

SUMMARY REPORT OF THE VIRGINIA SCIENTIFIC ADVISORY COMMITTEE'S SUBCOMMITTEE ON FAMILIAL SEARCHES

A subcommittee was tasked by the Scientific Advisory Committee with investigating the feasibility of the Department of Forensic Sciences conducting familial searches as an investigative tool during the course of their on-going DNA profiling activities. This subcommittee met on two occasions, on May 8, 2007, and on August 6, 2007 and its members were Dr. Fred Bieber, Dr. Arthur Eisenberg, Dominic Denio, Dr. Dan Krane, Demris Lee (May 8 meeting only), and Dr. Norah Rudin (August 6 meeting only). This summary report was discussed and approved by the subcommittee at the conclusion of the August 6 meeting for presentation to the Scientific Advisory Committee at its meeting in Richmond, Virginia on August 7, 2007.

A perfect match between the STR DNA profile of an evidence sample and an individual whose genotype has been entered into a database has clear utility as an investigative tool. Lack of concordance between the alleles of a single source profile derived from an evidence sample and an individual's DNA profile is also of utility in that it excludes the individual as a source of the biological material in the evidence sample. Very similar but nonetheless non-matching DNA profiles between an evidence sample and an individual in a DNA database also have the potential to provide useful information by suggesting that a close relative of the individual may be the actual source of the evidence sample (Paoletti et al., 2006; Bieber et al., 2006). CODIS software was not designed to conduct familial searches of DNA databases in criminal cases. Absent any additional investigative data, a database search approach that relies upon a minimum number of matching alleles across all loci would only identify a small fraction of true familial associations unless the threshold was set so low that numerous false investigative leads are generated. A kinship analysis-likelihood ratio approach (Paoletti et al., 2006) is much better suited for familial searches, particularly for parent/child and sibling relationships.

The subcommittee received a memorandum (dated August 2, 2007) from Dr. Thomas Callaghan, Chief of the FBI's CODIS Unit, stating that a "Next Generation CODIS" that will have a search engine is currently under development. The new search engine will be dedicated to missing person searches. It will utilize a "Joint Pedigree Likelihood Ratio." The subcommittee expects that approach will not only increase parent-child search efficiency but also allow other relatives to be incorporated into the pedigree searches.

The subcommittee also heard a presentation from Dr. Krane regarding on-going research into the use of a kinship analysis-likelihood ratio approach using extensive computer simulations. Dr. Krane suggested that two parameters needed to be considered to make familial searches feasible: 1) what is an acceptable rate of false positive investigative leads (which will be inversely related to a false negative rate)?; and 2) what is the size of the pool of reasonable, alternative suspects to those who are identified by a database search (to establish prior odds for a likelihood ratio)? Dr. Eisenberg suggested, and Dr. Krane agreed, that the size of the alternative suspect pool could be reduced to workable levels by "pre-screening by performing Y-STR searches." Such searches would eliminate individuals who are not from the same paternal lineage.

The Department of Forensic Science performed a feasibility study regarding the establishment of a Y-STR database for new entries into the Commonwealth's DNA databases at the request of the subcommittee. Mr. Jeff Ban responded to that request with a presentation at the August 6 meeting of the subcommittee and reported that Y-STR testing of all new DNA database entries would entail: approximately \$40 per sample (over \$11 million to do all 286,000 currently in database) and approximately \$750,000 per year to do all incoming samples to the database from this point forward. Generation of individual Y-STR profiles would cost approximately \$75 per sample. Jeff Ban thought that there may be 30 cases per year that autosomal profiles suggested involved a close relative.

The subcommittee also discussed some of the legal, policy and civil libertarian implications of familial searches at both of its meetings. Dr. Sheldon Krinsky, a Visiting Scholar with the American Civil Liberties Union, kindly provided a memorandum entitled the "Ethical, civil liberties and societal considerations of familial searches" to the subcommittee. While it was determined that these issues were outside of the purview of the subcommittee itself, it was also the consensus of the subcommittee that they needed to be seriously addressed by policy makers prior to the implementation of a familial search program.

The subcommittee talked at some length about the need for familial searches to be case driven rather than something that was driven by the database administrators. Such an approach would diminish many of the potential legal, policy, and civil libertarian issues associated with familial searches and would also have the potential to reduce the size of the effective alternative suspect pool (even without Y-STR pre-screening). Dr. Bieber suggested that a natural extension of this subcommittee would be a series of workshops aimed at educating investigators and criminal justice attorneys about the possible utility of familial searches.

The Commonwealth of Virginia has provided leadership in the implementation and utilization of DNA databases. This subcommittee was established to help continue leadership in forensic science. While no requests have been received to date, the investigation of familial associations has been shown to be a useful tool for humanitarian identification of human remains and missing persons and to solve serious crimes.

References:

F. R. Bieber, C. H. Brener and D. Lazer. "Finding criminals through DNA of their relatives." *Science*. 2006; 213(5778):1315-1316.

D. Paoletti, T. Doom, M. Raymer, and D. Krane. "Assessing the implications for close relatives in the event of similar but non-matching DNA profiles." *Jurimetrics*. 2006; 46(2):161-175.