Wood identification: an overview of current and past methods

José Luís Silva[1]; Rui Bordalo[2]; José Pissarra[3]

[1] Universidade Católica Portuguesa, School of Arts, Ph.D. researcher CITAR/
FCT in Art Conservation and Restoration, Portugal
[2] Universidade Católica Portuguesa, School of Arts, Research Center for the
Science and Technology of the Arts, Portugal
[3] Green UPorto and Department of Biology - Faculty of Sciences, University of Porto, Portugal

Abstract

Wood identification is an expertise vital in a variety of fields, from industry to art. Identification of the wood in works of art is usually underappreciated but it is as important as difficult. This article aims to provide heritage professionals with a brief overview of wood identification procedures available today, as well as, from an historical point of view, the methodologies that paved the way to the new approaches used nowadays. It also discusses some techniques that the general public usually relate with wood identification but that are meant to determine wood original location (stable isotopes), specimens dating (Dendrochronology) and geological dating (Radiocarbon, 14C). The final aim is to clarify the diverse procedures, with its advantages and limitations, that can be used for wood identification in works of art.

Keywords

Wood identification, Works of Art, Techniques, Preservation, Conservation & Restoration.

Introduction

The scientific identification of wood has an increasing economic, commercial, social and ecological importance and its application extends to diverse areas such as Biology, Timber Industry, Civil and Structural Engineering, Criminology, Art History, Ethnography, Archaeology, and Conservation and Restoration among many other disciplines.

The methods that allow the identification of wooden materials are several and range from the observation at naked eye to the most advanced DNA procedures. In between, there are many common suppositions and misunderstandings by the non-specialist professional that makes the subject of wood identification something very complex and apparently difficult to reach to most people.

This article presents an overview of the methods used for wood identification, ranging from the most primitive systems to the most advanced technical approaches used nowadays. Although there are many other methods, it was decided to focus this article exclusively in methodologies used with some regularity and with publications in the specialised literature. With this, the goal is also to clarify techniques that apparently may allow the identification of wood but are intended for other purposes such as wood dating, geographic origin of the wood, among others.

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Evidently, in an overview article, the descriptions of each technique are necessarily brief and focused in giving the basic information and possibilities of each method and, when necessary, direct the reader to in depth literature about each subject.

Principles of identification of wood

Wood its present all around the world and it is a human resource since the dawn of mankind.

The distinction between a conifer and a deciduous tree is accessible for most people, as is the interpretation that wood is constituted as a unified tissue. However, this could not be further from reality.

Wood is a complex tissue constituted by a multiplicity of different cells with different purposes and visual aspects and is through the analysis of the microstructure as the identification and quantification of the chemicals accumulated in this tissue that we can access to the comprehension and manipulation of this extraordinary material.

Specifically, the identification of a tree or shrub through its leaves, flowers and bark is much less problematic than when we have only access to a small wood sample. In this case, the identification has to resort to macroscopic characteristics such as colour, density, or weight to microscopic structures as cell distribution, diameter and length, and their functions as storage or support. Additionally, we may also resort to methods that analyse DNA, radiocarbon or identify particular chemical components specific or representative of the family, the genus or the species to which that wood belongs.

Problems in identification of biological materials

In Biology, every organism is classified according to a taxonomic hierarchy. For this, they are grouped in organizational levels according to several of their shared characteristics. These levels go from the most generalist to the most particular ones. For example, in the case of the European Oak (*Quercus robur)*, its taxonomic classification is as follows (adapted from ITIS, 2020):

- Kingdom: Plantae (plants)
  - Subkingdom: Viridiplantae (green plants)
    - Infrakingdom: Streptophyta (land plants)
      - Superdivision: Embryophyta
        - Division: Tracheophyta (vascular plants)
          - Subdivision: Spermatophytina (seed plants)
            - Class: Magnoliopsida
              - Order: Fagales
                - Family: Fagaceae
                  - Genus: *Quercus* L. (oak)
                    - Species: *Quercus robur* L. (European oak)

Thus, as it can be seen above, the final objective when identifying a certain wood sample is always to determine the species (the most specific level possible) to which the sample belongs. However, often only the determination of the genus, or even family, is possible. Not being able to reach an accurate identification is a shared problem in the many fields of Biology and not a specific wood identification issue. The difficulties and the reasons behind it are the same as for any other biological material (Fortuner, 1993).

