# Tracing the world's timber: the status of scientific verification technologies for species and origin identification

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**Summary** – Illegal logging and illegal timber trade is a global problem. Anatomical, genetic, and chemical techniques support illegal logging legislation by verifying the species and geographic origin of timber. In principle, these methods can be used to identify timber species and the origin of harvest, however, the availability of specific tests for important timber species is unclear. We review the status of these methods for the top 322 global priority timber taxa. Our results show that for species identification, reference data exist for 100% of taxa using wood anatomy, 86% using genetics, 41% for using DART TOFMS, and 6% using NIRS. For origin identification, data exist for 24% of taxa, with most studies applying genetic approaches (23%). No studies have developed forensic-ready tests for the global priority timber taxa. The review highlights that the current potential for identifying species is greater than for geographic origin and more research focused on determining the geographical origin of timber is required. Based on the current rate, it will take approx. 27 years to generate geographic data for all 322 priority taxa. Finally, we identify research opportunities to improve global timber tracing efforts. Our findings indicate more research is needed, and quickly so that scientific verification can support regulators to combat illegal logging.

**Keywords** – illegal logging, timber tracking, DNA barcoding, wood anatomy, DART TOFMS, NIRS, stable isotopes.

## Introduction

Illegal logging is a major global issue that has negative environmental, economic, and social impacts including deforestation and loss of biodiversity (Nellemann & INTERPOL 2012; Hoare 2015; Kleinschmit *et al.* 2016; Vijay *et al.* 2016). In this review, the term illegal logging encompasses 'all practices relating to the harvesting, processing, and trading of timber inconsistent with national and sub-national law' as per the definition given by Kleinschmit *et al.* (2016). It has been estimated that illegally logged products may account for 15–30% of the total global trade in timber (Nellemann & INTERPOL 2012) and is worth tens of billions of dollars per year (Hoare 2015; Jianbang 2016). For example, in 2014 illegal logging was considered more profitable than any other natural resource crime, including wildlife trafficking, illegal fishing, illegal mining, and crude oil theft (May 2017). Illegal logging is most problematic in the tropical forests of Southeast Asia, Central Africa, and South America, where, depending on country, illegal logging accounts for 50–90% of the volume of all forestry (Nellemann & INTERPOL 2012), the boreal forests of Russia's Far East are also a hot spot where up to 50% of logging is illegal in some regions (Wyatt 2014).

In response to the mounting threat and activity surrounding illegal logging, several countries have introduced, or are in the process of developing, legislation aimed at eliminating, or at least reducing, the trade of illegally harvested timber and timber products. For example, Canada (Wild Animal and Plant Protection and Regulation of International and Interprovincial Trade Act 1992), the United States (Lacey Act 2008), Australia (Illegal Logging Prohibition Act 2012), the European Union (European Union Timber Regulation 2013), Japan (Japanese Clean Wood Act 2017) and the United Kingdom (United Kingdom Timber Regulation 2021) have implemented legislative measures to combat the trade in illegally logged timber and wood products (Lowe *et al.* 2016). More recently Indonesia, Japan, South Korea, Malaysia, and China have taken steps to develop laws to prevent the import of illegally logged timber, and combined with the US, EU, and Australia these markets represent approximately 90% of the internationally traded timber in 2016 (Norman & Saunders 2017). Along with forest management measures such as selective logging (Edwards & Laurance 2013) and plantation forestry (Bremer & Farley 2010), legislation developed to combat illegal logging and the illegal timber trade is fundamental in the plight to preserve biodiversity worldwide.

### Scientific verification techniques for tracing timber

The accurate determination of species and timber origin are key to both demonstrating compliance in timber supply chains and policing illegal logging practices where a perpetrator is not 'caught in the act' of cutting down a tree (Dormontt *et al.* 2015). The taxonomic identification of timber products is often challenging as timber lacks the diagnostic features required for plant identification such as leaves, flowers, and fruits. To ascertain legality or compliance, however, identifying or verifying the species or genus of the timber is required. Under national laws or international agreements such as the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES), some but not all species in a genus may be protected and hence need to be differentiated. The determination of timber origin is called for where timber species are protected or trade-restricted, in the case of some species in CITES Appendix III, from certain areas (e.g., country, state, logging concession, plantation) of their geographic range. There are several common methods used to incorporate illegally sourced timber into otherwise legal supply chains, including forgery of compliance documentation presented at customs inspections, audits, or required by certification schemes; and mixing of illegal timber with legal timber (INTERPOL 2016). The ability to use characteristics inherent in the timber itself to accurately trace back through the supply chain to the geographic origin of timber (e.g., region, country, plantation, or even to a specific tree from which timber has come) enables the verification of claims made by compliance documentation and hence the legality of timber supply chains (Dormontt *et al.* 2015; Lowe *et al.* 2016).

