TEXAS DEPARTMENT OF PUBLIC SAFETY

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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
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AMERICAN SOCIETY OF CRIME LABORATORY DIRECTORS
LABORATORY ACCREDITATION BOARD

June 15, 2015

Notification from the ASCLD/LAB Board of Directors to Laboratories and Interested Parties Concerning Amendments to the 1999 and 2001 FBI STR Population Data

In late May 2015, ASCLD/LAB top management became aware that discrepancies had been discovered by the FBI in the 1999 and 2001 FBI STR Population Data. As reported by the FBI, "*The discrepancies discovered were attributable to (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). The published genotype data (3,4) from which allele frequencies were calculated also include sample or data processing errors (e.g., genotype duplications).*"[1] In addition, and very transparently, appropriate individuals ensured that a correction (*ERRATUM*) to previously reported journal data will be published in the *Journal of Forensic Sciences*.[2]

In its June 3, 2015 notice to CODIS State Administrators, the FBI acknowledged that the allele frequencies in question "*have been used by … many forensic laboratories for calculating match statistics in criminal investigations and other types of human identification applications since 1999. Given that statistical estimates based on these data have been included in thousands of laboratory reports and testimonies, the FBI Laboratory believes the discrepancies require acknowledgement.*"

Further, the FBI reported that the ERRATUM article "*describes these errors and their effect on profile probability calculations. Empirical testing described in this publication supports 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 amended allele frequency tables are now publicly available for anyone to compare the calculations made using the previously published data against the amended allele frequencies.

The ASCLD/LAB Board of Directors has not, and will not, make any scientific determination about what effect the population data errors may have had on previous calculations. As an accrediting body, that is not the role of ASCLD/LAB. However, this notice serves to remind the management of all ASCLD/LAB accredited laboratories that they are required by specific accreditation requirements to appropriately consider and effectively address any potential nonconforming test results that are not in conformance with those requirements. Although other accreditation requirements may also be relevant, those which are most relevant are found in the following:

1 Excerpt from the "*Notice of Amendment of the FBI's STR Population Data Published in 1999 and 2001*" released by the FBI to CODIS State Administrators on June 3, 2015.

2 http://onlinelibrary.wiley.com/doi/10.1111/1556-4029.12806/abstract

2008 ASCLD/LAB Legacy Accreditation Manual
For laboratories accredited in the ASCLD/LAB Legacy program

The laboratory must have a written procedure which it uses to initiate a review and to take corrective action when the laboratory has an indication of a significant problem with a technical procedure or the work of an analyst.

1.4.2.25 (E) IF THE LABORATORY HAS AN INDICATION OF A SIGNIFICANT TECHNICAL PROBLEM, IS THERE A PROCEDURE IN WRITING AND IN USE WHEREBY THE LABORATORY INITIATES A REVIEW AND TAKES ANY CORRECTIVE ACTION REQUIRED?

ISO/IEC 17025:2005
For laboratories accredited or seeking accreditation in the ASCLD/LAB-*International* program

4.9.1 The laboratory shall have a policy and procedures that shall be implemented when any aspect of its testing and/or calibration work, or the results of this work, do not conform to its own procedures or the agreed requirements of the customer. The policy and procedures shall ensure that:

a) the responsibilities and authorities for the management of nonconforming work are designated and actions (including halting of work and withholding of test reports and calibration certificates, as necessary) are defined and taken when nonconforming work is identified;
b) an evaluation of the significance of the nonconforming work is made;
c) correction is taken immediately, together with any decision about the acceptability of the nonconforming work;
d) where necessary, the customer is notified and work is recalled;
e) the responsibility for authorizing the resumption of work is defined.

Where DNA analysis is included in the scope of accreditation, the ASCLD/LAB Board of Directors expects laboratory management in all ASCLD/LAB accredited and applicant laboratories to evaluate the notice from the FBI and, if applicable, take any appropriate action in accordance with accreditation requirements. The management of ASCLD/LAB accredited and applicant laboratories should anticipate that ASCLD/LAB assessment teams will be instructed to confirm that appropriate action has been taken on this matter during future assessment activities.

