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Frequency data for the STR locus SE33 in a population sample from Brescia (northern Italy)

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Abstract. To establish a database for SE33 locus for an Italian population sample from Brescia (northern Italy), 90 unrelated individuals were typed. DNA samples were amplified using a commercial kit with subsequent automatic detection using capillary electrophoresis. The obtained data are very useful in our practice and they give a contribution to the definition of Italian population STRs allelic and genotypic frequencies for the locus analysed. © 2005 Published by Elsevier B.V.

Keywords: SE33 locus; Frequency data; Italy

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1. Introduction

Short tandem repeat (STR) markers are widely used in forensics as well in paternity testing, but before a new locus can be introduced in the current practice, a database for the relevant population must be established to evaluate its effectiveness in forensic identification and paternity testing [1]. Indeed it is well known that different ethnic group have different allelic frequencies and therefore different kind of genotypes [2,3]. In Italy, there are already data regarding a lot of STR, but few data about SE33 [4]. This locus is one of the most informative tetranucleotide short tandem repeat loci used for human identification and paternity testing. Due to its extensive polymorphism, the Federal Criminal Police Office of Germany has included SE33 as one of the eight core genetic loci with witch to establish a database [5].

2. Materials and methods

A total of 90 unrelated individuals from Brescia region (northern Italy) were typed. Genomic DNA was extracted using Chelex-100 procedure from whole blood or buccal

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swabs. PCR was performed in a GeneAmp PCR System 2400 (PE) using the commercial kit AmpFlSTR®SEfiler™ (Applied Biosystems, Foster City, CA, USA) according to manufacturer's recommendations. Typing was performed by capillary electrophoresis (ABI Prism 310 Genetic Analyzer, ABI). Allele scoring for this locus was obtained by comparison to AmpFlSTR®SEfiler™ Allelic Ladder (Applied Biosystems, Foster City, CA, USA).

3. Results and discussion

This work provides a picture of allelic and genotypic frequencies for the SE33 locus from Brescia region (northern Italy). As expected, the preliminary results in the distribution of allelic and genotypic frequencies in our population sample are close to those found in the Caucasian population [4,6,7]. On 90 individuals, a total of 32 different alleles and 70 different genotypes were found. The allele the most represented was "19" (frequency 0.133) and the genotype the most recurrent was "19–27.2" (frequency 0.044). Observed heterozygosity was 0.8889 while expected heterozygosity was 0.9387; the power of discrimination was 0.9828. These data are very useful in our practice and they give a contribution in the definition of Italian population STRs allelic and genotypic frequencies for the SE33 locus.

Genotypes frequencies

1	12–15	0.011
2	12–23.2	0.011
3	13–15	0.011
4	14–15	0.022
5	14–16	0.011
6	14–20	0.022
7	14–28.2	0.011
8	15–18	0.011
9	15–19	0.011
10	15–20	0.011
11	15–22.2	0.011
12	15–26	0.011
13	15–29.2	0.011
14	15–31.2	0.011
15	15.2–16	0.011
16	16–16	0.022
17	16–18	0.022
18	16–19	0.022
19	16–20	0.011
20	16–21	0.011
21	16–24.2	0.011
22	16–28.2	0.033
23	16–29	0.011
24	16–29.2	0.022
25	17–17	0.011
26	17–19	0.033
27	17–20	0.011
28	17–22.2	0.011
29	17–23.2	0.022
30	17–24	0.011
31	17–25.2	0.011
32	17–33	0.011
33	18–18	0.011
34	18–19	0.011
35	18–20	0.011
36	18–23.2	0.011
37	18–24.2	0.022
38	18–30.2	0.011
39	19–19	0.033
40	19–21	0.011

41	19–22	0.011
42	19–22.2	0.011
43	19–24.2	0.011
44	19–27.2	0.044
45	19–28.2	0.022
46	19–30.2	0.011
47	19.2–29.2	0.011
48	20–24.2	0.011
49	20–27.2	0.011
50	20–29.2	0.011
51	20.2–29.2	0.011
52	21–27.2	0.011
53	21–28.2	0.011
54	21.2–28.2	0.011
55	21.2–30.2	0.011
56	22–25.2	0.011
57	22.2–30.2	0.011
58	23–23.2	0.011
59	23.2–25.2	0.022
60	23.2–30.2	0.011
61	25.2–30.2	0.011
62	26.2–26.2	0.011
63	26.2–32.2	0.011
64	27.2–27.2	0.011
65	27.2–29.2	0.022
66	27.2–32.2	0.011
67	28.2–30.2	0.011
68	28.2–31.2	0.011
69	29.2–30.2	0.011
70	29.2–35	0.011

Allelic frequencies		Allelic frequencies	
12	0.011	23	0.005
13	0.005	23.2	0.044
14	0.033	24	0.005
15	0.061	24.2	0.027
15.2	0.005	25.2	0.027
16	0.105	26	0.005
17	0.066	26.2	0.016
18	0.061	27.2	0.061
19	0.133	28.2	0.055
19.2	0.005	29	0.005
20	0.05	29.2	0.055
20.2	0.005	30.2	0.044
21	0.022	31.2	0.011
21.2	0.011	32.2	0.011
22	0.011	33	0.005
22.2	0.022	35	0.005

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