Scientific techniques for timber tracking based on inherent characteristics (as opposed to externally introduced markers) include structural (wood anatomy, manual or machine vision), chemical (mass spectrometry and near-

infrared spectroscopy), and genetic methods (DNA barcoding, population genetics, and phylogeographic studies and DNA profiling). These techniques vary in (i) what they can identify (i.e., species, genus, geographical origin, individual), (ii) their potential to be used for screening on the front-line (in the field or at customs) or as diagnostic laboratory methods, and (iii) logistics such as cost, processing speed, equipment, and technical expertise required and have been reviewed and compared by Dormontt *et al.* (2015), Schmitz *et al.* (2020) and Schmitz (2020). The identification of species and geographical origin may be used to verify compliance documentation and the integrity of timber supply chains or, if the impetus exists, as forensic evidence in a court of law. To be used as forensic tools, techniques need to have undergone the rigorous process of forensic validation (see Glossary), e.g., Best Practice Guide for Forensic Timber Identification by the United Nations Office on Drugs and Crime (UNODC 2016). In addition to its value as a forensic tool used to curb the illegal logging and trade of timber, the forensic identification of timber can be useful in biosecurity and pest management control across borders.

The application of scientific techniques to support the legal timber trade has been gaining increased attention in the last five years, with reviews on timber identification and illegal logging published (Dormontt *et al.* 2015), the release of a Best Practice Guide for Forensic Timber Identification by the United Nations Office on Drugs and Crime (UNODC) in 2016 and a guide for different timber tracking methods (Schmitz *et al.* 2020). In addition, several initiatives exist to bring together scientists, policy makers, and industry stakeholders who work on technologies and policies to reduce illegal logging, including the Forest Legality Alliance (FLA, forestlegality.org) and World Forest ID (Gasson *et al.* 2021; worldforestid.org). World Forest ID aims at creating extensive global reference databases for the techniques discussed here.

Reviewing the global capacity to trace timber is pertinent as legislation increases worldwide. In the present review, we comprehensively assess the current status, and success to date, of genetic, chemical, and anatomical techniques for species identification and determining the geographic origin of tree species that are widely traded and/or highly vulnerable to illegal trade. For species identification, we use reference databases to determine if the capacity to identify species exists and for the determination of geographic origin, we interrogate the scientific literature to determine for which species geographic origin can be identified or have the potential to be identified.

## Materials and methods

### Reviewing the global capacity to trace timber

We assessed the current capacity for identifying species and geographic origin using genetic, chemical, and anatomical techniques in August 2021. For our target taxa, we used the GTTN Tree Species Priority List 2019 (hereafter 'GTTN list') (Cramm & Van Brusselen 2019). The priority species list includes 322 taxa susceptible to, or already impacted by, illegal logging and trade across the world (36 genera, 286 species).

*Species identification: review methodology*

For species identification, we searched reference databases to give us a snapshot of the current status of reference data for genetic (DNA barcoding), chemical (Direct Analysis in Real-Time Time-Of-Flight Mass Spectrometry, DART TOFMS), Near-Infrared Spectroscopy (NIRS) and microscopic wood anatomy methods. There is no NIRS database available at the time of this writing so we relied on the literature to establish which species can be identified using this method. Stable isotope ratio analysis is not considered here as this technique has not been used yet for species identification (Dormontt *et al.* 2015). When searching reference databases we relied on the presence of genetic markers, DART TOFMS spectra, or wood anatomical descriptions for the target taxa as indicators of the potential for species identification. This approach assumes that the existence of reference data for a species, in a given database, is sufficient to allow species-level identification of timber samples using the respective method. In reality, this assumption is not always met. Wood anatomy is generally conserved between species of the same genus, making it

