PROBABILITY DISTRIBUTION OF ALLELE BANDS FOR MULTI-PERSON STR MIXTURES

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When interpreting STR mixture samples, it is very helpful to know how many individuals may have contributed to the mixture. A related question to ask is: When the number of contributors is known, what is the expected distribution of the number of loci (of a typical 13 CODIS core-loci profile) that harbors 1, 2, 3, or more alleles per locus, as well as the total number of allele bands observed. This information can be useful in investigations possibly involving genetically related suspects and victims, and would also be useful in checking for possible occurrence of excessive allele dropouts, null alleles, and possible mixture status. When the contributors are closely related, or the sample has suffered excess allele dropout, the distribution of the loci that harbors 1, 2, 3, or more alleles per locus and the number of allele bands observed will be skewed from those when the contributors are not related.

Using the allele probability distributions from Budowle *et. al.* [1] for each of the three major ethnic groups: American Caucasian, African-American, and Hispanics, the report presents the various distributions associated with bands per locus, bands per 13-loci mixtures sample, as well as n-allele loci per 13-loci mixture profile (n=1,2,3, 4, …, 2p, where p is the number of contributors to the mixture), for mixtures with two or more contributors from the same ethnic population. The work is a theoretical development using only the allele probability distribution data, and with the assumption that the contributors to a mixture are unrelated individuals. A general method has been developed to analyze mixtures comprised of up to seven unrelated individuals. Study shows that for single-source samples, 99% of the American Caucasian population contains 20 to 26 allele bands in a 13 core CODIS loci profile with an average of 23 bands; 92% contains between 8 and 12 heterozygous loci, with an average of ~10. For 2-person 13-loci mixtures, almost all samples will contain between 30 and 45 bands with a mean of 38 bands. For 3-person 13-loci mixtures, almost all samples will contain between 39 and 57 bands with a mean of 48 bands. Distributions for various other allele-loci attributes are available and will be presented at the symposium. An observation very different from these average distribution profiles for mixtures comprised of unrelated contributors would indicate the probability that the contributors are either genetically related, or that allele dropouts have occurred.

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[1] Budowle, B, B. Shea, S. Niezgoda, and R. Chakraborty. CODIS STR Loci Data from 41 Sample Populations. J. Forensic Sci., 2003:46(3):453-489.