FOR THE RECORD

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AMPF/STR® Identifiler™ STR Allele Frequencies in Tanzania, Africa

POPULATION: Identifiler—Employees and students of Muhimibili University College of Health Sciences in Dar es Salaam representing 19 widely distributed administrative districts and 42 tribes within the country.

KEYWORDS: forensic science, DNA identification testing, short tandem repeats, Identifiler, paternity testing, D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, THO1, TPOX, CSF1PO, D2S1338, D19S433, Tanzania

Allele frequencies of the fifteen AMPLF/STR® Identifiler™ STR loci were determined for the population of Tanzania, East Africa. Two hundred and seventy-two saliva samples were gathered from unrelated healthy student or employee volunteers at Muhimibili University College of Health Sciences in Dar es Salaam, Tanzania during the summer of 2003. The tribal affiliation of each donor was recorded to ensure that representative sampling was achieved, and a total of 19 widely distributed administrative regions of the country and 42 tribes were represented in the final genotypic data. DNA was extracted using the QIAamp spin column protocol for saliva (Qiagen, Valencia, CA) and quantitated using the Quantiblot® colorimetric system (Applied Biosystems, Foster City, CA). Approximately 1 ng of DNA was amplified from each sample using the Identifiler™ system (Applied Biosystems) and subjected to capillary electrophoresis on a 310 Genetic Analyzer (Applied Biosystems). Raw data was collected, sorted, and sized using ABI Gene Collection® and Genescan® software (Applied Biosystems), and alleles were assigned using ABI Genotyper® software (Applied Biosystems).

Allele frequencies were calculated using GENEPOP© online software, v. 3.4 (1). Table 1 lists the frequencies of the alleles at each locus, indicates the total number of samples used to generate the table, and provides the database validation statistics.

A Fisher Exact Test was used to test adherence to Hardy Weinberg Equilibrium (HWE) at all loci (2,000 shufflings, GENEPOP© online software, v 3.4). Twelve of the 15 loci yielded *p*-values of >0.05, and thus failed to reject the hypothesis that the population is in HWE at these loci. The remaining three loci, D8S1178, D3S1358, and D2S1338, yielded *p*-values <0.05; however, a truncated product test for adherence of all loci yielded a *p*-value of 0.0654, thus validating the database for general use (2).

The complete dataset is available upon request through electronic mail from the corresponding author at ballardr@csus.edu and on the corresponding author's academic webpage at http://www.csus.edu/indiv/b/ballardr/index.htm.

References

1. Chang T, Hendrie R, Abercrombie-Higgins J, Maddocks R, Morgan E. Genepop, Version 3.4, 2004. Free program distributed by authors over the internet from http://genepop.curtin.edu.au/. Accessed 22 Jan. 2006.
2. Zaykin D, Zhivotovsky L, Weir BS. Exact tests for association between alleles at arbitrary numbers of loci. Genetica 1995;96:169–78.

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TABLE 1—Allele frequencies for ABI Identifier™ loci in the population of Tanzania, Africa.

