



Population genetics of the Identifiler system in Poland

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Abstract. Allele frequency data and forensic efficiency parameters for 15 Identifiler STR loci: D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA, were estimated from a sample of 125 unrelated individuals in central Poland. The accordance with the Hardy and Weinberg equilibrium (HWE) for all analyzed loci was proven. The combined power of discrimination (PD) and probability of identity (DI) were greater than 0.9999999999999999 and 6.7×10^{-18} , respectively, which proves that this multiplex system is an excellent tool for forensic casework. © 2003 Elsevier B.V. All rights reserved.

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1. Introduction

One of the two commercially available multiplex systems enabling a simultaneous variability analysis of the 15 different autosomal loci and AMG on the basis of the five-color detection is the Identifiler system [1,2]. The purpose of this work was to establish the allele frequencies for the 15 STR-loci included in this system, i.e., D3S1358, vWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01 and FGA in a Polish population sample. The evaluation of Hardy–Weinberg equilibrium (HWE) and the calculation of statistical parameters were another aim of this study.

2. Materials and methods

The database was obtained from blood samples taken from 125 unrelated healthy individuals at the Department of Forensic Medicine, Medical University of Lodz, Poland. Genomic DNA was isolated by the salt extraction procedure as described by Lahiri and Numberger [3]. Amplification was carried out using the Identifiler kit according to the User's Manual (Applied Biosystems). PCR products were detected in 5-dye florescent system and genotyped using GeneScan version 3.7 on the ABI Prism 377 sequencer with

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Table 2

The HWE evaluation and the forensic efficiency parameters for the 15 STR loci included in the Identifiler system in the population of central Poland

Locus	D8S1179	D21S11	D7S820	CSF1PO	D3S1358	TH01	D13S317	D16S539	D2S1338	D19S433	vWA	TPOX	D18S51	D5S818	FGA
HWE	0.08156	0.47375	0.38188	0.35000	0.96938	0.21688	0.41250	0.85938	0.72500	0.51750	0.53750	0.15063	0.85500	0.82750	0.19625
H _{obs}	0.80500	0.83200	0.78400	0.74400	0.81600	0.72800	0.78400	0.76800	0.86400	0.76000	0.81600	0.61600	0.85600	0.76000	0.84800
H _{exp}	0.79868	0.85899	0.80553	0.73173	0.79598	0.77671	0.77725	0.74210	0.88103	0.76517	0.80064	0.60392	0.87271	0.72623	0.86786
PIC	0.76796	0.83934	0.77447	0.68069	0.76076	0.73815	0.74380	0.69543	0.86494	0.73354	0.76856	0.55090	0.85492	0.67866	0.84942
PD	0.93065	0.96292	0.93308	0.87834	0.92503	0.91329	0.91865	0.88824	0.97243	0.91484	0.93009	0.79056	0.96860	0.87878	0.96664
DI	0.02707	0.05171	0.08323	0.11430	0.06148	0.12784	0.08323	0.09516	0.03448	0.10138	0.06148	0.23829	0.03849	0.10138	0.04270

HWE (Hardy and Weiberg equilibrium)—probability values of exact test based on 2300 shufflings, PIC polymorphism information content, H_{obs}—observed heterozygosity, H_{exp}—expected heterozygosity, PD—power of discrimination, DI—discrimination index. The combined values for the 10 loci of: PD>0.9999999999999999, DI=6.729 × 10⁻¹⁸.

GeneScan-500 LIZ as internal lane standard. Allele frequencies were calculated from the number of each genotype obtained in the sample set. Pairwise interclass correlation tests were performed for all possible two-locus combination. The evaluation of HWE was tested by the exact test with the computer programme GDA [4]. The evaluation of forensic efficiency parameters was estimated according to the appropriate designs: heterozygosity observed (H_{obs}), heterozygosity expected (H_{exp}) [5], polymorphism information content [6], power of discrimination [7], discrimination index [8].

3. Results and discussion

The data on the allele frequencies of the ten STR loci in the sample of population from central Poland are collected in Table 1. No pairwise correlation (not shown) was observed between the alleles of the 15 loci. Based on the results of the exact test, no deviation from the HWE was observed at any of the 15 loci. The 10 investigated loci proved to be highly polymorphic, but the most informative seems to be the following loci: D2S1338, D18S51, D21S11 and FGA (Table 2). All of the 15 loci possess the combined power of discrimination greater than 0.9999999999999999 and a combined probability that two randomly selected individuals share the same 10-locus profile is 6.7×10^{-18} . The observed heterozygosities ranged from 0.616 (TH01) to 0.864 (D2S1338) are close to those expected.

4. Conclusion

The 15 DNA STR loci included in the Identifiler multiplex possess a highly discriminating power in forensic casework in the population of central Poland. The allele frequency data will be applied for statistical evaluation of the DNA evidence in human identification as well as healthy population database for clinical studies.

Acknowledgements

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References

- [1] Paternity testing workshop of the English Speaking Working Group of the ISFG, 2003 (draft report).
- [2] A. Barbaro, P. Cormaci, G. Falcone, A. La Marca, A. Barbaro, Population genetic study of 15 STRs loci using AmpF/STR Identifiler™ kit, *Prog. Forensic Genet.* 9 (2003) 259–266.
- [3] D.K. Lahiri Jr., J.I. Nurnberger, A rapid non enzymatic method for RFLP studies, *Nucleic Acids Res.* 19 (1991) 5444.
- [4] P.O. Lewis, D. Zaykin, Genetic Data Analysis, Version 1.1, 2003, available at: <http://lewis.eeb.unconn.edu/lewishome/sofftware.html>.
- [5] M. Nei, A.K. Roychoudhury, Sampling variances of heterozygosity and genetic distance, *Genetics* 76 (1974) 379–390.
- [6] D. Botstein, R.L. White, M. Skolnick, R.W. Davis, Construction of genetic linkage map in man using restriction fragment length polymorphism, *Am. J. Hum. Genet.* 32 (1980) 314–331.
- [7] The Evaluation of Forensic DNA Evidence, National Research Council Report, vol. II, National Academy Press, Washington, DC, 1996, pp. 96–97.
- [8] Z. Wong, V. Wilson, I. Patel, S. Povey, A.J. Jeffreys, Characterization of a panel of highly variable minisatellites cloned from human DNA, *Ann. Hum. Genet.* 51 (1987) 269–288.