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Preliminary studies of individual genetic identification of domestic dogs (*Canis familiaris*)

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Abstract. Biological traces from dogs and other domestic animals can be found in a crime scene related to suspects or victims being themselves the protagonists of the forensic case. According to Portuguese Legislation, the individual identification of dogs dangerous or potentially dangerous is obligatory. It seems important to follow this subject with the implementation of genetic identification. So, this work has the aim to study STRs of DNA for individual genetic identification of dogs. DNA extracted from saliva of different dogs breed was amplified with StockMarks® Kit—Canine Genotyping.

Keywords: *Canis familiaris*; Canine STR; Animal identification

1. Introduction

Biological traces from dogs can be collected from a crime scene related to suspects or victims being themselves the protagonists of the forensic case.

According to Portuguese Legislation (D.L. 313/2003 of 17 of December art 6th), the individual identification of dogs dangerous or potentially dangerous is obligatory. It seems important to follow this subject with the implementation of genetic identification due to the increasing number of forensic incidents.

So, this work has the aim to study STRs of DNA for individual genetic identification of domestic dogs (*Canis familiaris*).

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2. Material and methods

DNA was extracted by Chelex™ 100 [1] from buccal swabs of 35 unrelated individuals of different dogs breeds (Rottweiler, Boxer, German Shepherd Dog, Labrador Retriever, Border Collie, Serra d'Aires, German Dogue, Airedaile Terrier, Beagle, Bernese Mountain Dog, Bordeaux Dogue, Doberman, Golden Retriever and dogs without breed).

The DNA was amplified 10 tetranucleotide STR loci with StockMarks® Kit—Canine Genotyping: Pez1, FHC2054, FHC2010, Pez5, Pez20, Pez12, Pez3, Pez6, Pez8 and FHC2079.

The detection was carried out on ABI Prism™ 310 Genetic Analyser with internal size standard (GeneScan 350 Rox) and fragment size was presented by alleles in comparison to the that described in [2,3]. Frequencies distribution and *P*-values were computed with software Genepop (version 3.1b).

3. Results

Table 1 presents the results of fragment size frequencies distribution in Pez1, Pez5 and Pez8. The allele frequencies distribution in Pez20, Pez6, Pez12, FHC2010, FHC2054 and FHC2079 are reported in Table 2.

Table 1
Fragment size frequency distribution in Pez1 ($P=0.0000$), Pez5 ($P=0.0037$) and Pez8 ($P=0.0137$)

Fragment size	Pez1			Pez5			Pez8		
	Min.	Max.	Freq.	Min.	Max.	Freq.	Min.	Max.	Freq.
101				100.96	101.93	0.516			
103				103.23	103.23	0.016			
104				104.09	104.83	0.032			
105				105.46	105.65	0.097			
106	105.93	106.05	0.048	106.91	106.91	0.016			
108				108.86	108.86	0.016			
109				109.39	109.85	0.274			
110	110.21	110.40	0.081						
112	112.17	112.17	0.016						
113				113.41	113.52	0.032			
114	114.06	114.52	0.177						
118	117.66	118.26	0.435						
122	121.78	122.24	0.194						
126	126.22	126.25	0.048						
215							215.53	215.53	0.016
219							219.41	219.41	0.031
223							223.41	223.95	0.156
224							224.49	224.49	0.016
225							225.03	225.03	0.016
227							227.48	227.55	0.078
228							228.47	229.04	0.141
231							231.47	231.76	0.063
232							232.19	233.09	0.063
233							233.64	233.64	0.047
235							235.46	236.05	0.172
236							236.17	236.57	0.047
239							239.61	239.81	0.094
243							243.62	243.68	0.031
247							247.79	247.84	0.031

Table 2
Allele frequency distribution in Pez20, Pez6, Pez12, FHC2010, FHC2054 and FHC2079

Allele	Pez20, $P=0.2189$	Pez6, $P=0.1164$	Pez12, $P=0.0024$	FHC2010, $P=0.0002$	FHC2054, $P=0.0185$	FHC2079, $P=0.0000$
7						0.214
8						0.400
9				0.107	0.052	0.257
10				0.375	0.034	
10.1			0.016			
11	0.076			0.161	0.293	0.043
11.1			0.032			
12	0.591		0.081	0.357	0.190	0.057
12.1			0.274			
12.2			0.016			
13	0.227		0.161		0.034	
13.1			0.113			
14	0.076		0.065		0.103	0.014
14.1			0.016			
15	0.015				0.172	
16	0.015		0.113		0.121	0.014
18.3			0.032			
19		0.033				
19.2			0.032			
20.2			0.048			
22.3		0.017				
24		0.067				
24.3		0.100				
25		0.017				
25.2		0.033				
25.3		0.167				
26.1		0.017				
26.3		0.200				
27		0.100				
27.3		0.100				
28		0.067				
28.3		0.017				
29		0.033				
30		0.033				

4. Discussion and conclusions

P-values show that Pez1, Pez5, Pez12, FHC2079 and FHC2010 are not in equilibrium of Hardy–Weinberg. The reduced size of the sample and the high heterogeneity of the breeds maybe the reason for this fact. Attending to the fewest results obtained for Pez3, this marker was not included in this study. This preliminary study is, according to other studies [4,5], prove that the degree of polymorphism of the 10 microsatellite markers seems to be sufficient for canine individual identification.

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