

Complex Mixtures and the Minimum Number of Contributors: A Case Study

Nathan D. Adams^a, BS; Ranajit Chakraborty^b, PhD; Carrie Rowland^a, MS; Dan E. Krane^c, PhD

^aForensic Bioinformatics, Inc., Fairbon, OH; ^bUniversity of North Texas Health Science Center, Fort Worth, TX; ^cWright State University, Dayton, OH

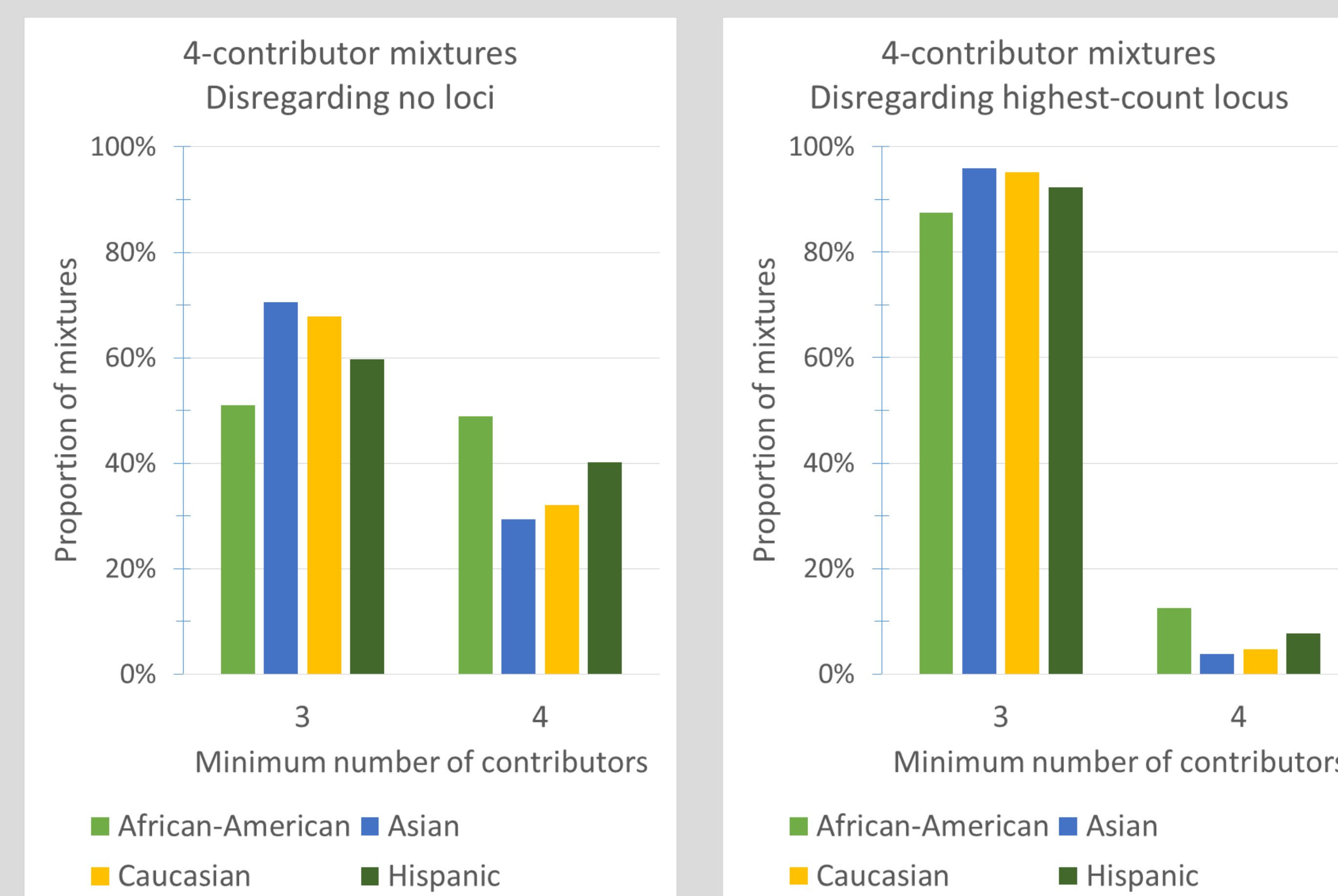
Overview

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, D13S317, D7S820, TH01, TPOX, CSF1PO, D19S433, D2S1338, D16S539) used by the AmpFISTR® Identifiler® PCR Amplification Kit from Applied Biosystems® were used.

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

Results



Discussion

Despite the observation of seven unique alleles at a single locus, a testing laboratory generated likelihood ratios under the assumption that only three individuals contributed to the observed DNA profile, suggesting that the single observation of a seventh allele at one locus across three injections may have been an artifact rather than an affirmative indication of a fourth contributor. The final reported LR supported the data under H1 (Hp; Defendant + 2 unknowns) as being 4,190 times more probable than under H2 (Hd; 3 unknowns).

The probabilistic genotyping system used for these analyses has not been validated for analyzing samples containing DNA from more than three individuals (as of January 2016). As a result, the testing laboratory was unable to evaluate the alternative hypotheses that four or more individuals contributed to the mixture.

The testing laboratory suggested that it was “more cautious” to consider the evidence sample to be a mixture of at least three individuals (presuming that allelic drop-in was likely to have occurred), though no quantitative support for such caution was provided. Known 3-person mixtures only presented as possible 4-person mixtures 2.5-4.0% of the time that a single additional allele was added randomly to one of the 15 loci in each of the 3-person mixtures.

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.

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.

Population	N	3-contributor	4-contributor
African-American	361	6,550,610	553,526,545
Asian	97	147,440	3,464,840
Caucasian	361	7,775,940	695,946,630
Hispanic	236	2,162,940	125,991,255

		Mischaracterization rate			
		3-contributor, disregarding:		4-contributor, disregarding:	
Population	N	0 loci	Highest-count	0 loci	Highest-count
African-American	361	1.0%	7.1%	51.1%	87.5%
Asian	97	2.8%	15.4%	70.6%	96.1%
Caucasian	361	2.7%	14.5%	67.9%	95.4%
Hispanic	236	1.4%	9.1%	59.8%	92.3%

References

- Hill, C.R., Diewer, D.L., Kline, M.C., Coble, M.D., Butler, J.M. (2013) U.S. population data for 29 autosomal STR loci. *Forensic Sci. Int. Genet.* 7: e82-e83. Available at - <http://www.cstl.nist.gov/strbase/NISTpop.htm>
- Paoletti, D. R., Doom, T. E., Krane, C. M., Raymer, M. L., & Krane, D. E. (2005). Empirical analysis of the STR profiles resulting from conceptual mixtures. *Journal of Forensic Sciences*, 50(6), 1361.