Next Generation Assays for Improved Performance on Compromised Samples

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Evidence submitted for DNA analysis can be recovered from a variety of biological samples including blood, saliva, or semen stains on different substrates, body surface swabs, hair, bones, and finger nail scrapings. Forensic analysts seek technologies to maximize the quality of results obtained and increase success rate of obtaining a DNA profile from these types of samples. Incorporating mini-STRs and/or more discriminating loci into a multiplex assay and modifying PCR reaction components and conditions are amongst the options available to help improve recovery of information from a biological sample.

This presentation will highlight the development of next generation STR assays which through the inclusion of new loci and improvements in amplification chemistry, deliver enhanced performance on the challenged and compromised samples most commonly encountered during casework investigations while still providing robust and reliable DNA profiles free of artifact peaks which may complicate interpretation.

An example of one such assay is the AmpFℓSTR® NGM™ PCR Amplification Kit, a 16-plex assay that incorporates primer sequences for 5 new ENFSI/EDNAP recommended loci for increased discrimination with a kit configuration optimized for improved allele recovery from degraded samples. Other improvements include modified PCR cycling conditions for faster amplification, improved performance with inhibited samples, and increased sensitivity when compared to previous kits. In addition, enhanced synthesis and purification processes are being applied to the amplification primers to minimize the potential for PCR artifacts.

These developments further expand the range of samples from casework and missing persons investigations which can yield probative DNA results and are designed to meet the stringent requirements of the global forensic DNA community. Data demonstrating the effectiveness of the multiplexes will be presented including sensitivity, mixtures, and models of inhibition and DNA degradation.