



B48 Considerations for Database Searching With Siblings

Lisa Sansom, BS, University of North Texas Center for Human Identification, Fort Worth, TX 76107; Melody Josserand, MS, University of North Texas Center for Human Identification, Fort Worth, TX 76107; Michael D. Coble, PhD, University of North Texas Health Science Center, Fort Worth, TX 76107-2690*

Learning Overview: After attending this presentation, attendees will be aware of the varying statistical results observed in kinship calculations when associations to a missing person found in the Combined DNA Index System (CODIS) include a single parent and sibling assembled into a pedigree tree and how these variations affect the outcomes of database searches.

Impact on the Forensic Science Community: This presentation will impact the forensic science and legal communities by highlighting the chance of missing an identification of a missing person when including a sibling reference into a pedigree search in CODIS. Recommendations to address this situation will be provided.

Since the release of CODIS v6.0 in 2008, missing persons searches performed in the software utilize pedigree trees to search for missing family members in the Unidentified Human (Remains) index of the database. First-order relatives are requested to optimize searching of CODIS, including siblings. Typically, the addition of a sibling to a single parent in a pedigree tree is beneficial for calculating kinship statistics such as a Likelihood Ratio (LR) when a genetic association is found in CODIS, as opposed to a parent alone. However, situations have been observed in which the addition of a sibling to a pedigree tree with a single parent (biological father or mother) has substantially reduced the statistical value of a genetic association compared to using the parent alone. This is attributable to the manner in which alleles are passed from parents to their offspring. Because it is possible that even full siblings may share two, one, or (especially) zero alleles in common, the statistical weight of a CODIS association can be negatively affected by the inclusion of the sibling data. The effect of allele sharing between siblings on statistical calculations can therefore mean that a valid association within the CODIS database may be missed due to search threshold requirements.

It is also possible that the submission of a sample purported to be from a full sibling is actually from a half-sibling. The information regarding the half-sibling relationship may be known, but not included in the submitted case information, or the true relationship is not known to the reference sample donor at all. In some scenarios observed, this is not the case. The addition of a full sibling to a pedigree tree has decreased the LR on more than one observed occasion, sometimes so low that the results are not above the lab threshold for reporting. This leads to the possibility that the addition of a full sibling to a pedigree tree in CODIS may actually depress the kinship LR just enough so that it does not meet the level required for reporting, resulting in a true association that is missed during a search of a large database.

Recommended solutions to address this situation will be presented. These solutions may include ignoring the submitted sibling reference sample when searching in the CODIS database. Sometimes, “less may be more” when calculating kinship LRs in missing persons cases wherein family reference samples include a single parent and sibling.

Kinship, Sibling, CODIS