Standards and guidelines for forensic botany identification

This document provides standards and guidelines for forensic botany identification, developed by the Society for Wildlife Forensic Science (SWFS)[1] in conjunction with members of the United Nations Office on Drugs and Crime (UNODC) Expert Group on Timber Identification[2]. The content is based on the Scientific Working Group for Wildlife Forensic Sciences (SWGWILD) Standards and Guidelines for wildlife forensic practitioners[3] but has been modified and updated for specific application to forensic botany. Scientists developing forensic botany identification methods and undertaking forensic botany identification case work should adhere to these recommendations in order to provide robust forensic evidence for court purposes. These standards and guidelines are intended to augment, not replace, current laboratory quality management systems. Consultation with relevant experts and authorities in applicable jurisdictions is recommended to ensure that all local requirements are also met.

1.0 Scope

This document provides minimum **standards** and additional **guidelines** for forensic analysts performing botany identifications using morphology, anatomy, DNA, or chemistry techniques. Forensic botany identifications include live specimens or parts and derivatives thereof. This document covers 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 botanical forensic science. The difference between standards and guidelines are defined in the Definitions section in 2.0

2.0 Definitions

Note: These definitions apply to General, DNA, Wood Anatomy and Wood Chemistry Standards and Guidelines. Definitions specific to DNA, Wood Anatomy and Wood Chemistry 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.

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[1] www.wildlifeforensicscience.org

[2] Specifically Eleanor Dormontt, Andrew Lowe and Bernd Degen.

[3] http://www.wildlifeforensicscience.org/documents/2013/01/swgwild-standards_and_guidelines_2-0_12192012.pdf

2.6 **Curated Collection** – An assemblage of reference materials acquired and maintained with associated data according to explicit quality control standards. In botanical forensic science it can consist of an herbarium or a xylarium.

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 forensic laboratories should consider implementation.

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 botanical identity or data derived from them, or from published sources. Voucher specimens are a subset of reference material (see Voucher Specimen)

2.15 **Reference Samples** – See Reference Material

2.16 **Reference Specimens** - See Reference Material

2.17 **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.

2.18 **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. The International Tropical Timber Organisation (ITTO) has defined a Standard as a document, established by consensus and approved by a recognized body that establishes common standards and repeated use, guidelines or characteristics for activities or their results, aimed at the achievement of the optimum degree of order in a given

context. The standards must be based on the consolidated results of science, technology and experience and must be aimed at the promotion of optimum benefits. A standard becomes an international standard if it is adopted by an international organization of standardization or normalization, and made available to the public (ISO and IEC 2001). A standard is of world importance if it can be used or applied widely by the affected industries and other stakeholders in markets around the world. Standards can be used as the technical basis for the trade of finished products between buyers and sellers and as a means of facilitating compliance with the technical regulations. Ideally, to be developed in a transparent process, open and based on consensus, that involves stakeholders and to define best practices for the processes (ITTO 2011).

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

2.20 **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.

2.21 **Voucher Specimen** – Biological specimen of known botanical identity and known geographical origin curated with associated field data in an appropriate herbarium/xylarium.

3.0 General Standards and Guidelines

3.1 Training and Personnel

3.1.1 *Standard:* Each laboratory conducting botanical 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 *Standard:* 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 signature or initials of all who handle the evidence

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

3.2.4 *Guideline:* Evidence subject to significant physical alteration in whole or part to assist identification should 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 *Guideline:* When physically altering evidence for the purpose of analysis, careful consideration should 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 should be consulted.

3.2.7 *Standard:* Research and casework reagents shall be kept separate. Equipment shall not be used for casework and research at the same time.

3.2.8 *Standard:* Evidence and derived data shall be stored and analysed 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 analysing casework samples, new instruments shall have their performance or function checked by analysing 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 *Standard:* 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 analysing 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 plant mixtures, tissue degradation, fungal or pathogen contamination, etc.) should be identified and evaluated.

3.4 Reference Materials and Collections

3.4.1 *Standard:* Laboratories conducting botanical forensic analyses shall consult reference materials.

3.4.2 *Guideline:* Reference materials should include voucher specimens curated in a herbarium and/or xylarium collection.