In any laboratory affected by the FBI announcement, accredited or not, the ASCLD/LAB Board of Directors stands firm that laboratory management has an ethical obligation, in consultation with the appropriate legal authorities, to consider the impact of this matter and, if deemed applicable and appropriate, to design and take corrective action.

The ASCLD/LAB Board encourages the top management, technical management and legal counsel of all affected laboratories to make the effort to maintain an awareness of the professional discussions regarding this subject that are ongoing in the forensic science and legal communities. As those discussions continue, and recognized scientific and legal authorities share conclusions, laboratory management should give due consideration to those conclusions as any needed corrective actions are planned and implemented.

Notice of Amendment of the FBI's STR Population Data Published in 1999 and 2001

Recently, new amplification kits that expand the number of loci in a multiplex reaction have become commercially available. To establish allele distributions for the additional loci, the FBI Laboratory retyped 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) using GlobalFiler (Thermo Fisher Scientific) and PowerPlex Fusion (Promega Corp.) (3). During a comparison of over 1100 DNA profiles from African Americans, Caucasians, Southwest Hispanics, Bahamians, Jamaicans, Trinidadians, Filipinos and Chamorros in the original (4,5) and new studies (3), genotyping discrepancies were discovered. 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). Genotypes from these populations thus could not be assessed for concordance.

The discrepancies discovered were attributable to (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). The published genotype data (3,4) from which allele frequencies were calculated also include sample or data processing errors (e.g., genotype duplications).

Allele frequencies cited across these publications (1,2) 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. Given that statistical estimates based on these data have been included in thousands of laboratory reports and testimonies, the FBI Laboratory believes the discrepancies require acknowledgement. The FBI Laboratory has submitted the attached erratum notice, which is scheduled to appear in the July issue of the Journal of Forensic Science. This article describes these errors and their effect on profile probability calculations. Empirical testing described in this publication supports 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 FBI Laboratory is additionally providing herein the amended allele frequency tables for use by anyone interested in performing comparisons between the multi-locus profile probabilities calculated using the previously published data and the amended allele frequencies.

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.

African American Amended Allele Frequency Table

Caucasian Amended Allele Frequency Table

Southwestern Hispanic Amended Allele Frequency Table

Bahamian Amended Allele Frequency Table

Jamaican Amended Allele Frequency Table

Trinidadian Amended Allele Frequency Table

Chamorro Amended Allele Frequency Table

Filipino Amended Allele Frequency Table

References

1. Budowle B, Moretti TR, Baumstark AL, Defenbaugh DA and 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;44:1277-1286.

2. Budowle B, Collins P, Dimsoski P, Ganong C, Hennessy L, Leibelt C, Rao-Coticone S, Shadravan F & Reeder D. Population data on the STR loci D2S1338 and D19S433. Forensic Sci Communications 2001;3(3).

3. Moretti TR, Moreno LI, Smerick JB, Pignone ML, Hizon RC , Onorato AJ, Bright J-A and Buckleton JS. Population data on the expanded CODIS core STR loci for eleven populations of significance for forensic DNA analyses in the United States. Forensic Sci International: Genetics 2015;(in preparation).

4. Budowle B and Moretti TR. Genotype Profiles for six population groups at the 13 CODIS short tandem repeat core loci and other PCR based loci. Forensic Sci Communications 1999;1(2).

5. Budowle B. Genotype profiles for five population groups at the short tandem repeat loci D2S1338 and D19S433. Forensic Sci Communications 2001;3(3).

6. Budowle B, Shea B, Niezgoda S and Chakraborty R. CODIS STR loci data from 41 sample populations. J Forensic Sci 2001;46:453–489.

7. Budowle B, Defenbaugh DA and Keys KM. Genetic variation at nine short tandem repeat loci in Chamorros and Filipinos from Guam. Legal Medicine 2000;2:26–30.

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 (a) human error, typically due to the limited software capabilities for genotyping with manual data editing and recording, and (b) 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 includes 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, 6 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 Figure 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 acknowledgement but are unlikely to materially affect any assessment of evidential value.

[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.

