Overview

**Aim:** To evaluate the reliability of assessing contributor count to 3- and 4-person complex mixtures when the highest-allele-count locus is disregarded.

**Methods:** All possible 3- and 4-person mixtures were generated using African-American, Asian, Caucasian, and Hispanic genotypes published by NIST [1]. The 15 STR DNA markers (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S17, D7S820, TH01, TPOX, CSF1PO, D19S433, D251338, D16S539) used by the AmpFISTR® Identifier® PCR Amplification Kit from Applied Biosystems® were used.

**Results:** Accuracy decreases from 97-99% to 85-93% for 3-contributore mixtures and from 29-49% to 4-13% for 4-contributore mixtures when the highest-allele-count locus is discarded.

Materials & Methods

**Genotypes:** One genotype (OT05588) was removed from the African-American dataset due to tri-allelism at the TPOX locus. Genotypes from African-American (N=341), Asian (N=97), Caucasian (N=361), and Hispanic (N=236) subpopulations were used.

**Combinations:** All possible 3- and 4-person combinations were generated using each subpopulation as in [2]. The number of conceptual mixtures where the minimum number of contributors was underestimated were counted for both when no loci were disregarded and for when the single locus with the largest number of unique alleles was disregarded.

**Conclusions:** While it has been long-established that the maximum allele count method is inaccurate for four-person mixtures [2], the results of this analysis demonstrate that ignoring the highest allele-count locus exacerbates this inaccuracy. The testing laboratory and prosecution chose to withdraw their conclusions regarding DNA testing in this case prior to a judge’s ruling in an admissibility hearing in a federal court.

**References**