3.4.3 *Guideline:* Laboratories should prepare a Standard Operating Procedure (SOP) covering curation and preservation of each type of biological reference material used for taxonomic identification. Topics to be covered include:

3.4.3.1 Documentation and curation procedures.

3.4.3.2 Protection of materials from degradation.

3.4.3.3 Taxonomic authorities and collection arrangement.

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

3.4.5 *Standard:* The identity of a botanical reference specimen must be verified before the material is used in casework. Verification of specimens is made with reference to other previously verified specimens at hand, to voucher specimens in a herbarium and/or xylarium, or to the professional literature (e.g. taxonomic monographs, identification keys, or field guides).

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

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

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

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

3.4.10 *Standard:* Geographic provenance assignments should only be attempted with robust databases containing accurate reference samples from the geographic areas in question.

3.4.11 *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 reviewed for technical accuracy by another scientist before the report is issued. The reviews shall be documented in the case file.

3.6.3 *Guideline:* If an administrative review is performed, it should be carried out by a person other than the analyst or 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:* 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 Training plan for both experienced and inexperienced analysts. The document should specify minimal training required before individuals are permitted to independently undertake casework and should include a mechanism to evaluate competency. (See section 3.1.)

3.7.1.4 Evidence receipt, tracking, storage, transfer, and post-analysis disposition. (See section 3.2.)

4.0 DNA Standards and Guidelines

Botanical DNA analysis is the discipline within forensics which uses genetic techniques to identify plants or plant parts and products to family, genus, species, population, or individual sources. These Standards and Guidelines refer to general considerations in the application of genetic techniques to analysing botanical forensic evidence. They also provide additional specific instructions for DNA analyses currently widely employed, such as DNA sequencing for the identification of class characters, DNA fragment analysis of short tandem repeats (STRs) and typing of single nucleotide polymorphisms (SNPs) for species identification, individualization or source origin identification. It is expected that these standards and guidelines will continue to evolve as the field develops.

4.1 DNA Definitions

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

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

4.1.3 Electropherogram – A plot of results from an electrophoretic analysis generated by a genetic analyser.

4.1.4 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.

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

4.1.6 Haplotype – A set of DNA variations, or polymorphisms, that tend to be inherited together. Particularly used when referring to haploid genotypes such as those derived from organellar DNA (primarily chloroplasts and mitochondria).

4.1.7 Low Copy Number Analysis – A genetic analysis to obtain a result from very low quality/quantity samples (e.g. timber), for example by using modified DNA extraction procedures, additional PCR cycles, differing reagent concentrations, etc.

4.1.8 PCR – Polymerase Chain Reaction.

4.1.9 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.

4.1.10 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.

4.1.11 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.

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

4.1.13 Single Nucleotide Polymorphism (SNP or Single Nucleotide Variant) - A specific nucleotide position at a target DNA locus that displays (usually bi-allelic) nucleotide variation. SNPs are often used for species identification, population/regional assignment, and individualization in timber due to their suitability for low copy number analysis.

4.1.14 Short Tandem Repeats (STRs) – (Microsatellites or SSRs) 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.

4.1.15 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:* 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 determination 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 analysed 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 undertake low copy number analysis (e.g. extraction and analysis of DNA from timber) 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 material, 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:* 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 haplotype frequencies shall consider the appropriateness and completeness of the reference materials used.

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

4.4 STR and SNP Standards and Guidelines

4.4.1 *Standard:* For STRs, an internal size standard shall be run with samples to normalize peak migration differences.

4.4.2 *Standard:* For STRs, 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.

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

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

4.4.5 *Standard:* All estimates of individualization probabilities shall incorporate an adjustment for population structure or report the most conservative within population probability adjusted for sibling relatedness.
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.

4.4.6 *Standard:* When performing a population/regional assignment, the reference database shall include representative geographic coverage and be of sufficient sample size. If an appropriate population cannot be included in the comparison, the conclusions shall reflect that fact.

4.4.7 Laboratories shall have SOPs to address the following:

4.4.7.1 *Standard:* Defining an analytical threshold for alleles used to assign genotypes. These threshold criteria are determined by generally accepted values based on the analysis platform or are determined empirically by internal validation.

