



Genetic analysis of the short tandem repeat loci D1S1656, D12S391, D18S535 and D22S683 in the Croatian population

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1. Introduction

Short tandem repeats (STR) polymorphisms are the standard genetic markers used not only in the field of forensic medicine and, population genetics, but can also be used as markers for following chimerism in allogeneic bone marrow transplantation [1]. The characterisation of new STR loci can provide additional data of population diversity. The aim of this work was to establish a representative data base of the Croatian population for four STR loci (D1S1656, D12S391, D18S535 and D22S683).

2. Material and methods

DNA was extracted from the peripheral blood of 150 unrelated donors from the wider area of the Croatian capital, Zagreb using a standard salting out method. PCR was performed with a PE thermal cycler with the following conditions: 95 °C—1 min, 60 °C—1 min, 72 °C—1 min and using primers detailed elsewhere [2]. After amplification samples were loaded on 6% polyacrylamide gels and detected using an ALFexpress (Pharmacia Biotech) sequencer. Statistical analysis, checking for Hardy–Weinberg equilibrium and comparisons of the allele frequencies between this and other populations were performed using Fisher's test [3].

3. Results and discussion

The distribution of the observed allele frequencies for the four STRs tested are shown in Table 1, while the genotypes observed four or more times are listed in Table 2. A

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Table 1
Allele frequency distribution at four STR loci in the Croatian population ($N=150$)

Allele	D1S1656	D12S391	D18S535	Allele	D22S683
9			0.099		
10			0.015		
11	0.075		0.051		
12	0.117		0.191	12	0.127
13	0.123	0.006	0.311	12.2	0.021
14	0.066	0.006	0.207	13	0.082
15	0.108	0.027	0.111	13.2	0.149
15.3	0.177	0.054		14	0.130
16	0.063	0.102		14.2	0.136
16.3	0.069	0.153		15	0.085
17	0.054	0.129		15.2	0.036
17.3	0.099	0.108		16	0.045
18	0.021	0.126		16.2	0.012
18.3	0.030	0.120		17	0.027
19		0.096		17.2	0.024
20		0.045		18	0.006
21		0.030		18.2	0.036
22				19	0.024
23				19.2	0.027
24				20	0.030
25				20.2	

comparison of the allele frequencies in Croatians with other European populations studied to date revealed no significant differences. For all markers, the observed genotype frequencies are in good agreement with expected distribution under the

Table 2
Genotypes observed four and more times at four STR loci in the Croatian population ($N=150$)

D1S1656 genotype	%	D12S391 genotype	%	D18S535 genotype	%	D22S683 genotype	%
11–12	0.030	15–15	0.012	9–9	0.012	12–12	0.036
11–14	0.012	15–19	0.012	9–12	0.030	12–13	0.012
11–15	0.024	16–19	0.018	9–13	0.060	12–13.2	0.018
11–15.3	0.024	16–20	0.018	9–14	0.030	12–14.2	0.036
11–16	0.012	16–23	0.012	11–13	0.042	12–15	0.024
12–13	0.036	17–17	0.018	11–15	0.012	12–15.2	0.012
12–15	0.024	17–18	0.024	12–12	0.072	12–16	0.012
13–14	0.018	17–19	0.018	12–13	0.138	12.2–13.2	0.012
13–15.3	0.036	17–20	0.012	12–14	0.042	13–13	0.012
13–16.3	0.024	17–22	0.030	12–15	0.018	13–13.2	0.030
13–17.3	0.036	17–23	0.012	13–15	0.072	13–14	0.030
14–15.3	0.012	18–18	0.030	13–13	0.084	13–18	0.012
14–16.3	0.012	18–19	0.048	13–14	0.078	13.2–13.2	0.042
14–17	0.012	18–21	0.024	14–14	0.078	13.2–14	0.054
14–17.3	0.030	18–22	0.042	14–15	0.060	13.2–14.2	0.012
15–15.3	0.042	18–23	0.048	15–16	0.018	13.2–15	0.030

Table 2 (continued)

D1S1656 genotype	%	D12S391 genotype	%	D18S535 genotype	%	D22S683 genotype	%
15–16.3	0.018	19–21	0.042			13.2–17	0.012
15–17	0.012	19–22	0.030			13.2–20	0.012
15–17.3	0.036	19–23	0.024			14–14	0.018
15–18	0.012	20–22	0.048			14–14.2	0.018
15.3–15.3	0.042	20–21	0.036			14–15	0.018
15.3–16	0.018	21–21	0.018			14–16	0.012
15.3–16.3	0.012	22–24	0.018			14–19	0.018
15.3–17	0.036	23–24	0.024			14–18.2	0.024
15.3–17.3	0.036					14–20	0.012
16–16	0.012					14.2–14.2	0.066
16–17	0.030					14.2–17	0.018
						14.2–19.2	0.012
						15–15.2	0.012
						15–17.2	0.012

Hardy–Weinberg law. Some of the statistic parameters of medicolegal interest are shown in Table 3. The cumulative power of exclusion for the four tested loci was calculated to be 99.99%.

Table 3

Statistic parameters of forensic interest calculated from the Croatian population data

	D1S1656	D12S391	D18S535	D22S683
Ob. H	0.8623	0.8742	0.7425	0.8545
Ex. H	0.8857	0.8832	0.7698	0.8973
PE	0.9799	0.9784	0.9317	0.9828
PIC	0.8933	0.8893	0.7819	0.9014
MP	0.0189	0.0216	0.0683	0.0172

Ob. H—observed heterozygosity; Ex. H—expected heterozygosity; PE—power of exclusion; PIC—polymorphic information content; MP—matching probability.

References

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