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2019

**Report Writing in Wildlife Forensics:  
Morphology and Genetics**



## **Report Writing in Wildlife Forensics: Morphology and Genetics**

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## Foreword

The wildlife forensic science community needs fit-for-purpose guidance to standardize reporting. Wildlife forensics differs from other disciplines in the breadth of species, substrates, and questions encountered in casework. This document describes the basic information to be provided in formal written reports of wildlife forensic examinations for uses in legal proceedings.

Each laboratory working in wildlife forensics reports on different taxonomic groups and often uses different markers, tests, and assays for analysis. This document provides guidance on the minimum information needed for reporting on wildlife forensic cases.

This standard was revised, prepared, and finalized by the Wildlife Forensics Consensus Body of the AAFS Standards Board. It was developed in the OSAC Wildlife Subcommittee Report Writing Task Group, reviewed by the OSAC Wildlife Subcommittee and presented to the Biology Scientific Area Committee for movement through the AAFS Standards Board. All hyperlinks and web addresses shown in this document are current as of the publication date of this standard.

**Keywords:** *wildlife forensics, reference collections, reporting*

**Abstract:** This document provides minimum standards and recommendations for report writing and report content for practicing wildlife forensic analysts. These minimum standards and recommendations are not intended to replace standards in ISO 17025, but are designed to guide analysts in proper report writing and report content. Notes and examples throughout this document offer clarifications and examples of how a lab may meet a specific standard.

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# Report Writing in Wildlife Forensics: Morphology and Genetics

## 1 Scope

This document describes the information to be provided in formal written reports of wildlife forensic examinations for use in legal proceedings. Requirements for both genetic and morphological examination reports are covered. Forensic reports serve a variety of audiences, and must provide a clear and concise summary of methods, results, and limitations.

## 2 Normative References

There are no normative reference documents. Annex C, Bibliography, contains informative references.

## 3 Report Content

### 3.1 General

Reports shall include information on administrative detail, chain of custody, examination requested, methods, results, and conclusions. Suggested section headings are given below. Additional materials and case information may be included, as appropriate to the particular case.

### 3.2 Administrative Information

**3.2.1** The report shall include the following.

- a) Title of report, specifying type of analysis being reported. This is distinct from the submitting investigator's case title, which may be noted separately.

EXAMPLE Genetics Examination Report

- b) Identity and location of the laboratory performing the analysis.
- c) A unique case identifier assigned by the laboratory.
- d) Pagination, including the total number of pages.
- e) Date of report.
- f) Name and signature of the author(s) of the report.

NOTE Verified digital signatures are acceptable.

### 3.3 Chain of Custody Information

**3.3.1** The report shall include the following.

- a) Investigator's case number.
- b) Name of submitter and (if appropriate) submitting agency.

- c) Date the evidence was received at laboratory.
- d) Name of laboratory functional unit or staff member who initially received the evidence into the laboratory.

EXAMPLE Evidence Unit

- e) The evidence item identifier(s) and submitted descriptions.
- f) Date the analyst received the evidence for the reported analysis.

### **3.4 Examination Requested**

The report shall include a section describing the investigator's request(s) for analysis.

EXAMPLE Species identification, individual matching, and minimum number of individuals.

### **3.5 Case Information**

Information provided by the investigator regarding the evidence that was used to formulate the analytical approach and subsequent interpretation shall be noted in the report.

### **3.6 Examination Conducted**

**3.6.1** The report shall include sufficient detail for another expert to be able to ascertain how the analyses were accomplished and conclusions drawn.

NOTE The report may note that complete documentation of the analyses conducted and data collected is maintained in the case record, which is available from the laboratory.

**3.6.2** The report shall state the technical methods used to reach the reported conclusion.

EXAMPLE Mitochondrial DNA sequencing or morphological examination.

**3.6.3** Names and roles of all persons who provided examinations that contributed to the conclusions shall be noted in the report.

**3.6.4** The report shall include information on the reference material on which analytical conclusions are based.

EXAMPLE Such reference material may include databases, specimen collections, and/or published literature.

**3.6.5** In the case of mtDNA analysis, the report shall include the name(s) of the loci on which the genetic conclusions are based.

### **3.7 Examination Results**

NOTE This section refers to results only, prior to their interpretation.

**3.7.1** The report shall include a statement of the results of the examination.

**3.7.2** If no results were obtained, a statement to that effect shall be included.

**3.7.3** Results that include a taxonomic category shall use currently accepted scientific names. Common names may be included as well.

**3.7.4** When DNA sequencing produces meaningful results, the following shall be reported.

- a) Total length of sequence used in comparison (base pairs).
- b) The unique identifier of the reference sequence used for comparison, along with the organism's scientific name.
- c) Percent identity or number of matching base pairs between the evidence sequence and the reference sequence used for comparison.