References

1. 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;44:1277-86.
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4. Budowle B. Genotype profiles for five population groups at the short tandem repeat loci D2S1338 and D19S433. Forensic Science Communications 2001;3(3).
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6. Budowle B, Defenbaugh DA, Keys KM. Genetic variation at nine short tandem repeat loci in Chamorros and Filipinos from Guam. Legal Medicine 2000;2:26-30.
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10. Budowle B, Monson KL, Giusti AM, Brown B. Evaluation of Hinf I-generated VNTR profile frequencies determined using various ethnic databases. J Forensic Sci 1994;39:988-1008.

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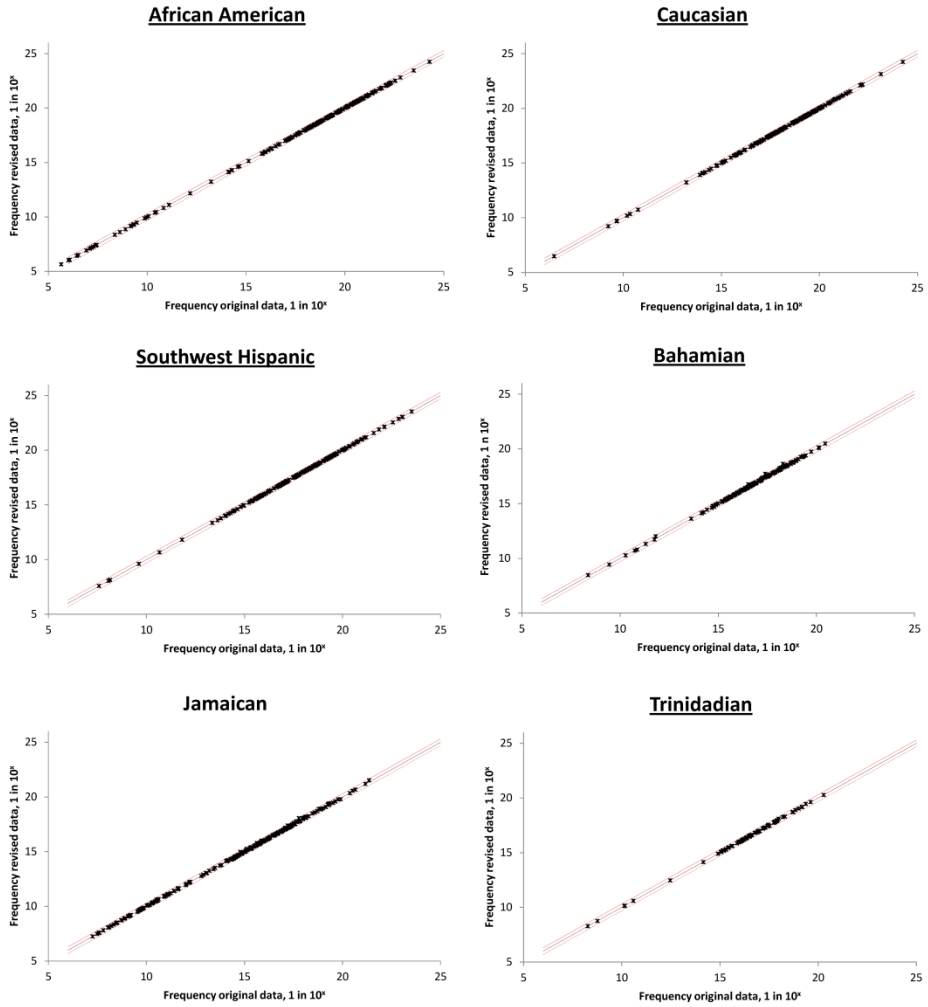

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85 FIG. 1—*The comparison of the log of the profile frequency for the original and amended data. The*
86 *x=y line and lines for a factor of two in either direction are given.*

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		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	-0.003123	<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	-0.003843	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	0.001805	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	0.004309	11.3	0.000058	11	0.004287	11	-0.018181	9.3	0.000605	13	-0.000470	-	-	-	-
	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	12	-0.003960	12	-0.004104	12	0.001138	10	-0.003084	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	-0.006250	-	-	<11	0.006410	-	-	-	-	-	-	-	-	-	-	-	-	12	0.006098	-	-	-	-
	-	-	-	-	-	-	15	0.006250	-	-	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	-	-