Specifically in wood identification, one of the most common reasons, among others, that prevent an accurate identification is the lack of critical features on the sample under analysis. This is even more frequent to occur when analysing increasingly smaller samples and when dealing with badly preserved fossil wood or decayed wood.

A deficient reference base that can extend to a non-existent or limited xylotheque, added to the fact that the true range of variability of a taxon might not be fully known (since probably not all species are present on the reference database that the user may have access to) are also common issues that hinder the identification.

The wood features recognition is another usual problem in this area, since it can include errors in the recognition of the visible features or misinterpreting the feature described or present on the database used by the researcher. The reason behind this difficulty is the lack of background or training on the users' side.

The use of different terms to refer to the same feature is an issue that has also been gradually disappearing since a common wood anatomical vocabulary has been defined by using the IAWA Features Lists (Wheeler, E.A., P. Baas & P.E. Gasson, 1989).

Finally, it is always necessary to take into consideration the inherent variability of internal wood anatomy being the boundaries between some features not precise; therefore, intermediates forms between two features can easily be interpreted by different anatomists in different ways by the different users.

The number of existing woody species is 281,621 described and, as a global estimate, including both described and undescribed, of 368,050 (Chapman, 2009). A considerable amount has never been anatomically described or, if so, are only based on a few or even on one single sample. This fact has a direct reflex on the range of variability that certain species have and that are not described.

It is common knowledge that there is intraspecific variability, for instance, the variation among individuals of the same species coming from different geographic locations, but there is, also, within-tree variation (like variation across organs -root, trunk, branches-, radial variation –sapwood/heartwood-, and axial variation -juvenile/mature wood). Examples of this are the ray size and cellular composition, which often varies with its position within the tree, the cells of the tree trunk that are bigger than the ones from the branches, or the cells from the root, which present different quantitative and qualitative features (as parenchyma abundance and distribution, porosity, ray type, etc) than the ones from the trunk (Panshin & de Zeeuw, 1980).

Identification Methods

There are several different methods to achieve the identification of any given wood. These range from visual methods that use distinct approaches to obtain information from the wood sample, to analytical techniques that provide distinct results and data.

Historical Identification Methods

Visual comparison is most likely the most frequently used method for wood identification. The main resource are atlases with high quality photographs illustrating the most defining characteristics of every specific wood. They usually contain photographs and a descriptive text of the wood anatomical characteristics, even though one of the most popular CSIRO Hardwood atlas (Ilic, 1990) only contains photographs. This extensive atlas provides good quality histological photographs (cross, radial and tangential sections) of nearly 1800 species. Other important atlases from around the world are summarised in Table 1.

Table 1 – *Main wood identification atlases for different regions of the world.*

Regions		**References**
Europe	**European species**	Schweingruber, 1990
	Mediterranean	Edlmann A.M.L., L. de Luca & S. Lazzeri., 1994
	Britain and Northern Europe	Cutler D.F., P.J. Rudall, P.E. Gasson & R.M.O. Gale., 1987
Middle East	**Israel and adjacent regions**	Fahn, A., E. Werker & P. Baas., 1986
	Iran	Parsa P.D. & EH. Schweingruber, 1985
North America	**General**	Furono, T., 1985
	Mexico	Barajas, M.J. & C.L. Gomez, 1989
South America	**Chile**	Rancusi, H.M., M. Nishida & H. Nishida, 1987
	Peru	Acevedo Mallque, M. & Y. Kikata, 1994
Africa	**General**	Nardi, B.R. & Edlmann, A.M.L., 1988
		Liu P., Jiang X. & Zhang L.F., 1996

Asia/ Australasia	**Southeast Asia and Pacific**	Ogata, K. 1985 Menon, P.K.B., 1993 Soerianegara, I. & R.H.M.J. Lemmens, 1993 Lemmens, R.H.M.J., 1995 Sosef, M.S.M., L.T. Hong & S. Prawirohatmodjo, 1998 Martawijaya, A., Kartasujana, K. Kadir & S.A. Prawira, 1986 Martawijaya, A., Kartasujana, Y. Mandang, S.A. Prawira & K. Kadir, 1989
	Papua New Guinea	Sudo, S., 1988
	Brunei	Ogata, K. & A. Kalat, 1997
	Korea	Lee Pil-Woo, 1994 Wong Yong Lee. 1997
	Himalayas	Suzuki, M. & S. Noshiro. 1988 Suzuki, M., S. Noshiro, A. Takahashi, K. Yoda & L. Joshi, 1991 Wheeler & Baas, 1998

