A86 How Distant Relatives Influence the Efficiency and Error Rate of Familial Searching

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After attending this presentation, attendees will gain a sophisticated understanding of familial searching arising from realistic population genetics and the presence of distant relatives in DNA databases. Since the utility of familial searching is predicated on relatives being present in these databases, it is important to consider how these relationships affect the practical application of familial searching techniques. Specifically, attendees will see how while familial searching effectively identifies first-degree relatives, distant relatives are also very commonly misidentified as first-degree relatives, calling into question the effectiveness of large database familial searching.

This presentation will impact the forensic science community by bringing to light important caveats affecting familial searching, which may lead to increased false identification rates. Depending on the demographics of DNA databases, these false identification rates may be unacceptably high, potentially influencing decisions about the use and implementation of familial searching methods. This is particularly relevant considering the continuing rapid rise in use of familial searching.

Familial searching is now being implemented in several states and is under consideration for national application as a tool to aid cold case investigations. The consequences of adopting the familial searching criteria used by the state of California, as described by Myers *et al*., (2011) are considered.[1] A simulation study, in which randomly generated profiles of related and unrelated individuals, comprising of a 13-locus CODIS genotype and YFiler® Y-chromosome haplotype, were considered for first-degree relationships as carried out through the Myers protocol for relative identification, was conducted. The Myers protocol powerfully identifies first-degree relatives who share a Y-chromosome, with an 80-99% probability, depending on the population background of the individuals in question. For unrelated individuals, there is a low probability of false identification as first-degree relatives. The Myers protocol showed low probabilities of falsely identifying totally unrelated individuals as first-degree relatives, supporting the method to distinguish first-degree relatives from unrelated individuals. However, for more distant Y-haplotype sharing relatives (half-siblings, first cousins, half-first cousins, or second cousins), there is a substantial probability of incorrect identification as first-degree relatives. For example, there is a 3-18% chance of identifying a first cousin as a full sibling, with the probability depending on the population genetic background of the individuals in question. The California familial search policy is likely to identify a first-degree relative if their profile is in the database and it poses little risk of falsely identifying an unrelated individual in a database as a first-degree relative. However, importantly, there is a substantial risk that a somewhat more distant Y-chromosome sharing relative whose profile is in the database will be wrongly identified as a first-degree relative, with the consequence that their immediate family will become the target for further investigation. In this outcome, the familial search is ineffective in identifying the true relative and may convincingly lead investigators to futilely consider distant relatives who may not even be aware of their relationships to the true relative in question. Importantly, this risk of unprovoked investigation falls disproportionately on those groups that are over-represented in state and federal databases, particularly African Americans and Latinos.

Reference:

1. S. Myers, M.D. Timken, M.L. Piucci, G.A. Sims, M.A. Greenwald, J.J. Weigand, K.C. Konzak, M.R. Buoncristiani, Searching for first- degree familial relationships in California's offender DNA database: Validation of a likelihood ratio-based approach, Forensic Science International: Genetics 5 (2011) 493–500.

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