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Allele frequencies of 15 STR loci in an Italian population

M. Lancia *, A. Coletti, G. Margiotta, L. Lottanti, E. Carnevali, M. Bacci

Section of Legal Medicine, University of Perugia, Italy

Abstract. STRs are today one of the most effective tools for individual and populational genetic characterization. This paper presents the results of a population study of 15 STR loci included in AmpFlSTR Identifiler kit (Applied Biosystems) that has the aim of creating a local database. Blood or oral swab samples were obtained from 100 unrelated individuals, who were born in Terni (in the center of Italy) and lived there for at least two generations. DNA was extracted from blood, using QIAamp, miniKit of Qiagen and from oral swab, using Chelex method. For each locus allele frequency was calculated and Hardy–Weinberg equilibrium was evaluated. The Expected Heterozygosity (He), the Observed Heterozygosity (Ho), the Polymorphic Information Content (PIC), the Power of Discrimination (PD) and the Power of exclusion (PE) were also calculated.

Keywords: Short tandem repeat; DNA polymorphism; Italian population database; AmpFlSTR Identifiler

1. Introduction

STRs are today one of the most effective tools for individual and populational genetic characterization. In the latest years, European countries began to plan studies whose purpose is to create national and local databases and to be acquainted with the expression frequency of a great number of these DNA loci. Our research has the aim of creating a local database, according to the recommendations published by the ISFG. Genetic analysis of 15 STRs loci, including the 13 CODIS core (D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, vWA, TPOX, D18S51, D5S818 and FGA) and 2 tetrameric STRs (D2S1338 and D19S433) present in AmpFlSTR Identifiler system (Applied Biosystems) were carried out [1,2].

* Corresponding author. Tel.: +39 744 205055; fax: +39 744 220236.
E-mail address: lancia.massimo@infinito.it (M. Lancia).

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2. Materials and methods

Blood or oral swab samples were obtained from 100 unrelated individuals, who were born in Terni and lived there for at least two generations. Extraction of the DNA from blood specimens was carried out using QIAamp DNA miniKit of Qiagen Company, oral swabs were processed through Chelex method. The 15 STR loci were electrophoresed

