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THE NATIONAL INSTITUTE OF JUSTICE'S EXPERT SYSTEMS TESTBED PROJECT: PHASE II, ANALYSIS OF CASEWORK SAMPLES

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The primary goal of the National Institute of Justice's Expert Systems Testbed (NEST) Project is to conduct a thorough evaluation of the commercially available software programs and report the results back to the forensic community. Phase I, the evaluation of expert systems for single source samples, is complete. The handbook, entitled "Forensic DNA Databasing: Expert Systems for High-Throughput Analysis of Single Source Samples," is now available. Phase II of the NEST Project is the evaluation of commercially available expert systems to evaluate two-person forensic DNA mixture data. Phase II studies the ability of different software systems to evaluate controlled mixture data for major and minor profiles and apply this information to casework analyses. The design of the mixture samples included varying ratios of male and female DNA including 30:1, 10:1, 3:1, 1:1, 1:3, 1:10, and 1:30 at various DNA input levels including 1.5, 1.0, 0.5 and 0.25 times the manufacturers' recommendations of total input DNA and amplified with PowerPlex 16 and AmpFLSTR Identifiler, Profiler Plus, COfiler, and SGM Plus PCR Amplification Kits. These experiments were conducted in duplicate with two different pairs of male and female DNA and processed on two multi-capillary instruments. The raw data were then analyzed using the FSS-i3™ Expert Systems Software version 4.1.2 (Promega Corporation, Madison, Wisconsin) in conjunction with GeneMapper® ID version 3.2 and TrueAllele™ System 3 (Cybergenetics, Pittsburgh, Pennsylvania). The results of these studies demonstrate that expert systems can positively identify a partial profile of a minor contributor even at ratios as low at 30:1 and 1:30 down to 0.25 ng of total input DNA. The expert systems can evaluate two-person DNA mixtures and produce best-fit major profiles. The experts systems interpret the mixed data based on mathematical modeling, identify the combinations of two DNA donors for each locus, report a weighted ratio, and produce objective, unbiased, and reproducible results. These expert systems can be adopted in the forensic laboratory to support the forensic DNA analyst in mixture deconvolution interpretation. The design of the mixed experiments, the evaluation criteria used for this study, and a summary of results obtained will be presented.