E. Raczek,<sup>1</sup> Ph.D.

## Population Data on Three STR Loci in the Upper Silesia (Poland)

**KEYWORDS:** forensic science, DNA typing, population genetics, short tandem repeat, Upper Silesia, Poland

Blood samples from unrelated individuals were extracted using Kunkel's et al. (1) method with small modifications. DNA samples (2 to 5 ng) were amplified and typed according to manufacturer's instructions (2). Data were analyzed using a program provided by P.M. Miller (Northern Arizona University, Flagstaff). Ht<sub>obs.</sub>, Ht<sub>exp.</sub>, PD, MEC, MEP and PIC were calculated using program provided by G.M. Dudek (HTS, Częstochowa, Poland). The parts of these data (for 101 individuals at the FESFPS locus and for 226 individ-

<sup>1</sup> Department of Forensic Medicine, Silesian Academy of Medicine, Katowice, Poland. uals at the VWA locus) were presented (3,4). The dataset can be accessed at: e-mail: medsad@slam.katowice.pl

## References

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Allele	F13A01	FESFPS	VWA
Ν	66	230	263
4	0.0758		
5	0.1591		
6	0.3106		
7	0.3939	0	
8	0.0227	0.0217	
9	0	0.0022	
10		0.2522	
11	0	0.4261	
12	0	0.2391	
13	0	0.0587	0.0057
14	0.0152	0	0.1027
15	0.0227		0.0951
16	0		0.1920
17			0.2738
18			0.2433
19			0.0760
20			0.0114
$X_{df}^2$ test	$X_{21}^2 = 19.94$ $p = 0.5245$	$X_{15}^2 = 17.36$ $p = 0.2975$	$X_{28}^2 = 33.33$ $p = 0.2235$
Exact test (Monte Carlo)	$p = 0.4637 \pm 0.0468$	p = 0.0837 = 0.0100	$p = 0.2268 \pm 0.0105$
Ht <sub>obs.</sub>	0.7215	0.7304	0.8555
Htexp	0.7424	0.6953	0.8050
PD	0.8728	0.8527	0.9334
MEC	0.4785	0.4388	0.6136
MEP	0.4623	0.4210	0.6083
PIC	0.6694	0.6403	0.7755

 TABLE 1—Allele frequencies in the Upper Silesian population (Poland).

N = Number of individuals analyzed.