difficult to tell them apart, however wood anatomy is the only method for which this discrepancy is well characterised and it is clear for each species whether the identification is to species or genus. For DNA barcodes and DART TOFMS, the situation is less clear. DNA barcodes are often shared between closely related species and the likelihood of between species discrimination is increased with the inclusion of additional loci. It has been reported that for plants species discrimination success of less than 70% is not uncommon with the standard barcoding loci (Hollingsworth *et al.* 2011). DART TOFMS success at distinguishing closely related, or look-a-like, species varies depending on the species group in question. Classification accuracies ranging from 50% (depending on the species; Deklerck *et al.*, 2019) to 100% (Cody *et al.* 2012) have been reported for DART TOFMS. NIRS has shown success for timber identification but only on a select group of species (see further). Despite these complexities, the existence of reference data for a given species does allow verification of whether the timber sampled is consistent with the claim, even if it cannot be ruled out that there may have been a substitution for a closely related species. Therefore, we have chosen to use the presence of genetic markers, DART TOFMS spectra, NIRS literature, and wood anatomical descriptions as proxies for species identification capacity.

The genetic reference database GenBank (Sayers *et al.* 2020) was searched for key DNA barcoding markers. Searches were carried out using the Matrix Maker script (Freyman & Thornhill 2016) in August 2021. For DART TOFMS we searched the Forensic Spectra of Trees (ForeST$^©$) database (curated by the US Fish and Wildlife Forensic Laboratory, Ashland, Oregon) which contains DART TOFMS spectra that have been used, or have the potential to be used, for species-level identification (search undertaken in July 2021). For wood anatomy, we focused on microscopic wood anatomy methods. The diagnostic identification of timber using wood anatomy, particularly to the species level, is usually only achieved through microscopic as opposed to macroscopic examination (Schmitz *et al.* 2020). We searched three databases and computerized identification keys that provide wood anatomical descriptions according to the terminology of the International Association of Wood Anatomists (IAWA) (Richter *et al.* 2004). The databases Commercial Timbers (Richter & Dallwitz 2000 onwards) and InsideWood (Wheeler 2011) were searched for hardwoods and Softwood ID (Richter & Dallwitz 2016 onwards) for softwoods (searches undertaken July 2021).

*Geographic origin determination: review methodology*

We assessed the current status and potential of scientific verification techniques for determining the geographic origin of the priority taxa on the GTTN list. We surveyed the peer-reviewed scientific literature that demonstrate the use, or the potential for use, of genetic (population genetics and phylogeography) and chemical (DART TOFMS, NIRS, and stable isotopes) methods for determining geographic origin for the target taxa. In particular, for the priority taxa we wanted to know (i) if geographical differences between genetic markers, DART TOFMS mass spectra, NIRS spectra, or isotopic signatures have been investigated, (ii) if assignment analyses (e.g., samples assigned to their geographic region of origin) have been undertaken, and (iii) if tests for determining geographic origin have been forensically validated.