**3.7.5** When DNA sequencing is used for haplotyping comparisons, the following shall be reported.

- a) The locus/loci with reported results, specifying which items have the same haplotype and which items have different haplotypes.
- b) For inclusions, indicate statistical support via confidence interval.

**3.7.6** Individual matching using short tandem repeats (STRs).

- a) When multiple evidence items are to be compared to one another, indicate which evidence items have the same genotype.
- b) For inclusions, indicate the likelihood ratio.

**EXAMPLE** Indicate the propositions and present the likelihood ratio for these propositions.

**3.7.7** When conducting population assignment analysis, include statistical metrics, such as confidence intervals, likelihood ratios, or probability estimates. When evaluating parentage, include combined parenting index (CPI) support for inclusions.

**NOTE** Statistical support is not necessary when determining minimum number of individuals using either morphology or sequencing or when determining exclusions. When conducting species identification using morphology or sequencing, statistical support is not appropriate.

### **3.8 Examination Conclusions**

**NOTE** Conclusions are an opinion statement requiring an expert's interpretation and evaluation of the results.

**3.8.1** The report shall include a statement of the conclusions based on the examinations conducted.

**3.8.2** Conclusions that include a taxonomic category shall use currently accepted scientific names. Common names may be included as well.

### **3.9 Optional Additional Information**

Depending on the circumstances of particular cases, additional report sections may be appropriate. These may include References Cited (when providing the published literature, databases, or other sources consulted would be helpful to the Court) or a Glossary/Definitions section, when terms used need to be defined to avoid misunderstanding by non-technical recipients of the report.

## **4 Conformance**

Conformance to the above standard will be reflected in the written case report.

## **Annex A** **(informative)**

### **Foundational Principles**

The 2009 National Academy of Sciences report “Strengthening Forensic Science in the United States: A Path Forward” stated:

*“Two very important questions should underlie the law’s admission of and reliance upon forensic evidence in criminal trials: (1) the extent to which a particular forensic discipline is founded on a reliable scientific methodology that gives it the capacity to accurately analyze evidence and report findings and (2) the extent to which practitioners in a particular forensic discipline rely on human interpretation that could be tainted by error, the threat of bias, or the absence of sound operational procedures and robust performance standards.”*

This report writing standard directly addresses both of the points above, describing the minimum information to be presented in a wildlife forensic report, and giving guidance on how to accurately present results and conclusions. Report writing is one of the most essential steps in the forensic science process, providing results of the analysis of evidence and the expert interpretation of those results for the court. These standards minimize the possibility of error, bias, and misrepresentation of results.

**Annex B**  
(informative)

**Example Reports**

The following are example analytical reports incorporating these standards. Reports have been annotated to cross-reference these standards with specific examples where they are implemented. Laboratories may use these example reports for guidance in developing their own reporting format.

**B.1 Individual Matching Using STRs**

LAB HEADER with address here<sup>3.2.1.b</sup>

August 10, 2016<sup>3.2.1e</sup>

**GENERIC GENETICS REPORT<sup>3.2.1.a</sup>**

**Agency:**

Submitting Agency<sup>3.3.1b</sup>

Street Address

City, State, ZIPCODE

**Lab Case #:** 10-000999<sup>3.2.1c</sup>

**Examiner:** W. E. Kiyote

**Agency Case #:** INV 2016123456<sup>3.3.1a</sup>

**Investigator:**

Trout<sup>3.3.1b</sup>

**Suspects:** Leghorn, F

**Case Title:** Unlawful Take of salmon

**EVIDENCE RECEIVED:**

The following evidence was received in the Evidence Unit<sup>3.3.1d</sup> of the Laboratory on March 17, 2010<sup>3.3.1c</sup>, and was transferred to the undersigned examiner on March 18, 2010:<sup>3.3.1f</sup>

LAB-1: "One of 2 salmon fillets from freezer search, Leghorn residence, 11-15-09." [Item# 1, ST#####]<sup>3.3.1e</sup>

LAB-2: "One of 2 salmon fillets from freezer search, Leghorn residence, 11-15-09." [Item# 2, ST#####]

LAB-3: "Bloody hook-removal tool from campsite." [Item# 3, ST#####]

**EXAMINATION REQUESTED:<sup>3.4</sup>**

The submitting investigator, Special Agent Bull Trout, requested analyses to determine the species origin of the evidence represented by LAB-1, LAB-2 and LAB-3, and whether the evidence represented by LAB-3 originated from the same individual as LAB-1 or LAB-2. Material was swabbed from LAB-3 and assigned item LAB-3A.

