ASB Standard 029, First Edition
2018

Report Writing in Wildlife Forensics

AAFS Standards Board

Report Writing in Wildlife Forensics

ASB Approved Xxxxx 2018

ANSI Approved Xxxxx 2018

410 North 21st Street
Colorado Springs, CO 80904

This document may be downloaded for free at: http://asb.aafs.org/

Foreword

The wildlife forensic science community needs fit-for-purpose guidance on report writing to standardize the reporting process. Wildlife forensics differs from other disciplines in the breadth of species, substrates, and questions encountered in casework. Guidance on reporting taxonomic identifications is not addressed by other existing standards, and is of particular importance to wildlife forensics.

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

This standard 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 Subject Area Committee for movement through the AAFS Standards Board. All hyperlinks and web addresses shown in this document are current as the publication date of this standard.

Keywords: *wildlife forensics, taxonomic identification, 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.

Table of Contents

Report Writing in Wildlife Forensics

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.

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, source evaluation, 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 Examinations 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.

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

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

EXAMPLE: Mitochondrial DNA sequencing or morphological examination.

3.6.4. Examinations conducted by any other person or persons shall be noted, including the identity of the person(s) and the nature of the examination.

3.6.5. The report shall include information on the reference material on which examination conclusions are based.

EXAMPLE: Such reference material includes databases, specimen collections, and published literature.

3.6.6. 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 most similar reference sequence.

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. Source evaluation for individuals 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 a confidence interval.

3.7.8. 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

This standard has no conformance requirements.

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."

These reporting writing standards directly address 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 essentials steps in the forensic science process, as 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 examples of a variety of different analytical reports incorporating the standards. They have been annotated with the sections in this document appropriate for each case. Laboratories may use these for guidance in developing their own reporting format.

B.1 Source Evaluation for Individuals Using STRs

LAB HEADER with address here[3.2.1.b]

August 10, 2016[3.2.1e]

GENERIC GENETICS REPORT[3.2.1.a]

Agency:
Submitting Agency[3.3.1b]
Street Address
City, State, ZIPCODE

Lab Case #: 10-000999[3.2.1c]
Examiner: W. E. Kiyote
Agency Case #:INV 2016123456[3.3.1.a]
Investigator: Trout[3.3.1b]
Suspects: Leghorn, F
Case Title: Unlawful Take of salmon

EVIDENCE RECEIVED:

The following evidence was received in the Evidence Unit[3.3.1d] of the Laboratory on March 17, 2010[3.3.1c], and was transferred to the undersigned examiner on March 18, 2010:[3.3.1.f]

LAB-1: "One of 2 salmon fillets from freezer search, Leghorn residence, 11-15-09." [Item# 1, ST######][3.3.1.e]
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:[3.4]

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[3.6.1]
A segment of the mitochondrial DNA (mtDNA) containing a portion of the cytochrome *b* gene[3.6.6.] 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 tschawytscha*), and Coho salmon (*Oncorhynchus kisutch*).[3.6.5]

_____
Examiner's Initials

Examination Report 10-000999 - Continued

August 10, 2016

Nuclear DNA Analysis[3.6.1]
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.[3.6.5]

EXAMINATION RESULTS:[3.7.1]
Mitochondrial DNA Analysis
The cytochrome *b* sequence obtained from LAB-1 and LAB-3A was identical to that of *Oncorhynchus tschawytscha*[3.7.3] reference sequence DNA A12345 at 430/430 base pairs (bp).[3.7.3]

The cytochrome *b* sequence obtained from LAB-2 was identical to that of *Oncorhynchus mykiss*[3.7.3] reference sequence DNA B40125 at 427/427 bp.[3.7.4a,b]

Nuclear DNA Analysis
The STR genotypes of LAB-1 and LAB-3A were the same[3.7.6a] at all ten loci.

The probability that LAB-1 and the material from LAB-3A originated from two different Chinook salmon from the Rogue River given that they share the same genotype is 1 in 120 billion. .[3.7.6b]

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

EXAMINATION CONCLUSIONS:[3.8]
There is strong support that LAB-1 and the material in LAB-3A originated from the same Chinook salmon, *Oncorhyncus tschawyscha*. [3.8.1, 3.8.2]

LAB-2 originated from *Oncorhynchus mykiss*.[3.8.1, 3.8.2]

DISPOSITION OF EVIDENCE:
All evidence items were transferred to the Evidence Unit pending return to the submitting agency. A complete record of the analysis may be obtained from the Laboratory.[3.6.2]

Validated Digital Signature here[3.2.1f]

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

2 of 2[3.2.1d]

B.2 Species Identification Using Morphology

FORENSIC MORPHOLOGY ASSOCIATES
101 FIRST AVENUE
BIRDVILLE, CA 95555 3.2.1b

August 10, 2016 3.2.1e

MORPHOLOGY EXAMINATION REPORT 3.2.1a

Agency: 3.3.1b
LE, Anytown
101 Main Street
Anytown, OR 97500

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

EVIDENCE RECEIVED:

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

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] 3.3.1e

EXAMINATION REQUESTED: 3.4

The submitting investigator, Special Agent Rhett Green, requested analysis to determine the species origin of the evidence and the minimum number of individuals represented.