We searched the literature using a search string and the snowball method. The search string was developed and refined in an iterative process based on its ability to capture several key journal articles and the quantity of non-target studies in the search results. The search string had three sections to retrieve studies that (i) included the priority taxa on the GTTN list, (ii) were relevant to the determination of geographic origin, and, (iii) contained search terms related to genetics, DART TOFMS, NIRS or stable isotopes. Wood anatomy was not included in the literature search as it is most commonly used for taxonomic identification and only occasionally used for geographic origin determination, where restricted distributions mean that a species ID also confers information on geographic origin (Dormontt *et al.* 2015). Separate literature searches were undertaken for each method. Literature searches were carried out for genetics, DART TOFMS, NIRS, and stable isotopes between June and September 2021 (see Appendix A at 10.6084/m9.figshare. 20268018 for a detailed description of the literature search methods).
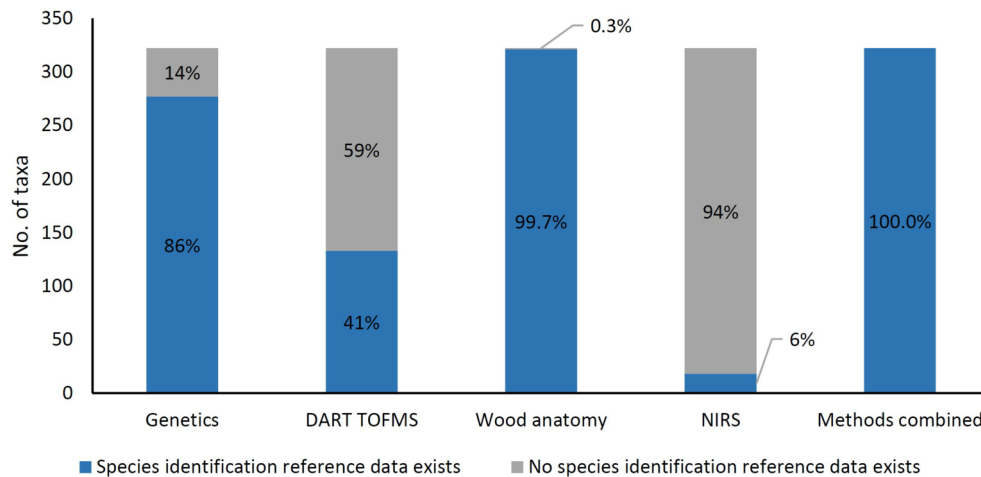
**Fig. 1.** Number and percentage of priority taxa for which species identification reference data exists in the genetic, DART TOFMS, and wood anatomy databases surveyed (i.e., presence of genetic markers in Genbank (presence of at least one of the nine barcoding markers: ITS, matK, psbA, rbcL, trnL, trnF, trnL-trnF, rpoB, and rpoC1), DART TOFMS spectra in ForeST and/or anatomical descriptions in Commercial Timbers, InsideWood or Softwood ID) or in the NIRS literature.

## Results

The following sections summarise our findings regarding the status of genetic, chemical, and microscopic wood anatomy verification techniques for species identification and geographic origin determination. See Appendix B at 10.6084/m9.figshare.20268018 for taxa-specific results.

### Species identification: status

Reference data with the potential for species identification exists for 100% of the priority taxa on the GTTN list (Fig. 1). Wood anatomy data was available for all but one priority taxa (99.7%), with 283 (88%) reliably identified to genus level and 38 (12%) to species level. One species, *Widdringtonia whytei,* could only be identified to family level. Genetic reference data exists for 277 priority taxa (86%), DART TOFMS reference data for 133 priority taxa (41%), and NIRS studies for 18 priority taxa (6%). The extent of species and/or genus level identification is unknown for genetic, DART TOFMS, and NIRS data (see *Species identification*: *review methodology* for further explanation).

All taxa on the GTTN list from Europe and North America had either genetic, DART TOFMS, or NIRS reference data, with the next highest number of taxa with reference data found in the Asia, Pacific, and Oceania region, followed by Africa and Central and South America (Fig. 2). A total of 12 priority taxa (23%) in Central and South America, nine priority taxa (17%) in Asia, Pacific and Oceania and six priority taxa (11%) in Africa had no genetic or DART TOFMS reference data.