**EXAMINATION CONDUCTED:**

*Mitochondrial DNA Analysis*<sup>3.7.4 a,b,c</sup>

A segment of the mitochondrial DNA (mtDNA) containing a portion of the cytochrome *b* gene<sup>3.7.4 a,b,c</sup> from LAB-1, LAB-2, and LAB-3A was amplified by PCR and subjected to DNA sequence analysis. The resulting sequences were compared to An Agency reference database and reference sequences from the GenBank database for Rainbow trout (*Oncorhynchus mykiss*), Cutthroat trout (*Oncorhynchus clarkii*), Chinook salmon (*Oncorhynchus tshawytscha*), and Coho salmon (*Oncorhynchus kisutch*).<sup>3.7.4 a,b,c</sup>

\_\_\_\_\_  
Examiner's Initials

## Examination Report 10-000999 - Continued

August 10, 2016

*Nuclear DNA Analysis*<sup>3.6.1</sup>

The DNA isolated from LAB-1, LAB-2, and LAB-3A was also characterized by STR analysis at ten nuclear loci designated as Loc01, Loc02, Loc03, Loc04, Loc05, Loc06, Loc07, Loc08, Loc09, and Loc10 to determine if the evidence items were of wild or hatchery origin. The resulting genotypes were compared to An Agency database of reference genotypes for salmon from rivers in southern Oregon.<sup>3.6.4</sup>

**EXAMINATION RESULTS:**<sup>3.7.1</sup>*Mitochondrial DNA Analysis*

The cytochrome *b* sequence obtained from LAB-1 and LAB-3A was identical to that of *Oncorhynchus tshawytscha*<sup>3.7.3</sup> reference sequence DNA A12345 at 430/430 base pairs (bp).<sup>3.7.4.abc</sup>

The cytochrome *b* sequence obtained from LAB-2 was identical to that of *Oncorhynchus mykiss*<sup>3.7.3</sup> reference sequence DNA B40125 at 427/427 bp.<sup>3.7.4abc</sup>

*Nuclear DNA Analysis*

The STR genotypes of LAB-1 and LAB-3A were the same<sup>3.7.6a</sup> at all ten loci.

The probability of observing the same genotype if the material from LAB-1 and the material from LAB-3A originated from two different Chinook salmon from the Rogue River is 1 in 120 billion.<sup>3.7.6b</sup>

The STR genotype of LAB-2 is not the same as that of LAB-1 and LAB-3A.

**EXAMINATION CONCLUSIONS:**<sup>3.8</sup>

There is strong support that LAB-1 and the material in LAB-3A originated from the same Chinook salmon, *Oncorhynchus tshawytscha*.<sup>3.8.1, 3.8.2</sup>

LAB-2 originated from *Oncorhynchus mykiss*.<sup>3.8.1, 3.8.2</sup>

**DISPOSITION OF EVIDENCE:**

All evidence items were transferred to the Evidence Unit pending return to the submitting agency.

Validated Digital Signature here<sup>3.2.1f</sup>

W.E. Kiyote, Ph.D.  
Senior Forensic Analyst

## B.2 Species Identification Using Morphology

**FORENSIC MORPHOLOGY ASSOCIATES  
101 FIRST AVENUE  
BIRDVILLE, CA 95555<sup>3.2.1b</sup>**

August 10, 2016<sup>3.2.1e</sup>

### **MORPHOLOGY EXAMINATION REPORT** <sup>3.2.1a</sup>

**Agency:**<sup>3.3.1b</sup>  
LE, Anytown  
101 Main Street  
Anytown, OR 97500

**Lab Case #:** 16-0111<sup>3.2.1c</sup>  
**Examiner:** Smith  
**Agency Case #:** 2015123456<sup>3.3.1a</sup>  
**Investigator:** Green<sup>3.3.1b</sup>  
**Suspects:** John Doe  
**Case Title:** Ex-birds

#### **EVIDENCE RECEIVED:**

The following evidence was received via FedEx by Evidence Technician Dusty Rhodes<sup>3.3.1d</sup> of the Laboratory on August 02, 2016<sup>3.3.1c</sup> and was transferred to the undersigned examiner on August 05, 2016:<sup>3.3.1f</sup>

LAB-1: One of "Three (3) individual bags of feathers" [ST#xxxxxx;Item#1]  
LAB-2: One of "Three (3) individual bags of feathers" [ST#xxxxxx;Item#1]  
LAB-3: One of "Three (3) individual bags of feathers" [ST#xxxxxx;Item#1]  
LAB-4: One of "Two (2) birds" [ST#xxxxxx;Item#2]  
LAB-5: One of "Two (2) birds" [ST#xxxxxx;Item#2]<sup>3.3.1e</sup>

#### **EXAMINATION REQUESTED:**<sup>3.4</sup>

The submitting investigator, Special Agent Rhett Green<sup>3.3.1b</sup>, requested analysis to determine the species origin of the evidence and the minimum number of individuals represented.

