TEXAS DEPARTMENT OF PUBLIC SAFETY

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September 10, 2015

The August 21, 2015 notification to the Texas Criminal Justice Community from the Texas Forensic Science Commission (TFSC) is specific to the combined probability of inclusion (CPI) method of calculating statistics for DNA mixtures. The reported statistic provides a probability that an unrelated individual in a population is a contributor to a DNA mixture profile recovered from evidentiary items. In other words, a probability is calculated to assist the trier of fact in understanding the strength or weight of the inclusionary statement. This method was utilized by the Texas DPS Crime Laboratory when we started short tandem repeat (STR) testing in 1999 until we changed our standard operating procedure on August 10, 2015.

The Texas DPS Crime Laboratory Service is committed to keeping and remaining current with guidance published by the Scientific Working Group on DNA Analysis Methods (SWGDAM). In 2010 when updated SWGDAM Interpretation Guidelines were published, the Crime Laboratory Service's DNA Advisory Board began evaluating and implementing the recommendations. From 2011 through 2014, in addition to implementing revised FBI Quality Assurance Standards and new instrument validations, the DPS DNA sections conducted implementation validation studies across eight laboratories, two amplification kits, three injection times, and two instrument models to further address the recommendations. Due to a lack of consensus in the forensic DNA testing community about the direction of the changes or clear instruction on the application of CPI, final changes to our interpretation guidelines were not implemented until that clear instruction was provided, in part, by Dr. John Butler. In October 2014, Dr. Butler published *Advanced Topics in Forensic DNA Typing: Interpretation.* In this book, Dr. Butler proposes some practices and guidelines for the application of CPI statistics. Colleague-to-colleague communications and training has given the DPS system the tools necessary to implement the data interpretation changes resulting in our protocol change on August 10, 2015.

The application of SWGDAM's DNA interpretation guidance will result in the data utilized for interpretation being more reliable. It is expected that with these new interpretation guidelines, a given sample will have lower "1 in" numbers that translate to more conservative statistics. The forensic community is moving in the direction of automating DNA data interpretation and a recommended software solution is being purchased by DPS. This move will also result in a conversion from CPI calculation to Likelihood Ratio (LR) calculation protocols. DPS anticipates that we will complete validation and implementation of this software solution and protocol conversion by the end of the calendar year.

While SWGDAM advises against retroactive re-analysis of past cases, DPS recognizes advances in forensic science and changes in scientific protocol may impact current and past criminal cases. In saying that, DPS also recognizes it may not be possible to re-evaluate data obtained prior to recent validation studies. While many questions remain, DPS believes it is important to provide as much information on potentially impacted criminal cases as soon as possible. A list of DNA cases potentially impacted by this protocol change, listed by county of offense, accompanies this letter.

The Texas DPS Crime Laboratory Service is working with the TFSC to develop a path forward. This path will need to cover three different types of cases: 1) cases with CPI interpretations that are currently pending trial; 2) cases that are completed and ready to report under our August 10, 2015 standard operating procedures; and 3) cases with CPI interpretations that have already been adjudicated. The third case type may also include post-conviction cases that were reexamined under a Chapter 64 motion for forensic DNA testing. Our first step is to engage a panel of national experts to assist the Texas crime laboratory community with this challenge. The TFSC has reached out and assembled this panel. The first meeting will be held September 18, 2015.

With the help of these experts, the Texas crime laboratory community will be able to develop a plan for each case type listed above. We are committed to considering requests for re-calculation on a case by case basis as suggested by the Texas Forensic Science Commission. We appreciate the support of the Commission in assisting all Texas laboratories in addressing this challenging area. Additional questions can be addressed by contacting my office.

Brady W. Mills
Deputy Assistant Director
Texas Department of Public Safety
Crime Laboratory Service

TEXAS FORENSIC
SCIENCE COMMISSION
Justice Through Science

1700 North Congress Ave., Suite 445
Austin, Texas 78701

August 21, 2015

Members of the Texas Criminal Justice Community:

This letter provides notification to the community regarding an issue of potential concern to judges, criminal prosecutors, criminal defense lawyers, victims and defendants in the Texas criminal justice system. The concerns involve the interpretation of DNA results where multiple contributors may be present, commonly referred to as DNA mixture interpretation. The attached document details the origin and scope of the concerns.

While the Commission assesses the issues described in the attached document, we recommend any prosecutor, defendant or defense attorney with a currently pending case involving a DNA mixture in which the results could impact the conviction consider requesting confirmation that Combined Probability of Inclusion/Exclusion (referred to as "CPI" or "CPE") was calculated by the laboratory using current and proper mixture interpretation protocols. If the laboratory is unable to confirm the use of currently accepted protocols for the results provided, counsel should consider requesting a re-calculation of CPI/CPE.

The extent to which any closed criminal cases may require re-analysis will be a subject of Commission review and subsequent notification to the stakeholder community.

If you have any questions regarding these issues, please contact the Commission's general counsel, Lynn Garcia, at 512-936-0649 or lynn.garcia@fsc.texas.gov.

Sincerely,

Vincent J.M. Di Maio, MD
Presiding Officer

Unintended Catalyst: the Effects of 1999 and 2001 FBI STR Population Data Corrections on an Evaluation of DNA Mixture Interpretation in Texas

1. FBI Data Corrections: What Do They Mean?

In May 2015, the Federal Bureau of Investigation ("FBI") notified all CODIS laboratories it had identified minor discrepancies in its 1999 and 2001 STR Population Database. Laboratories across the country have used this database since 1999 to calculate DNA match statistics in criminal cases and other types of human identification. The FBI attributed the discrepancies to two main causes: (a) human error, typically due to manual data editing and recording; and (b) technological limitations (*e.g.,* insufficient resolution for distinguishing microvariants using polyacrylamide gel electrophoresis), both of which were known limitations of the technology. The FBI has provided corrected allele frequency data to all CODIS laboratories.