### *Studies using genetic methods*

Examples of studies retrieved from the literature that demonstrate the utility of genetic barcoding markers to identify and discriminate timber species on the GTTN list are as follows. The gene region ITS was used to identify species in the mahogany family (Muellner *et al.* 2011) and *Araucaria* tree species (Bolson *et al.* 2015). It is often the case with plants that a combination of markers is required to discriminate between species (Lowe & Cross 2011). The rbcL + matK barcode was used to discriminate among *Dalbergia* species (Hartvig *et al.* 2015) and among 136 species in a tropical dry evergreen forest in India (Nithaniyal *et al.* 2014). Other studies have used ITS2 + trnH-psbA to resolve *Dalbergia* species (He *et al.* 2019). The trnL-trnF and ITS1 regions were used to discriminate *Aquilaria* species
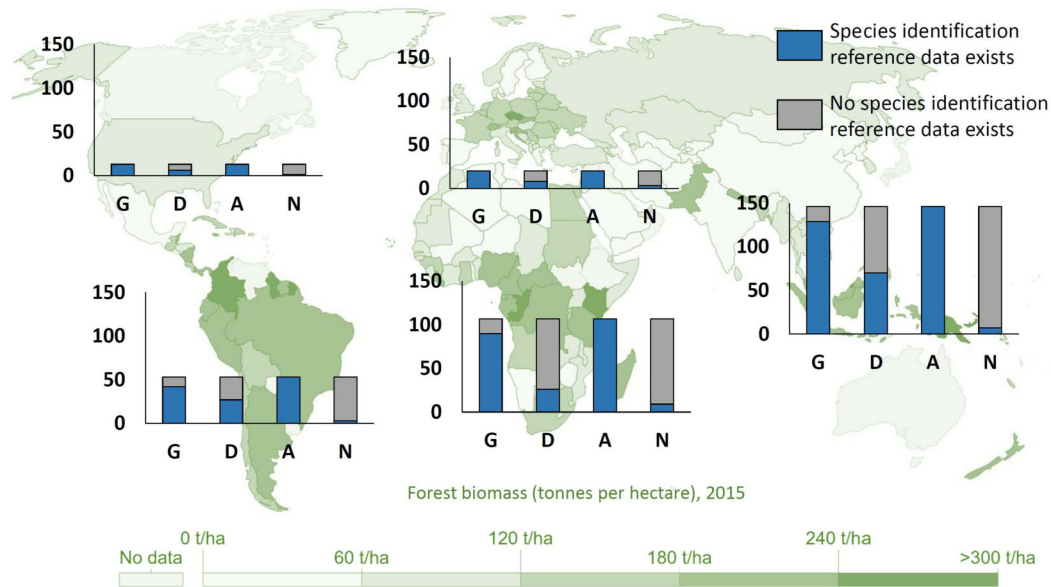
**Fig. 2.** Number of priority taxa in Africa; Asia, Pacific and Oceania, Central and South America, Europe, and North America for which species identification reference data exists in the genetic (G), DART TOFMS (D), and wood anatomy (A) databases surveyed and the NIRS (N) literature (i.e., presence of genetic markers in Genbank (presence of at least one of the nine barcoding markers: ITS, matK, rbcL, trnL, trnF, trnL-trnF, psbA-trnH, rpoB, and rpoC1), DART TOFMS spectra in ForeST and/or anatomical descriptions in Commercial Timbers, InsideWood or Softwood ID). Forest biomass figure published online at OurWorldInData. org. Retrieved from https://ourworldindata.org/grapher/above-ground-biomass-in-forest-per-hectare.

from other closely related species (Jiao *et al.* 2014; Lee *et al.* 2019). The combination of psbA-trnH + trnK was able to discriminate between five *Santalum* species with 100% success (Jiao *et al.* 2019). Ng *et al.* (2016) achieved species-level identification of *Gonystylus* using ITS2, trnh-psbA, and trnL regions with a 90% success rate. The applicability of genetic barcoding markers to identify and discriminate timber will increase immensely with the application of cutting-edge hybrid capture technologies. Hybrid capture is a targeted approach that can identify 100s of DNA markers that can be recovered for approximately 90% of samples, compared to other methods which rely on random loci that are not guaranteed for all samples (Waycott *et al.* 2021).

*Studies using chemical methods – DART TOFMS*

Similarly, here we discuss some of the studies that use DART TOFMS spectra to discriminate among timber species on the GTTN list. Cody *et al.* (2012) discerned *Quercus alba* and *Quercus rubra* with a 100% classification accuracy based on Linear Discriminant Analysis (LDA) with Leave-One-Out Cross-Validation (LOOCV). Lancaster and Espinoza (2012) differentiated several *Dalbergia* species and achieved a 91.2% accuracy using LDA with LOOCV. In addition, 15 out of 16 blind samples were correctly identified. McClure *et al.* (2015) also differentiated between several *Dalbergia* species and achieved a classification accuracy of 97.2% using Kernel Discriminant Analysis (KDA) and LOOCV. Musah *et al.* (2015) hypothesized that *Dalbergia granadillo* and *Dalbergia retusa* were synonyms of the same species due to the similarities in their chemotypes, and by grouping the two species into a single class were able to separate them from species of *Platymiscium* and *Caesalpinia* using KDA and LOOCV (98.98%). Evans *et al.* (2017) differentiated several *Araucaria* species and achieved a 94.8% accuracy using KDA with LOOCV. *Pericopsis* species and their look-alikes were differentiated by Deklerck *et al.* (2017). The accuracy ranged from 88.89% to 95.79% depending on species, via either KDA with LOOCV or random forest. Paredes-Villanueva *et al.* (2018) differentiated between *Cedrela angustifolia*, *C. balansae*, *C. fissilis*, *C. odorata* and *C. saltensis*. The success rate (KDA or random