92 TABLE 2—*The ratio of profile probability produced during testing of the original and amended data.*
93 *The profile probabilities of all samples in the original data set were calculated using the original and*
94 *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	2.00	1.32
Min (new frequency is less)	0.87	0.92	0.92	0.81	0.79	0.84

95

African American Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
6											0.0861	0.1095				6
7							0.0028		0.0071	0.0429	0.0215	0.4405				7
8				0.0028			0.0500	0.0335	0.1738	0.0857	0.3684	0.1857	0.0359			8
9				0.0056			0.0139	0.0279	0.1571	0.0333	0.1818	0.1452	0.1986			9
9.3												0.1048				9.3
10				0.0250			0.0639	0.0503	0.3238	0.2714	0.0933	0.0143	0.1100		0.0150	10
<11						0.0056										<11
11		0.0028		0.0361		0.0056	0.2611	0.2374	0.2238	0.2048	0.2249		0.2943		0.0689	11
<12	0.0048															<12
12	0.0024			0.1083		0.0587	0.3556	0.4832	0.0905	0.3000	0.0239		0.1866		0.1138	12
12.2															0.0808	12.2
13	0.0119	0.0056		0.2222		0.0559	0.2444	0.1257	0.0190	0.0548			0.1651		0.2964	13
13.2						0.0056									0.0509	13.2
14	0.1214	0.0667		0.3333		0.0642	0.0056	0.0391	0.0048	0.0071			0.0096		0.1946	14
14.2															0.0539	14.2
15	0.2905	0.2361		0.2139		0.1676		0.0028							0.0419	15
15.2															0.0389	15.2
16	0.3071	0.2694		0.0444		0.1872								0.0449	0.0210	16
>16							0.0028									>16
16.2															0.0180	16.2
17	0.2000	0.1833		0.0083		0.1620								0.1018		17
17.2			0.0028												0.0030	17.2
18	0.0548	0.1361	0.0083			0.1313								0.0659		18
18.2			0.0083												0.0030	18.2
19	0.0048	0.0722	0.0528			0.0782								0.1377		19
>19	0.0024															>19
19.2			0.0028													19.2
20		0.0278	0.0722			0.0559								0.0629		20
21			0.1250			0.0112								0.1527		21
22			0.2250			0.0056								0.1377		22
22.2			0.0056													22.2
23			0.1250			0.0056								0.0988		23
24			0.1861											0.0928		24
24.2					0.0028											24.2
25			0.1000											0.0838		25
26			0.0361		0.0028									0.0210		26
27			0.0222		0.0615											27
28			0.0167		0.2151											28
29			0.0056		0.1899											29
29.3					0.0028											29.3
30			0.0028		0.1788											30
30.2			0.0028		0.0084											30.2
31					0.0922											31
31.2					0.0754											31.2
32					0.0084											32
32.2					0.0698											32.2
33					0.0084											33
33.2					0.0335											33.2
34					0.0084											34
34.2					0.0028											34.2
35					0.0279											35
36					0.0056											36
37					0.0056											37
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
N	210	180	180	180	179	179	180	179	210	210	209	210	209	167	167	

