FOR THE RECORD

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

KEYWORDS: forensic science, DNA typing, population genetics, short tandem, 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, AZ). $Ht_{obs.}$, $Ht_{exp.}$, PD, MEC, MEP, and PIC were calculated using program provided by G. M. Dudek (Technical University of Częstochowa, Poland). The dataset can be accessed at: e-mail: medsad@slam.katowice.pl.

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References

1. Kunkel LM, Smith KD, Bayer SH, Borgaonkar DS, Wachtel SS, Miller OJ, et al. Analysis of human Y-chromosome—specific reiterated DNA in chromosome variants. Proc Natl Acad Sci 1977;74:1245–9.
2. Promega Corp. GenePrint™ STR Systems (Silver Stain Detection), Revised ed., June, 1998.

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

Allele	D13S317	D7S820	D16S539
N	178	178	154
7	…	0.0084	…
8	0.1236	0.2051	0.0130
9	0.0983	0.1517	0.0812
10	0.0618	0.2416	0.0292
11	0.3511	0.2079	0.3312
12	0.2191	0.1545	0.3149
13	0.0815	0.0309	0.2011
14	0.0646	…	0.0260
15	…	…	0.0032
X^2_{df} test	$X^2_{21} = 20.46$ $p = 0.4918$	$X^2_{21} = 16.57$ $p = 0.7367$	$X^2_{28} = 24.85$ $p = 0.6359$
exact test (Monte Carlo)	$p = 0.5977 \pm 0.02$	$p = 0.6555 \pm 0.00$	$p = 0.4920 \pm 0.00$
$Ht_{obs.}$	0.7809	0.7865	0.7662
$Ht_{exp.}$	0.7914	0.8108	0.7447
PD	0.9290	0.9348	0.8908
$PD_{combined}$	…	0.9995	…
MEC	0.6017	0.6159	0.5120
$MEC_{combined}$	…	0.9253	…
MEP	0.5831	0.6192	0.5008
PIC	0.7626	0.6159	0.6995

N = number of individuals analyzed.