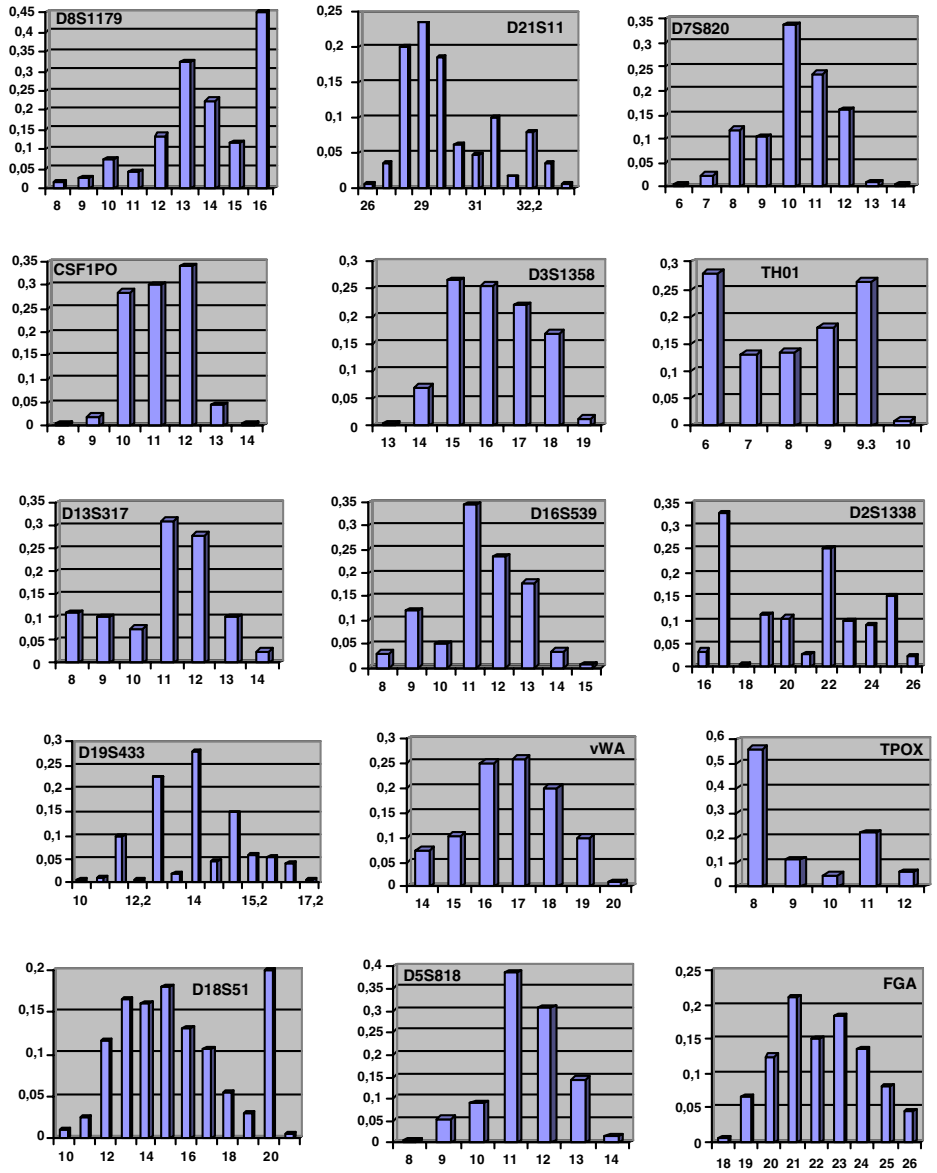

Fig. 1. Allele frequencies of 15 STR loci analyzed.

Table 1
Statistical parameters for the 15 STR loci in our population

	No. alleles	He	Ho	P.I.C.	P.D.	P.E.
D8S1179	9	0.810	0.820	0.780	0.923	0.637
D21S11	12	0.850	0.860	0.830	0.951	0.715
D7S820	9	0.840	0.860	0.750	0.905	0.715
CSF1PO	7	0.755	0.780	0.660	0.843	0.562
D3S1358	7	0.750	0.740	0.750	0.909	0.493
TH01	6	0.850	0.850	0.750	0.905	0.695
D13S317	7	0.790	0.790	0.760	0.922	0.581
D16S539	8	0.760	0.750	0.740	0.911	0.510
D2S1338	11	0.870	0.870	0.820	0.955	0.735
D19S433	13	0.830	0.810	0.810	0.947	0.618
vWA	7	0.710	0.720	0.770	0.929	0.460
TPOX	5	0.630	0.600	0.570	0.798	0.291
D18S51	12	0.940	0.940	0.850	0.957	0.878
D5S818	7	0.760	0.780	0.680	0.868	0.562
FGA	9	0.915	0.910	0.840	0.947	0.816

using ABI Prism 310 Genetic Analyzer and alleles were typed using GeneScan and Genotyper Analysis Software.

3. Results and discussion

For each locus allele frequency was calculated and Hardy–Weinberg equilibrium was evaluated [3]. The following table shows some statistical values useful in forensic caseworks and in paternity tests: Expected Heterozygosity (He), Observed Heterozygosity (Ho), Polymorphic Information Content (PIC), Power of Discrimination (PD) and Power of Exclusion (PE). All statistical values were calculated using Software PowerStats v 2.1 [4,5].

4. Conclusions

Fig. 1 shows the allelic classes for every STR and his respective frequencies in our population. The allelic range changes among the 5 alleles that presents TH01 and the 13 alleles detected in case of D19S433. In Table 1 statistical parameters for the 15 STR loci in our population sample are shown. The observed and expected heterozygosity rates showed similar values. All 15 loci were in Hardy–Weinberg equilibrium and all loci were highly polymorphic. In spite of that, there are some important differences among analyzed loci, as regards Heterozygosity and PIC terms, TPOX is the fewest polymorphic STR and D18S51 is the most polymorphic one. The results indicate that these 15 loci are useful genetic markers for forensic personal identification and paternity testing in our population.

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