

## FOR THE RECORD

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# Allele Frequencies for the 13 CODIS STR Loci in a Sample of Southern Croatians

**POPULATION:** Croatian ( $n = 105$ ) results obtained on 101 or 103.

**KEYWORDS:** forensic science, DNA typing, short tandem repeat, polymerase chain reaction, population genetics, Split Croatia, D3S1358, vWA03, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX, CSF1PO

Whole blood obtained by venipuncture was collected in EDTA vacutainer tubes from individuals attending Split Hospital, Split, Croatia. Blood was dried onto clean cotton cloth, sealed in individual plastic bags and transported to the United States for testing. Approximately 3 mm squares were extracted using Chelex (1). The DNA was not quantified. PCR amplification was performed using the AmpF $\ell$ STR Profiler Plus<sup>TM</sup> and Cofiler<sup>TM</sup> PCR amplification kits (PE-Biosystems, Foster City, CA) following the manufacturer's protocol using 2  $\mu$ L of sample. The amplified products were separated and detected using the ABI Prism<sup>TM</sup> 377 DNA sequencer (PE-Biosystems, Foster City, CA). Allele frequencies and goodness of fit tests were performed using Excel spread sheets. Each locus ( $n = 13$ ) was tested for the following: Hardy-Weinberg Global Chi-square goodness of fit using all genotypes with expected values greater than 1.0, all other genotypes were pooled to form a residual class ( $df = \text{number of genotypes minus the number of al-$

leles)(p1);  $T$  statistic testing  $\theta = 0$  recommended by NRC 2 (2)(p2); and the Chi-square comparing expected and observed total homozygosity and heterozygosity ( $df = 1$ )(p3). The Bonferroni corrected threshold was 0.0038. No loci exceeded the Bonferroni threshold; only one locus (D8S1179) was significant ( $p < 0.05$ ) for one of three tests of deviation from Hardy-Weinberg equilibrium due to an excess of heterozygotes and deficiency of homozygotes prior to the Bonferroni correction for multiple tests.

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Complete data sets can be obtained by contacting [mschanfield@netscape.net](mailto:mschanfield@netscape.net)

### References

1. Walsh PS, Metzger DA, Higuchi R. ChelexR 100 as a medium for simple extraction of DNA for PCR-based typing from forensic material. *Bio Techniques* 1991;10:506-13.
2. Robertson A, Hill WG. Deviations from Hardy-Weinberg proportions: sampling variances and use estimation of inbreeding coefficients. *Genetics* 1984;107:703-18.

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TABLE 1—Allele frequencies in a Southern Croatian sample (n = 105).

D3S1358 (n = 101)		vWA031 (n = 102)		FGA (n = 103)		D8S1179 (n = 103)		D21S11 (n = 103)		D18S51 (n = 103)			
14*	0.0693	14*	0.1520	18*	0.0146	8*	0.0340	26*	0.0049	10*	0.0194		
15*	0.2673	15*	0.0931	19*	0.0777	9*	0.0146	27*	0.0291	11*	0.0097		
16*	0.3218	16*	0.1961	20*	0.1019	10*	0.0728	28*	0.1553	12*	0.1214		
17*	0.1683	17*	0.2696	21*	0.1699	11*	0.0388	29*	0.1942	13*	0.1117		
18*	0.1683	18*	0.1765	22*	0.1845	12*	0.1165	29.2*	0.0049	14*	0.1893		
19*	0.0050	19*	0.0980	22.2*	0.0194	13*	0.3107	30*	0.2136	15*	0.1456		
		20*	0.0147	23*	0.1408	14*	0.2573	30.2*	0.0534	16*	0.1408		
				23.2*	0.0146	15*	0.1359	31*	0.0534	17*	0.1019		
				24*	0.1359	16*	0.0194	31.2*	0.1117	18*	0.0680		
				25*	0.0874			32*	0.0146	19*	0.0534		
				26*	0.0388			32.2*	0.1214	20*	0.0097		
				27*	0.0097			33.2*	0.0388	21*	0.0291		
				28*	0.0049			34.2*	0.0049				
p1	0.529	0.626		0.599		0.011*		0.108		0.668			
p2	0.569	0.560		0.709		0.756		0.428		0.328			
p3	0.501	0.653		0.463		0.461		0.840		0.491			
D5S818 (n = 103)		D13S317 (n = 103)		D7S820 (n = 101)		D16S539 (n = 101)		TH01 (n = 101)		TPOX (n = 103)		CSF1PO (n = 101)	
7*	0.0049	8*	0.0922	7*	0.0198	8*	0.0099	6*	0.1980	8*	0.5446	9*	0.0347
9*	0.0340	9*	0.0922	8*	0.1782	9*	0.0891	7*	0.1287	9*	0.0941	10*	0.2228
10*	0.0437	10*	0.0874	9*	0.1634	10*	0.0446	8*	0.1733	10*	0.0495	11*	0.2921
11*	0.3447	11*	0.3786	9.1*	0.0050	11*	0.3317	8.3*	0.0050	11*	0.2871	12*	0.3564
12*	0.3981	12*	0.2379	10*	0.2228	12*	0.2723	9*	0.2129	12*	0.0248	13*	0.0743
13*	0.1748	13*	0.0534	11*	0.1931	13*	0.2228	9.3*	0.2673			14*	0.0099
		14*	0.0534	12*	0.1782	14*	0.0297	10*	0.0149			15*	0.0099
		15*	0.0049	13*	0.0347								
				15*	0.0050								
p1	0.657	0.378		0.869		0.872		0.510		0.660		0.469	
p2	0.450	0.217		0.487		0.772		0.098		0.905		0.380	
p3	0.525	0.593		0.694		0.530		0.063		0.260		0.797	

\* Bonferroni correction for multiple tests ( $n = 13$ ) is  $0.05/13 = 0.0038$ . No value exceeds that threshold.