forest) varied between 53.9% and 95.6%. Deklerck *et al.* (2019) differentiated between several *Meliaceaea species* using DART TOFMS data and achieved an accuracy of 82.2% using random forest with cross-validation. Zhang *et al.* (2019) differentiated between *Pterocarpus tinctorius* and *P. santalinus* wherein a 100% classification accuracy was achieved using Orthogonal Partial Least Squares-Discriminant Analysis (OPLS-DA). Deklerck and Price *et al.* (2021) showed that *Baillonella toxisperma* can be separated from other Sapotaceae species (*Autranella congolensis, Tieghemella africana* and *T. heckelii*) via DART TOFMS data and Discriminant Analysis of Principal Components (DAPC) (LOOCV = 96.61%). Kitin *et al.* (2021) utilized DAPC to separate *Afzelia bipindensis* from *A. pachyloba* with a LOOCV accuracy of 78%; the low accuracy of the model was linked to the variability of mass spectra within each species group. Finally, Price *et al.* (2021) separated seven species of *Pterocarpus* including *P. erinaceus, P. soyauxii, P. santalinus, P. dalbergioides, P. indicus, P. macrocarpus* and *P. tinctorius* using support vector machine (SVM) and DAPC; LOOCV accuracy of the models was 94% and 95%, respectively, and blind test accuracy was 100% for both models.

These studies have shown that wood analysis using DART TOFMS allows for rapid and reliable identification to genus or species level, and, once initial equipment costs are met, analysis is relatively straightforward and cheap (Dormontt *et al.* 2015; Kitin *et al.* 2021). DART TOFMS has been proven to be a clear contender as a means of supporting law enforcement agencies in the US, with leading Customs and Border Protection (CBP) to procure three of the instruments for testing different substances and materials including wood (Clark 2017).

*Studies using chemical methods: NIRS*

NIRS has shown promise in identifying some species or even varieties of species (Bergo *et al.* 2016; Pastore *et al.* 2011; Snel *et al.* 2018). It should be noted, however, that the identification potential has to be seen within the species group that is used, and the ability to identify a species could change when other species are compared against. One of the earliest NIRS papers on timber identification is Brunner *et al.* (1996), where species are discriminated in two series of species groups, with series 1: *Andira inermis, Liriodendron tulipifera, Manilkara bidentata, Sextonia rubra, Pouteria guianensis* and *Trattinickia rhoifolia* and series 2: *Carapa guianensis, Cedrela odorata, Jacaranda copaia, Laetia procera, Pinus ponderosa* and *Pinus sylvestris.* The study indicates a high potential for differentiating the species within their series. Tsuchikawa *et al.* (2003) used NIR and Mahalanobis' generalized distance to discriminate between the following species: *Cryptomeria japonica, Pseudotsuga menziesii, Picea sitchensis, Tectona grandis, Quercus mongolica, Paulownia tomentosa, Quercus gilva* and *Fagus crenata.* When using the second derivative spectra ranging from 800 to 2500 nm in the discriminant analysis, their results seemed most promising. The highest number of publications on NIRS for timber identification is on the same species group. Pastore *et al.* (2011) investigated the feasibility of NIRS in combination with Partial Least Squares for Discriminant Analysis (PLS-DA) for wood discrimination of *Swietenia macrophylla, Carapa guianensis, Cedrela odorata* and *Micropholis melinoniana.* The observed root mean square errors of predictions were 86%, 91%, 88%, and 94% for discriminations of *Swietenia macrophylla, Carapa guianensis, Cedrela odorata* and *Micropholis melinoniana,* respectively. The study by Braga *et al.* (2011) explored the efficacy of a fibre optic NIRS scan of solid wood surfaces (transverse, radial, and tangential) to separate the same species as Pastore *et al.* (2011). The PLS discriminant models showed small errors for each species. Bergo *et al.* (2016) discriminated the same species as Pastore *et al.* (2011) and Braga *et al.* (2011) using NIRS and PLS-DA on solid block and mill samples. The correct classification rate was higher than 96.8%. Ma *et al.* (2019) used NIR spatially resolved spectroscopy (SRS) based on hyperspectral imaging (HIS) for the rapid identification of 15 species (five softwoods and 10 hardwoods). The species were: *Agathis alba, Araucaria heterophylla, Thuja plicata, Chamaecyparis obtusa, Cryptomeria japonica, Triplochiton scleroxylon, Ochroma pyramidale, Hevea brasiliensis, Liriodendron tulipifera, Cercidiphyllum japonicum, Paulownia tomentosa, Kalopanax pictus, Fraxinus mandshurica, Eusideroxylon zwageri* and *Fagus sylvatica.* The identification accuracy of the quadratic discriminant analysis (QDA) under the five-fold cross-validation method was 94.1%. We should note here that four subsamples coming from one sample were allocated to the training set while one subsample from the same sample was allocated to the testing set; this process was then repeated five times. In

