FORENSIC BIOLOGY PROTOCOLS FOR FORENSIC STR ANALYSIS

PATERNITY ANALYSIS		
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Paternity Analysis

Kinship Analysis tests alternate or competing hypotheses of kinship. In the forensic context, it is useful for determining familial relationships, the identification of unknown bodies, and the identification of the donor of bloodstains when the donor/body is missing or unavailable, and the identification of the biological father or mother of products of conception/babies, which result from a sexual assault or are abandoned. All calculations are performed according to the Parentage Testing Standards of the American Association of Blood Banks. The DNA from the subject/stain in question is compared to the DNA of close biological relatives.

For parent(s)/child comparisons, the loci are first evaluated to determine whether the individual in question can be excluded as a biological relative of the other individual(s) (see below). If the individual cannot be excluded, or for comparisons not involving a parent(s)/child relationship, a PI (traditionally called a paternity index, but this could be a maternity or kinship index), is calculated for each locus using the DNAVIEW program of Dr. Charles Brenner. The formulas for parent/child comparisons are listed in Appendices 6 and 11 of Parentage Testing Accreditation Requirements Manual, 3rd edition, AABB.

If there is an exclusion at a single locus in a parent/child comparison, The PI is calculated according to the formula in Appendix 11 ($PI=\mu/PE$) where

> μ (locus specific mutation rate) is obtained from Appendix 14 of Parentage Testing Accreditation Requirements Manual, Fourth Edition, AABB and
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> $PE = h^2 (1-2hH^2)$ where H is the frequency of homozygosity and h is the frequency of heterozygosity. PE is calculated by the DNAVIEW program.

An overall CPI (combined paternity index) is calculated by multiplying all of the individual PIs. A probability of paternity (maternity/kinship) is then calculated using Bayes' theorem and assuming a prior probability of 50%. The individual loci PI, the CPI, and probability of paternity (W) are calculated by the DNAVIEW program. The report printed out from DNAVIEW should be included in the case file as the statistics sheet. The DNAVIEW calculations should be performed for each race.

The Forensic Biology case report should report the results for ONE race, preferably the race of the individual in question (e.g., the race of the tested man in a paternity case). The case report must list the PI for each locus, the race used for the calculations, the CPI, the probability of paternity, and the assumed prior probability. It must also state the final conclusion. The three possible final conclusions are exclusion, inconclusive, or inclusion, of the tested hypothesis of kinship.

Exclusions occur when either 2 or more loci exclude in a parent/child comparison, or when the CPI < 0.1.

Inconclusive occurs when the CPI is between 0.1 and 10, and for individual loci in mixtures of parent/child combinations when there are other peaks visible which could potentially exclude or include but cannot be genotyped by the software.

Inclusions occur when either 0 or 1 loci exclude in parent/child combinations, and when for all cases the CPI > 10. The analyst should bear in mind and report the strength of the inclusion based on the CPI. When the CPI is greater than 2000 (probability of paternity > 99.95%, 50% prior probability), the hypothesis of kinship should be accepted (considered proven). When the CPI is between 100 and 2000, the hypothesis is supported by the data. When the CPI is between 10 and 100, the hypothesis should not be rejected, and should be considered a weak inclusion.