

Research article

Assessing the frequency of somatic mutation from single dog hairs—Forensic testing of StockMarks[®] Canine I Ver3 kit

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Abstract

As dogs are widespread and popular pets they have overriding importance from criminal point of view. The relevancy exists not only in cases of dog attacks or in traffic accidents, but also the scattered, shaded hairs can often provide indirect evidence in crime scene—person relation as well. © 2008 Elsevier Ireland Ltd. All rights reserved.

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1. Introduction

Up-till-date only a few human reports exist on somatic mutation study of hair roots in an individual [4], however the reasons for anomalous patterns during STR profiling are increasingly investigated [1,3]. Due to intense mitotic activity, somatic mutations are believed to occur with higher chance in the integument than in other tissues. In this study we tested the success revealing the right profile from single dog hairs.

2. Materials and methods

We collected 393 plucked hairs from different parts of bullmastiff donor (Table 1). Buccal swab of this individual was sampled for control analysis. In case of hairs the DNA was isolated from the 0.3–0.5 cm long root ends after the microscopic examination. Standard organic phenol/chloroform extraction method was performed. The DNA was quantified on agarose yield gel. StockMarks[®] Canine I. Ver3 kit, ABIPrism 310 Genetic Analyzer, Genescan 3.1 and Genotyper 2.5.2. softwares were used for standard amplification, electrophoresis and genotyping.

3. Results

It appeared that 73.8% – 290 samples – of total samples provided complete genetic profile with no locus dropout (Table 1). There 44 aberrant – imbalance, allelic dropout or “triallelic” – patterns were found in 290 complete profiles. All aberrant loci were re-checked by monoplex and new multiplex amplification. Consequently, one sample resulted homozygote – instead of heterozygote – genotype at PEZ1 locus (Fig. 1).

4. Discussion

The majority of the hair samples (73.8%) provided apparently complete genetic profile at all 10 loci. The 15.2%

Table 1
Number of collected hairs from four different areas, success of PCR reaction and the occurrence of aberrant alleles

	Total attempted	PCR product	Complete profile	Number of aberrant alleles	Frequency
Back hairs	249	206	187	35	0.187165
Chops hairs	64	46	43	5	0.116279
Front foots hairs	26	19	16	0	0
Hind foots hairs	54	44	44	4	0.090909
Hairs total	393	315	290	44	0.151724

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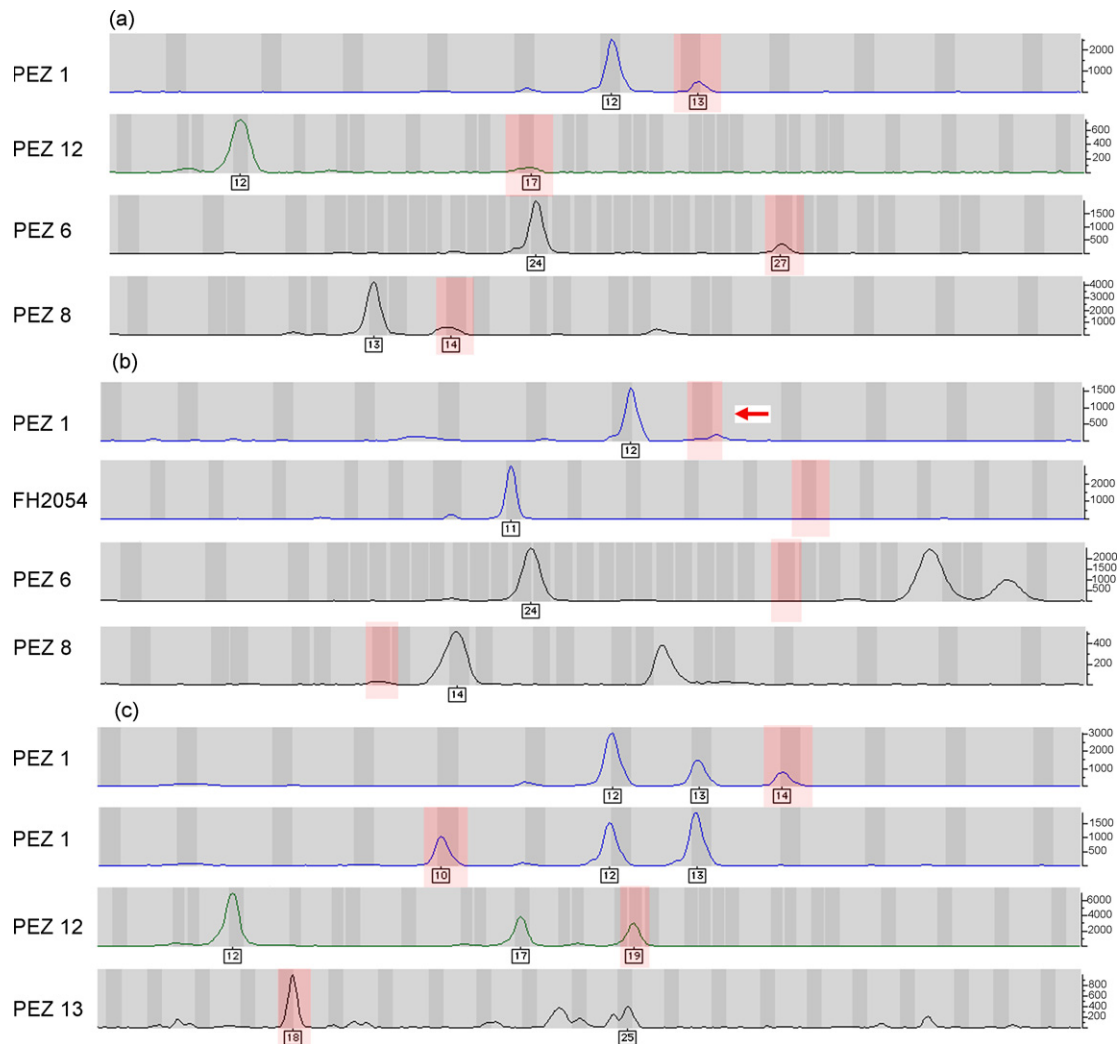


Fig. 1. There are three types (a) imbalance, (b) dropout and (c) artifacts of aberrant loci after the first multiplex amplification. The highlights show the false negative or positive positions and fragments. The arrow shows the only one real mutant locus.

of this profiles resulted divergent genotypes from the original ones. In spite of the repeated analysis of one sample (0.345%) obtained different genotype consequently. This fact can support the hypothesis of a somatic mutation [2]. The results above suggest a careful use of this kit for hairs as well as low copy number DNA sample analysis.

Conflict of interest

None.

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