SWGWILD Standards and Guidelines

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1.0 Scope

This document provides minimum standards and additional guidelines for wildlife forensic analysts in the subdisciplines of DNA and morphology. This document covers good laboratory practices, evidence handling, and training which are central to all forensic laboratories. They also include critical considerations of phylogeny, taxonomy, and reference collections that are specific to wildlife forensic science.

2.0 Definitions

Note: These definitions apply to General, DNA and Morphology Standards and Guidelines. Definitions specific to DNA and Morphology are located in those respective sections.

2.1 **Accuracy –** The ability to obtain a correct result, e.g. the degree of conformity of a measured quantity to its actual (true) value.

2.2 **Administrative Review –** An evaluation of the report and supporting documentation for consistency with laboratory policies and for editorial correctness

2.3 **Analyst –** An individual who conducts and/or directs the analysis of forensic casework samples, interprets data, reaches conclusions, and/or issues reports concerning conclusions.

2.4 **Chain of Custody –** The chronological documentation or paper trail, showing the seizure, custody, control, transfer, analysis, and disposition of evidence.

2.5 **Competency –** The demonstration of technical skills and knowledge necessary to perform certain tasks.

2.6 **Curated Collection** – An assemblage of reference materials acquired and maintained with associated data according to explicit quality control standards.

2.7 **Guidelines –** Suggestions to optimize the accuracy and precision of methods. Guidelines are not mandatory, but represent a “best-case-scenario” for analysts and laboratories with the means to achieve them. Laboratories that encounter forensic casework occasionally may not be able to implement all guidelines, however, dedicated wildlife forensic laboratories should consider implementation. Guidelines have a wider tolerance in operational parameters within which the accuracy and precision of analyses is assured.

2.8 **Known –** In the context of evidence, the material for which the character under investigation (e.g. individual identity, geographic source) is unquestioned. This serves as the basis for comparison to questioned material for the purpose of individual matching.

2.9 **Identification –** Analyses to establish the taxonomic classification of the sample. These analyses are based on class characters diagnostic for the taxonomic level in question.

2.10 **Individualization –** Analyses that attempt to match a questioned to a known sample to the exclusion of all others.

2.11 **Laboratory** –The entity providing the analysis, including the staff and the physical facility.

2.12 **Notes –** Clarifications and explanations of Standards and Guidelines. These are not standards or guidelines and should not be treated as such.

2.13 **Precision –** The degree of mutual agreement among a series of individual measurements, values, and/or results.

2.14 **Reference Material** – Biological specimens of known identity or data derived from them, or from published sources.

2.15 **Standard Operating Procedure (SOP) –** Written documentation maintained by the laboratory including laboratory policies, procedures and protocols or methods for specific forensic procedures. SOPs are controlled documents with a mechanism for ensuring SOPs are implemented in the laboratory, content is current and authorized with previous or invalid versions being archived for reference.

2.16 **Standards –** Mandatory minimum practices necessary to ensure analysts produce accurate, precise analytical findings, and convey these findings in an unbiased, objective manner. Some standards are accompanied by methods for evaluating accuracy and objectivity, e.g., tracking performance of reagents and equipment, or through technical review of analytical products and reports. Standards are non-negotiable, and every analyst shall abide by them whether in a research laboratory or a dedicated forensic facility. Standards and guidelines can be modified in response to new information, innovations, and perspectives.

2.17 **Technical Review –** An evaluation of reports, notes, data, and other documents to ensure there is an appropriate and sufficient basis for the scientific conclusions.

2.18 **Validation –** The process of performing a set of experiments that establishes the reliability of a technique or procedure or modification thereof. Method validation demonstrates that an analytical method is acceptable for its intended purpose.

2.19 **Voucher Specimen –** Biological specimen of known identity and known geographical origin curated with associated field data, such as life history stage and sex.

3.0 General Standards and Guidelines

3.1 **Training and Personnel**

3.1.1 *Standard:* Each laboratory conducting wildlife forensic analyses shall have an ethical code by which all staff must abide. All laboratory staff shall make explicit efforts to conduct their work in a professional, confidential, and unbiased manner.

3.1.2 *Guideline:* All analysts and supervisors should have a documented training program.

3.1.3 *Standard:* All members of the laboratory who handle evidence shall have training in chain of custody, evidence handling, ethics, bias and safety before assuming independent duties.