In May and June 2015, Texas laboratories notified stakeholders (including prosecutors, the criminal defense bar and the Texas Forensic Science Commission) that the FBI allele frequency data discrepancies were corrected. The immediate and obvious question for the criminal justice community was whether these discrepancies could have impacted the outcome of any criminal cases. The widely accepted consensus among forensic DNA experts is the database corrections have *no impact* on the threshold question of whether a victim or defendant was *included or excluded* in any result. The next questions were whether and to what extent the probabilities associated with any particular inclusion changed because of the database errors.

The FBI conducted empirical testing to assess the statistical impact of the corrected data. This testing concluded the difference between profile probabilities using the original data and the corrected data is less than a two-fold difference in a full and partial profile. Testing performed by Texas laboratories also supports the conclusion the difference is less than two-fold. For example, in an assessment performed by one Texas laboratory, the maximum factor was determined to be 1.2 fold. In other words, after recalculating cases using the amended data, the case with the *most substantially affected* Combined Probability of Inclusion/Exclusion ("CPI")[1] statistical calculation (evaluated for a mixed sample) changed from a 1 in 260,900,000 expression of probability to a 1 in 225,300,000 expression of probability.

Amended allele frequency tables are publicly available for anyone to compare the calculations made using the previously published data and the amended allele frequencies, though expert assistance may be required to ensure effective use of the tables.[2]

2. The Impact of FBI Database Errors on DNA Mixture Interpretation Using CPI

As part of their ongoing commitment to accuracy, integrity and transparency, many Texas laboratories offered to issue amended reports to any stakeholder requesting a report using the corrected FBI allele frequency data. Some prosecutors have submitted such requests to laboratories, particularly for pending criminal cases. As expected, the FBI corrected data have not had an impact exceeding the

[1] The Combined Probability of Inclusion/Exclusion is commonly referred to as either "CPI" or "CPE." They are referred to jointly in this document as "CPI" for ease of reference.

[2] https://www.fbi.gov/about-us/lab/biometric-analysis/codis/amended-fbi-str-final-6-16-15.pdf

two-fold difference discussed above. However, because analysts must issue *signed amended reports* with the new corrected data, they may only issue such reports if they believe *the analyses and conclusions in the report comply with laboratory standard operating procedures*. For cases involving DNA mixtures, many laboratories have changed their interpretation protocols and related procedures using CPI. To reiterate, changes in mixture interpretation protocols are unrelated to the FBI allele frequency data corrections discussed above. However, when issuing new reports requested because of the FBI data corrections, the laboratory's use of current mixture protocols may lead to different results if the laboratory had a different protocol in place when the report was originally issued. Changes in mixture interpretation have occurred primarily over the last 5-10 years and were prompted by several factors, including but not limited to mixture interpretation guidance issued in 2010 by the Scientific Working Group on DNA Analysis ("SWGDAM").

The forensic DNA community has been aware of substantial variance in mixture interpretation among laboratories since at least 2005 when the National Institute of Standards and Technology ("NIST") first described the issue in an international study called MIX05. Though NIST did not expressly flag which interpretation approaches were considered scientifically acceptable and which were not as a result of the study, it has made significant efforts to improve the integrity and reliability of DNA mixture interpretation through various national training initiatives. These efforts have ultimately worked their way into revised standard operating procedures at laboratories, including laboratories in Texas. Based on the MIX05 study, we know there is variation among laboratories in Texas and nationwide, including differences in standards for calculation of CPI that could be considered scientifically acceptable. However, we also know based on a recent audit of the Department of Forensic Sciences ("DFS") in Washington, DC that some of the "variation" simply does not fall within the range of scientifically acceptable interpretation. This finding does not mean laboratories or individual analysts did anything wrong intentionally or even knew the approaches fell outside the bounds of scientific acceptability, but rather the community has progressed over time in its ability to understand and implement this complex area of DNA interpretation appropriately.

While in many cases the changed protocols may have no effect, it is also possible changes to results may be considered material by the criminal justice system, either in terms of revisions to the population statistics associated with the case or to the determination of inclusion, exclusion or an inconclusive result. The potential range of interpretive issues has yet to be assessed, but the potential impact on criminal cases raises concerns for both scientists and lawyers. We therefore recommend any prosecutor, defendant or defense attorney with a currently pending case involving a DNA mixture in which the results could impact the conviction consider requesting confirmation that CPI was calculated by the laboratory using current and proper mixture interpretation protocols. If the laboratory is unable to confirm the use of currently accepted protocols for the results provided, counsel should consider requesting a re-analysis of CPI.

The Texas Forensic Science Commission is currently in the process of assembling a panel of experts and criminal justice stakeholders to determine what *guidance and support* may be provided to assist Texas laboratories in addressing the challenging area of DNA mixture interpretation. In particular, a distinction must be made between acceptable variance in laboratory interpretation policies and protocols and those approaches that do not meet scientifically acceptable standards. An emphasis on statewide collaboration and stakeholder involvement will be critical if Texas is to continue to lead the nation in tackling challenging forensic problems such as those inherent in DNA mixture interpretation.

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June 30, 2015

The Texas Department of Public Safety Crime Laboratory system was informed by the Federal Bureau of Investigation in May 2015 of errors in the FBI-developed population database. This database has been used by the Texas DPS Crime Laboratory system as well as many other crime laboratories across the country for calculating match statistics in criminal investigations and other types of human identification applications since 1999.

Upon notification, the forensic DNA community immediately began corrective action. During implementation of corrective measures, minor discrepancies were discovered in additional data used exclusively by the Texas Department of Public Safety. All of the errors have been corrected and the changes have empirically demonstrated minimal impact on the calculations used to determine the significance of an association. **Further, the database corrections have no impact on the inclusion or exclusion of victims or defendants in any result.**

If requested in writing, the Texas DPS Crime Laboratory System will recalculate and report statistics previously reported in individual cases.

If you have any questions, please contact your local crime laboratory.

