Allele frequencies of the STR-loci F13A01, F13B, TPOX in population sample from the Ukraine

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Before installation of PCR-technique to expert practice of such region forensic service for which genetic-population research is absent, preliminary analysis of alleles and genotype distribution in concrete population is necessary. This analysis includes the evaluation of individual genotype distribution correspondence to the equilibrium law of Hardy–Weinberg, the estimation of expected loci heterozygote (H_{exp}) and the following parameters of self-descriptiveness in selected loci: probability of casual concurrence of two unrelated persons' genotypes (probability of random match, pM), probability of distinguishing of two unrelated persons' genotypes (power of discrimination, PD), average probability of typing sample exception (mean exclusion chance, W), self-descriptiveness of a given locus polymorphism (polymorphism information content, PIC).Until now, analysis data on allele frequencies matching and polymorphism information contents of researched loci in Ukraine populations are, in general, absent, which hinders the use of DNA-typing technique for person identification.

We estimated the allele frequencies of F13A01, F13B, TPOX loci in Ukrainian population among the unrelated representatives.

Distribution of alleles and genotype frequencies is shown in Tables 1 and 2. In the investigated population, the availability 14 alleles in locus F13A01 (sample size $n = 88$) was shown. Most of those distributed have appeared the allele 7 with cleanness matching 0.3238. On locus F13B ($n = 103$) is revealed seven alleles most widespread from 9 and 10 with frequency 0.233 and 0.392, accordingly. In locus F13B ($n = 100$), eight alleles were found with the greatest frequency of 0.43 and 0.17 for alleles 8 and 11, respectively.

The alleles' frequency distributions of the F13A01, F13B and TPOX loci are rather similar to those in population groups related to other European populations in the USA and Europe.

The observable frequencies matching the genotype-investigated loci were checked upon deviation from Hardy–Wainberg equilibrium on criterions $\times 2$ and *G*-statistics.

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Character of allele inheriting and the valuation of individual genotype distribution correspondence of investigated loci are submitted to the equilibrium law of Hardy–Weinberg.

Table 1
The alleles' frequency matching loci F13A01, F13B and TPOX in Ukrainian population

Allele designation	F13A01		F13B		TPOX	
	Size (bp)	Frequency	Size (bp)	Frequency	Size (bp)	Frequency
	$n = 88$		$n = 103$		$n = 100$	
3.2		0.034				
4	283	0.1136				
5	287	0.1477				
6	291	0.1875	169	0.0873	224	0.0400
7	295	0.3238	173	0.0145	228	0.0750
8	299	0.1363	177	0.1893	232	0.4300
9	303	0.0113	181	0.2330	236	0.1550
10	307	0.0000	185	0.3920	240	0.0950
11	311	0.0056	189	0.0436	244	0.1700
12	315	0.0000	193	0.0242	248	0.0250
13	319	0.0000			252	0.0100
14	323	0.0795				
15	327	0.0284				
16	331	0.0000				
Parameters	F13A01	F13B	TPOX			
H_{obs}	0.659	0.7572	0.63			
H_{exp}	0.86547	0.85628	0.8516			
PM	0.0759	0.11735	0.1247			
PD	0.9241	0.88267	0.8753			
PIC	0.7978	0.72264	0.7392			

Table 2
Genotype frequency matching loci F13A01, F13B. TPOX

Frequency matching			Frequency matching			Frequency matching		
Genotype	Observed	Expected	Genotype	Observed	Expected	Genotype	Observed	Expected
F13A01			TPOX			F13B		
						6−6	0.0097	
3.2−3.2	0.0114		6−6	0.03		6−8	0.0291	
3.2−4	0.0114		6−8	0.02		6−9	0.0679	
3.2−5	0.0114		6−9	0.03		6−10	0.0679	
3.2−6	0.0114		7−7	0.04		7−9	0.0194	
3.2−15	0.0114		7−8	0.02		7−10	0.0097	
4−4	0.0114		7−10	0.02		8−8	0.0291	
4−5	0.0227		8−8	0.2		8−9	0.0582	
4−6	0.0568		8−9	0.09		8−10	0.2135	
4−7	0.1023		8−10	0.03		8−11	0.0097	
5−5	0.0455		8−11	0.24		8−12	0.0097	
5−6	0.0682		8−12	0.03		9−9	0.0485	
5−7	0.0568		9−9	0.07		9−10	0.1747	
5−8	0.0227		9−10	0.04		9−11	0.0291	
5−15	0.0227		9−11	0.05		9−12	0.0194	
6−6	0.0682		9−12	0.01		10−10	0.1456	
6−7	0.0795		9−13	0.02		10−11	0.0291	
6−8	0.0341		10−10	0.02		10−12	0.0194	
6−15	0.0114		10−11	0.05		11−11	0.0097	
7−7	0.1591		11−11	0.01				
7−8	0.1023		11−12	0.01				
8−8	0.0341							
8−9	0.0227							
8−11	0.0114							
15−15	0.0114							