#### **EXAMINATION CONDUCTED:** <sup>3.6.1</sup>

The evidence was examined visually, and identification was made by macroscopic comparison with known reference specimens in the collection of the Forensic Morphology Associates Laboratory. In all cases, similar species were considered and excluded, based on the external morphological characters exhibited by the evidence. <sup>3.6.3</sup>

**EXAMINATION RESULTS:**<sup>3.7.1</sup>

- LAB-1: The evidence consisted of tail feathers exhibiting diagnostic morphological characters of Northern Mockingbird, *Mimus polyglottos*,<sup>3.7.3</sup> as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory. <sup>3.6.4</sup>
- LAB-2: The evidence consisted of tail feathers exhibiting diagnostic morphological characters of Northern Mockingbird, *Mimus polyglottos*, as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory.
- LAB-3: The evidence consisted of tail feathers exhibiting diagnostic morphological characters of Red-tailed Hawk, *Buteo jamaicensis*, as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory.
- LAB-4: The evidence consisted of a carcass exhibiting diagnostic morphological characters of Hairy Woodpecker, *Picoides villosus*, as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory.
- LAB-5: The evidence consisted of a carcass exhibiting diagnostic morphological characters of Killdeer, *Charadrius vociferus*, as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory.

**EXAMINATION CONCLUSIONS:**<sup>3.8</sup>

- LAB-1: Tail feathers of NORTHERN MOCKINGBIRD (*Mimus polyglottos*<sup>3.8.2</sup>)
- LAB-2: Tail feathers of NORTHERN MOCKINGBIRD (*Mimus polyglottos*)
- LAB-3: Tail feathers of RED-TAILED HAWK (*Buteo jamaicensis*)
- LAB-4: Carcass of HAIRY WOODPECKER (*Picoides villosus*)
- LAB-5: Carcass of KILLDEER (*Charadrius vociferus*)

**SUMMARY OF MINIMUM NUMBER OF INDIVIDUALS** <sup>3.8.1</sup>

The evidence consisted of a minimum of two Northern Mockingbirds (*Mimus polyglottos*), based on the presence of twenty tail feathers. All other species in this evidence were represented by a minimum of one individual each.

**DISPOSITION OF EVIDENCE:**

All evidence item(s) were transferred to the Evidence Unit pending return to the submitting agency.

**John J. Smith** <sup>3.2.1f</sup>

John J. Smith  
Senior Forensic Scientist

**B.3 Species Identification Using Sequencing**

**US Ocean Agency**<sup>3.2.1b</sup>  
**Agency Address**<sup>3.2.1b</sup>

**Genetics Examination Report**<sup>3.2.1a</sup>

**INVESTIGATOR:** SA LOTS A FISH<sup>3.3.1b</sup>      **LAB CASE #:** 12335<sup>3.2.1c</sup>  
**AGENCY:** US OCEAN AGENCY<sup>3.3.1b</sup>      **AGENCY CASE #:** 6789<sup>3.3.1a</sup>

**Administrative Information****Evidence received**

**Date:** DD/MM/YYYY<sup>3.3.1cf</sup>  
**From:** SA Lotsa Fish<sup>3.3.1b</sup>  
US Ocean Agency<sup>3.3.1b</sup>  
Street Address  
City, State Zip Code  
**Via:** UPS Next Day Air (tracking #123 45 6789)  
**By:** Receiver's name<sup>3.3.1d</sup>  
**Brief Description:** One sealed package of frozen suspected whale meat.

**Analysis Performed by:** Analyst name<sup>3.6.3</sup>

**Case summary and examination requested:** SA Lotsa Fish requested "DNA analysis to confirm that the imported meat, identified by passenger as whale meat (species unknown) is a marine mammal product."<sup>3.4, 3.5</sup>

**Disposition of Evidence:** Evidence will be held at the laboratory pending further instruction from SA Fish.

**Conclusions**<sup>3.8.1</sup>

I identified the submitted evidence item as originating from *Balaenoptera acutorostrata*, Minke whale.<sup>3.8.2</sup>

**Conclusions Table.** Laboratory item number, sample information, and identification conclusion for the submitted evidence.

Laboratory Item #	Submitter's Item #	Seized Prop. #	Laboratory Description	Identification
Smp01	1	1234 <sup>3.3.1e</sup>	suspected whale meat	<i>Balaenoptera acutorostrata</i> <sup>3.8.1, 3.8.2</sup>



## **Annex C** **(informative)**

### **Bibliography**

This is not meant to be an all-inclusive list, as the group recognizes other publications on this subject exist. Any mention of a particular software tool or vendor as part of this bibliography is purely incidental, and any inclusion does not imply endorsement by the authors of this document.

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