Brady W Mills
Deputy Assistant Director
Law Enforcement Support
Crime Laboratory Service

Position statement for Texas DPS Crime Laboratory System DNA discipline on the Amendment of the 1999 and 2001 FBI STR Population data and Minimum Allele Frequencies Error

June 12, 2015

A CODIS bulletin (BT050815) was released on May 8, 2015 (e-mail distribution on May 11, 2015) indicating an identification of errors of the original population database samples published in the Journal of Forensic Sciences in 1999. The bulletin notified CODIS users that an erratum notice will be published as a Letter to the Editor in the July 2015 issue of the Journal of Forensic Sciences. This notice will contain data showing the minimal effect these errors would have on profile probabilities calculated using this data. The bulletin stated the errors were attributable to clerical mistakes and limitations of the old technology and software.

The Texas DPS DNA advisory board (DAB) discussed this issue via electronic correspondences to determine a course of action. In these discussions, it was noted that the Texas DPS system only uses a portion of the loci noted in the publication. These errors were reviewed and the effect on the statistics would be nominal and unlikely to have an impact on evidentiary samples. The errors are only going to affect profiles that contain the alleles with the errors in certain population groups. The majority of the errors occurred in subpopulations that the Texas DPS system does not report. Additionally, a change in statistics would not change a conclusion of included or excluded as that conclusion is made prior to statistics being calculated. Not all reports contain statistics therefore not every case worked in the system is affected. It was also noted though this bulletin was released in early May, specific data regarding the errors and the updated population data was not made available until May 27, 2015 making it impossible to correct or update the databases prior to this announcement. The performance checks of the updated database demonstrated small changes in the rarity. These results verify the FBI assessment that the changes are unlikely to materially affect the statistical estimates.

During the review of the population data it was discovered that the frequency for allele 15 at loci D19S433 for the African American population and the minimum allele frequencies for loci D2S1338 and D19S433 for African American, Caucasian and Hispanic population groups (updated in 2004) were calculated incorrectly. The minimum allele frequency for the Caucasian population group at D13S317 was incorrect in one version of our statistical software. On June 1, 2015 when this was discovered, the DPS system stopped releasing DNA reports that contained statistical calculations. As this error affects statistical analysis as well, it is noted that this is unlikely to have a large impact on evidentiary profiles for the same reason listed above for the amended database. Additionally, it is noted that the minimum allele frequency error should not affect a large number of cases as these alleles are rare. Profiles were generated to

test this theory, and no instances of a greater than 5 fold difference occurred for single source. A mixture profile was generated to test the limits of the minimum allele frequency and showed a greater than a 10 fold difference; however, a statistical test was run and demonstrated this change was still not statistically significant. This is further corroborated by The Evaluation of Forensic DNA Evidence by the National Research Council (1996 publication) that discusses uncertainty for profile frequencies.

A review of all DNA cases released in the entire Texas DPS system from 1999 until present was conducted to determine the potential number of cases affected by these errors. The total number of DNA reports released is 29,376. The total number of DNA reports that contained inclusions is 24,166. The total number of DNA reports released in which statistics were calculated is 18,144. This means about 60% of the DNA reports released statewide since 1999 contain statistics.

As a result of these discussions, the DAB has agreed statistics for released cases calculated from 1999 until June 1, 2015 will only be recalculated if requested in writing and an amended report will be issued. The statistical tools were updated system wide on June 4, 2015 and all subsequent statistical calculations will use the updated population data. If a lab was unable to update the statistical tools by this date, no reports containing statistics were issued until the update was completed. Additionally our customers will be notified.

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ERRATUM

Reference: Budowle B, Moretti TR, Baumstark AL, Defenbaugh DA, Keys KM. Population data on the thirteen CODIS core short tandem repeat loci in African Americans, US Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. J Forensic Sci 1999;44(6):1277–86.

Since the development in the late 1990s of the original short tandem repeat (STR) typing systems that included the 13 CODIS core loci, new amplification kits that expand the number of loci to 24 in a multiplex reaction are now commercially available. To establish allele distributions for the additional loci, population samples that were originally genotyped using AmpFlSTR Profiler Plus, COfiler, Identifiler (Thermo Fisher Scientific, South San Francisco, CA), and/or GenePrint PowerPlex (Promega Corp., Madison, WI) (1,2) were retyped using GlobalFiler (Thermo Fisher Scientific) and PowerPlex Fusion (Promega Corp.). For any sample where a given locus is typed with different amplification kits, concordant genotypes should be obtained irrespective of the kit(s) used, with the exception of genotype differences due to rare primer binding site variants and improvements in allelic ladders that expand allele identification capabilities (e.g., an allele may be designated as <11 in one system and as 9 in another).

During a comparison of the 1100 profiles from African Americans, Caucasians, Southwest Hispanics, Bahamians, Jamaicans, Trinidadians, Filipinos, and Chamorros in the original (3,4)[1] and new studies, genotyping discrepancies were revealed. Discrepancies were attributable to (i) human error, typically due to the limited software capabilities for genotyping with manual data editing and recording, and (ii) technological limitations (e.g., insufficient resolution for distinguishing microvariants by polyacrylamide gel electrophoresis). The published genotype data (3,4) from which allele frequencies were calculated also include data or sample processing errors (e.g., known genotype duplications).

Genotyping errors were made in 27 samples, affecting the reported frequencies of 51 alleles. Additionally, six samples exhibited full or partial genotype duplications, which affected all allele frequencies at the duplicated loci in the respective populations due to the change in N that resulted from removal of duplicate genotypes. The minimum allele frequency (5/2N) was amended accordingly. For alleles requiring a frequency correction, the magnitude of the change in frequencies ranged from 0.000012 to 0.018 (average 0.0020 ± 0.0025). See Table 1.

The published allele frequencies (1,2) have been used in the past to generate profile probabilities for autosomal STR typing results using FBI PopStats software. Empirical testing suggests that any discrepancy between profile probabilities calculated using the original and corrected data is expected to be less than a factor of two in a full profile. The actual minimum ratio that we could obtain for a constructed profile in the direction of the profile probability being more rare in the original as compared to the amended data was for a highly homozygous partial profile in the Jamaica dataset. It was 0.76, which is well within the factor of 10 suggested by previous studies and the National Research Council (7–10). See Fig. 1 and Table 2. Amended data will be available at fbi.gov and through FBI PopStats. The authors are of the view that these discrepancies require acknowledgment but are unlikely to materially affect any assessment of evidential value.

