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Allele Frequencies of 15 STR Loci in the Population of the City of Quito, Ecuador

POPULATION: Quito City Population (Ecuador, South America, $n = 116\text{--}207$).

KEYWORDS: forensic science, DNA typing, Quito population, short tandem repeats, population genetics, D3S1358, THO1, D21S11, D18S51, PENTA E, D5S818, D13S317, D7S820, D16S539, CSF1PO, PENTAD, VWA, D8S1179, TPOX, FGA

Whole blood obtained by venipuncture was collected from unrelated individuals residing in Quito City, Ecuador, South America, using one 1.2-mm micropunch of bloodstains collected on FTA Classic Cards (Whatman FTA[®]), and the DNA was extracted following the manufacturer's directions. PCR amplification of the 15 STR loci (D3S1358, THO1, D21S11, D18S51, PENTA E, D5S818, D13S317, D7S820, D16S539, CSF1PO, PENTAD, VWA, D8S1179, TPOX, FGA) was performed using the PowerPlex[®]16 System kit (Promega Corp., Madison, WI) (1) (PE-Biosystems, Foster City, CA) following the manufacturer's protocol. The amplified products were separated and detected using the ABI Prism[®] 310 genetic analyzer (Applied Biosystems, Foster City, CA) using the ABI Prism GeneScan analysis software version 3.1 and Genotyper DNA fragment analysis software version 2.5.2 (2).

The data were analyzed using Power-Stats (3). Allele frequencies and other relevant information from analysis of the 15 STR loci are given in Table 1. The complete dataset is available to any interested researcher upon request, or can be downloaded from the following World Wide Web site: <http://www.fcv.unlp.edu.ar/info-general/publicaciones/pdf/supplementary.pdf>.

Acknowledgment

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TABLE 1—STR allele frequencies of the 15 loci in the population of the city of Quito (Ecuador).

Allele	D3S1358	THO1	D21S11	D18S51	PENTA E	D5S818	D13S317	D7S820	D16S539	CSFIPO	PENTAD	VWA	D8S1179	TPOX	FGA
5	—	—	—	—	2.3%	—	—	—	—	—	—	—	—	—	—
6	—	36.1%	—	—	—	0.3%	—	—	—	—	—	—	—	—	—
7	—	33.2%	—	—	5.6%	10.3%	—	0.3%	—	—	0.6%	—	—	—	—
8	—	7.7%	—	—	1.0%	0.7%	8.2%	4.4%	1.3%	0.7%	1.6%	—	—	50.0%	—
9	—	7.4%	—	—	0.3%	6.0%	25.2%	4.0%	20.5%	1.0%	21.1%	—	0.7%	4.3%	—
9.3	—	14.8%	—	—	—	—	—	—	—	—	—	—	—	—	—
10	—	0.6%	—	2.2%	2.3%	4.3%	9.9%	23.8%	20.1%	24.3%	27.3%	—	7.2%	2.6%	—
11	—	—	—	2.9%	6.3%	50.7%	14.9%	38.6%	25.2%	28.8%	11.4%	—	6.5%	27.6%	—
12	0.6%	—	—	8.4%	18.4%	—	21.3%	25.8%	21.8%	35.8%	16.2%	—	16.4%	15.5%	—
13	—	—	—	9.5%	4.9%	—	14.9%	3.0%	8.7%	8.3%	14.3%	—	33.3%	—	—
14	8.1%	—	—	24.8%	3.9%	—	5.3%	—	2.3%	1.0%	5.8%	3.6%	20.3%	—	—
15	47.4%	—	—	13.9%	16.4%	—	0.4%	—	—	—	1.3%	7.5%	11.8%	—	—
16	26.3%	—	—	14.6%	7.9%	—	—	—	—	—	0.3%	37.7%	3.6%	—	—
17	12.7%	—	—	12.4%	6.3%	—	—	—	—	—	—	34.4%	—	—	1.3%
18	4.9%	—	—	6.6%	7.9%	—	—	—	—	—	—	13.3%	—	—	0.9%
18.2	—	—	—	—	—	—	—	—	—	—	—	—	—	—	—
19	—	—	—	2.2%	3.9%	—	—	—	—	—	—	2.6%	—	—	9.9%
20	—	—	—	1.1%	6.6%	—	—	—	—	—	—	1.0%	—	—	6.9%
21	—	—	—	0.4%	3.0%	—	—	—	—	—	—	—	—	—	9.1%
22	—	—	—	0.4%	3.0%	—	—	—	—	—	—	—	—	—	12.1%
23	—	—	—	0.4%	—	—	—	—	—	—	—	—	—	—	13.8%
24	—	—	—	0.4%	—	—	—	—	—	—	—	—	—	—	14.7%
25	—	—	—	—	—	—	—	—	—	—	—	—	—	—	15.5%
26	—	—	—	—	—	—	—	—	—	—	—	—	—	—	10.3%
27	—	—	1.70%	—	—	—	—	—	—	—	—	—	—	—	2.6%
28	—	—	7.50%	—	—	—	—	—	—	—	—	—	—	—	2.2%
29	—	—	20.80%	—	—	—	—	—	—	—	—	—	—	—	0.9%
29.2	—	—	0.80%	—	—	—	—	—	—	—	—	—	—	—	—
30	—	—	17.50%	—	—	—	—	—	—	—	—	—	—	—	—
30.2	—	—	1.70%	—	—	—	—	—	—	—	—	—	—	—	—
31	—	—	11.70%	—	—	—	—	—	—	—	—	—	—	—	—
31.2	—	—	18.30%	—	—	—	—	—	—	—	—	—	—	—	—
32	—	—	0.80%	—	—	—	—	—	—	—	—	—	—	—	—
32.2	—	—	14.20%	—	—	—	—	—	—	—	—	—	—	—	—
33.2	—	—	5%	—	—	—	—	—	—	—	—	—	—	—	—
<i>n</i>	154	155	119	137	152	151	141	149	149	144	154	154	207	152	116
<i>h_o</i>	62.30	71.00	81.50	81.00	86.80	65.60	87.20	77.50	77.2	71.50	79.90	69.50	79.70	63.80	86.20
<i>h_e</i>	68.33	72.79	84.40	85.09	90.58	68.46	83.06	72.55	80.35	72.53	82.02	71.67	80.74	64.93	89.08
PD	0.852	0.877	0.9491	0.960	0.977	0.859	0.943	0.872	0.931	0.870	0.938	0.873	0.930	0.821	0.9686
PE	0.320	0.443	0.6274	0.618	0.731	0.363	0.739	0.468	0.548	0.452	0.597	0.420	0.594	0.339	0.7188

—, allele not detected or not applicable; *n*, sample size; *h_o*, observed heterozygosity (%); *h_e*, expected heterozygosity (%); PD, power of discrimination; PE, power of exclusion.