3.1.4 *Guideline:* All analysts should have training in relevant laws and expert witness testimony before undertaking casework that may lead to court proceedings.

3.2 Evidence Handling

3.2.1 *Standard:* Laboratories shall have standard operating procedures (SOPs) in place to assure evidence integrity at all times, addressing the prevention of evidence loss, contamination, cross-contamination, and tampering during storage, processing, and examination.

3.2.2 *Standard:* A chain of custody shall be maintained. All evidence shall be marked with a unique identifier and the analyst's signature or initials.

3.2.3 *Guideline:* A portion of each evidence sample should be retained to enable possible future independent analysis.

3.2.4 *Standard:* Evidence subject to significant physical alteration in whole or part to assist identification (e.g., parts removed for molecular analyses, skeletonized) shall be photographed prior to alteration.

3.2.5 *Standard:* Care shall be taken to minimize the consumption or alteration of all the submitted evidence. If consumption of the entire amount of evidence is necessary, the pertinent party (e.g., case officer or submitting entity) shall be consulted.

3.2.6 *Standard:* When physically altering evidence for the purpose of analysis, careful consideration shall be given to the effects the alteration(s) may have on possible subsequent analyses. If alteration that will affect subsequent analysis is necessary, the pertinent party shall be consulted.

3.2.7 *Standard:* Research and casework reagents shall be kept separate.

3.2.8 *Standard:* Research and casework samples shall be physically or temporally separated when processed on the same instrument.

3.2.9 *Standard:* Evidence and derived data shall be stored and analyzed in a controlled and secure manner at all times.

Note: Controlled access includes secure evidence storage, restrictions to forensic analytical spaces, and digital data protection. Access to analytical and evidence areas by non-forensic personnel should be with escort or under supervision at all times.

3.3 Equipment and Methods

3.3.1 *Standard:* Before use in analyzing casework samples, new instruments shall have their performance or function checked by analyzing representative samples (case-type samples, positive controls) and assessing whether the expected results are achieved. Thereafter, performance shall be checked on a regular basis (at least as frequently as indicated by the instrument manufacturer). Additionally, instruments that have been shared or loaned out shall have their performance tested before being used again in casework.

3.3.2 *Standard:* Protocols used in casework shall be validated prior to use. New methods shall be science-based (i.e., based on peer-reviewed literature and methods) and extensively documented.

3.3.3 *Standard:* Use of an analytical method derived from procedures validated at another laboratory or from a method published in the peer-reviewed literature shall undergo an internal validation. The validation shall be of sufficient rigor and detail to confirm that the expected results of the analysis can be achieved at the testing laboratory before the method is used in casework.

3.3.4 *Standard:* Statistical methods used shall be documented in the case file.

3.3.5 *Guideline:* The following validation criteria should be addressed if appropriate:

3.3.5.1 Literature review of the relevant issue. A list of relevant references should be available.

3.3.5.2 Accuracy of the analysis. Accuracy can be determined by analyzing a traceable control sample.

3.3.5.3 Precision of the analysis: Precision can be determined by repeated testing of known samples.

3.3.5.4 Specificity of the analysis: Specificity can be evaluated by the analysis of individuals from related but non-target species or populations, likely contaminant species, or substitute species. Alternative sources (tissue types or substrates) can also be tested.

3.3.5.5 Limitations to accurate interpretation (e.g., contaminants in blood mixtures, substrate, etc.) shall be identified and evaluated.

3.4 Reference Materials and Collections

3.4.1 *Standard:* Laboratories conducting wildlife forensic analyses shall maintain reference materials in curated collections.

3.4.2 *Standard:* Laboratories shall prepare an SOP covering curation and preservation of each type of biological reference material used for taxonomic identification. Topics to be covered include:

3.4.2.1 Documentation and curation procedures

3.4.2.2 Protection of materials from degradation

3.4.2.3 Taxonomic authorities and collection arrangement

3.4.3 *Standard:* Specimens and databases used in casework shall be uniquely identified and documented in the case file.

3.4.4 *Standard:* The identity of a biological reference specimen must be verified before the material is used in casework. Validation of morphological specimens is made with reference to verified specimens at hand, to specimens in a larger natural history collection (e.g., major museums), or to the professional literature (e.g., taxonomic monographs, identification keys, or field guides). Reference samples for DNA analysis must be sourced from morphologically validated specimens.

