



Forensic and population genetic analysis of Serbian population using 21 STR loci of GlobalFiler™ PCR amplification kit

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ABSTRACT

Autosomal short tandem repeats (STRs) have been widely used in forensic investigations. Prior to the application of any DNA based identification method, it is essential to estimate the allele frequencies and forensic statistical parameters of targeted STR loci in each population in order to provide a more precise reference database for forensic investigation. The GlobalFiler™ Kit is a multiplex assay that combines the 13 original CODIS loci with 7 non-overlapping loci from the expanded European Standard Set (ESS), as well as the highly discriminating SE33 locus, two Y-based loci and the sex determining maker, Amelogenin. The full complement of loci in the GlobalFiler™ Kit are: D13S317, D7S820, D5S818, CSF1PO, D1S1656, D12S391, D2S441, D10S1248, D18S51, FGA, D21S11, D8S1179, vWA, D16S539, TH01, D3S1358, AMEL, D2S1338, D19S433, DYS391, TPOX, D22S1045, SE33 and a Y-specific insertion/deletion locus (Yindel). The 6-dye GlobalFiler™ PCR Amplification kit (ThermoFisher Scientific) comprises 21 autosomal STRs have already been proven to be able to provide reliable DNA profiling results and enhance the power of discrimination between individuals. In this study, we are presenting an analysis of GlobalFiler STR loci on 209 unrelated individuals from Serbia.

1. Introduction

Evaluating STR allelic frequencies is an essential prerequisite to start applying such analysis in the forensic casework, as it has been shown before that, each population will have its own composition of alleles distribution and therefore, it will facilitate the correct calculations of weight of evidence. By utilizing one of the most powerful commercially available STR amplification kits (GlobalFiler™) can aid development of allelic frequency database to enhance knowledge about patterns of genetic diversity and to have further understanding about population genetic structure [1].

2. Materials and methods

Total of 209 DNA samples was extracted and purified from blood stains or buccal swabs by using the Chelex 100 extraction method [2] from unrelated individuals from Serbia, following informed consent.

DNA was amplified using the GlobalFiler™ Kit (ThermoFisher Scientific) in a thermal cycler GeneAmp 9700 PCR system (Applied Biosystems), according to manufacturer's recommendations, but reducing the PCR final volume to half (12.5 µl) of the recommended quantity. The electrophoresis was carried out on 3500 Genetic Analyzer (Applied Biosystems, USA) and the fragment analysis was performed with GeneMapper ID-X v.1.4 software (Applied Biosystems). Arlequin version 3.5 [3] was used to calculate allele frequencies, expected heterozygosity (He), observed heterozygosity (Ho), probability value of the Hardy-Weinberg equilibrium (HWE) exact test. Population genetics statistical parameters were calculated using PowerStats version 1.2.

3. Results

Allele frequencies and resulting statistical parameters are given in Table 1. No significant deviations from Hardy-Weinberg equilibrium and linkage disequilibrium were detected within and between the 21

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Table 1
Allele frequencies and statistical parameters of 21 autosomal STRs loci in a population sample from Serbia (N = 209).

Allele/ Locus	D3S1358	vWA	D16S539	CSF1PO	TPOX	D8S1179	D21S11	D18S51	D2S441	D19S433	TH01	FGA	D22S1045	D5S818	D13S317	D7S820	SE33	D10S1248	D1S1656	D12S391	D2S1338	
6					0.002																	
6.2					0.010					0.251												
7					0.555	0.012				0.153						0.026						
8		0.014	0.002	0.002	0.079	0.012		0.002	0.002	0.093					0.139	0.175						
9		0.136	0.031	0.031	0.079	0.012		0.196	0.196	0.196				0.043	0.055	0.179						
9.3										0.285												
10		0.067	0.285	0.285	0.057	0.055		0.007	0.335	0.019				0.069	0.062	0.282						
11		0.292	0.297	0.297	0.280	0.074		0.005	0.067	0.002			0.148	0.333	0.361	0.177	0.007	0.112				
12		0.301	0.325	0.325	0.017	0.144		0.134	0.053	0.014			0.022	0.380	0.268	0.129	0.005	0.022				
13	0.005	0.148	0.053	0.053		0.323		0.136	0.026	0.096			0.031	0.160	0.089	0.024	0.010	0.256				
13.2										0.232												
14	0.093	0.112	0.033	0.007		0.225		0.191	0.268	0.012			0.388	0.007	0.026	0.007	0.024	0.266	0.072			0.005
14.2										0.038							0.002					
14.3																	0.055	0.234	0.002			
15	0.242	0.100	0.007			0.139		0.139	0.045	0.165			0.285	0.007			0.055	0.234	0.134	0.065		0.002
15.2								0.002		0.038												
15.3																						
16	0.268	0.222				0.017		0.139	0.007	0.043			0.100				0.063	0.175	0.041	0.026		0.053
16.2										0.031									0.141			
16.3																						
17	0.206	0.278						0.112		0.002			0.024				0.077	0.029	0.053	0.100		0.234
17.2										0.005												
17.3												0.022	0.002				0.077	0.010	0.100	0.002		0.093
18	0.167	0.187						0.074		0.002							0.002		0.002	0.199		
18.2																						
18.3																						
19	0.019	0.081						0.033		0.002			0.108	0.148			0.060	0.002	0.060	0.129		0.086
19.2												0.002					0.002		0.014	0.134		0.146
19.3																						
20												0.105	0.105				0.072		0.014	0.014		0.146
20.2												0.002					0.010					
20.3																						
21												0.177					0.024		0.002	0.002		0.029
21.2												0.005					0.002		0.093			
22												0.184					0.007		0.105			
22.2												0.010					0.041		0.105			
23												0.144					0.048		0.065			
23.2												0.002					0.048		0.110			
24												0.120					0.029		0.012			
24.2												0.053					0.029		0.105			
25												0.005					0.048		0.017			
25.2												0.005					0.048		0.017			
26							0.005					0.050					0.048		0.017			
26.2												0.002					0.043		0.002			
27												0.007					0.043		0.002			
27.2												0.007					0.058		0.007			
28												0.002					0.087		0.012			
28.2												0.002					0.087		0.012			
29												0.002					0.046		0.012			
29.2												0.002					0.046		0.012			
30												0.208					0.046		0.012			
30.2												0.041					0.046		0.012			
31												0.055					0.002		0.007			

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