

## PARENTAGE TESTING

### Considerations for the interpretation of STR results in cases of questioned half-sibship

*Robert W. Allen, Jun Fu, Thomas M. Reid, and Michael Baird*

Likelihood ratios (LRs) were calculated for a cohort of 60 pairs of true half-sibs and compared with LR values calculated for unrelated, paired children. STR results for the half-sib group were obtained from 60 archived cases involving a true mother, two children, and an alleged father subjected to typing with a multiplex STR kit (Identifier multiplex, Applied Biosystems) and in which the alleged father was excluded as the father of only one of the two children (half-sib pairs). The distribution of LR values among true half-sibs was compared to those produced from paired, unrelated children selected in two ways: One method for producing unrelated pairs was to randomly select Identifier profiles from children in 120 distinct paternity cases and group them into 60 ethnically matched pairs (random pairs). In a second approach, the children in the true half-sib group were shuffled and ultimately paired with someone from a different case. A total of 49 ethnically matched, unrelated pairs were created (shuffled pairs). In the shuffled pairs group, comparisons were thus based on a constant set of phenotypes. LRs comparing the probability of half-sibship versus being unrelated were produced for all groups with standard methods. Among pairs of known half-sibs, LRs ranged from a low of 0.1 to a maximum of 3763. Among random and shuffled pairs, LRs ranged from a low of 0.0001 to 12 for shuffled pairs or 42 for random pairs. LRs of greater than 2 were produced in 8 instances among random pairs and in 4 instances among the shuffled pairs. Overall, results suggest that half-sib indices of 30 or greater are fairly characteristic of individuals who are related as half-sibs. In contrast, half-sib indices of 0.1 or less are fairly characteristic of unrelated individuals who claim to be half-sibs. LRs falling between 0.1 and 10.0 are uninformative, as this region represents the overlap in the LR distributions produced from the true and false half-sib groups when the Identifier multiplex kit is used for testing.

(b)(4)

(b)(4)