3.4.5 *Standard:* The provenance and taxonomic identity of reference specimens or DNA sequences used for comparison to evidence items shall be documented.

3.4.6 *Standard:* Taxonomic identification reports shall include currently accepted scientific names.

3.4.7 *Standard:* Authoritative sources (published literature or databases) shall be used in determining whether a taxonomic classification is scientifically accepted, and each laboratory shall maintain an updated list of the taxonomic authorities used.

3.4.8 *Guideline:* Each analyst should be prepared to address synonymies and other potential taxonomic issues.

3.4.9 *Guideline:* Subspecies determination of wild taxa should only be attempted with accurate and current data concerning geographic origin.

3.4.10 *Standard:* Assumptions of geographical origin used in taxonomic identification shall be documented in the case file.

3.5 Case Documentation

3.5.1 *Standard:* The case file shall include chain of custody, submittal request, bench notes, location of any electronic data, documentation of technical and administrative reviews, and final report.

3.5.2 *Guideline:* The case file should additionally include any other pertinent documents, such as raw data files, emails, records of other external communications regarding the case, shipping and receiving documentation, and/or photographic documentation of the evidence or packaging.

3.5.3 *Standard:* Details in bench notes shall be sufficient to enable another analyst competent in the reporting subject to repeat the analysis conducted under the same methodology and testing conditions.

3.6 Reporting

3.6.1 *Standard:* Reports shall include information on general methods, results, and conclusions. The report shall contain sufficient detail for another expert to be able to ascertain how the analyses were accomplished and conclusions drawn.

3.6.2 *Standard:* Each case file and report shall be technically and administratively reviewed before the report is issued. All reports shall be reviewed for technical accuracy by another scientist competent in the reporting subject. The reviews shall be documented in the case file.

3.6.3 *Guideline:* The administrative review should be carried out by a person other than the analyst and the technical reviewer.

3.6.4 *Standard:* All reports shall identify the analyst(s) involved in generation and interpretation of forensic data.

3.6.5 *Standard:* Terms used in the conclusion, such as “match,” “consistent with,” etc., shall be defined by each reporting laboratory.

3.6.6 *Standard:* Statistical tests used to support conclusions shall be reported.

3.7 **Standard Operating Procedures/Protocols (SOP) Needed:**

3.7.1 *Standard:* Each Laboratory shall have the following SOPs in place:

3.7.1.1 Acceptance criteria, storage conditions, and methods for validation, documentation and tracking of critical reagents or reference material whose activity directly influences the success of a reaction or test. (See standards related to validation in Sections 3.3 and 3.4.)

3.7.1.2 Data analysis. (See section 3.3.5.5.)

3.7.1.3 Evidence receipt, tracking, storage, transfer, and post-analysis disposition. (See section 3.1.2.)

4.0 DNA Standards and Guidelines

Wildlife DNA Analysis is the discipline within wildlife forensics using genetic techniques to identify wildlife parts and products to family, genus, species, population, or individual source. Analysis of genetic characters is the method of choice for individualization and classification when morphological characters are absent, particularly with trace evidence (blood, body fluids), partial organisms (gut piles, crafted items, bones, antlers, horn), degraded or processed tissues (cooked meats, fish filets, timber, Traditional Chinese Medicines).

These Standards and Guidelines refer to general considerations in the application of genetic techniques in analyzing wildlife forensic evidence (e.g., restriction fragment length polymorphisms, single nucleotide polymorphisms, or protein analysis). They also cover specific wildlife DNA analyses currently widely employed, such as DNA sequencing for the identification of class characters, and DNA fragment analysis of short tandem repeats (STRs) for establishing individual identity. It is expected that these standards and guidelines will continue to evolve as the field develops.

4.1 **DNA Definitions and Abbreviations**

4.1.1 **Analytical Thresholds –** In STR analysis, minimum and maximum peak amplitudes acceptable for peaks intended to be assigned allele designations.

4.1.2 **Bin –** In STR analysis, a “window” around the size obtained for each allele (determined for each different species with empirical data).

4.1.3 **Contamination –** The unintentional introduction of exogenous DNA into a sample or PCR reaction.

4.1.4 **Electropherogram –** A plot of results from an electrophoretic analysis generated by a genetic analyzer.

