J Forensic Sci, Sept. 2005, Vol. 50, No. 5
Paper ID JFS2005185
Published 3 Aug. 2005
Available online at: www.astm.org

FOR THE RECORD

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Allele Frequency Distribution of the D1S80 VNTR Locus in a Tunisian Population

POPULATION: Tunisian, Arab, North African

KEYWORDS: forensic science, DNA typing, population genetics, Tunisia, VNTR, polymerase chain reaction, D1S80 locus, alleles distribution

EDTA blood samples were collected from 200 unrelated Tunisian healthy adults coming from different regions of the country. All subjects gave their informed consent. DNA was extracted from leucocytes by the standard phenol chloroform technique. Amplification of the D1S80 was carried out by polymerase chain reaction (PCR) using the primers described by Kasai et al. (1). Reaction was performed in a total volume of 50 μL containing 200 ng genomic DNA, 10 mM Tris-Hcl (pH 8.3), 50 mM Kcl, 1.5 mM MgC12, 2.5 units of AmplitaqTM polymerase (Perkin Elmer-Cetus USA), 200 μM dNTP and 1μM of each primer. The thermocycling used GeneAmpR PCR System 9700 PE Applied Biosystems. PCR fragments were analysed using a 3% agarose gel electrophoresis (Agarose LE Promega, France); a D1S80 allelic ladder (Perkin Elmer Cetus) was applied on the gel at two-lane intervals to allow correct sizing of the amplified fragments. DNA fragments were visualised by ethidium bromide staining. Statistical analysis was performed using The TFPGA program version 1.3 (2).

The discrimination power (DP) and the exclusion power (EP) were calculated as previously reported (3). A trimodal pattern was observed, the most frequent alleles were those of 24, 18 and 28 repeats. These results are different from most population reports that show two peaks at alleles 18 and 24. The distribution of D1S80 genotypes does not deviate from HWE ($p > 0.05$) based on the homozygosity test (Chi-square = 102.521; df = 210; $P = 1$), log likelihood ratio test (G-square = 0.2961; df = 1; $P = 0.5864$) and the exact test ($p = 0.9401$, SE = 0.00807). We have also tested for HWE by calculating the unbiased estimate of expected heterozygote frequency. The observed heterozygosity was 79% that was comparable to expected heterozygosity of 81.3%, thus providing evidence that the population followed the Hardy-Weinberg equilibrium expectation. The DP (0.946) and the EP (0.581) confirm that this locus is very informative for forensic discrimination.

The complete dataset is available to any interested party at http://www.websamba.com/genetique-chaabouni/genotype.asp

TABLE 1—*D1S80 alleles frequency data for Tunisian population (n = 200).*

Allele	Number	Frequency	SD*	Allele	Number	Frequency	SD
13		...		28	52	13.00	0.0168
14		...		29	40	10.00	0.0150
15		...		30	3	00.75	0.0043
16				31	8	02.00	0.0070
17	5	01.25	0.0055	32	3	00.75	0.0043
18	59	14.75	0.0177	33	1	00.25	0.0024
19				34	13	03.25	0.0088
20	5	01.25	0.0055	35	2	00.50	0.0035
21	7	01.75	0.0065	36			
22	18	04.50	0.0103	37	1	00.25	0.0024
23	1	00.25	0.0024	38	1	00.25	0.0024
24	146	36.50	0.0240	39			
25	10	02.50	0.0078	40			
26	7	01.75	0.0065	>41	16	04.00	0.0097
27	2	00.50	0.0035				

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TABLE 2—*D1S80 genotypes frequency data for Tunisian population (n = 200).*

Genotype	Observed	Expected	Frequency	Genotype	Observed	Expected	Frequency	Genotype	Observed	Expected	Frequency
17-24	3	1.825	0.0150	21-34	1	0.227	0.0050	25-25	1	0.125	0.0050
17-28	1	0.650	0.0050	22-22	1	0.405	0.0050	25-28	1	1.300	0.0050
17-29	1	500	0.0050	22-24	8	6.570	0.040	26-28	2	0.910	0.010
18-18	6	4.361	0.030	22-28	1	2.340	0.0050	26-29	1	0.700	0.0050
18-20	1	0.737	0.0050	22-29	2	1.800	0.010	26->41	2	0.280	0.010
18-21	1	1.032	0.0050	22-34	1	0.585	0.0050	28-28	4	3.380	0.020
18-22	3	2.655	0.0150	22->41	1	0.720	0.0050	28-29	5	5.200	0.0250
18-24	22	21.535	0.1100	23-24	1	0.365	0.50%	28-31	1	1.040	0.0050
18-25	2	1.475	0.0100	24-24	25	26.645	0.1250	28-34	2	1.690	0.010
18-26	1	1.032	0.0050	24-25	4	3.650	0.020	28-38	1	0.130	0.0050
18-28	5	7.670	0.0250	24-26	1	2.555	0.0050	28->41	3	2.080	0.015
18-29	5	5.900	0.0250	24-27	2	0.730	0.010	29-29	2	2.000	0.010
18-30	1	0.442	0.0050	24-28	19	18.980	0.095	29-31	1	0.800	0.0050
18-34	1	1.917	0.0050	24-29	18	14.600	0.090	29-32	1	0.300	0.0050
18->41	5	2.360	0.0250	24-30	2	1.095	0.010	29-35	1	0.200	0.0050
20-24	1	1.825	0.0050	24-31	2	2.920	0.010	29->41	1	1.600	0.0050
20-28	2	0.650	0.0100	24-32	2	1.095	0.010	31-31	1	0.080	0.0050
20-34	1	0.162	0.0050	24-33	1	0.365	0.0050	31-34	1	0.260	0.0050
21-24	2	2.555	0.0100	24-24	4	4.745	0.020	34-34	1	0.211	0.0050
21-25	1	0.175	0.0050	24-35	1	0.730	0.0050	>41->41	1	0.320	0.0050
21-28	1	0.910	0.0050	24-37	1	0.365	0.0050				
21-31	1	0.140	0.0050	24->41	2	5.840	0.010				

Homozygosity test (Chi-square = 102.521; df = 210; $P = 1$),
Log likelihood ratio test (G-square = 0.2961; df = 1; $P = 0.5864$)
Exact test ($p = 0.9401$, SE = 0.00807).
Observed heterozygosity: 79%. Expected heterozygosity: 81.3%.