Dichotomous keys

The most frequent identification keys to identify organisms in the natural world are dichotomous keys. The word "Dichotomous", meaning "divided into two parts", is a clear indicator of the mechanism used for this method of identification. A Dichotomous key works by giving the user two choices, or a couplet. Each question or describable characteristic leads the observer to the next question until all the questions are answered, leading the user to a correct identification of the item in question, which for wood could be the species, genus, group of genera or family.

A dichotomous key is a single-access key system, where its developer guides the observer to look for characteristics that the developer finds important and with distinguishing capabilities. The effectiveness and speed of results of any dichotomous key is directly related to those choices. The smaller the number of matches, the more effective are the keys. Although the absence of specific features does not inevitably compromise the identification, it may compromise the desired results when these shortcomings represent referential and fundamental characteristics.

The longer the key, however, the more likely there will be an error in choosing the correct descriptor at any one couplet. As a reference, keys with over 200 taxa are particularly prone to mistakes (Pankhurst, 1978, 1991).

Computer software can be of great help on the development of dichotomous keys by calculating the information content of features, and how to use the features to divide the species into groups (Wheeler & Baas, 1998).

Multi-access keys

A Multi-access key overcomes the issue imposed by single-access keys, such as the previously described dichotomous key, where the user is limited to a structured path of predetermined steps. In fact, Multi-access keys enable the user to freely choose the individual characteristics that are considered more adequate to describe the item to be identified and to adapt the key to the item and circumstances of identification.

The term Multiple-entry key is frequently used as an alternative term to Multi-access key, but in fact it is not the same. A Multi-entry key allows the user to freely choose only the first step while in a Multi-access key, the choice of characteristics by the user can be repeated multiple times, reducing thus the number of remaining taxa each time (Pankhurst, 1991).

A variation of this is the synoptic key where the sequence of features surveyed is inspired by the sample to be identified and not by the author of the key, since it is the key itself that names first each diagnostic feature and then identifies the taxa that have that same diagnostic feature.

The above key systems are based in cards, where there is one card per taxon. Each card has sequentially numbered perforated edges where each perforation represents a feature. Usually, if a given wood has a particular feature, the edge of the card will be notched to indicate the presence of that feature.

To identify an unknown sample, a needle is passed through a stack of cards at the perforation representing a feature seen in the wood. Thus, cards of species with the feature absent stay on the needle, the cards with the feature present fall out. The sorting process is repeated until a single or only a few cards remain.

Despite only one feature is used at a time in multi-entry keys, the sequence and the total number of features used are a choice of the expert, being this capability a characteristic that turns the type of keys particularly useful when the objective is to identify wood samples where some features are not present. In these identification systems with cards, the number of features present was limited to the number of holes that the card could fit along the margins, which was generally less than 100. This limitation obviously was surpassed when this type of keys were computerized.

The capability of obtaining one single name when using a multi entry key is one of the advantages over the dichotomous keys exposed above. However, species not included in the key or one or more features that are not present may occur. In this case, comparing similar features of the unknown sample allow to narrow down the possibilities as well as the expert to decide which features are identifiable or closer to those present on the unknown sample.

Visual Identification Methods

· Macroscopy

Even though it is, without any doubt, the oldest wood identification method, macroscopy cannot be discarded as an unreliable method. Nowadays, instead of being considered a method of identification of wood samples, it should be regarded as a way to discard possible species. It is especially useful used *in loco*, such as when a customs officer has to determine if certain woods are from illegal logging or not. After this preliminary but very decisive identification step, a more advanced methodology is necessary to reach the species level of identification (UN *et al*., 2016).