Caucasian Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
6									0.0025			0.2252				6
7									0.0173	0.0025		0.1733				7
8				0.0179				0.0995	0.1634	0.0050	0.5470	0.1262	0.0199			8
8.3												0.0025				8.3
9				0.0102			0.0308	0.0765	0.1460	0.0198	0.1238	0.1658	0.1045			9
9.3												0.3045				9.3
10				0.1020			0.0487	0.0510	0.2896	0.2525	0.0371	0.0025	0.0647			10
10.3										0.0025						10.3
<11						0.0128										<11
11				0.0587		0.0128	0.4103	0.3214	0.2030	0.2995	0.2550		0.2736			11
12				0.1454		0.1276	0.3538	0.3061	0.1411	0.3267	0.0371		0.3383		0.1086	12
12.2															0.0066	12.2
13	0.0025	0.0051		0.3393		0.1224	0.1462	0.1097	0.0297	0.0718			0.1642		0.2829	13
13.2															0.0263	13.2
14	0.1386	0.1020		0.2015		0.1735	0.0077	0.0357	0.0074	0.0149			0.0323		0.3355	14
14.2															0.0033	14.2
15	0.2475	0.1122		0.1097		0.1276	0.0026			0.0050			0.0025		0.1349	15
15.2															0.0263	15.2
16	0.2327	0.2015		0.0128		0.1071								0.0296	0.0428	16
16.2															0.0263	16.2
17	0.2104	0.2628		0.0026		0.1556								0.1941		17
17.2															0.0033	17.2
18	0.1634	0.2219	0.0306			0.0918								0.0526		18
18.2															0.0033	18.2
19	0.0050	0.0842	0.0561			0.0357								0.1447		19
20		0.0102	0.1454			0.0255								0.1546		20
20.2			0.0026													20.2
21			0.1735			0.0051								0.0197		21
22			0.1888			0.0026								0.0296		22
22.2			0.0102													22.2
23			0.1582											0.1349		23
24			0.1378											0.1217		24
24.2					0.0051											24.2
25			0.0689											0.0954		25
26			0.0179											0.0230		26
27			0.0102		0.0459											27
28					0.1658											28
29					0.1811											29
30					0.2321											30
30.2					0.0383											30.2
31					0.0714											31
31.2					0.1020											31.2
32					0.0153											32
32.2					0.1097											32.2
33.2					0.0306											33.2
35.2					0.0026											35.2
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
N	202	196	196	196	196	196	195	196	202	202	202	202	201	152	152	

Southwest Hispanic Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
5												0.0024				5
6									0.0024		0.0048	0.2321				6
7							0.0616		0.0215	0.0024	0.0048	0.3373				7
8				0.0025			0.0025	0.0665	0.0981		0.5550	0.0813	0.0168			8
9				0.0025			0.0542	0.2192	0.0478	0.0072	0.0335	0.1029	0.0793		0.0035	9
9.3												0.2416				9.3
10				0.0936			0.0640	0.1010	0.3062	0.2536	0.0335	0.0024	0.1755			10
<11						0.0049										<11
11		0.0025		0.0616		0.0123	0.4261	0.2020	0.2895	0.2656	0.2727		0.3149		0.0035	11
12				0.1207		0.1059	0.2882	0.2167	0.1914	0.3923	0.0933		0.2885		0.0563	12
12.2															0.0211	12.2
13	0.0024			0.3251		0.1700	0.0961	0.1379	0.0383	0.0646	0.0024		0.1010		0.1620	13
13.2															0.1092	13.2
14	0.0789	0.0616		0.2463		0.1700	0.0049	0.0567	0.0048	0.0096			0.0240		0.3204	14
14.2															0.0458	14.2
15	0.4258	0.0714		0.1158		0.1379	0.0025			0.0048					0.1197	15
15.2															0.0810	15.2
16	0.2656	0.3645		0.0246		0.1158								0.0176	0.0423	16
16.2															0.0352	16.2
17	0.1268	0.2217		0.0074		0.1379								0.2218		17
18	0.0837	0.1946	0.0025			0.0517								0.0423		18
19	0.0144	0.0714	0.0813			0.0369								0.2606		19
>19	0.0024															>19
20		0.0123	0.0690			0.0172								0.1408		20
20.2			0.0025													20.2
21			0.1305			0.0197								0.0106		21
21.2			0.0025													21.2
22			0.1773			0.0074								0.0704		22
>22						0.0123										>22
22.2			0.0049													22.2
23			0.1404											0.1232		23
23.2			0.0074													23.2
24			0.1256											0.0669		24
24.2					0.0025											24.2
25			0.1379											0.0387		25
26			0.0837											0.0070		26
27			0.0320		0.0099											27
28			0.0025		0.0690											28
29					0.2044											29
29.2					0.0025											29.2
30					0.3300											30
30.2					0.0320											30.2
31					0.0690											31
31.2					0.0862											31.2
32					0.0123											32
32.2					0.1355											32.2
33.2					0.0419											33.2
34.2					0.0049											34.2
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	D2S1338	D19S433	Allele
N	209	203	203	203	203	203	203	203	209	209	209	209	208	142	142	