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*Names of commercial manufacturers are provided for identification purposes only, and inclusion does not imply endorsement of the manufacturer or its products and services by the FBI. The views are those of the authors and do not necessarily reflect the official policy or position of the FBI or the US government.

[1]Electronic genotype data corresponding to the published allele frequencies are not available for the Southeast Hispanic, Apache, Navaho, and Minnesota Native American populations (6), as well as Filipino and Chamorro populations (except for D2S1338 and D19S433) (7), and could not be assessed for concordance with GlobalFiler and Fusion genotypes.

TABLE 1—*The effect of change in allele counts and/or sample size (N) on allele frequencies. All alleles with incorrect allele counts derived from the original data are shown with the difference in frequency between the original and amended values. Negative and positive values reflect a decrease and increase, respectively, in allele frequency.*

	D3S1358		vWA		FGA		D8S1179		D21S11		D18S51		D5S818		D13S317	
	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference
African American	–	–	–	–	–	–	–	–	29.2	−0.002793	<11	0.000031	–	–	8	−0.002793
	–	–	–	–	–	–	–	–	29.3	0.002793	11	0.000031	–	–	14	0.002793
	–	–	–	–	–	–	–	–	–	–	12	0.000326	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	13	0.000310	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	13.2	0.000031	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	14	0.000357	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	15	0.000931	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	16	−0.001738	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	17	−0.001878	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	18	0.000729	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	19	0.000435	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	20	0.000310	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	21	0.000062	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	22	0.000031	–	–	–	–
Caucasian	13	0.000012	–	–	–	–	–	–	–	–	>22	0.000031	–	–	–	–
	14	−0.001780	–	–	–	–	–	–	31.2	0.002551	–	–	–	–	11	0.002551
	15	0.001219	–	–	–	–	–	–	32.2	−0.002551	–	–	–	–	12	−0.002551
	16	0.001146	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	17	−0.001427	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	18	0.000805	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	19	0.000024	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
Southwest Hispanic	–	–	15	−0.004926	19	0.002463	–	–	–	–	–	–	–	–	–	–
	–	–	16	0.004926	20	−0.002463	–	–	–	–	–	–	10	−0.002463	–	–
	–	–	–	–	–	–	–	–	–	–	–	–	11	0.004926	–	–
	–	–	–	–	–	–	–	–	–	–	–	–	12	−0.002463	–	–
Bahamian	14	−0.001758	11	0.000175	<18	0.000248	9	0.000062	24.3	−0.003123	<11	0.000186	8	0.001339	7	0.000058
	15	−0.003536	13	0.000524	18.2	0.000248	10	−0.002812	27	0.001365	11	0.000186	9	0.000175	8	−0.005765
	15.2	0.000062	14	0.001165	19	0.001117	11	0.000993	28	0.004281	12	0.000931	10	0.001106	9	0.000582
	16	0.003329	15	0.002853	20	0.001427	12	−0.000703	29	0.000165	13	0.000993	11	−0.004833	10	0.000466
	17	0.000600	16	0.001805	21	−0.001075	13	0.003660	30	0.000227	13.2	0.000062	12	0.000699	11	−0.000524
	18	0.001241	17	−0.005532	21.2	0.000062	14	−0.003164	30.2	0.000186	14	0.000869	13	0.001106	12	0.004309
	19	0.000062	18	0.000291	22	0.002792	15	0.000352	30.3	0.000062	15	−0.000207	14	0.000291	13	−0.000116
	–	–	19	0.001339	22.3	0.000062	16	0.001179	31	−0.001386	15.2	0.000062	15	0.000116	14	0.000990
	–	–	20	−0.002621	23	−0.006204	17	0.000434	31.2	−0.002254	16	−0.006452	–	–	–	–
	–	–	–	–	24	−0.002585	–	–	32	−0.002875	17	0.000352	–	–	–	–
	–	–	–	–	25	0.001861	–	–	32.2	−0.001324	18	−0.000765	–	–	–	–
	–	–	–	–	26	0.000620	–	–	33	0.000062	19	0.001861	–	–	–	–
	–	–	–	–	27	0.000993	–	–	33.2	0.000744	20	0.000931	–	–	–	–
	–	–	–	–	28	0.000186	–	–	34	0.003371	21	0.000434	–	–	–	–
	–	–	–	–	29	0.000124	–	–	34.2	0.000062	21.2	0.000062	–	–	–	–
	–	–	–	–	–	–	–	–	35	0.000434	22	0.000496	–	–	–	–

TABLE 1—*Continued.*

	D3S1358		vWA		FGA		D8S1179		D21S11		D18S51		D5S818		D13S317	
	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference
Jamaican	–	–	–	–	24	0.002577	12	0.002577	–	–	15	0.012887	–	–	–	–
	–	–	–	–	24.2	−0.002577	13	0.007732	–	–	16	0.002577	–	–	–	–
	–	–	–	–	–	–	14	0.005155	–	–	17	−0.005155	–	–	–	–
	–	–	–	–	–	–	15	−0.002577	–	–	18	0.007732	–	–	–	–
	–	–	–	–	–	–	16	−0.012887	–	–	20	−0.010309	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	21	−0.007732	–	–	–	–
Trinidadian	–	–	–	–	–	–	13	−0.006250	–	–	<11	0.006410	–	–	–	–
	–	–	–	–	–	–	15	0.006250	–	–	13	−0.006410	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	16	−0.006410	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	19	0.006410	–	–	–	–
Filipino	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–
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	D7S820		CSF1PO		TPOX		TH01		D16S539		D2S1338		D19S433	
	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference
African American	–	–	–	–	–	–	–	–	–	–	–	–	14	−0.002989
	–	–	–	–	–	–	–	–	–	–	–	–	15	0.003016
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TABLE 1—*Continued.*