4.1.5 **Extraction Negative Control –** (or Reagent Blank) An analytical control sample that contains no template DNA and is used to monitor contamination from extraction to final fragment or sequence analysis. This control is included in the analysis alongside the questioned and/or known samples.

4.1.6 **Genotype –** The genetic constitution of an organism or cell; also refers to the specific allele(s) inherited at nuclear or mitochondrial loci.

4.1.7 **Heterozygous –** In STR analysis, alleles that appear as a two-peak pattern and, on average, have similar peak height relative to each other.

4.1.8 **Homozygous –** In STR analysis, alleles that appear as single peaks.

4.1.9 **Low Copy Number Analysis –** An analysis to obtain a result from very low quality/quantity samples, for example by using additional PCR cycles, differing reagent concentrations, etc.

4.1.10 **Mitochondrial Haplotype –** A DNA sequence that has been identified at a specific mitochondrial DNA region.

4.1.11 **PCR –** Polymerase Chain Reaction.

4.1.12 **PCR Negative Control –** An analytical control used to detect DNA contamination of the amplification reagents. This control consists of only amplification reagents without the addition of template DNA. This control is included in the analysis alongside the questioned and/or known samples.

4.1.13 **PCR Positive Control** – An analytical control sample that is used to determine if the PCR performed properly. This control consists of the amplification reagents and a known DNA sample, and is included in the analysis alongside the questioned and/or known samples.

4.1.14 **Peak** – A distinct triangular section of an electropherogram that projects above the baseline. In STR analysis, the designation of a peak as an allele is determined primarily by the parameters set in the equipment's analytical software.

4.1.15 **Peak Height** – (or Peak Amplitude) The point at which the signal intensity of the peak is greatest.

4.1.16 **Peak Height Ratios** – In STR analysis, the ratio of the height of the lower peak to the height of the higher peak, expressed as a percentage.

4.1.17 **Short Tandem Repeats (STRs)** – (or Microsatellites) Polymorphic fragments of DNA containing a repeated sequence of generally 2-5 nucleotides. STRs are commonly used for individualization, as the number of repeats is typically highly variable in a population.

4.1.18 **Theta (θ) –** An estimator of Wright's F_{ST} statistic (NRC, 1996) which is used to represent population genetic structure; incorporated as a correction into match probability equations where population reference data contains multiple subpopulations.

4.2 General DNA Standards and Guidelines

4.2.1 Laboratory

4.2.1.1 *Standard:* Areas of the laboratory shall be designated post-PCR and pre-PCR.

4.2.1.2 *Standard:* Equipment, PCR products, and supplies shall not be transferred from post-PCR to pre-PCR areas unless decontaminated using generally accepted laboratory practices established through a defined SOP.

4.2.2 DNA Extraction

4.2.2.1 *Standard:* Each DNA extraction set shall include at least one extraction negative control.

4.2.2.2 *Standard:* Extraction of DNA from reference material shall be physically or temporally separated from extraction of DNA from evidence. Casework and research shall not be conducted simultaneously in the same physical location.

4.2.2.3 *Standard:* When multiple evidence items are to be compared for DNA matching, e.g., questioned vs. known evidence, the items shall be processed at different times or in different places.

4.2.2.4 *Guideline:* Trace samples should be extracted and amplified before samples with high copy number DNA, and questioned samples should be extracted before related reference material and known samples.

4.2.2.5 *Guideline:* In analyses that are sensitive to template concentration, samples should be quantified prior to amplification.

4.2.3 Amplification

4.2.3.1 *Standard:* Primers used for species identification shall be documented in the case file.

4.2.3.2 *Standard:* Routinely used primers shall have been tested on a wide variety of likely species to determine specificity. They shall likewise be validated with varying dilutions of template, reagent concentrations, annealing temperatures, and cycle numbers to delimit the range of acceptable PCR conditions and to evaluate the likelihood of encountering false positives and false negatives.

4.2.3.3 *Standard:* Each PCR shall include an extraction negative control and PCR negative and positive controls.

4.2.3.4 *Guideline:* A positive control should produce a distinctive genotype, to allow one to readily determine that it is not a source of contamination.

4.2.3.5 *Standard:* PCR negative and positive controls and extraction negative controls should be analyzed with evidence samples through the final step (sequencing or fragment size determination).

