ERROR RATES IN SIBLINGSHIP DETERMINATIONS

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Multiple methods exist for calculating siblingship. Of these, the “index” and “likelihood” methods have gained popularity. The calculations provided by these methods are pivotal in the determination of a siblingship match as opposed to providing only statistical weight. Potential discordance exists between these methods and is likely complicated by the use of discordant allele frequency databases. This combination may culminate into an incorrect siblingship determination. Actual siblingship DNA profiles obtained from full-sibling, half-sibling, and unrelated individuals were used; and their relationship was conclusively established through paternity testing. In addition, computer software was designed to generate simulated sibling profiles based upon published allele frequency data. The profiles from the practical data and the simulated data were individually analyzed for sibling relationship using both the index and the likelihood methods. The relationship call success and error rates were computed and compared. Further, the simulated data was also investigated for the effect that increasing the number of utilized genetic markers may have on the error rate. The resulting data suggests that both calculation methods are prone to significant error in siblingship determination. The index method was 4.5% more accurate than the likelihood method when calculating true full siblings and 1.8% more accurate when unrelated pairs were tested, but 9.7% less accurate when testing theoretical half siblings. Varying the number of genetic markers and testing true full siblings resulted in a rate of error ranging between 1.9% (36 loci) and 11.6% (13 loci). When testing true unrelated individuals the error ranges between 3.4% (36 loci) and 10.3% (13 loci). When testing true half siblings the error is significantly higher, ranging from 16.4% (36 loci) to 35.3% (13 loci). The error rates are observed to be inversely proportional to the number of loci tested. According to this data, using 15 STR markers and potentially non-concordant databases for siblingship testing gave results that are prone to significant error. The use of more loci, concordant databases, and multiple calculation methods for comparison should assist in obtaining the most accurate siblingship results using the available STR technology.