	D7S820		CSF1PO		TPOX		TH01		D16S539		D2S1338		D19S433	
	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference
Caucasian	6	0.000012	7	0.000012	7	−0.002463	6	−0.001353	8	0.000099	–	–	–	–
	7	0.000085	8	0.000024	8	0.002695	7	0.000854	9	0.000517	–	–	–	–
	8	0.000805	9	0.000098	9	0.000610	8	0.000622	10	−0.002155	–	–	–	–
	9	−0.001744	10	−0.001219	10	0.000183	8.3	0.000012	11	0.001355	–	–	–	–
	10	−0.001036	10.3	0.000012	11	0.001256	9	0.000817	12	−0.000800	–	–	–	–
	11	0.001000	11	−0.000988	12	−0.002280	9.3	−0.000963	13	0.000813	–	–	–	–
	12	0.000695	12	0.001610	–	–	10	0.000012	14	0.000160	–	–	–	–
	13	0.000146	13	0.000354	–	–	–	–	15	0.000012	–	–	–	–
	14	0.000037	14	0.000073	–	–	–	–	–	–	–	–	–	–
	–	–	15	0.000024	–	–	–	–	–	–	–	–	–	–
Southwest Hispanic	–	–	–	–	–	–	–	–	10	0.002404	–	–	–	–
	–	–	–	–	–	–	–	–	12	0.002404	–	–	–	–
	–	–	–	–	–	–	–	–	13	−0.002404	–	–	–	–
	–	–	–	–	–	–	–	–	15	−0.002404	–	–	–	–
Bahamian	7	0.000233	6	0.000061	6	0.002172	5	0.000020	8	0.000735	–	–	–	–
	8	0.002853	7	0.001225	7	0.000827	6	0.000968	9	−0.005451	–	–	–	–
	9	−0.003843	8	0.001102	8	0.007281	7	−0.000766	10	0.001899	–	–	–	–
	10	0.003203	9	−0.002246	9	0.003868	8	0.001451	11	0.002593	–	–	–	–
	11	0.000990	10	0.001307	10	0.002896	9	0.000806	12	0.000143	–	–	–	–
	11.3	0.000058	11	0.004287	11	−0.018181	9.3	0.000605	13	−0.000470	–	–	–	–
	12	−0.003960	12	−0.004104	12	0.001138	10	−0.003084	14	0.000490	–	–	–	–
	13	0.000466	13	−0.001878	–	–	–	–	15	0.000061	–	–	–	–
	–	–	14	0.000184	–	–	–	–	–	–	–	–	–	–
	–	–	15	0.000061	–	–	–	–	–	–	–	–	–	–
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Jamaican	–	–	–	–	–	–	–	–	–	–	–	–	–	–
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Trinidadian	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	–	–	–	–	–	–	–	–	12	0.006098	–	–	–	–
	–	–	–	–	–	–	–	–	13	−0.006098	–	–	–	–
	–	–	–	–	–	–	–	–	13.3	0.006098	–	–	–	–
Filipino	–	–	–	–	–	–	–	–	14	−0.006098	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	16	0.000402	12	0.000402
	–	–	–	–	–	–	–	–	–	–	17	0.001107	13	−0.003016
	–	–	–	–	–	–	–	–	–	–	18	0.000805	13.2	−0.006536
	–	–	–	–	–	–	–	–	–	–	19	0.003119	14	0.002213
	–	–	–	–	–	–	–	–	–	–	20	0.001107	14.2	0.000704
	–	–	–	–	–	–	–	–	–	–	21	−0.013679	15	0.001509
	–	–	–	–	–	–	–	–	–	–	22	0.000905	15.2	0.003521
	–	–	–	–	–	–	–	–	–	–	23	0.001911	16	0.000201
	–	–	–	–	–	–	–	–	–	–	24	0.003722	16.2	0.000905
	–	–	–	–	–	–	–	–	–	–	25	0.000503	17.2	0.000101
	–	–	–	–	–	–	–	–	–	–	26	0.000101	–	–