Macroscopic identification evaluates features such as weight, density (Bessa, 2009), hardness, texture (Esteves, 2001), characteristic colours such as purple heart (*Peltogyne* spp.), pink ivory (*Rhamnus zeyheri* Sand.), or boxelder maple (*Acer negundo*) (Burger & Richter, 1991), and visual anatomical characteristic features. On the latter case, for example, the *Quercus* species has a very distinct ring porous arrangement but, in particular, it has a very notorious presence of the radial structure (Wheeler & Baas, 1998).

Odours are also a relevant feature, especially for certain particularly odorous woods as pine (*Pinus* spp.), stink wood (*Ocotea bullata* E. Meyer), cedar (*Cedrela* spp.), sandalwood (*Santalum album* L.). However, odour is ephemeral and woods may acquire smells of its surroundings (Wheeler & Baas, 1998).

The amount of obtained information increases exponentially with the aid of hand lenses. In this case, the anatomist may observe features like porosity, vessel arrangement, axial parenchyma arrangement, ray size and height, presence and abundance of tylosis, vessel diameter (Wheeler & Baas, 1998) as well as other observable features at the surface of the sample.

The level to which an identification can be done varies within and between families. For example, in *Annonaceae* usually is not possible to identify individual genera; in *Betulaceae* (Birch family) it is possible to identify individual genera, but not species; in *Ulmaceae* (Elm family) native to the United States, it is not possible to distinguish any one ring-porous species of *Celtis* from another, but it is possible to distinguish *Ulmus americana* from *Ulmus rubra* and from the hard Elm group (Wheeler & Baas, 1998).

· Microscopy

Wood identification trough microscopic analysis of the wood anatomy is the most common, recognised and enduring method for wood identification available at the moment. This methodology has already a long history and is still the most frequently used technique nowadays when identification is needed.

The "traditional" method requires three cubes of 1 cubic centimetre, being each one exclusively used to obtain transverse, tangential and radial histological sections (Hather, 2000).

However, when dealing with art objects, the size of the samples must be the smallest possible and, more often than not, only one sample can be removed from the art piece. Therefore, it is possible that the sample is too small or fragile to handle and sectioning. In this case, it is necessary to embed the sample in an appropriated resin that, after several steps that include the gradual penetration of the resin in the sample through a vacuum chamber, will result in a solid object ready for sectioning with a microtome (Hamann, Smets & Lens, 2011). The sections should vary between 8 and 30 micrometres in thickness (Carlquist, 2001).

From there, the histological sections go through a series of cleaning, clarifying and colouring procedures. These coloured histological sections are mounted in a microscope slide with a cover slip and after drying are ready for microscopic analysis and storing.

This methodology allows the anatomist to observe and compare the structure of the sample, referring to characteristics such as vessel arrangements, parenchyma type, number and typology of ray cells and numbers. Beyond that, it is literally possible to analyse the interior of the wood sample through the transparency provided by the thinness of the histological sections. With this, the anatomist has access to elements such as the perforation plates, punctuations, and thickenings, that may be difficult to analyse by other ways (Esteban *et al*., 2003).

The limitation of this methodology is mostly related with the lack of anatomical differentiation characteristics between species of the same family (such as *Larix* and *Picea*, both from the *Pinacea* family) and, although not very commonly, between different family's (such as *Lonicera xylosteum* (*Caprifolliaceae*) and *Ligustrum vulgare* (*Oleaceae*) (Hather, 2000).

Other constraint of this method is that the anatomist must be highly trained to recognize and interpret the sample's features to compare them with the available bibliography. At the same time, the advantage is that computer programs already available are, in a way, relieving the anatomist of most of the comparison processes and gradually providing more accurate identification.

The great strength of identifying wood through its anatomy is that unknown samples can be identified with a cheap and fast methodology, at least to the genus level, facilitating in that way sub-sequential analysis that may reach the species level (Dormontt, 2015).

· Scanning Electron Microscopy

Unlike common optical microscopy, Scanning Electron Microscopy (SEM) is capable of magnifications from 20x to up to 30,000x and spatial resolution of 50 to 100 nm by which it is an outstanding technique to image the sample's topography in high detail (Esteban *et al.*, 2003).

When compared with results obtained with the microscopic analyses of wood structure (Carlquist, 2001), this technique allows a characteristic three-dimensional appearance, given by the large depth of field achieved, producing surprising results. This is very useful when the objective is to understand the sample's surface structure or specific details.

