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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 $\pm$ 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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[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	–	–	–	–
	–	–	–	–	–	–	–	–	–	–	>22	0.000031	–	–	–	–
Caucasian	13	0.000012	–	–	–	–	–	–	31.2	0.002551	–	–	–	–	11	0.002551
	14	−0.001780	–	–	–	–	–	–	32.2	−0.002551	–	–	–	–	12	−0.002551
	15	0.001219	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	16	0.001146	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	17	−0.001427	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	18	0.000805	–	–	–	–	–	–	–	–	–	–	–	–	–	–
	19	0.000024	–	–	–	–	–	–	–	–	–	–	–	–	–	–
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Southwest Hispanic	–	–	15	−0.004926	19	0.002463	–	–	–	–	–	–	10	−0.002463	–	–
	–	–	16	0.004926	20	−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	–	–	–	–	–	–	–	–	–	–	–	–	14	−0.002989
American	–	–	–	–	–	–	–	–	–	–	–	–	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	–	–	–	–	–	–	–	–	10	0.002404	–	–	–	–
Hispanic	–	–	–	–	–	–	–	–	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	–	–	–	–
	–	–	–	–	–	–	–	–	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	–	–

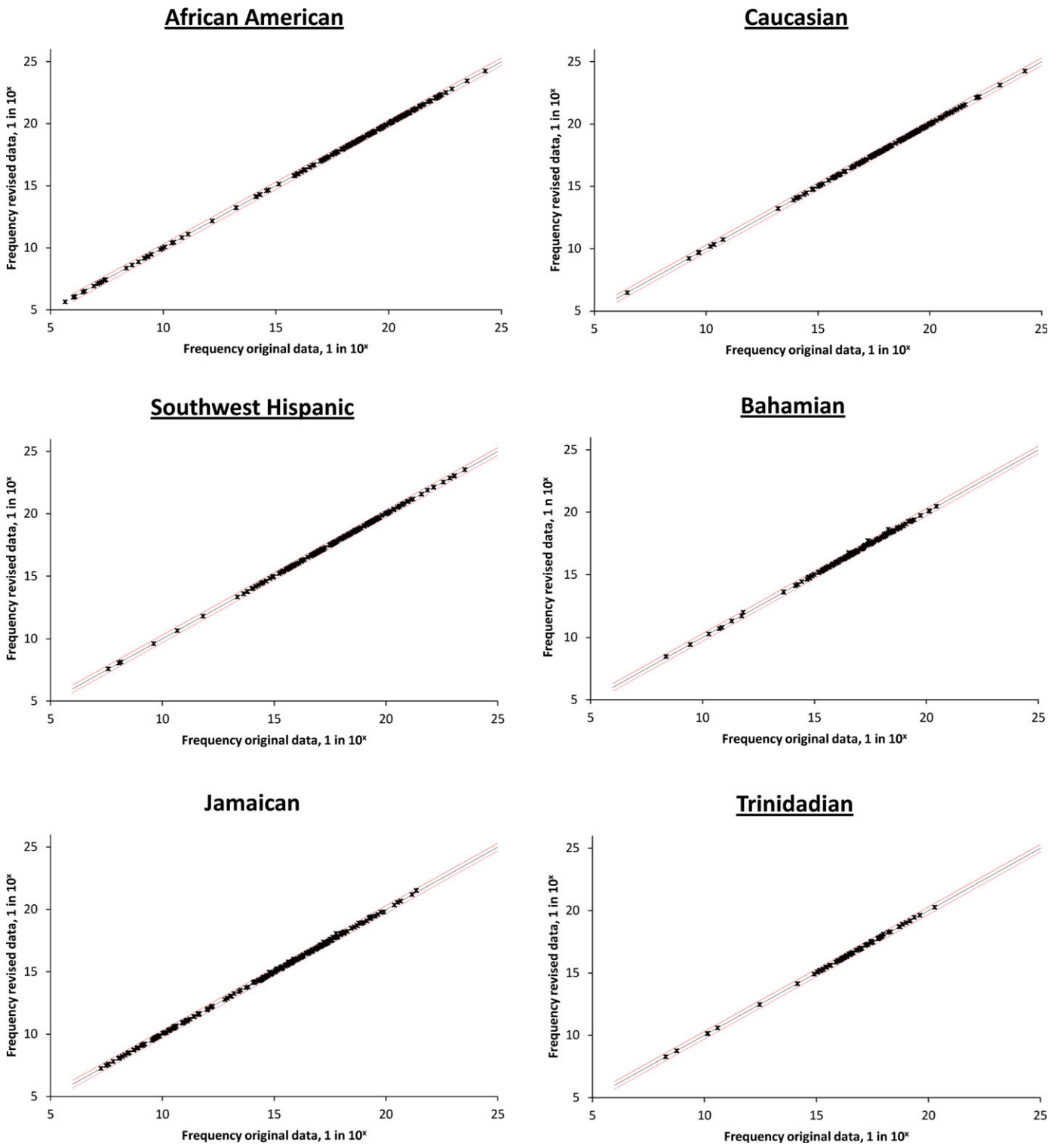

FIG. 1—*The comparison of the log of the profile frequency for the original and amended data. The* x = y *line and lines for a factor of two in either direction are given.*

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