Bahamian Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
5												0.0032		5
6										0.0032	0.0673	0.1538		6
7								0.0031	0.0126	0.0641	0.0256	0.3846		7
8							0.0723	0.0220	0.1541	0.0577	0.3237	0.2276	0.0385	8
9				0.0032			0.0094	0.0314	0.1258	0.0481	0.2212	0.1282	0.2147	9
9.3												0.0897		9.3
10				0.0194			0.0597	0.0252	0.3396	0.2340	0.0897	0.0128	0.0994	10
<11						0.0097								<11
11		0.0094		0.0516		0.0097	0.2390	0.3050	0.2201	0.2244	0.2372		0.3013	11
11.3									0.0031					11.3
12				0.1290		0.0484	0.3711	0.3994	0.1195	0.2853	0.0353		0.1731	12
13		0.0283		0.1903		0.0516	0.2264	0.1604	0.0252	0.0705			0.1442	13
13.2						0.0032								13.2
14	0.0742	0.0629		0.3387		0.0452	0.0157	0.0535		0.0096			0.0256	14
15	0.3194	0.1541		0.1839		0.1548	0.0063			0.0032			0.0032	15
15.2	0.0032					0.0032								15.2
16	0.3387	0.2642		0.0613		0.1645								16
17	0.1968	0.2013		0.0226		0.1871								17
<18			0.0129											<18
18	0.0645	0.1824				0.1258								18
18.2			0.0129											18.2
19	0.0032	0.0723	0.0581			0.0968								19
20		0.0252	0.0742			0.0484								20
21			0.1129			0.0226								21
21.2			0.0032			0.0032								21.2
22			0.1452			0.0258								22
22.3			0.0032											22.3
23			0.1774											23
24			0.1968											24
24.3					0.0065									24.3
25			0.0968											25
26			0.0323											26
27			0.0516		0.0710									27
28			0.0097		0.2226									28
29			0.0065		0.1742									29
30					0.1774									30
>30			0.0065											>30
30.2					0.0097									30.2
30.3					0.0032									30.3
31					0.0935									31
31.2					0.0484									31.2
32					0.0194									32
32.2					0.0968									32.2
33					0.0032									33
33.2					0.0387									33.2
34					0.0097									34
34.2					0.0032									34.2
35					0.0226									35
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
N	155	159	155	155	155	155	159	159	159	156	156	156	156	

Jamaican Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
5												0.0024		5
6									0.0041		0.0673	0.1394		6
7								0.0020	0.0061	0.0481	0.0313	0.3558		7
8							0.0533	0.0205	0.1988	0.0625	0.3822	0.2548	0.0340	8
9				0.0077			0.0102	0.0246	0.1393	0.0313	0.2644	0.1587	0.2087	9
9.3												0.0841		9.3
10				0.0129			0.0553	0.0246	0.3443	0.2716	0.0745	0.0048	0.1092	10
10.1									0.0020					10.1
<11						0.0026								<11
11		0.0041		0.0309		0.0052	0.2049	0.2766	0.1844	0.2332	0.1538		0.3131	11
12	0.0052			0.1160		0.0438	0.3996	0.4549	0.1025	0.2933	0.0264		0.1869	12
13	0.0155	0.0082		0.2139		0.0258	0.2561	0.1434	0.0123	0.0529			0.1383	13
13.2						0.0052								13.2
14	0.0670	0.0738		0.3273		0.0412	0.0143	0.0533	0.0061	0.0072			0.0097	14
14.2						0.0026								14.2
15	0.3376	0.2275		0.2165		0.1572	0.0061							15
15.2	0.0026													15.2
16	0.3067	0.2910		0.0670		0.1907								16
17	0.2113	0.1824		0.0052		0.1830								17
<18			0.0077											<18
18	0.0464	0.1311		0.0026		0.1237								18
18.2			0.0206											18.2
19	0.0077	0.0533	0.0670			0.0954								19
19.2			0.0077											19.2
20		0.0225	0.0464			0.0696								20
21		0.0061	0.0747			0.0284								21
21.2						0.0026								21.2
22			0.1881			0.0155								22
23			0.1959			0.0052								23
24			0.1469			0.0026								24
24.3			0.0026		0.0026									24.3
25			0.1160											25
26			0.0412											26
27			0.0515		0.0644									27
28			0.0155		0.2732									28
29			0.0077		0.1830									29
30					0.1649									30
>30			0.0103											>30
30.2					0.0180									30.2
31					0.0644									31
31.2					0.0490									31.2
32					0.0155									32
32.1					0.0026									32.1
32.2					0.0619									32.2
33					0.0052									33
33.2					0.0309									33.2
34					0.0077									34
34.2					0.0026									34.2
35					0.0412									35
36					0.0103									36
37					0.0026									37
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
N	194	244	194	194	194	194	244	244	244	208	208	208	206	

