

E54 Strategies for Reconciliation of Personal Identifying Information and DNA Profile Data at a State DNA Index System (SDIS) Databasing Laboratory

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Learning Overview: After attending this presentation, attendees will be aware of how the Texas State Combined DNA Index System (CODIS) Offender Databasing Laboratory addresses unique challenges with known offender samples to include: (1) sex/gender discrepancies between reported biographical data and DNA profile data; (2) twins in the Texas State CODIS Offender Database; and (3) multiallelic offenders and/or chimeric DNA profiles.

Impact on the Forensic Science Community: This presentation will impact the forensic science community by highlighting the complexities of known offenders' biographical data and DNA profile data and how these complexities can affect casework and/or law enforcement interpretations.

The Texas Department of Public Safety (DPS) CODIS Offender DNA Databasing Laboratory (Texas SDIS Lab) encounters challenges that differ from traditional forensic DNA casework laboratories. Because the main role of CODIS is to provide law enforcement with investigative leads, accurate identifying information is emphasized. Biographical data provided with each sample is compared with crime record data to verify identification prior to processing their DNA sample. In some cases, the information obtained from the DNA profile leads to questions about the offender's reported biographical data. The following discrepancies are rare but important to investigate for internal laboratory quality assurance: accurate familial searching and providing accurate identifying information associated with a CODIS hit.

Sex/gender discrepancies are queried in the internal Laboratory Information Management System (STACS-DB from STACS DNA, Inc.) to yield discrepancies between biological sex data collected during DNA analysis and biological sex data manually entered into the database during sample data entry. Data entry errors were resolved without retesting. Retested samples included 81 Fast Technology for Analysis (FTA) blood samples, 67 non-FTA blood samples, 40 buccal samples, and nine samples on GenTegra® GenPlates®. All samples were retested using GlobalFiler® Express amplification kit and a portion tested for Y-chromosomal Short Tandem Repeat (Y-STR) using the Y Filer® kit. Following processing, amelogenin, DYS391, and Y-chromosome insertion/deletion (Y-indel) loci results for each sample were compared with the reported biological sex. While the project is ongoing, results suggest that there are sex-typing issues as a result of genetic insertions, deletions, and primer site polymorphisms at amelogenin, or other genetic anomalies, such as XXY females. Of the portion tested for Y-STR, 12% of male samples exhibiting apparent female STR profiles produced a Y-STR profile consisting of 12, 14, and 15 null loci. Results also suggest that reported sex may contradict with DNA sex based on an individual's self-identification. Many discrepancies were in fact updates to reported sex in crime records as an individual changes the way they report their identity at arrest, such as in a case of gender dysphoria.

Texas currently has over 950,000 offender and arrestee samples in SDIS and receives approximately 3–7 sets of identical twins each month. Possible sets of twins are initially identified when two individuals in Texas SDIS appear to have identical DNA profiles. First, the samples are researched to rule out duplicate samples that were accidently processed as two separate individuals due to biographical data errors within crime records. The possibility of twins is then researched through contacting supervising agencies and sporadically analyzing requested vital records. As of 2018, over 800 sets of identical twins exist in Texas SDIS. Currently, there is no method within CODIS to differentiate individuals from a set of identical twins. When a match occurs with twins, both individuals are reported to the investigating agency and the local lab working their forensic case.

Chimeric offender samples are rare in Texas SDIS, with just 22 chimeric samples identified as of 2018. However, a chimeric profile could mislead an investigation if the sample is interpreted as a mixture and devolution is performed, when in fact the source of the DNA is from one contributor. Explanations vary from embryonic development to bone marrow transplants. Chimeric or mixed profile offender samples are initially identified at analysis. Once contamination is ruled out, an additional DNA sample is requested from a supervising agency, if possible. If the original sample was a blood sample, a buccal sample is requested to compare DNA derived from different biological material. Once confirmation testing of the mixed profile is performed with a second collection, the sample is uploaded into CODIS to be searched in the Multi-Allelic Offender (MAO) specimen category. Information about the research into these samples is documented internally.

Databasing, Gender, Chimeras

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