

Hungarian population data for 11 PCR-based polymorphisms

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INTRODUCTION

Before introducing any new genetic marker into forensic casework, population surveys are needed in the relevant population samples. The legal DNA work requires highly informative polymorphic markers, and also requests sufficiently large database for the systems used. Considering these demands, we carried out population genetic surveys for 11 PCR-based polymorphic loci LDLR, GYPA, HBGG, D7S8, GC, HLA-DQ α , D1S80, ApoB3', HUMVWFA31, HUMTH01, and HUMFES/FPS. In this study we present data for these systems in population samples of at least 244 unrelated Hungarian Caucasian individuals.

MATERIALS AND METHODS

DNA was obtained from whole liquid blood samples of 661 unrelated individuals. Amplification and typing of PM and HLA-DQ α loci were performed according to the Perkin Elmer protocol. The rest of the systems were amplified in singleplex ways [1,2], and were analysed on horizontal non-denaturing/high-resolucional PAGE followed by silver staining except ApoB3', for which agarose gel electrophoresis and ethidium bromide staining was used [3]. The Hardy-Weinberg expectations (HWE) were checked by using the heterozygosity-test [4] and the χ^2 -analysis, where the allele binning strategy [5] was applied for VNTRs and STRs.

RESULTS AND DISCUSSION

The allele frequency distributions for the 11 polymorphic loci are shown in Table 1. In Table 1 we also denoted the allele counts (n) for each system.

LDLR: We could observe all the 3 possible genotypes, the most common one was AB (50%). Statistical analyses were performed as follows: χ^2 (1df) = 0.186, P = 0.666; observed heterozygosity (h^{obs}) = 0.5000.

GYPA: All the 3 possible genotypes were found, the most common one was AB (48.8%). The results of statistical analyses: χ^2 (1df) = 0.066, P = 0.798; h^{obs} = 0.4877.

HBGG: We encountered 4 out of 6 possible genotypes with the genotype AB being the most frequent (47.1%). The statistics was calculated as follows: χ^2 (1df) = 0.441, P = 0.507; h^{obs} = 0.4877.

D7S8: All the 3 possible genotypes were detected, the most common one was AB (50%). The results of statistical calculations: χ^2 (1df) = 0.469, P = 0.493; h^{obs} = 0.5000.

GC: All the 6 possible genotypes were encountered with the genotypes AC and CC the most common ones (33.6% for both). Statistical analyses resulted as follows: χ^2 (3df) = 0.692, P = 0.875, h^{obs} = 0.5656. The 5 PM loci result a combined discrimination power (PD) of

0.994. Similarly, the combined chance of exclusion (CE) value for the 5 systems in the Hungarian Caucasian population is 0.692.

HLA-DQ α : We observed all the 21 possible genotypes with the genotype 4-4 being the most frequent (11.8%). In the statistical computations we obtained the following results: χ^2 (14df) = 9.87, $P = 0.772$; $h^{obs} = 0.793$, PD = 0.930, CE = 0.602.

D1S80: We obtained 103 different genotypes and the genotype 18-24 was the most frequent (17.2%). Statistical analyses were performed as follows: χ^2 (10df) = 8.24, $P = 0.606$; $h^{obs} = 0.8321$; PD = 0.942, CE = 0.645.

ApoB3': 56 distinct genotypes could be typed in this survey. We noticed the genotype 35-37 most frequently (18%). The results of statistical analyses: χ^2 (6df) = 1.55, $P = 0.956$; $h^{obs} = 0.7734$, PD = 0.923, CE = 0.587.

HUMVWFA31: In this population sample we distinguished between 30 genotypes with the genotype 16-17 being the most common (13.2%). Statistical results: χ^2 (21df) = 11.30, $P = 0.957$; $h^{obs} = 0.8151$, PD = 0.935, CE = 0.621.

HUMTH01: In the TH01 analysis 22 different genotypes were detected. The genotype 6-9.3 was most frequently observed (14.4%). Statistical analyses were performed as follows: χ^2 (15df) = 12.13, $P = 0.669$; $h^{obs} = 0.7847$, PD = 0.917, CE = 0.575.