Trinidadian Amended Allele Frequencies

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
5												0.0061		5
6											0.0976	0.1829		6
7							0.0118		0.0060	0.0671	0.0122	0.3110		7
8				0.0063			0.0235	0.0536	0.2083	0.0549	0.3232	0.2073	0.0610	8
9							0.0294	0.0476	0.1131	0.0244	0.1646	0.2073	0.1646	9
9.3												0.0732		9.3
10				0.0500			0.1529	0.0536	0.3333	0.2744	0.0671	0.0122	0.1280	10
<11						0.0064								<11
11		0.0059		0.0750		0.0256	0.2941	0.2798	0.2202	0.2134	0.2866		0.2866	11
12				0.1563		0.0833	0.3235	0.3214	0.1012	0.2744	0.0488		0.1829	12
13		0.0059		0.2250		0.0962	0.1353	0.1607	0.0179	0.0793			0.1402	13
13.2						0.0064								13.2
13.3													0.0061	13.3
14	0.0563	0.0882		0.2500		0.1090	0.0235	0.0833		0.0122			0.0305	14
15	0.3125	0.1412		0.1813		0.1538								15
16	0.3188	0.2941		0.0563		0.2051	0.0059							16
17	0.2000	0.2647				0.0513								17
18	0.1125	0.1353	0.0125			0.0577								18
19		0.0471	0.0563			0.0962								19
20		0.0176	0.0938			0.0705								20
21			0.1000			0.0385								21
22			0.1688											22
23			0.1625											23
24			0.2063											24
25			0.1063											25
26			0.0438											26
27			0.0188		0.0625									27
28			0.0125		0.2250									28
29			0.0063		0.2000									29
29.2					0.0063									29.2
30					0.1750									30
>30			0.0125											>30
30.2					0.0125									30.2
31					0.0500									31
31.2					0.0813									31.2
32					0.0313									32
32.2					0.0688									32.2
33					0.0063									33
33.2					0.0500									33.2
34					0.0188									34
35					0.0125									35
Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	CSF1PO	TPOX	TH01	D16S539	Allele
N	80	85	80	80	80	78	85	84	84	82	82	82	82	

Chamorro Amended Allele Frequencies

Allele	D2S1338	D19S433	Allele
12		0.0347	12
12.2		0.0139	12.2
13		0.3542	13
13.2		0.0417	13.2
14		0.2292	14
14.2		0.0972	14.2
15		0.0903	15
15.2		0.0972	15.2
16	0.0278		16
16.2		0.0139	16.2
17	0.1042		17
17.2		0.0278	17.2
18	0.0833		18
19	0.1875		19
20	0.1111		20
21	0.0139		21
22	0.0972		22
23	0.1736		23
24	0.1319		24
25	0.0556		25
26	0.0069		26
27	0.0069		27
Allele	D2S1338	D19S433	Allele
N	72	72	

Filipino Amended Allele Frequencies

Allele	D2S1338	D19S433	Allele
12		0.0286	12
13		0.2857	13
13.2		0.0357	13.2
14		0.1571	14
14.2		0.0500	14.2
15		0.1071	15
15.2		0.2500	15.2
16	0.0286	0.0143	16
16.2		0.0643	16.2
17	0.0786		17
17.2		0.0071	17.2
18	0.0571		18
19	0.2214		19
20	0.0786		20
21	0.0286		21
22	0.0643		22
23	0.1357		23
24	0.2643		24
25	0.0357		25
26	0.0071		26
Allele	D2S1338	D19S433	Allele
N	70	70	