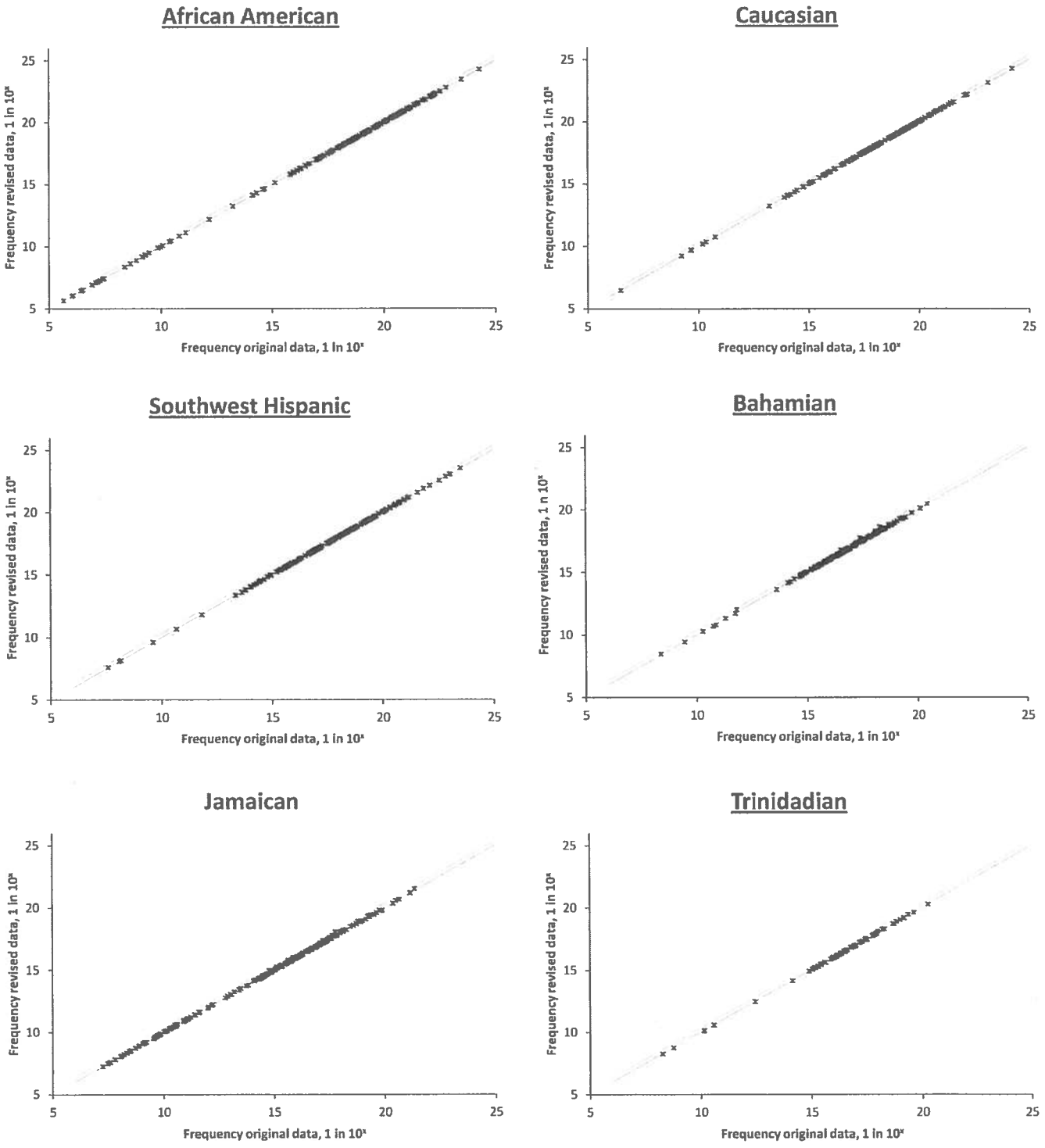

FIG. 1—*The comparison of the log of the profile frequency for the original and amended data. The* x = y *line and lines for a factor of two in either direction are given.*

TABLE 2—*The ratio of profile probability produced during testing of the original and amended data. The profile probabilities of all samples in the original dataset were calculated using the original and the amended data.*

Original Data Frequency/ Amended Data Frequency	African American	Caucasian	Southwest Hispanic	Bahamian	Jamaican	Trinidadian
Max (new frequency is more)	1.18	1.17	1.14	2.15	2	1.32
Min (new frequency is less)	0.87	0.92	0.92	0.81	0.79	0.84

CODIS
COMBINED DNA INDEX SYSTEM

CODIS Bulletin

Bulletin #: **BT052915** Date Distributed: **05/29/15**

UPDATE ON THE AMENDMENT OF THE 1999 AND 2001 FBI STR POPULATION DATA

As reported in the CODIS Bulletin BT050815, the FBI Laboratory has identified some errors in the data published in the Journal of Forensic Sciences *Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans and Trinidadians*, Journal of Forensic Sciences 1999 44(6):1277-86. The FBI Laboratory has now been advised by the publisher of the Journal of Forensic Science (JFS) that the electronic version of the JFS, July 2015, Volume 60, Issue 4 containing the erratum notice containing the empirical data demonstrating their nominal effect on profile probabilities will be published as a Letter to the Editor in electronic form on July 1, 2015 and with the print version to follow on July 7, 2015.

Because this timeframe is substantially different than that originally provided by John Wiley and Sons, Inc. (http://onlinelibrary.wiley.com/), please see the table provided for more information regarding the changes in allele frequencies between the original and amended 1999 and 2001 FBI data sets. All alleles with incorrect allele counts derived from the original data are shown with the difference in frequency between the original and amended values. Negative and positive values reflect a decrease and increase, respectively, in allele frequency.

If you have any questions, please contact Anthony J. Onorato of the FBI's DNA Support Unit at Anthony.Onorato@ic.fbi.gov or 703-632-7572.