EXAMINATION CONDUCTED: 3.6.1

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. 3.6.3 Complete documentation of the analyses conducted and data collected is maintained in the case record, which is available from the laboratory. 3.6.2

EXAMINATION RESULTS:[3.7.1]

LAB-1: The evidence consisted of tail feathers exhibiting diagnostic morphological characters of Northern Mockingbird, *Mimus polyglottos*,[3.7.3] as verified by comparison with reference specimens in the collection of the Forensic Morphology Associates Laboratory. [3.6.5]

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:[3.8]

LAB-1: Tail feathers of NORTHERN MOCKINGBIRD (*Mimus polyglottos*[3.8.2])
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 [3.8.1]

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 [3.2.1f]
John J. Smith
Senior Forensic Scientist

B.3 Species Identification Using Sequencing

US Ocean Agency[3.2.1b]
Agency Address[3.2.1b]

Genetics Examination Report[3.2.1a]

INVESTIGATOR: SA LOTSA FISH[3.3.1B] **LAB CASE #:** 12335[3.2.1C]

AGENCY: US OCEAN AGENCY[3.3.1B] **AGENCY CASE #:** 6789[3.3.1A]

Administrative Information

Evidence received

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

Analysis Performed by: Analyst name

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."[3.4, 3.5]

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

Conclusions

I identified the submitted evidence item as originating from *Balaenoptera acutorostrata*[3.8.2], Minke whale.[3.8.2]

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

Laboratory Item #	Item #	Seized Prop. #	Laboratory Description	Identification
Smp01	1	1234[3.3.1e]	suspected whale meat	*Balaenoptera acutorostrata*[3.8.1, 3.8.2]

Genetics Examination Report

INVESTIGATOR:	SA LOTSA FISH	**LAB CASE #:**	12345
AGENCY:	US OCEAN AGENCY	**AGENCY CASE #:**	6789

Details of Examination

Methods[3.6.1]**:** A small tissue subsample was taken from the submitted item. Standard laboratory protocols were used for molecular genetic analysis[3.6.3]. DNA was extracted from the evidence. The mtDNA control region [3.6.6] was amplified from the extracted DNA and controls and sequenced. Resulting sequences were evaluated for quality, edited, aligned, and compared to appropriate reference sequences, following standard procedures.

The sequence data from the unknown sample was compared with reference sequences and identifications were made based on sequence similarity and phylogenetic reconstruction. A full record of the work is available from the laboratory.[3.6.2]

Results:[3.7.1]
Evidence sequences produced a 445[3.7.7a] bp contig, which shared 99.8% identity [3.7.4c] with an Ocean Agency Forensic Laboratory reference sequence for *Balaenoptera acutorostrata.*[3.7.3]

Results Table. Laboratory item and evidence bag numbers, most similar reference sequence and source species, and the number of base pairs (bp) in the evidence sequence identical to those in the most similar reference sequence.

Laboratory Item #	Item #	Most similar species	Most similar reference sequence(s)	# Identical bp/ Total # bp (%)
Smp01		*Balaenoptera acutorostrata*[3.7.4b]	Bacu001[3.7.4b]	444/445[3.7.4c] (99.8%)

Reference Material: Forensics Laboratory internal database "Cetacean standards dlp V1" and DNA Surveillance databases "All cetaceans Vs4.3" and "Mysticetes Vs4.3"[3.6.5].

Analyst name[3.2.1f]
Analyst's signature
Certified Wildlife Forensic Scientist

-END-

MM/DD/YYYY[3.2.1E] | PAGE X OF Y[3.2.1D]

Annex C
(informative)

Bibliography

This is not meant to be an all-inclusive list as the group recognizes other publications on this subject may exist. At the time these standards were drafted, these were the publications available to the working group members for reference. Additionally, 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.

1] American Society of Crime Lab Directors/Laboratory Accreditation Board. ASCLD/LAB-*International Supplemental Requirements for the Accreditation of Forensic Testing Laboratories*. 2011.

2] ASTM E620-11, Standard Practice for Reporting Opinions of Scientific or Technical Experts

3] Forensic Quality Services. *Forensic Requirements for Accreditation* (FRA-1:2008/1) 2008.

4] International Laboratory Accreditation Cooperation. ILAC Guide 19: *Modules in a Forensic Science Process*. 2014. 37pp.

5] International Organization for Standardization, 2005. ISO/IEC 17025:2005 *General Requirements for the Competence of Testing and Calibration Laboratories*

6] International Organization for Standardization. National Commission of Forensic Science. *2015. Views Document on Documentation, Case Record and Report Contents*

7] ISO/IEC 17025:2005 *General Requirements for the Competence of Testing and Calibration Laboratories*. International Organization for Standardization. 2005. 28 pp.

8] Moore, M. K. and I. L. Kornfield *Best practices in wildlife forensic DNA. In, Wildlife forensics: methods and applications*, 2012. 1st ed. Edited by J.E. Huffman and J.R. Wallace, pp. 201-236. Chichester: Wiley-Blackwell.

9] National Research Council/National Academy of Sciences. *Strengthening Forensic Science in the United States: A Path Forward*. National Research Council, 2009. Washington, DC.

10] SWGWILD Standards and Guidelines v2.0, 2012

Academy Standards Board
410 North 21st Street
Colorado Springs, CO 80904

http://asb.aafs.org/