These microphotographs have an extremely high-resolution that allow the observation of the smallest details, spatial configuration and architectonic morphology (Esteban *et al*., 2003), which is the anatomist's objective (Carlquist, 1988). These features occasionally lead to the identification of not just of the genus but also the species level.

This method uses, ideally, a cubic sample of around 10 mm wide x 15 mm high already cut with the three sections plans exposed (transverse, tangential and radial). Because of the extreme detail that this technique allows, these cuts should be made with a microtome or a ultramicrotome to avoid that the flaws of the blade interfere with the observation.

Since this method traditionally requires a vacuum chamber, the sample is submitted to a great negative pressure, being advisable special care when dealing with fragile samples. Good examples of this effect are found when observing samples from softwoods where the torus of the areolate punctuations can collapse, or from hardwoods the lactiferous tubes or mucilages can form big bobbles coming out from these tubes, which naturally will affect greatly the observation capacity of the sample (Esteban *et al*., 2003). To avoid such situations, a Variable Pressure SEM may be used instead since the pressure upon the sample can be controlled (Cartwright *et al*., 2012b).

· Computer-assisted wood identification

Long before the emergence of personal computers and the technological revolution that came with them (Wheeler & Baas, 1998) the use of computers as an aide for wood identification was first discussed in 1980 (Miller, 1980). Since then, several wood identification software and databases are available with different levels of efficiency.

Two of the first truly relevant computer programs were GUESS and CSIROID program (Wheeler & Baas, 1998). The GUESS program is based on the OPCN database (an 1986 database whose acronym reflects its sources of information: Oxford, Princes Risborough, Centre Technique Forestier Tropical, North Carolina State University) (InsideWood, 2004). By its turn, OCPN is based on the Oxford Key cards collected by Chalk during the preparation of 'Anatomy of the Dicotyledons' (Metcalfe & Chalk, 1950).

This program proved to be very practical by presenting lists of species that have a specific set of characteristics or by indicating which family or genus may be related to the sample under analysis. It also proved to be particularly useful for the identification of uncommon woods or specimens that are very difficult to identify such as woods with unknown geographic origin or geologically ancient woods, in which an individual match may be unlikely due to the evolutionary differences between fossils and existing species. However, for common commercial woods in Europe and North America, it would probably be quicker to use keys in speciality books or to compare the sample with illustrations and descriptions in atlases.

The GUESS program aimed at reducing the process of comparative identification and, when necessary, to direct the researcher to the relevant literature, whether a publication, specific group of texts or regional atlases (Wheeler & Baas, 1998).

The CSIROID program was developed to use the CSIRO key (Ilic, 1993) but it also includes the Family key (Ilic, 1987), the Macro key (Ilic, 1990) and the Eucalyptus key (Dadswell & Eckersley 1941). It is an interactive program that allows the introduction of more than one feature at a time. It also presents the possibility for the user to define the "best subsequent feature" which allows the definition of what are the best and more effective features that might be useful for eliminating other taxa. Another very effective advantage is that the "best subsequent feature" option offers on-screen text descriptions of the features.

By recognizing that the features identification is the main problem for most users, the CSIRO books possess high quality illustrations and descriptions of the key features and, as mentioned already, an on-screen help.

The CSIROID program does not allow for mismatched features and so does not have required absence or required presence. This allows a different level of confidence in the databases; however, Wheeler (1986) recognized the presence of some misidentified woods on the Oxford card data (OPCN key). For that reason, an option to allow for mismatches to accommodate variability, especially important when dealing with geologically ancient woods is present on the GUESS program.

The best-known wood identification program available is probably the DELTA-Intkey. The DELTA system (Dallwitz & Paine, 1986) is structured as a general system for processing taxonomic descriptions, and, for that end, has several programs, being the Intkey focused on wood identification.

This is an interactive program that allows the entry of one or more features at a time and can suggest which features can be useful for distinguishing between remaining taxa. Is also possible to obtain a list of matches at any point.

Unlike GUESS or CSIROID programs, the DELTA format uses both numeric characters and text characters. These are not used to identify the wood, but are useful information in text descriptions (Wheeler & Baas, 1998).

More recently, some other software has been developed, especially focused on *in loco* identification of commercial timber.