	D3S1358		VWA		FGA		D8S1179		D21S11		D18S51		D5S818		D13S317		D7S820		CSF1PO		TPOX		TH01		D16S539		D2S1338		D19S433	
	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference	Allele	Frequency Difference
African American	-	-	-	-	-	-	-	-	29.2	-0.002793	<11	0.000031	-	-	8	-0.002793	-	-	-	-	-	-	-	-	-	-	-	-	14	-0.002989
	-	-	-	-	-	-	-	-	29.3	0.002793	11	0.000031	-	-	14	0.002793	-	-	-	-	-	-	-	-	-	-	-	-	15	0.003016
	-	-	-	-	-	-	-	-	-	-	12	0.000326	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	13	0.000310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	13.2	0.000031	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	14	0.000357	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	15	0.000931	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	16	-0.001738	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	17	-0.001878	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	18	0.000729	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	19	0.000435	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	20	0.000310	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	21	0.000062	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	22	0.000031	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	>22	0.000031	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Caucasian	13	0.000012	-	-	-	-	-	-	31.2	0.002551	-	-	-	-	11	0.002551	6	0.000012	7	0.000012	7	-0.002463	6	-0.001353	8	0.000099	-	-	-	-
	14	-0.001780	-	-	-	-	-	-	32.2	-0.002551	-	-	-	-	12	-0.002551	7	0.000085	8	0.000024	8	0.002695	7	0.000854	9	0.000517	-	-	-	-
	15	0.001219	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	0.000805	9	0.000098	9	0.000610	8	0.000622	10	-0.002155	-	-	-	-
	16	0.001146	-	-	-	-	-	-	-	-	-	-	-	-	-	-	9	-0.001744	10	-0.001219	10	0.000183	8.3	0.000012	11	0.001355	-	-	-	-
	17	-0.001427	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10	-0.001036	10.3	0.000012	11	0.001256	9	0.000817	12	-0.000800	-	-	-	-
	18	0.000805	-	-	-	-	-	-	-	-	-	-	-	-	-	-	11	0.001000	11	-0.000988	12	-0.002280	9.3	-0.000963	13	0.000813	-	-	-	-
	19	0.000024	-	-	-	-	-	-	-	-	-	-	-	-	-	-	12	0.000695	12	0.001610	-	-	10	0.000012	14	0.000160	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	13	0.000146	13	0.000354	-	-	-	-	15	0.000012	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	14	0.000037	14	0.000073	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	15	0.000024	-	-	-	-	-	-	-	-	-	-
Southwest Hispanic	-	-	15	-0.004926	19	0.002463	-	-	-	-	-	-	10	-0.002463	-	-	-	-	-	-	-	-	-	-	10	0.002404	-	-	-	-
	-	-	16	0.004926	20	-0.002463	-	-	-	-	-	-	11	0.004926	-	-	-	-	-	-	-	-	-	-	12	0.002404	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	12	-0.002463	-	-	-	-	-	-	-	-	-	-	13	-0.002404	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	15	-0.002404	-	-	-	-
Bahamian	14	-0.001758	11	0.000175	<18	0.000248	9	0.000062	24.3	-0.005123	<11	0.000186	8	0.001339	7	0.000058	7	0.000233	6	0.000061	6	0.002172	5	0.000020	8	0.000735	-	-	-	-
	15	-0.003536	13	0.000524	18.2	0.000248	10	-0.002812	27	0.001365	11	0.000186	9	0.000175	8	-0.005765	8	0.002853	7	0.001225	7	0.000827	6	0.000968	9	-0.005451	-	-	-	-
	15.2	0.000062	14	0.001165	19	0.001117	11	0.000993	28	0.004281	12	0.000931	10	0.001106	9	0.000582	9	-0.003643	8	0.001102	8	0.007281	7	-0.000766	10	0.001899	-	-	-	-
	16	0.003329	15	0.002853	20	0.001427	12	-0.000703	29	0.000165	13	0.000993	11	-0.004833	10	0.000466	10	0.003203	9	-0.002246	9	0.003868	8	0.001451	11	0.002593	-	-	-	-
	17	0.000600	16	0.001825	21	-0.001075	13	0.003660	30	0.000227	13.2	0.000062	12	0.000699	11	-0.000524	11	0.000990	10	0.001307	10	0.002896	9	0.000806	12	0.000143	-	-	-	-
	18	0.001241	17	-0.005532	21.2	0.000062	14	-0.003164	30.2	0.000186	14	0.000869	13	0.001106	12	0.004909	11.3	0.000058	11	0.004287	11	-0.018181	9.3	0.000605	13	-0.000470	-	-	-	-
	19	0.000062	18	0.000791	22	0.002792	15	0.000352	30.3	0.000062	15	-0.000207	14	0.000291	13	-0.000116	12	-0.003960	12	-0.004104	12	0.001138	10	-0.003064	14	0.000490	-	-	-	-
	-	-	19	0.001339	22.3	0.000062	16	0.001179	31	-0.001386	15.2	0.000062	15	0.000116	14	0.000990	13	0.000466	13	-0.001878	-	-	-	-	15	0.000061	-	-	-	-
	-	-	20	-0.002621	23	-0.006204	17	0.000434	31.2	-0.002254	16	-0.006452	-	-	-	-	-	-	14	0.000184	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	24	-0.002585	-	-	32	-0.002875	17	0.000352	-	-	-	-	-	-	15	0.000061	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	25	0.001861	-	-	32.2	-0.001324	18	-0.000765	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	26	0.000620	-	-	33	0.000062	19	0.001861	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	27	0.000993	-	-	33.2	0.000744	20	0.000931	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	28	0.000186	-	-	34	0.003371	21	0.000434	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	29	0.000124	-	-	34.2	0.000062	21.2	0.000062	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	35	0.000434	22	0.000496	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Jamaican	-	-	-	-	24	0.002577	12	0.002577	-	-	15	0.012887	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	24.2	-0.002577	13	0.007732	-	-	16	0.002577	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	14	0.005155	-	-	17	-0.005155	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	15	-0.002577	-	-	18	0.007732	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	16	-0.012887	-	-	20	-0.010309	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	21	-0.007732	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
Trinidadian	-	-	-	-	-	-	13	-0.006150	-	-	<11	0.006410	-	-	-	-	-	-	-	-	-	-	-	-	12	0.006098	-	-	-	-
	-	-	-	-	-	-	15	0.006150	-	-	13	-0.006410	-	-	-	-	-	-	-	-	-	-	-	-	13	-0.006098	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	16	-0.006410	-	-	-	-	-	-	-	-	-	-	-	-	13.3	0.006098	-	-	-	-
	-	-	-	-	-	-	-	-	-	-	19	0.006410	-	-	-	-	-	-	-	-	-	-	-	-	14	-0.006098	-	-	-	-
Filipino	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	16	0.000402	12	0.000402
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	17	0.001107	13	-0.003016
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	18	0.000805	13.2	-0.006536
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	19	0.003119	14	0.002213
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	20	0.001107	14.2	0.000704
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	21	-0.013679	15	0.001509
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	22	0.000905	15.2	0.003521
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	23	0.001911	16	0.000201
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	24	0.003722	16.2	0.000905
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	25	0.000503	17.2	0.000101
	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	26	0.000101	-	-

TABLE 1—*The effect of change in allele counts and/or sample size (N) on allele frequencies. All alleles with incorrect allele counts derived from the original data are shown with the difference in frequency between the original and amended values. Negative and positive values reflect a decrease and increase, respectively, in allele frequency.*

EXPANSION OF
FBI STR POPULATION DATA

Allele distributions for the autosomal short tandem repeat (STR) loci D1S1656, D2S441, D2S1338, D3S1358, D5S818, D7S820, D8S1179, D10S1248, D12S391, D13S317, D16S539, D18S51, D19S433, D21S11, D22S1045, CSF1PO, FGA, Penta D, Penta E, SE33 TH01, TPOX and vWA have been determined in the following FBI populations: Caucasians, Southwestern Hispanics, Southeastern Hispanics, African Americans, Bahamians, Jamaicans, Trinidadians, Chamorros, Filipinos, Apaches, and Navajos. An announcement of population data will be submitted for publication under the title "*Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States.*" The Expanded FBI STR files contain all the corrections made to the recent Amended FBI STR data of the original 1999 population database files. The new expanded FBI population data will be made available immediately on the CJIS WAN (Expanded FBI STR) and then via publication and in a future update to Popstats.

