FOR THE RECORD

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Population Data on the D1S80 Locus in the Upper Silesia (Poland)

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Blood samples from unrelated individuals were extracted using Kunkel's et al. (1) method with small modifications. DNA samples (10 to 15 ng) were amplified and typed according to manufacturer's instructions (2). Data were analyzed using a program provided by M.P. Miller (Northern Arizona University, Flagstaff). $Ht_{obs.}$, $Ht_{exp.}$, PD, MEC, MEP, and PIC were calculated using a program provided by G.M. Dudek (HPS, Częstochowa, Poland). A part of these data (for 260 individuals) was published (3). The dataset can be accessed at: e-mail: medsad@slam.katowice.pl.

References

1. Kunkel LM, Smith KD, Bayer SH, Borgaonkar DS, Wachtel SS, Miller OJ, et al. Analysis of human Y-chromosome—specific reiterated DANN in chromosome variants. Proc Natl Acad Sci 1977;74:1245–9.
2. AmpliFLP™ D1S80 PCR Amplification Kit, Perkin Elmer, 1995.
3. Raczek E. Polimorfizm ukladu D1S80 w populacji Górnego Śląska; jego przydatność w badaniach spornego ojcostwa. Arch Med Sąd i Krym 2000;50:57–65.

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

Allele	D1S80
N	665
14	0.0008
15	0.0008
16	0.0015
17	0.0038
18	0.2203
19	0.0023
20	0.0301
21	0.0143
22	0.0519
23	0.0143
24	0.3556
25	0.0805
26	0.0211
27	0.0045
28	0.0496
29	0.0308
30	0.0150
31	0.0729
32	0.0015
33	0.0030
35	0.0008
36	0.0053
37	0.0180
39	0.0008
44	0.0008

X_{df}^2 test: $X_{300}^2 = 288.2194$, p = 0.6773
Exact test (Markov chain): p = 0.5228

$Ht_{obs.} = 0.8075$	PD = 0.9422	MEP = 0.6089
$Ht_{exp.} = 0.8053$	MEC = 0.6416	PIC = 0.7850

N = Number of individuals analyzed.