

## FOR THE RECORD

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# Eight Short Tandem Repeats (STR) Frequencies for Descendants from Terena Indigenous Brazilian Group

**POPULATION:** descendants from Terenas an indigenous group

**KEYWORDS:** forensic science, short tandem repeats, population data, Terena, Brazil

Allele distribution on the basis of eight short tandem repeats (STR) loci CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317, and D5S818 has been performed for direct descendants from Terena population (a Brazilian ethnic group). Terenas are classified as from guaná ethnic group, speaking Aruak language (1). They live in Mato Grosso do Sul, a Brazil's Central State.

DNA was extracted from buccal swab samples from 81 individuals by organic extraction methods and ethanol precipitation according to Budowle et al. (2). DNA quantification of each sample was performed using the GeneQuant pro RNA/DNA/calculator

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(Amersham Pharmacia Biotech). PCR amplification reactions were prepared using 5 ng human genomic DNA, 10X Taq Gold Buffer, 10X PowerPlex primers (CSF1PO, TPOX, TH01, vWA, D16S539, D7S820, D13S317 and D5S818) Fluorescent Systems (Promega Corporation, Madison, WI) and 2U Taq Gold to 25  $\mu$ L final volume.

The amplifications were performed in a Perkin-Elmer GeneAmp PCR System 9600 Thermal Cycler. The electrophoretical separation of STR-PCR reaction products was performed in a 34 cm long, 0.4 mm thick 4.5% polyacrylamide denaturing gel. Allelic Ladder standard was loaded between each two samples and internal standard was included in each sample for size determination. The fluorescent signals were detected using FMBIO II Fluorescent Scanner (Hitachi Software Engineering American, LTD., San Francisco, CA).

TABLE 1—Allele frequencies of eight STR loci in the descendants from Terena population.

Allele	CSF1PO	TPOX	TH01	vWA	D16S539	D7S820	D13S317	D5S818
6	...	0.015	0.247					
7	0.021	0.000	0.482		0.019			0.077
8	...	0.477	0.050		0.153	0.042	0.088	0.021
9	0.043	0.053	0.031		0.211	0.118	0.233	0.035
9,3	...	...	0.181		...	...	...	...
10	0.239	0.022	0.010		0.192	0.271	0.008	0.042
11	0.347	0.325			0.326	0.389	0.120	0.366
12	0.282	0.106			0.038	0.161	0.330	0.190
13	0.065				0.057	0.016	0.161	0.267
14				0.226			0.056	
15				0.073				
16				0.413				
17				0.213				
18				0.033				
19				0.040				
No. of Chr	46	132	162	150	52	118	124	142
H <sub>(ob)</sub>	0.739	0.727	0.645	0.693	0.730	0.898	0.822	0.690
H <sub>(Ex)</sub>	0.751	0.675	0.693	0.749	0.803	0.738	0.797	0.758
P	0.208	0.068	0.166	0.001	0.221	0.003	0.012	0.157

H<sub>(ob)</sub>: observed heterozygozity.

H<sub>(Ex)</sub>: Expected heterozygozity.

P-Hardy-Weinberg equilibrium, exact test.

The relative allele frequencies as well as the observed heterozygosity rates for each locus were calculated from the observed number of each genotype in the sample set. Some DNA samples could not be optimally amplified at some loci, and consequently, sample sizes differ from one locus to the other. Possible divergence from Hardy-Weinberg Expectation (HWE) was calculated by exact test using Arlequin package (3).

The complete dataset is available upon request.

#### *Acknowledgments*

We thank directors from Sullivan Silvestre Oliveira Elementary School for providing permission to samples collection. This research was supported by FAPERJ grant # E26-170.412/99.

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