Abstract 41

THE FORENSIC IDENTIFICATION OF AN INDIVIDUAL USING INDIRECT FAMILIAL REFERENCE DNA: COMPARISON OF TWO SOFTWARE PACKAGES

Danna Bicknell[1] and Daniele Podini[2]
[1]United States Secret Service, 245 Murray Lane, SW, Bldg. T-5, Washington, DC 20223
[2]Department of Forensic Sciences, The George Washington University, 2036 H St., Washington, DC 20052

Kinship analyses can be of vital importance in the identification of victims of mass disasters, such as terrorist attacks, environmental assaults, and war. In such disasters, remains are often severely fragmented and can be commingled with those of other individuals. In events such as these, as well as those of a smaller scale, such as missing persons cases and aircraft crashes, conventional methods of identification are often not sufficient to identify victims, and other procedures must be utilized. DNA from family members must often be obtained and compared with that of victims in order to make identifications possible. The objective of this research was the investigation of applications for kinship analyses focusing on two software packages used to calculate the likelihood that a victim is related to a particular family.

DNA-VIEW and Familias software programs were evaluated in order to determine the differences in likelihood ratios (LRs) returned for a known pedigree consisting of 21 members. One family member was designated as a missing person for whom identification was sought. DNA was extracted from buccal swabs that were obtained from each family member, and samples were amplified using the AmpFISTR® Identifiler™ kit and analyzed after capillary electrophoresis on an ABI 310 Genetic analyzer, using Genescan™ and Genotyper™ software. A total of 26 scenarios were evaluated in which various family members were designated as available for sampling and comparison. This pedigree consisted of distantly-related relatives in order to simulate scenarios in which parents, offspring, or siblings of the victim are not available for sampling. This study sought to compare the significance of the LRs returned by both DNA-VIEW and Familias in each of the simulated scenarios.

Through this research, Familias returned higher LRs for all scenarios than did DNA-VIEW, ranging from a value of 1.0221 to 471,732.6639. DNA-VIEW, for some scenarios, returned LRs that were less than 1.0 and generally generated more conservative results ranging from 0.4233 to 69,201.5. Additionally, Familias required less processing time, despite being installed on a much older computer system. Four scenarios were not resolvable using DNA-VIEW, and the calculation for each was terminated after 24 hours of computation. However, DNA-VIEW yielded distinct advantages when compared to Familias with regard to disaster victim identification in that Familias lacks sufficient database structure for compilation and analysis of this extended kinship information. The capability of DNA-VIEW to store direct, indirect, and victim reference samples having been analyzed using both autosomal and non-autosomal markers makes it ideal for use in mass fatality incidents. Through analysis with both programs, it was found that one cannot necessarily define a standard set of relations for which to test when extending to third degree relatives and beyond, because of significant importance is the number of alleles

that they share and their corresponding frequencies. As expected, for both Familias and DNA-VIEW, the more the markers that were examined, the greater their polymorphism, and the lesser the population frequencies of the shared alleles, the higher the LRs that were returned.