A110 Are They Full Siblings? The Distribution of the Sibship Index and Its Application in Forensic Identification

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After attending this presentation, attendees will understand the basic concepts of DNA profiling and the significance and challenges of using autosomal Short Tandem Repeat (STR) DNA in forensic identification.

This presentation will impact the forensic science community by providing a baseline dataset to assist in the interpretation of the sibship index to increase the chances of identifying missing people with no self-DNA references.

The Department of Defense has collected DNA samples for all American service members since 1992 to ensure reliable self DNA samples are obtained. Due to the absence of self DNA reference for the missing servicemen from the conflicts prior to 1992, the DNA sequences from bone samples are compared to the missing person's Family Reference Samples (FRSs). Mitochondrial DNA (mtDNA) has been most commonly used as the missing person shares the same mtDNA with his/her maternal relatives; however, an mtDNA sequence is not individual specific and can be shared by thousands of unrelated people. If the missing person has an mtDNA sequence common in a population, additional evidence may be required to establish identification. One such evidence is nuclear DNA, both Y-chromosome Short Tandem Repeat (Y-STR) and autosomal-STR (auto-STR). If the missing person is a male and has brother FRSs, the paternally inherited Y-STR is used for comparison. If the missing person is a male and has sister FRSs, auto-STR analysis is used. Unlike mtDNA or Y-STR, auto-STR is unique to an individual. The individual specific nature of the auto-STR poses a challenge for comparison because even full siblings do not have the same auto-STR profile. This is where the sibship index comes into play.

The sibship index is the likelihood that the auto-STR results obtained from a sample support the hypothesis that the sample and the included reference sample are biological siblings, rather than if the sample is a full sibling of an unrelated individual. For example, a sibship index of 100 means that it is 100 times more likely that the bone sample and the FRS are biological siblings, rather than if the bone is a full sibling of a random person. If the sibship index is in the millions, a full sibling relationship can convincingly be established as it is highly unlikely that two unrelated individuals have significant overlap in their auto-STR profile; however, a low sibship index may not necessarily indicate that the two individuals are unrelated due to the chance of two full siblings inheriting two complete different sets of auto-STR from their parents. The sibship index frequently falls into a gray area that neither supports nor refutes full sibling relationship. This is a problem because auto-STR is often the only way to identify a missing serviceman. The goal of this study is to document the distribution of the sibship index for: (1) full siblings; and, (2) unrelated individuals. The focus is on discovering the degree of overlap of the tales of these two distributions.

In this study, the auto-STR comparison data obtained from the following four scenarios were used to generate sibship index distributions (N = 1,000): (1) the bone of an identified soldier to the full siblings of the identified soldier; (2) the bone of an identified soldier to the excluded soldiers (unrelated individuals); (3) two known full siblings in the FRS database; and, (4) two unrelated individuals in the FRS database. The number of obtained auto-STR loci was also documented to see how significantly the sibship index can change based on the quality

of the auto-STR data. The study found that when two samples are full siblings, the average sibship index was in the millions but indices lower than 0.05 were also observed (Negatively skewed curve; Mean 5,073,370; Median 10,635). When two samples are unrelated individuals, the average sibship index was in the hundredths but indices between zero and ten were also observed (Normal distribution curve; Mean 0.0598; Median 0.0005755). There was minimal overlap between the two curves. As predicted, the number of obtained auto-STR loci affected the sibship index significantly: the higher the number of loci, the stronger the sibship index to confirm/refute the sibling relationship. The current research will be expanded to increase the sample size as additional results are obtained from more bones and FRS samples.

Sibship Index, Autosomal STR, DNA Profiling