summary, subsamples coming from the same specimen were used both in the training and in the test set. The highest misclassification was between *Chamaecyparis obtusa* and *Ochroma pyramidale* (22%).

There are some developments recently that could aid in field identifications. Soares *et al.* (2017) evaluated a NIR handheld device for the discrimination of the following species: *Swietenia macrophylla, Cedrela odorata, Carapa guianensis, Erisma uncinatum, Micropholis melinoniana*, and *Hymenaea coubaril*. The efficiency rates were higher than 90% for all species, showing that the handheld NIR combined with PLS-DA succeeded in discriminating between species. Snel *et al.* (2018) explored the option of hand-held NIRS technology to discriminate between different high-value *Dalbergia* species in combination with either PLS-DA or soft independent modelling of class analogies (SIMCA). Overall PLS-DA performed better compared to SIMCA with efficiency rates of over 90%. The main success was in discriminating *Dalbergia nigra* from other *Dalbergia* species. Law enforcement agents could now be trained to use the device to identify *Dalbergia nigra*, without having to study the spectra or develop the model as it will be implemented in the device (Snel *et al.* 2018).

*Studies using wood anatomy methods*

Since wood anatomy has been routinely described and applied for more than 100 years a substantial amount of literature in the field of microscopic wood identification is available (Wheeler & Gasson 1989; Wheeler *et al.* 1989; Wheeler 2011). Despite wood anatomy being the most frequently used method for taxonomic identification, for many taxa, it can only achieve genus-level identification with misidentifications common at the species level (Schmitz *et al.* 2020). Fundamental developments in the field of wood anatomy will be forthcoming through the design of digital computerized/automated identification systems (deep learning or machine learning). The first portable digital systems are currently available such as Xylotron (http://xylotron.org/), Xylorix (https://www.xylorix.com/), and MyWood-ID (http://mywoodid.frim.gov.my/), and several basic studies have been published in this rapidly moving field of computer-assisted wood identification using neural network methods (Ravindran *et al.* 2018, 2020; He *et al.* 2020; Lens *et al.* 2020;). However, more sophisticated systems, based on morphometric analyses of cell shapes and mathematical analysis of texture patterns based on an extensive worldwide wood image reference dataset must be further developed to allow global species identification in ways unavailable so far (Lens *et al.* 2020). Important to note here is that XyloTron is also part of the World Forest ID initiative, so we expect to see that database expand soon.

For the development of automated image identification systems, different methodological approaches can be applied, which have to be specifically adapted for the individual requirements.

 (i) Deep learning (often synonymously referred to as artificial intelligence): based on the generation of annotated training images, a "black box procedure" learns which images belong to a defined wood species or not. Therefore, an (extremely) large number of images is required and a human must train the algorithms.
 (ii) Classification: here, the developer predetermines specific characters for the learning procedure to distinguish individual wood species. This method requires much less image material but is not easy to implement due to the manifold (diverse) anatomical structures on a macroscopic and microscopic level.
(iii) Stochastic structural models describe material properties based on "few" defined parameters. By comparing these parameters, similar materials or material types can be recognized.

The current (practical) experiences show that a combination of the described approaches offer the best solution for the development of machine learning systems (Sun *et al.* 2021). The advantages of "classification" and "structural model" are based on a direct calculation of why an image is assigned to a certain class. This is not possible in "deep-learning", but this method allows a better (targeted) application with sufficiently secured image material.