XiloTron (Ravindran *et al*., 2020), for example, is an open-source, Image-Based Macroscopic Field Identification program that is described as a platform for identification and metrology of materials that show useful macroscopic variability, in the specific case, wood and charcoal. It provides controlled visible light and UV illumination capacity, adjustable illumination positioning and all the necessary software to control the device, capture images, and deploy trained classification models for field screening. Performs trough the capture of high-quality images of the wood or charcoal samples with visible or UV light. The identification success rate for wood is assumed on the 97.7% and 99.1% with the use of UV light (e.g. identification doubts between *Robinia* spp. and *Morus* spp. and between *Ulmus rubra* and *Ulmus americana*), being of 98.7% for charcoal (Ravindran *et al*., 2020). New applications are being developed also to provide identification on wood veneers and various types of synthetic products. It is particularly focused on the ability of being used on the field in real time (Ravindran *et al*., 2020).

Most of these software are based on automated machine vision, that is automatic recognition of patterns, from an image provided by the user, decomposed and processed by the computer in order to establish a description scheme to which the unknown sample image will be referenced (Martins, Marcal & Pissarra, 2019).

Automated machine vision algorithms are able to detect and quantify variations on the wood structure that are not perceptible under a strictly human analysis, and is plausible that better and more precise data will be achieved with future research (Hermanson & Wiedenhoeft, 2011; Martins, Marcal & Pissarra, 2019). However, it is important to refer that for the system to interpret the sample's specificities with such a precision level, an integration of reference material is required into the image database to allow that the wood structure natural variations of a specific sample are captured (Dormontt *et al*., 2015).

Several approaches are underway, being one of the most relevant the integration of image classification based on deep learning, more specifically, Convolutional Neural Networks (CNNs). These are an artificial neural network class of feed-forward type, having been successfully applied for digital image processing analysis, which has made possible to increase the correct identification rate up to 95.6% (Lens *et al*., 2020).

· Dendrochronology

Dendrochronology studies the growth rings for dating purposes. It is so well developed that the study of the ring increments from a specimen of a temperate area provides data concerning the environment where the tree had grown, when it was cut and its life span. It can also provide a valuable record of the general and specific environmental conditions such as fire, diseases, climate variations and other external occurrences (Speer, 2010).

Even though very useful to study wood development, dendrochronology cannot be widely used for wood identification. At most, it can give a specific match if the objective is to identify a specific individual age by comparing the tree rings of the sample (ideally a log) with the pattern present on a specific stump (UN *et al.*, 2016).

Although it is mainly used when dealing with archaeological wood from temperate regions with visible annual rings, it is possible to compare tree ring series to reference chronologies to conclude if the pattern is consistent with a particular area/region (Haneca *et al*., 2005).

Analytical Identification Techniques

The analyses of the chemicals present on the wood of a sample can, in many cases, be more relevant for its identification that other identification methodologies (Dormontt *et al*., 2015). Below are some of the most used analytical techniques for wood identification.

· Mass spectrometry

Mass spectrometry, in essence, ionizes chemical compounds to generate charged molecules in order to measure the mass-to-charge ratios. In wood science, it is used to characterize phytochemicals present in the heartwood, determining if they are extractives, exudates, or metabolites (UN *et al*, 2016). After measured, it generates a chemical profile that through statistical analysis can group taxonomically related individuals. This chemical profile grouping can be used to point unknown samples to reference groups and, depending on the natural variation in extractives present in the wood samples, different levels of taxonomic identification may be achieved as demonstrated in several key publications, e.g. genera level (Lancaster & Espinoza, 2012), species level (McClure, Chavarria, & Espinoza, 2015) and even wild vs. cultivated (Espinoza *et al*., 2014). However, it is important to note that classification models are only valid for taxa included in the reference dataset.

The usual methodology of mass spectrometry involves extensive sample preparation steps due to the requirement for ionization in vacuum (Cody *et al*., 2012). However, ambient atmospheric ionization techniques, minimizing sample preparation steps and providing very fast results, specifically the Direct Analysis in Real Time, Time of Flight Mass Spectrometer (DART TOFMS) (Cody, & Dane, 2010), have shown great promise when used for timber identification (Musah *et al*., 2015).

· Near infrared spectroscopy

Near infrared spectroscopy (NIRS) technique measures the absorption spectra of materials when exposed to near infrared electromagnetic energy (UN *et al.*, 2016).

