiler, obtaining complete results at only 6 loci, and partial results at 3 loci. The ski slope effect seen in the original electropherogram was indicative of degradation, and PCR inhibition was observed from the qPCR quantitation results. When the DNA from the victim's bone sample was typed using MiniFiler, a complete profile that complemented the Identifiler results was obtained. Combining the results obtained from both MiniFiler and Identifiler allowed for a more powerful statistical analysis in comparison of the DNA profile of the bone to that of the DNA profile from the putative son of the crash victim, ultimately identifying the remains.

Data obtained from the eight validation experiments evaluating the performance of the AmpF/STR[®] MiniFiler[™] PCR Amplification Kit demonstrates the MiniFiler kit, when used in conjunction with the Identifiler kit, provides an increased power to obtain genetic profiles from challenged samples. This validation study supports the use of the MiniFiler kit on forensic casework samples that are degraded and/or contain PCR inhibitors, and also demonstrates that these recent advances in DNA technology can provide answers for cases that have remained unsolved for years.

MiniFiler[™], Validation, Identification of Human Remains