4.2.4 Analysis and Interpretation

4.2.4.1 *Standard:* The results shall be rejected if a negative control shows amplification and the genotype is identical to an evidence sample.

4.2.5 *Standard:* Laboratories shall have SOPs to address the following:

4.2.5.1 Contamination detected in positive controls, negative controls, or in the case samples.

4.2.5.2 Analysis, interpretation, and minimum thresholds for acceptance of data. Examples of data quality indicators include PHRED scores, signal intensities or peak heights.

4.2.5.3 Cleaning and decontaminating facilities and equipment.

4.2.6 *Guideline:* Laboratories that work with degraded or low copy number DNA should have an SOP specifically addressing analysis of such samples and subsequent data interpretation.

4.3 Sequencing Standards and Guidelines

4.3.1 *Standard:* Taxonomic identification based on sequence data shall include considerations of:

4.3.1.1 The appropriateness of the reference data, including suitable representation of closely related species

4.3.1.2 Distribution of genetic distances among closest relatives

4.3.1.3 Organism's biogeography, life history and taxonomy

4.3.1.4 Published phylogenies

4.3.2 *Standard:* Sequences from public databases (e.g., the National Center for Biotechnology Information's GenBank) shall be used with caution.

4.3.3 *Guideline:* An identification should not rest on a single sequence from a public database. In the rare instance where additional data are unavailable, limitations of the conclusion should be stated in the report.

4.3.4 *Standard:* Statistical estimates of mitochondrial haplotype frequency shall consider the appropriateness and completeness of the reference data.

4.3.5 *Standard:* Laboratories shall have SOPs to address the following:

4.3.5.1 Nucleotide sequence editing and comparison

4.3.5.2 Sequence contamination or mixtures

4.3.5.3 Heteroplasmy

4.4 STR Standards and Guidelines

4.4.1 *Standard:* An internal size standard shall be run with samples to normalize peak migration differences. The sample allele designation shall only be used if the largest and smallest alleles for that sample fall within the range covered by the internal size standard.

4.4.2 *Standard:* When data are shared between laboratories, allele calls shall be harmonized by the use of quality control samples of known genotype.

4.4.3 *Standard:* Each laboratory shall use internally validated panels of loci.

4.4.4 *Standard:* All estimates of individualization probabilities shall incorporate an adjustment for population structure.

Note: For taxa with limited mobility or species with non-panmictic breeding, relevant estimates of population structure should be acquired. When θ *is not known for a particular*

species, a conservative adjustment shall be incorporated based on data available from taxa expected to have similar population structure.

4.4.5 *Standard:* When doing a population assignment, it is essential that the database include representative geographic coverage and sufficient sample size. If an appropriate population cannot be included in the comparison, the conclusions shall reflect that fact.

4.4.6 Laboratories shall have SOPs to address the following:

4.4.6.1 *Standard:* Defining a threshold of signal intensity for alleles used to assign genotypes. These signal intensity criteria are determined by generally accepted values based on the collection platform or are determined empirically by internal validation.

4.4.6.2 *Standard:* Defining a set of minimum criteria for allele designation and genotypes to be included in the final report.

4.4.6.3 *Standard:* Defining bin designation for alleles.

4.4.6.4 *Standard:* Distinguishing artifacts, stutter peaks and pull-up peaks, where applicable, from true allele peaks.

4.4.6.5 *Standard:* Distinguishing between single source, multiple source and partial profile genotypes.

4.4.6.6 *Standard:* Use of established formulae (e.g., NRC, 1996) to calculate individualization probability.

5.0 Morphology Standards and Guidelines

Morphology is the study of form. In a wildlife forensic context, it is the discipline using morphological comparison to identify wildlife parts and products, typically to the family, genus, or species source. Depending on the nature of the evidence, a variety of macroscopic and microscopic comparison techniques may be employed.

It is essential to recognize that almost all analyses performed by a forensic wildlife morphologist are based on class characters, not individual characters. Shared quantitative and/or qualitative morphological characteristics are used by scientists to specify, or define, taxonomic groups, such as families, genera, and species. These class characters are reliably associated with evolutionary lineages down to the species level. Individualization, in contrast, requires the recognition of characters uniquely identifying a particular individual. Individualization based on morphological characters is rarely conducted in wildlife cases.