Allele	D8S1179 n = 225	D21S11 n = 224	D7S820 n = 225	CSF1PO n = 172	D3S1358 n = 225	THO1 n = 172	D13S317 n = 225	D16S539 n = 172	D2S1338 n = 172	D19S433 n = 172	vWA n = 225	TPOX n = 169	D18S51 n = 225	D5S818 n = 225	FGA n = 225
6.00			0.0044			0.1424						0.0976		0.0022	
7			0.0022	0.0436		0.3663						0.0148		0.0022	
8			0.1956	0.0552		0.2326	0.0067	0.0291				0.2367		0.0844	
9	0.0044		0.1156	0.0669		0.2006	0.0133	0.2122		0.0087		0.284		0.0378	
9.3						0.0581									
10			0.3911	0.2878			0.0267	0.1599		0.0116		0.0858	0.0067	0.0756	
10.2													0.0067		
11	0.0489		0.1956	0.1919			0.3067	0.3401		0.0727	0.0044	0.2574	0.0156	0.2022	
12	0.1267		0.0822	0.2791	0.0044		0.4044	0.1366		0.1076		0.0178	0.0333	0.38	
12.2										0.0436					
13	0.2067		0.0111	0.061	0.0067		0.1956	0.1163		0.2645	0.0089	0.0059	0.0333	0.2067	
13.1			0.0022												
13.2										0.0814			0.0067		
14	0.2978			0.0087	0.0644		0.0467	0.0058		0.2238	0.06		0.0622	0.0067	
14.2										0.0669			0.0022		
15	0.2067			0.0058	0.2333					0.0523	0.2422		0.1289	0.0022	
15.2										0.0378			0.0022		
16	0.0978				0.4267				0.061	0.0058	0.2622		0.1956		
16.1															0.0022
16.2										0.0203			0.0022		
17	0.0111				0.1956				0.0756		0.14		0.1867		0.0022
17.1															0.0022
17.2										0.0029			0.0022		
18					0.0622				0.0552		0.1733		0.1444		0.0067
18.2															0.0044
19					0.0067				0.1773		0.0778		0.0956		0.0556
19.2															0.02
20									0.0669		0.0244		0.04		0.0444
20.2															0.0022
21									0.186		0.0044		0.0267		0.0667
21.2															0.0022
22									0.1512		0.0022		0.0067		0.1778
23									0.0814				0.0022		0.1556
24									0.0465						0.2111
24.3		0.0045													
25									0.061						0.1089
25.2															0.0022
25.3															
26		0.0022							0.0233						0.0622
27		0.0022							0.0145						0.0333
28		0.0804													0.0044
29		0.2567													0.0044
29.1		0.192													
30		0.1272													0.0022
30.2		0.0134													
31		0.1161													0.0022
31.1		0.0022													
31.2		0.0536													0.0067
32		0.0201													
32.2		0.0402													
33		0.0067													0.0044
33.1		0.0022													0.0067

TABLE 1—*continued.*

Allele	D8S1179 n = 225	D21S11 n = 224	D7S820 n = 225	CSF1P0 n = 172	D3S1358 n = 225	THO1 n = 172	D13S317 n = 225	D16S539 n = 172	D2S1338 n = 172	D19S433 n = 172	vWA n = 225	TPOX n = 169	D18S51 n = 225	D5S818 n = 225	FGA n = 225
33.2		0.0268													
34		0.0089													
34.2		0.0022													
35		0.0379													
36		0.0022													
39		0.0022													
43.2															0.0022
44.2															0.0067
45.2															
P	0.0223	0.5288	0.8680	0.6626	0.0358	0.0824	0.6276	0.0656	0.0195	0.9407	0.2209	0.6227	0.4634	0.8337	0.7538
H(obs)	0.8400	0.8438	0.7777	0.8023	0.6800	0.8198	0.7378	0.7674	0.8895	0.8837	0.8311	0.8107	0.8844	0.7244	0.8667
H(exp)	0.7977	0.8537	0.7502	0.7892	0.7171	0.7478	0.7010	0.7807	0.8809	0.8453	0.8126	0.7796	0.8714	0.7577	0.8726
PD	0.9063	0.9510	0.8487	0.8968	0.8023	0.8498	0.7842	0.8872	0.9688	0.9445	0.9298	0.8887	0.9634	0.8581	0.9638
PE	0.5544	0.6511	0.4837	0.5411	0.4394	0.4804	0.4192	0.5280	0.7042	0.6355	0.5786	0.5264	0.6852	0.4942	0.6875
PIC	0.7687	0.8385	0.7144	0.7591	0.6747	0.7072	0.6487	0.7492	0.8695	0.829	0.787	0.7452	0.8584	0.7234	0.8601
MAF	0.0111	0.0112	0.0111	0.0145	0.0111	0.0145	0.0111	0.0145	0.0145	0.0145	0.0111	0.0148	0.0111	0.0111	0.0111

P, *p*-value for HWE exact test; H, heterozygosity; PD, power of discrimination; PE, power of exclusion; PIC, polymorphism information content; MAF, minimum allele frequency for this locus.