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

4.4.7.3 *Standard:* Distinguishing artefacts (including for STRs, stutter peaks and pull-up peaks where applicable) from true allele calls.

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

5.0 Wood Anatomy Standards and Guidelines

Wood anatomy involves the study of the structure of timber at the micro- and macroscopic levels. Determinations are based on a large set of wood anatomical characters. Each anatomical character has a relative degree of environmental and genetic influence, and as such, specific combinations of characters can serve as diagnostic identifiers of certain taxonomic groups. Wood anatomy is concerned with the observation of wood characters in three different planes, the transverse, radial and tangential, and primarily focuses on examination of the shape, size, arrangement and contents of the various cell and tissue types found in wood. For more information on the history of wood anatomy as a discipline, see Carlquist (2001) and references therein.

Wood anatomical characters can be examined at both the macroscopic and microscopic levels. Macroscopic examination can be undertaken with the naked eye, or with the aid of a small magnifying hand lens. Microscopic identification requires sectioning a sample, staining of those

sections where required and observation under a light microscope. In order to achieve a definitive identification, usually to the genus level, microscopic examination is required in most instances.

5.1 General Wood Anatomy Standards and Guidelines

5.1.1 *Standard:* The analyst shall examine, interpret, and document wood character similarities between the evidence item and reference specimens, using additional information from scientific references, as appropriate.

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

5.1.3 *Guideline:* Taxonomic determinations made on the basis of wood anatomy should be verified by an independent analyst to ensure consensus.

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

5.1.5 *Guideline:* In the absence of physical comparative reference materials, databases of taxonomically verified reference materials should be used (e.g. wood anatomy descriptions and/or images). Databases may also be used in conjunction with physical comparative reference materials.

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

5.1.7 *Guideline:* Analytical documentation and data interpretation in wood anatomy 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 where possible.

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

5.1.9 *Standard:* Identifications shall be made with reference to collections (e.g., herbariums, xylariums, etc.) of specimens of known taxonomic source or, if not available, to scientific references as defined in Section 5.1.3 and 5.1.4 above.

5.2 Documentation Standards and Guidelines

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

5.2.1.1 Type of material received as evidence (e.g., log, disc, veneer, crafted item, etc.).

5.2.1.2 Intactness and condition of the evidence.

5.2.1.3 Wood anatomy characters used to make the identification.

5.2.1.4 Other wood characters used to aid the identification: wood density of the sample, color, etc.

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

6.0 Wood Chemistry Standards and Guidelines

Analyses of wood chemistry can provide information on timber identification that cannot otherwise be determined by wood anatomy alone. Trees and other plants synthesize phytochemical compounds that are often a distinctive feature of a species or higher taxonomic group. These phytochemicals can be characterized using chemical instruments such as infra-red spectroscopes and mass spectrometers.

6.1 General Wood Chemistry Standards and Guidelines

6.1.1 *Standard:* The analyst shall examine, interpret, and document chemical profile similarities between evidence items and reference specimens.

6.1.2 *Standard:* The analyst shall consider the diagnostic value of key molecules and inter- and intraspecific variability of the characters being analysed.

6.1.3 *Guideline:* Scientific references used in wood chemistry analyses shall include primary scientific literature and taxonomic monographs.

6.1.4 *Standard:* Identification that relies on data from a public database should not be based on a single chemical profile, single chemical spectra or compound. In the rare instance where additional data are unavailable, limitations of the conclusion should be stated in the report.

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

6.1.6 *Standard:* Taxonomic identification based on chemical fingerprint data shall include considerations of:

6.1.6.1 The appropriateness and completeness of the reference material, including suitable representation of closely related species and look–alike timbers.

6.1.6.2 The plant's biogeography, life history and taxonomy

6.1.6.3 Relevant published phylogenies

6.2 Documentation Standards and Guidelines

6.2.1 *Standard:* In making a taxonomic identification or geographic assignments using wood chemistry characters, the analyst shall document the following in the case file:

6.2.1.1 Type of material received as evidence (e.g., log, disc, veneer, crafted item, etc.)

6.2.1.2 Intactness and condition of the evidence.

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

7.0 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.

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