Traditionally, NIRS has been used to estimate wood properties, but less frequently for wood identification (Tsuchikawa & Schwanninger, 2013).

As a great advantage, NIRS can be used either in solid wood as well as small particles such as pulp. When used on solid wood, the information obtained derived from both the chemical and physical structure of the wood.

It is important to note that the raw spectroscopic outputs usually are not directly informative and must be used in conjunction with appropriate multivariate analyses to obtain meaningful results (Pastore *et al.*, 2011).

NIRS has the potential to return accurate results with minimal sample processing and specialized skills required of the operator (UN et al, 2016). Research results indicated that is possible to distinguish between individuals of different genera (Pastore *et al.*, 2011; Braga *et al.*, 2011), different species within the same genus (Adedipe *et al*., 2008), and between the same species in different regions (Sandak, Sandak, & Negri, 2011). Despite its advantages, NIRS to be used for wood identification still has to improve and evolve, and further research is needed.

· Stable isotopes

Every chemical element has one or more isotopes. These vary from the regular atom in the number of neutrons, making it have a similar behaviour but a different atomic mass and physical properties.

Their unique characteristics allows its use in a wide variety of areas, including its detection and identification when they are present in chemical compounds that are synthesized by trees to acquire their raw constituent elements from the surrounding environment (UN et al, 2016). These various stable isotopes ratios fluctuate in nature and can be correlated with various climatological, biological and geological variables (UN *et al*., 2016).

By the analysis of informative stable isotopes that commonly include bioelements such as carbon, hydrogen, oxygen, nitrogen (Fry, 2007) and other elements such as sulphur (Thode, 1991) and strontium (Voerkelius *et al*., 2010), an isotopic signature of a given area can be determined (Dormontt *et al*., 2015).

The oxygen isotope ratio of plant tissues reflects the isotopic composition of the water source for plants as well as the effect of transpiration, which is influenced by climate (Barbour, 2007).

After the analysis of these ratios of a given area, an isotopic “fingerprint” of a location can be determined making possible to use stable isotopes to identify the region of origin of a wood sample, which means that this technique is mostly suited to draw conclusions when it comes to geographic provenance at the broad regional level where appropriate reference databases exist (Förstel *et al*., 2011).

· Radiocarbon

Such as the stable isotopes, carbon occurs naturally in nature as the radioactive isotope ^{14}C, better known as Radiocarbon[14].This isotope decays naturally to ^{14}N, a stable nitrogen isotope, during which one of the neutrons in the carbon atom becomes a proton. The time it takes for ^{14}C to radioactively decay to half of the original amount, is defined by its half-life. ^{14}C has a half-life of 5730±40 years (Godwin, 1962).

The formation of this isotope occurs in his greater part in the upper atmosphere trough natural nuclear processes.

After oxidation to $CO_{2,}$ ^{14}C spreads through the atmosphere and ends being present in the earth soil and oceans. After its formation, this element starts to decay following its half-life and the balance between production, mixing and decay will result in quasi-constant ^{14}C concentrations in various carbon pools of Earth's system (UN *et al*., 2016).

Specifically, carbon is retained by plants from atmospheric CO_2 via photosynthesis and is in that moment that it is no longer exchanged with the surrounding environment through processes as respiration, and by remaining in the organism body (e.g. tree trunk) starts consequently its expected decay to ^{14}N (Dormontt *et al.*, 2015; UN *et al.*, 2016).

It is by the decay measurement and after comparison with known standards that the radiocarbon age of the organism in analysis can be calculated.

The conversion of radiocarbon age into calendar age, being IntCal04 (northern hemisphere) and SHCal04 (southern hemisphere) two internationally agreed calibration curves (data sets) (UN *et al.*, 2016), is based in data sets obtained from independently dated tree ring and marine samples (Reimer *et al.*, 2004).

In conclusion, radiocarbon dating can be used only to determine the age of the wood sample in analysis (Uno *et al.*, 2013).

· DNA barcoding

DNA analysis is seen, very justifiably, as the last and most precise method of identification of any organic material and the ability of this technique to give specific and very accurate result when wood identification is needed is not an exception.

