

Wildlife Forensics Method- Collection of Known Samples from Live Animals (domestic)

Wildlife Forensic Biology

Biology

Organization of Scientific Area Committees (OSAC) for Forensic Science





OSAC Proposed Standard

Wildlife Forensics Method- Collection of Known Samples from Live Animals (domestic)

Prepared by
Wildlife Forensic Biology
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Disclaimer:

This document has been developed by the Wildlife Forensic Biology subcommittee of the Organization of Scientific Area Committees (OSAC) for Forensic Science through a consensus process and *proposed* for further development through a Standard Developing Organization (SDO). This document is being made available so that the forensic science community and interested parties can consider the recommendations of the OSAC pertaining to applicable forensic science practices. The document was developed with input from experts in a broad array of forensic science disciplines as well as scientific research, measurement science, statistics, law, and policy.

This document has not been published by a SDO. Its contents are subject to change during the standards development process. All interested groups or individuals are strongly encouraged to submit comments on this proposed document during the open comment period administered by the AAFS ASB <http://www.asbstandardsboard.org/notice-of-standard-development-and-coordination/>.

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Foreword

This document addresses the particular need in the domestic animal forensic science community for a defined sampling protocol for genetic known evidence samples for individual matching or parentage comparison purposes from dog, cat, and livestock. This document provides methods for investigators to facilitate consistent sampling of domestic animals.

This method document was developed and reviewed by the OSAC Wildlife Subcommittee and presented to the Biology Subject Area Committee for movement through the American Academy of Forensic Sciences' Academy Standards Board.

Keywords: *sample collection, DNA sample, individual matching, parentage, domestic animal, dog, cat, horse, cattle, livestock recommendations*

43 Wildlife Forensics Method- Collection of
44 Known Samples from Live Animals
45 (domestic)

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41 **1 Scope**

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47 This standard provides the protocol for obtaining genetic known evidence samples (buccal swabs and pulled
48 hair) for the purpose of individual matching or parentage comparison from live domestic animals such as
49 dogs, cats, or livestock. This standard does not address sampling of non-domesticated animals.

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52 **2 Normative Reference**

53 N/A

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55 **3 Terms and Definitions**

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57 **3.1**

58 **Buccal swab**

59 A cotton swab or similar collection substrate; used in a relatively non-invasive sample collection
60 technique for scraping the inside of a mouth to collect cells from the inner cheek lining; this is a
61 common method for collecting and preserving samples for DNA testing from known individuals.

62

63 **3.2**

64 **Genetic known evidence samples**

65 Biological material for which the identity of the donor is established and used for individual matching
66 or parentage comparison purposes.

67

68 **3.3**

69 **Individual matching**

70 An individual match refers to genetic profiles that have the same alleles at all loci tested in common; a
71 match statement does not confirm that an individual is the source of the DNA.

72

73 **3.4**

74 **Livestock**

75 Domestic animals raised in an agricultural setting, including horses, cattle, and pigs.

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77 **3.5**

78 **Nuclear DNA**

79 The DNA contained within a nucleus of eukaryotic organisms comprising the majority of the genome.

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81 **3.6**

82 **Parentage**

83 Comparison of genetic profiles of two or more individuals to evaluate for a parent/offspring
84 relationship.

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4 Requirements

4.1 General

4.1.1 All genetic known evidence samples submitted shall contain a sample identifier (for example, name), and an agency case number.

4.2 Buccal swabs

4.2.1 Buccal swabs are the preferred sample type for domestic cat and dog genetic known evidence samples. Buccal swabs should be sterile.

4.2.2 Preparing to sample

- a) Sample one animal at a time. If there is more than one animal to be sampled, complete the process for one animal before sampling the next and then change gloves (if gloves are worn) or clean hands (if gloves are not worn).
- b) Use at least 2 buccal swabs to collect cheek cells from each animal. These are intended to be replicate samples.
- c) Before collecting the sample, the dog or cat should not have nursed or had anything to eat or drink recently (for example, 15 minutes for dogs, 30 minutes for cats).
- d) Prepare a paper envelope (or equivalent) for each animal being sampled, by labeling it with the name or identification of the animal being sampled.

