



Y-chromosome haplotypes in an Albanian population sample

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Abstract

Seven Y-STR polymorphisms (DYS19, DYS385, DYS389I/II, DYS390, DYS391, DYS392 and DYS393) were analyzed by means of two multiplex PCR reactions and capillary electrophoresis in a population sample of 72 unrelated Albanian males residing in Piedmont (northwest Italy) and 47 different haplotypes were observed. The combination of all seven STR systems revealed a haplotype diversity of 0.952.

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1. Introduction

Analysis of microsatellite systems located on the nonrecombining portion of the human Y chromosome is a powerful tool in male identification and paternity testing. Y haplotypes can display a remarkable degree of population specificity, therefore, detailed population data are required when using these markers in forensic studies. In recent years, Italy has experienced a strong migration flow from Albania. As a consequence, the number of cases of DNA analysis involving Albanians has been constantly increasing. At the moment, published data on Y-STR polymorphisms in the Albanian population are extremely limited [1]. With this in mind, seven of the most commonly used Y-chromosomal STRs (DYS19, DYS385, DYS389I/II, DYS390, DYS391, DYS392 and DYS393) were investigated in Albanians residing in northwest Italy.

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Table 1
Haplotypes detected in the Albanian population sample ($n=72$)

<i>n</i>	Multiplex PCR I				Multiplex PCR II			
	DYS19	DYS391	DYS392	DYS393	DYS385	DYS389I	DYS389II	DYS390
1	12	10	11	14	16, 18	13	30	24
1	13	10	11	13	14, 18	13	30	24
4	13	10	11	13	15, 18	13	30	24
1	13	10	11	13	16, 17	13	31	24
1	13	10	11	13	16, 17	14	31	23
9	13	10	11	13	16, 18	13	30	24
3	13	10	11	13	16, 18	13	30	25
1	13	10	11	13	16, 18	13	31	24
1	13	10	11	13	16, 18	14	31	24
1	13	10	11	13	16, 19	12	30	24
1	13	10	11	13	16, 19	13	30	25
2	13	10	11	13	17, 18	13	30	25
1	13	10	11	13	17, 18	14	31	24
1	13	10	11	13	17, 19	13	30	24
1	13	10	11	13	17, 19	13	30	25
1	13	10	12	13	15, 17	13	30	24
1	13	11	11	13	15, 19	13	30	24
1	14	10	11	12	12, 16	13	30	23
1	14	10	11	12	13, 18	12	28	24
1	14	10	11	12	14, 15	12	28	24
1	14	10	11	12	14, 17	13	29	25
1	14	10	12	12	14, 17	12	28	24
1	14	10	12	13	13, 14	12	28	24
1	14	10	13	12	12, 14	13	29	25
4	14	10	13	13	11, 11	13	29	24
1	14	10	13	13	11, 11	13	29	25
9	14	11	13	13	11, 11	13	29	24
1	14	11	13	13	11, 14	13	29	24
1	14	12	13	13	11, 14	13	28	24
1	15	10	11	12	13, 17	12	28	24
1	15	10	11	12	13, 17	13	29	24
1	15	10	11	12	14, 17	12	28	24
1	15	10	11	12	14, 17	13	29	24
1	15	10	11	12	14, 19	12	29	24
1	15	10	12	15	16, 16	13	29	24
1	15	11	11	13	12, 14	13	31	25
1	15	11	11	13	14, 15	13	31	24
1	15	11	11	13	14, 16	13	31	24
1	15	11	13	12	10, 15	13	29	25
1	15	11	14	12	11, 15	14	30	24
1	16	10	11	12	13, 14	13	29	22
1	16	10	11	13	11, 14	13	30	24
1	16	10	11	13	11, 15	13	30	27
1	16	11	11	13	12, 14	14	31	25
1	16	11	11	13	14, 15	13	31	24
1	16	12	11	13	14, 15	13	31	24
1	17	11	11	13	11, 13	13	30	25

2. Material and methods

Saliva samples were obtained from 72 unrelated Albanian males residing in the region of Piedmont (northwest Italy). DNA was isolated by standard phenol/chloroform extraction. The seven Y-chromosomal STRs were co-amplified using two multiplex PCRs: the primer sequences used were those described by Kayser et al. [2], while multiplex PCRs were performed according to the conditions described by Anslinger et al. [3]. The amplified products were detected with the 310 Genetic Analyzer (Perkin-Elmer, Foster City, CA). Genotype classification was carried out in comparison to self-made allelic ladders generated through sequence analysis of amplified products [4–6]. Nomenclature was according to Kayser et al. [2], with the exclusion of locus DYS398I/II, where a mostly monomorphic (GATA)₃ block was included in the repeat counting (+3 repeats compared to the nomenclature given by Kayser et al.). Gene and haplotype diversity was calculated according to the formula $P(Y) = 1 - \sum(P_i)^2$.

3. Results and discussion

Y-haplotype distribution in the Albanian population sample is shown in Table 1, and 47 different haplotypes were seen in all. The combined haplotype diversity calculated for this set of Y polymorphisms was 0.952. The obtained population data allowed to establish the core of a reference database to be used in forensic casework.

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