The FBI Laboratory recently announced an expansion of the original thirteen short tandem repeat (STR) loci that have been the core of the National DNA Index System (NDIS) since 1997 (D.R. Hares (2015) Selection and Implementation of Expanded CODIS Core Loci in the Unites States. Forensic Sci. Int. Genet. http://dx.doi.org/10.1016/j.fsigen.2015.03.006 page 33 – page 34). Seven additional STR loci were selected by the CODIS Core Loci Working Group and, following an implementation phase concluding on January 1, 2017, will also be required for upload and searching of DNA profiles at NDIS. Collectively, these loci provide greater discrimination potential for human identification applications and enhance kinship analyses typically used in missing person inquiries. Since many of these loci are included in databases globally, the expanded STR locus set facilitates international law enforcement and counterterrorism endeavours.

The twenty STR loci (the original set: D3S1358, D5S818, D7S820, D8S1179, D13S317, D16S539, D18S51, D21S11, CSF1PO, FGA, TH01, TPOX and vWA; and the additional set: D1S1656, D2S441, D2S1338, D10S1248, D12S391, D19S433 and D22S1045) can be simultaneously genotyped with either the AmpFlSTR® GlobalFiler® (GlobalFiler, Life Technologies, Inc., Carlsbad, CA) or PowerPlex® Fusion™ (Fusion, Promega Corporation, Madison, WI) multiplex amplification systems. These kits also enable the genotyping of SE33

and a Y indel locus (GlobalFiler), Penta D and Penta E (Fusion), and DYS391 (GlobalFiler and Fusion), as well as Amelogenin for sex determination.

The FBI Laboratory has generated allele frequencies for the autosomal STR loci with both the GlobalFiler and Fusion kits in the following FBI population groups: African Americans, Caucasians, Southeast Hispanics, Southwestern Hispanics, Bahamians, Jamaicans, Trinidadians, Apaches, Navajos, Chamorros and Filipinos. Concordance studies on these populations demonstrate genotyping accuracy and identified instances of non-concordance due to rare kit-specific primer binding site variants. Additionally, the results of population genetic analyses support the usage of these loci and the associated allele frequencies for estimating match statistics in human identity testing. All of these studies will be described in an announcement of population data that will be submitted for publication under the title "*Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States.*"

If you have any questions, please contact Anthony J. Onorato of the FBI's DNA Support Unit at Anthony.Onorato@ic.fbi.gov or 703-632-7572.

CODIS
COMBINED DNA INDEX SYSTEM

CODIS Bulletin

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AMENDMENT OF THE 1999 AND 2001 FBI STR POPULATION DATA

In the evaluation of original population database samples with the new expanded CODIS core loci, the FBI Laboratory has identified some errors in the data published in the Journal of Forensic Sciences *Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans and Trinidadians*, Journal of Forensic Sciences 1999 44(6):1277-86. An erratum notice will be published as a Letter to the Editor in the July 2015 issue of the Journal of Forensic Sciences containing the empirical data demonstrating their nominal effect on profile probabilities. The new amended population data will be available at FBI.gov (http://www.fbi.gov/about-us/lab/biometric-analysis/dna-casework-unit-dcu-1), on the CJIS WAN, and in a future update to Popstats.

Since the development in the late 1990s of the original short tandem repeat (STR) typing systems that included the 13 CODIS core loci, new amplification kits that expand the number of loci to 24 in a multiplex reaction are now commercially available. To establish allele distributions for the additional loci, population samples that were originally genotyped using AmpFlSTR Profiler Plus, COfiler, Identifiler (Thermo Fisher Scientific, South San Francisco, CA) and/or GenePrint PowerPlex (Promega Corp., Madision, WI) were retyped using GlobalFiler (Thermo Fisher Scientific) and PowerPlex Fusion (Promega Corp.). For any sample where a given locus is typed with different amplification kits, concordant genotypes should be obtained irrespective of the kit(s) used, with the exception of genotype differences due to rare primer binding site variants and improvements in allelic ladders that expand allele identification capabilities (e.g., an allele may be designated as <11 in one system and as 9 in another).

The FBI Laboratory has identified errors in the data published in the Journal of Forensic Sciences and has submitted erratum notice regarding "Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians,

Jamaicans and Trinidadians," Journal of Forensic Sciences 1999 44(6):1277-86. DNA samples that were used in the published study were recently genotyped again with new commercial products. A concordance assessment of the 1999 and recent data revealed errors in the original data that are attributable to clerical mistakes in transcription of the genotypes and to limitations of the old technology and software.

Erroneous allele frequencies cited in this publication have been used by the FBI and many forensic laboratories for calculating match statistics in criminal investigations and other types of human identification applications since 1999. We are of the view that these discrepancies are unlikely to materially affect any assessment of evidential value. However, given that statistics based on these data have been included in thousands of laboratory reports and testimonies, we believe the discrepancies require acknowledgement and wish to inform on an erratum informing on the existence of these errors, along with the empirical data demonstrating their nominal effect on profile probabilities, which was accepted on March 29, 2015 for publication in the Journal of Forensic Sciences (the journal in which the erroneous data were published) as a Letter to the Editor. According to the current publishing schedule this erratum should appear in the July 2015 issue of the JFS. This issue will be posted on the web at www.aafs.org (for AAFS members) or www.wiley.com (for non-members) in the 60-day period prior to publication of the printed issue. Additionally, amended data will be available at FBI.gov, on the CJIS WAN, and in a future update to Popstats.

If you have any questions, please contact Anthony J. Onorato of the FBI's DNA Support Unit at Anthony.Onorato@ic.fbi.gov or 703-632-7572.