NOTE: Other packaging options can be appropriate as long as collected samples are stored in a way that minimizes mold and bacterial growth and sample degradation.

4.2.3 Taking the sample

- a) Open the swab packaging and remove the swab by its handle.
- b) Place head of the swab against the inside of the cheek and gums, and swirl/wipe vigorously 8 - 10 times.
- c) Place the swabs in the labeled envelope (or equivalent). Seal the envelope and sign and date the seal.

4.2.4 Prior to processing, store swabs at room temperature for the short term (i.e. days to weeks); freeze them for long term (i.e. months to years) storage.

4.3 Pulled hair

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123 4.3.1 Pulled hair is the preferred sample type for livestock. Nuclear DNA is only present in high
124 quantities in the root of the hair so cutting the hair is not acceptable since no root is obtained.

125 4.3.2 Preparing to sample

126 a) Sample one animal at a time. If there is more than one animal to be sampled, complete the
127 process for one animal before sampling the next and then change gloves (if gloves are worn)
128 or clean hands (if gloves are not worn) and clean pliers (if using).

129 b) Prepare a paper envelope (or equivalent) for each animal being sampled, by labeling it with
130 the name or identification of the animal being sampled.

131
132 NOTE: Other packaging options can be appropriate as long as collected samples are stored in a way that
133 minimizes mold and bacterial growth and sample degradation.
134

135 4.3.3 Taking the sample

136 a) Pull thick hairs such as hairs from the mane or tail. The area on the animal from which hairs
137 are pulled should be dry and should not contain excess dirt or debris. Brush the area if
138 necessary to remove dirt and debris.

139 b) Use fingers or pliers to grasp hair close to the skin and pull approximately 10 hairs at once
140 (do not cut). Repeat this until 20-30 hairs with roots have been obtained.

141
142 NOTE: For pigs, which have very thick hairs, 5-10 hairs with roots is sufficient.
143

144 c) Place the hairs in the labeled paper envelope (or equivalent). Seal the labeled paper envelope,
145 and then sign and date the seal.
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147 4.3.4 Prior to processing, store hair at room temperature for the short term (i.e. days to weeks); freeze
148 it for long term (i.e. months to years) storage.
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172 **Annex A**
173 (informative)

174 **Bibliography**

- 175 1] Chang ML, Terrill RL, Bautista MM, Carlson EJ, Dyer DJ, Overall KL, Hamilton SP. Large-scale
176 SNP genotyping with canine buccal swab DNA. *J Hered.* 2007;98(5):428-37.
177
- 178 2] Deedrick DW, Koch SL. *Microscopy of Hair Part II: A Practical Guide and Manual for Animal*
179 *Hairs, Forensic Science Communications, July 2004, Vol 6 Number 3.*
- 180 3] Mitsouras K, Faulhaber EA. Saliva as an alternative source of high yield canine genomic DNA for
181 genotyping studies. *BMC Res Notes.* 2009 Oct 29;2:219.
- 182 4] Pfeiffer I, Volkel I, Taubert H, Brenig B. Forensic DNA-typing of dog hair: DNA-extraction and
183 PCR amplification. *For Sci Int.* 2004. 141:149-151.
- 184 5] Natonek-Wiśniewska M, Krzyścin P. Evaluation of the suitability of mitochondrial DNA for
185 species identification of microtraces and forensic traces. *Acta Biochim Pol.* 2017;64(4):705-
186 708.
- 187 6] Oberbauer AM, Grossman DI, Eggleston ML, Irion DN, Schaffer AL, Pedersen NC, Belanger JM.
188 Alternatives to blood as a source of DNA for large-scale scanning studies of canine genome
189 linkages. *Vet Res Commun.* 2003 Jan; 27(1):27-38.
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