The method of morphological comparison is the basis for classic studies of biological structure and evolution, and is essential in the scientific work of taxonomists, anatomists, paleontologists, and archaeologists, as well as forensic anthropologists. An extensive body of peer-reviewed literature exists that establishes the scientific rigor and utility of morphological comparison techniques.

5.1 General Morphology Standards and Guidelines

5.1.1 Bases for Morphological Determinations

5.1.1.1 *Standard:* The analyst shall examine, interpret, and document morphological similarities between the evidence item and specimens of known species source, using additional information from scientific references, as appropriate.

5.1.1.2 *Standard:* The analyst shall consider the diagnostic value and inter- and intraspecific variability of the characters being analyzed.

5.1.1.3 *Guideline:* Scientific references used in morphological examinations should include primary scientific literature, taxonomic monographs, morphometric datasets, identification keys, field guides, and reliable image databases.

5.1.1.4 *Guideline:* In the absence of physical comparative reference materials, metric and non-metric data (e.g., anatomical descriptions and osteological identification guides) should be used. Metric and non-metric data may also be used in conjunction with physical comparative reference materials.

5.1.1.5 *Guideline:* If a species' geographical origin is of particular importance in the interpretation of morphological characters, the most relevant reference specimens should be selected.

5.1.1.6 *Guideline:* Analytical documentation and data interpretation in morphology should follow the hierarchy of taxonomy, with characteristics of the order noted first, followed by family-specific characters, and finally those diagnostic to particular genera and species.

5.1.2 Process of Morphological Examination – External Remains

5.1.2.1 *Standard:* The analyst shall consider the completeness and condition of the evidence, and the presence/absence of taxonomically informative characters.

5.1.2.2 *Standard:* When the evidence item does not represent a complete organism, the analyst shall evaluate the appropriate taxonomic level to which identification can be made.

5.1.2.3 *Standard:* Age and sex characters of the evidence shall be evaluated, and the analyst shall determine whether available reference materials are appropriate for correct data interpretation and species identification. For example, a morphometric dataset based on adult mammals is usually not useful to identify remains of a juvenile individual.

5.1.3 Process of Morphological Examination – Osteological Remains

5.1.3.1 *Standard:* Skeletonization shall not be undertaken without consulting the pertinent party.

5.1.3.2 *Guideline:* Laboratories should have in place an SOP covering any required cleaning of skeletal evidence.

5.1.3.3 *Standard:* Evidence analysis shall include a description of the osteological elements examined, their physical condition, and any taphonomic or anthropogenic alterations.

5.1.3.4 *Guideline:* To determine relative age (adult, subadult, juvenile, or neonate), the analyst should first assess if sufficient material is available for analysis, then assess relevant calibrated characters for the taxon in question (e.g., epiphyseal fusion of skeletal elements or relative completeness of dental eruption or wear in mammals).

5.1.4 Process of Morphological Examination – Microscopic Structures

5.1.4.1 *Standard:* Where detailed examination of integumentary structures (such as hair and feathers) is required, macroscopic examinations shall document gross features such as color, pattern, size, or shape, while microscopic examination shall document details of external and/or internal structures.

5.1.4.2 *Standard:* Identifications shall be made with reference to collections of specimens of known taxonomic source (e.g., mounted hairs or feather barbs), or, if not available, to scientific references as defined in Section 5.1.1.3, above.

5.1.4.3 *Guideline:* If microscopic characteristics are examined or compared, evidentiary and reference hairs/feathers/scales should be mounted on glass slides in mounting media of a refractive index close to that of keratin (e.g., xylenes or xylene substitute).

5.1.4.4 *Guideline:* When morphological evidence consists of mammal hair, taxonomic identification should be determined using informative hairs, typically guard hairs.

5.2 Documentation Standards and Guidelines

5.2.1 *Standard:* In making a taxonomic identification based on morphological characters, the analyst shall document the following in the case file:

5.2.1.1 Type of material received as evidence (e.g., whole or partial organism, bone, tooth, feather, hair, ivory carving, leather, crafted item, etc.).

5.2.1.2 Intactness and condition of the evidence.

5.2.1.3 Morphological characters used to make the identification.

5.2.1.4 Reference materials and/or data sources used to verify identification.

Appendix- References

The references listed here include the key materials upon which these standards and guidelines are based, and some additional references for context or specific issues covered. This is not intended to be an exhaustive list of relevant literature.

References for General Section

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