J Forensic Sci, March 2006, Vol. 51, No. 2
doi:10.1111/j.1556-4029.2006.00091.x
Available online at: www.blackwell-synergy.com

FOR THE RECORD

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Population Data on Eight Short Tandem Repeat Loci in the Barbadian Population

POPULATION: Barbadian ($n = 186$).

KEYWORDS: forensic science, DNA typing, short tandem repeats, polymerase chain reaction, population genetics, Barbados, D16S539, D7S820, D13S317, D5S818, CSF1PO, TPOX, TH01, vWA

Whole blood drawn in EDTA vacutainer tubes from 200 unrelated individuals was kindly donated from the Queen Elizabeth Hospital blood bank and stored on Ultrastain Cards (Whatman® Inc., Newton Center, MA). DNA extraction was performed using the QIAamp DNA mini kit (Qiagen, Valencia, CA) dried blood spot protocol, according to the manufacturer's instructions. The Quantiblot® Human DNA Quantitation kit (Applied Biosystems, Foster City, CA) was used to determine the quantity of extracted DNA, as per manufacturer's instructions. Amplification was performed using the reagents contained in the PowerPlex® 1.1 System (Promega, Madison WI), according to the manufacturer's instructions. Postelectrophoresis amplified products were detected using the Hitachi FMBIO® II Fluorescent Scanner (Hitachi Software Engineering Ltd., San Francisco, CA). Results were

TABLE 1—*Allele frequency data on eight STR loci in a sample population from Barbados.*

Allele	D16S539 ($n = 167$)	D7S820 ($n = 182$)	D13S317 ($n = 184$)	D5S818 ($n = 183$)	CSF1PO ($n = 173$)	TPOX ($n = 183$)	TH01 ($n = 181$)	vWA ($n = 184$)
5	—	—	—	—	—	—	0.009	—
6	—	—	—	—	0.003	0.09	0.169	—
7	—	0.009	—	0.006	0.075	0.025	0.398	—
8	0.045	0.209	0.019	0.060	0.075	0.358	0.202	—
9	0.186	0.110	0.014	0.022	0.029	0.189	0.119	—
9.3	—	—	—	—	—	—	0.088	—
10	0.177	0.363	0.035	0.087	0.251	0.082	0.017	—
11	0.299	0.217	0.283	0.243	0.257	0.221	—	0.009
12	0.219	0.082	0.399	0.344	0.266	0.036	—	—
13	0.111	0.0137	0.174	0.224	0.035	—	—	0.022
14	0.024	—	0.073	0.014	0.009	—	—	0.054
15	—	—	0.003	—	—	—	—	0.171
16	—	—	0.003	—	—	—	—	0.285
17	—	—	—	—	—	—	—	0.193
18	—	—	—	—	—	—	—	0.163
19	—	—	—	—	—	—	—	0.065
20	—	—	—	—	—	—	—	0.030
21	—	—	—	—	—	—	—	0.009
MP	0.069	0.094	0.124	0.096	0.087	0.084	0.100	0.058
PD	0.931	0.906	0.876	0.904	0.913	0.916	0.900	0.942
PIC	0.77	0.72	0.68	0.72	0.75	0.74	0.72	0.79
PE	0.608	0.542	0.491	0.535	0.575	0.571	0.538	0.638
HWE								
Exact test	0.050	0.735	0.134	0.790	0.342	0.275	0.370	0.629
χ^2	0.644	0.998	0.522	0.999	0.995	0.934	0.984	0.206
Homozygosity test	0.001	0.546	0.371	0.933	0.225	0.033	0.690	0.412

MP, match probability; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion.

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analyzed using the STaR Call™ Allele Calling Software. The genotypes obtained from the STaR Call™ Software were imported into the Power Stats V12 program for each locus.

Possible divergence from Hardy–Weinberg expectations (HWE) was tested by calculating the unbiased estimate of the expected homozygote/heterozygote frequencies (1) and the exact test (2), based on 2,000 shuffling experiments. An interclass correlation criterion (3) for two-locus associations was used for detecting disequilibrium between the STR loci.

The program to perform these tests (DNA type) was developed and kindly provided by R. Chakraborty (University of Cincinnati). Table 1 displays the results of the study. Based on the exact test there were no detectable departures from HWE.

The complete data are available to any interested researcher upon request.

Acknowledgments

We are thankful to the staff of the DNA section of the Forensics Sciences Centre. In particular, the contributions of Joy Forde for carrying out the sample preparation and Tamara Forde for technical advice and assistance. This study was funded by the Barbados Forensic Sciences Centre.

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