The foundation of the technique is that a particular gene region presents distinguishable genetic variation that allows the differentiation between species (Hebert, Cywinska, & Ball, 2003).

In natural forests, individuals of the same species that are present in a specific area, frequently show a greater genetic proximity the closer they are geographically and this phenomenon is called spatial genetic structure (Hardy *et al.*, 2006).

This genetic "portrait" in natural populations is shaped by several factors such as migration and extinction history (Hardy *et al.*, 2013) and genetic variability via pollen and seed dispersal (Loveless & Hamrick, 1984).

According to the International Consortium on Combating Wildlife Crime (UN *et al.*, 2016), only 70% of plants can be identified through the two gene regions that are the standard markers for plants, while the remaining species determination requires additional gene regions, known as local barcodes.

DNA barcoding can be used as part of a species discovery process or for specimen identification (Collins & Cruickshank, 2013), although species discovery utilizing DNA barcoding will very much constitute the main background to substantiate robust species identification (UN et al, 2016). With this, DNA barcoding is a technique that gives solid information concerning the phylogeographic (regional) level within species, but most importantly concerning this article, allows the identification to the species level or higher.

Discussion

Although most of the methods used for wood identification mentioned here are based in high-tech solutions, and hence out of reach for most heritage professionals on a daily basis, there are still some that can be used on a regular basis with positive results for these professionals.

Where the macroscopic examination shines on as quick on the field preliminary identification, microscopy stands out as the most well established, well known and economically efficient method nowadays as a regular resource for wood identification. Despite that, improvements can be made on the sample size required for identification and on the adaptation of this technique to specific subjects as wood identification of works of art.

Techniques as near infrared spectroscopy, mass spectrometry and DNA barcoding clearly stand as on the rise methods with solid results that, with future research, will improve the precision of the information obtained presently and naturally become more accessible, available and well known.

However, it is unavoidable to assume Computer-assisted wood identification technology as the spearhead of nowadays approach to wood identification science; nonetheless, as seen above, the most promising software (Lens *et al*., 2020) still needs to have access to histological wood sections, showing that no method is 100% independent in wood identification.

Conclusions

The combination of disciplines is no longer an option but a necessity in what concerns to obtaining a correct, time efficient and legally binding wood identification.

Although multiple methods can respond to the same questions, the accuracy may be improved if more than one method is used. This do not exclude that nowadays most of these techniques present a notorious gap between its potential and real applications, which is the reason for wood anatomy analysis through microscopy and DNA to be the only mature disciplines capable of being applied in a more frequent basis.

The fact that the identification through wood anatomy is the oldest, most common, fastest and cheapest method do not diminish or invalidate any of the new approaches since, as seen above, every technique has its benefits and limitations.

The palpable value of each approach for wood identification is that when one technique finds its limit, another one can give its contribution from that same point forward, for the ultimate goal is achieving a correct identification of the wood sample in analysis. For all these reasons, it becomes clear that the view is changing and a new way of collaborative thinking is emerging.

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Author’s *Curriculum Vitae*

José Luis Silva initiated his superior education in 2000 with a Bachelor degree on Arts, Communication and Design, variant Landscape Design at Instituto Politécnico de Viana do Castelo, following from 2010 to 2015 a Graduation and Master’s degree in Conservation-restoration at Universidade Católica Portuguesa, Oporto. He started his professional career as a conservator-restorer specialist in wood in 2007, working for several companies. He is presently working at FRESS - Fundação Ricardo do Espírito Santo Silva, Lisbon and being CEO at the conservation and restoration and decorative arts company Cádmio - Decorative Systems. His main investigation line is focused on conservation of wood works of art, wood technology and wood identification adapted to art objects.

Contact: jl_6@hotmail.com

Rui Bordalo (cienciavitae: EE16-F237-8016) is graduated in Art Conservation (2003). He holds a PhD in the area of Heritage Sciences by the Courtauld Institute of Art (2011), specialized in the analytical characterization of artistic materials. At present, he is an integrated member of CITAR where he is developing research within the GEO-SR project.

Contact: rbordalo@porto.ucp.pt

José Pissarra (cienciavitae: EE1F-B3CE-1FA1) is a national specialist in plant anatomy and physiology and an associate professor in the Department of Biology of the Faculty of Sciences of the University of Oporto.

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