FOR THE RECORD

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Distribution of HumTPOX, HumvWA, HumTH01 Alleles in a Turkish Population Sample

Population: Marmara Region, Turkey

Keywords: forensic science, DNA typing, population genetics, short tandem repeats, polymerase chain reaction, TPOX, vWA, TH01, Marmara Region, Turkey

The samples were collected from unrelated individuals randomly selected from criminal cases. The DNA was extracted from fresh blood leucocytes, bloodstains, and single hairs by Chelex 100 method (1).

The quantity of DNA was determined (2) by using the Quantiblot® Human DNA Quantitation Kit (Perkin Elmer, Norwalk, CT).

DNA samples (1 to 2 ng) were amplified by using reagents provided in Gene Print® STR System kit (Promega, Madison, WI) according to the technical manual (Part#TMD004). PCR amplifications were carried out in a Perkin-Elmer 9700. The amplified products were separated in denaturing polyacrylamide gels according to the technical manual and visualized by silver staining (3).

Exact tests were performed by using the computer program GDA (Genetic Data Analysis, Lewis PO, Zaykin D) for checking the Hardy-Weinberg expectations. Data were analyzed by The Promega Software, POWERSTATS.

The dataset can be accessed at http://w3.gazi.edu.tr/~leyacik

References

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TABLE 1—*Observed allele frequencies and genotype values for TPOX in 80 unrelated Turkish individuals.*

Allele Frequencies		
6	1	0.006
8	81	0.506
9	15	0.094
10	10	0.063
11	47	0.294
12	12	0.038

Genotype Frequencies		
Genotypes	Number	Proportion
6–12	1	0.013
8–8	19	0.238
8–9	7	0.088
8–10	7	0.088
8–11	25	0.313
8–12	4	0.050
9–9	2	0.025
9–10	1	0.013
9–11	3	0.038
10–11	2	0.025
11–11	8	0.100
11–12	1	0.013

Ho (observed heterozygosity): 0.638.
He (expected heterozygosity): 0.647.
P* (heterozygosity): 0.856.
P† (exact test): 0.403.
PD (power of discrimination): 0.815.
PEP (excluding probability of paternity): 0.338.
MP (matching probability): 0.185.
TPI (typical paternity index): 1.38.
PIC (polymorphism information content): 0.59.
*$\chi^2 |_{df}$ based on unbiased estimate with 3200 shufflings.
† based on 3200 shufflings.

TABLE 2—*Observed allele frequencies and genotype values for VWA in 105 unrelated Turkish individuals.*

Allele Frequencies		
14	18	0.086
15	14	0.067
16	58	0.276
17	63	0.300
18	43	0.205
19	10	0.048
20	2	0.001
21	2	0.001

Genotype Frequencies		
Genotypes	Number	Proportion
14–14	2	0.019
14–16	8	0.076
14–17	2	0.019
14–18	2	0.019
14–19	2	0.019
15–15	1	0.009
15–16	3	0.029
15–17	4	0.038
15–18	5	0.048
16–16	5	0.048
16–17	20	0.190
16–18	14	0.133
16–19	3	0.029
17–17	11	0.105
17–18	11	0.105
17–19	3	0.029
17–20	1	0.009
18–18	4	0.038
18–19	2	0.019
18–20	1	0.009
21–21	1	0.009

Ho (observed heterozygosity): 0.771.
He (expected heterozygosity): 0.781.
P* (heterozygosity): 0.806.
P† (exact test): 0.146.
PD (power of discrimination): 0.906.
PEP (excluding probability of paternity): 0.547.
MP (matching probability): 0.094.
TPI (typical paternity index): 2.19.
PIC (polymorphism information content): 0.74.
*$\chi^2 |_{df}$ based on unbiased estimate with 3200 shufflings.
† based on 3200 shufflings.

TABLE 3—*Observed allele frequencies and genotype values for TH01 in 95 unrelated Turkish individuals.*

Allele Frequencies		
6	56	0.295
7	28	0.147
8	35	0.184
9	44	0.232
9.3	5	0.026
10	22	0.116

Genotype Frequencies		
Genotypes	Number	Proportion
6–6	10	0.105
6–7	6	0.063
6–8	8	0.084
6–9	14	0.147
6–9.3	2	0.021
6–10	6	0.063
7–7	2	0.021
7–8	4	0.042
7–9	7	0.074
7–10	7	0.074
8–8	4	0.042
8–9	9	0.095
8–9.3	2	0.021
8–10	4	0.042
9–9	4	0.042
9–9.3	1	0.011
9–10	5	0.053

Ho (observed heterozygosity): 0.789.
He (expected heterozygosity): 0.794.
P* (heterozygosity): 0.847.
P† (exact test): 0.831.
PD (power of discrimination): 0.921.
PEP (excluding probability of paternity): 0.580.
MP (matching probability): 0.079.
TPI (typical paternity index): 2.38.
PIC (polymorphism information content): 0.76.
*χ^2 |$_{df}$ based on unbiased estimate with 3200 shufflings.
† based on 3200 shufflings.