HUMFES/FPS: In the course of the typing for FES/FPS we did not distinguish between the alleles 10 and 10a as well as between the alleles 11 and 11a on non-denaturing PAGE, thus 17 distinct genotypes were counted. The most frequent genotype was 10-11 with 26.5%. The results of statistical analyses: χ^2 (10df) = 9.79, $P = 0.460$; $h^{obs} = 0.6872$, PD = 0.833, CE = 0.417.

There was no significant deviation from HWE for the 11 systems based on the χ^2 -analysis and the heterozygosity-test. In a different survey [6] there was found little evidence for departures from expectations of independence of alleles across 7 loci (LDLR, GYPA, HBGG, D7S8, GC, HLA-DQ α , D1S80) in a Hungarian population sample. Validation of the independence across all the 11 loci is under investigation. Since the high degree of polymorphisms of the 11 PCR-based markers led to a combined PD = 0.999999998 and a combined CE value of 0.998 in the Hungarian population, the joint application of these systems gives an extremely informative tool to the hand of the forensic scientist.

REFERENCES

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Table 1 Allele frequency distributions for 11 PCR-based loci in Hungarian Caucasian population samples

| <i>DIS80</i> Allele | (n=1322) Frequency | <i>ApoB3'</i> Allele | (n=1156) Frequency | <i>PM loci</i> Allele | (n=488) Frequency |
|---------------------------|-----------------------|--------------------------|-----------------------|--|----------------------|
| 14 | 0.0015 | 29 | 0.0009 | LDLR A | 0.4180 |
| 16 | 0.0023 | 31 | 0.0969 | LDLR B | 0.5820 |
| 17 | 0.0045 | 33 | 0.0580 | GYPA A | 0.6004 |
| 18 | 0.2451 | 35 | 0.2457 | GYPA B | 0.3996 |
| 19 | 0.0030 | 36 | 0.0026 | HBGG A | 0.5102 |
| 20 | 0.0257 | 37 | 0.3746 | HBGG B | 0.4816 |
| 21 | 0.0242 | 39 | 0.0450 | HBGG C | 0.0082 |
| 22 | 0.0424 | 41 | 0.0112 | D7S8 A | 0.6025 |
| 23 | 0.0106 | 43 | 0.0017 | D7S8 B | 0.3975 |
| 24 | 0.3404 | 45 | 0.0095 | GC A | 0.2766 |
| 25 | 0.0620 | 47 | 0.0597 | GC B | 0.1934 |
| 26 | 0.0166 | 49 | 0.0735 | GC C | 0.5840 |
| 27 | 0.0061 | 51 | 0.0147 | | |
| 28 | 0.0620 | 53 | 0.0051 | | |
| 29 | 0.0378 | 55 | 0.0009 | | |
| 30 | 0.0113 | | | | |
| 31 | 0.0620 | | | | |
| 32 | 0.0061 | | | | |
| 33 | 0.0045 | | | | |
| 34 | 0.0023 | | | | |
| 35 | 0.0015 | | | | |
| 36 | 0.0083 | | | | |
| 37 | 0.0121 | | | | |
| 38 | 0.0008 | | | | |
| 39 | 0.0008 | | | | |
| 40 | 0.0030 | | | | |
| 41 | - | | | | |
| >41 | 0.0030 | | | | |
| | | | | <i>HLA-DQα</i> Allele | (n=726) Frequency |
| | | | | 1.1 | 0.1983 |
| | | | | 1.2 | 0.1556 |
| | | | | 1.3 | 0.0964 |
| | | | | 2 | 0.1019 |
| | | | | 3 | 0.1185 |
| | | | | 4 | 0.3292 |
| <i>HUMVWA31</i> Allele | (n=1136) Frequency | <i>HUMTH01</i> Allele | (n=734) Frequency | <i>HUMFES/FPS</i> Allele | (n=748) Frequency |
| 13 | 0.0009 | 5 | 0.0041 | 8 | 0.0134 |
| 14 | 0.1039 | 6 | 0.2139 | 9 | - |
| 15 | 0.1206 | 7 | 0.1621 | 10 | 0.2500 |
| 16 | 0.1998 | 8 | 0.1158 | 11 | 0.4532 |
| 17 | 0.2879 | 9 | 0.1853 | 12 | 0.2313 |
| 18 | 0.1954 | 9.3 | 0.3106 | 13 | 0.0481 |
| 19 | 0.0757 | 10 | 0.0082 | 14 | 0.0040 |
| 20 | 0.0132 | | | | |
| 21 | 0.0026 | | | | |