The very dynamic progress in the field of automated machine learning offers also a high potential for the identification of pulp and paper components as well as those of fibreboards which are also subject to the controls of timber regulations (Koch *et al.* 2015). The identification of the macerated cell elements requires special expertise

due to the restricted number of available characters (Helmling *et al.* 2016, 2018) and is currently limited to genus and family level (Schmitz *et al.* 2020).

In conclusion, these new developments in the field of automated machine learning do not eliminate the need for wood anatomical experts but provide alternative methods of identification in the current reality of the declining population of expert anatomists despite the increased global trade in wood products (Gasson *et al.* 2021).

### GEOGRAPHIC ORIGIN DETERMINATION: STATUS

The literature searches showed that 78 (24%) of the 322 priority taxa on the GTTN list have been the focus of genetic, DART TOFMS, stable isotope, and/or NIRS studies aimed to determine some level of geographical origin, e.g., forest concession, region within a country, country (Fig. 3). Genetic studies determining geographical origin captured the highest number of priority taxa (75 taxa, 23%), compared to DART TOFMS (5 taxa, 2%), stable isotopes (5 taxa, 2%) and NIRS (3 taxa, 1%) (Fig. 3).

Of the 244 taxa for which no geographic origin data could be found (76% of total priority taxa on the GTTN list), 108 taxa (74%) were from the Asia, Pacific, and Oceania region, 84 species (79%) from Central and South America, 42 species (79%) from Africa, 9 species (69%) from North America and 4 species (20%) from Europe (Fig. 4). None of the priority taxa from the GTTN list identified in studies retrieved in the literature have been the focus of tests used for forensic purposes, i.e., no tests for determining geographic origin have been forensically validated. A genetic individualisation test, also known as DNA profiling, which differs from previously mentioned origin determination as they use genetic markers to trace an unknown sample back to an individual, rather than a geographic location was validated for *Acer macrophyllum* and demonstrates validation of individualisation tests for timber is possible (Dormontt *et al.* 2020). Cronn *et al.* (2021) reengineered the SNP-based assay developed by Dormontt *et al.* (2020) for individualisation of *A. macrophyllum* grown in the Pacific Northwest and Northern California using a sample size of 1188. In addition, Cronn *et al.* (2021) provided a method for geolocalization of *A. macrophyllum* that resulted in an error rate of 8.5–11.7% for those trees originating from Southern California, and 36– 80% for trees originating from the Pacific Northwest. The individualisation method created by Cronn *et al.* (2021) was used in a law enforcement case wherein the likelihood of the match being erroneous was one in one undecillion ($10^{36}$) (Peiser in press).
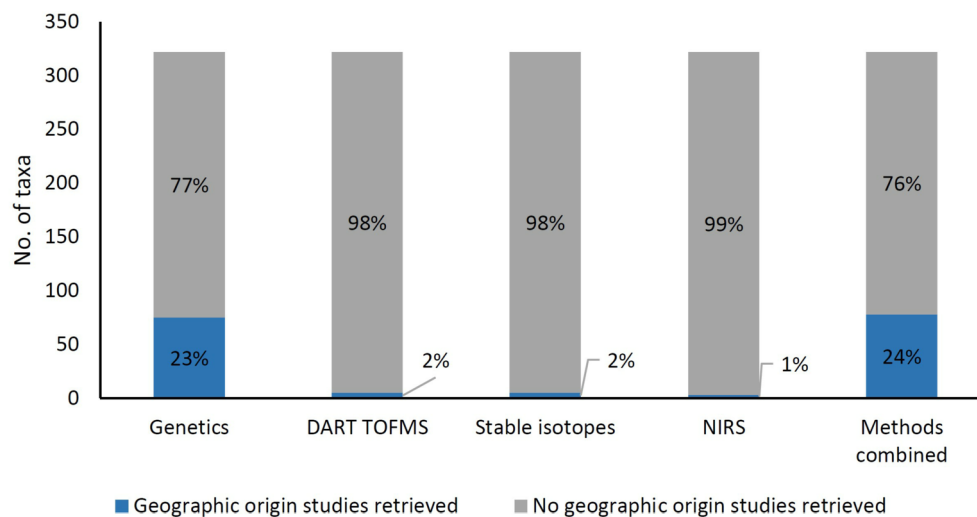


**Fig. 3.** Number and percentage of priority taxa for which genetic, DART TOFMS, NIRS, and/or stable isotope studies relevant to the determination of geographic origin were retrieved in the literature search results.
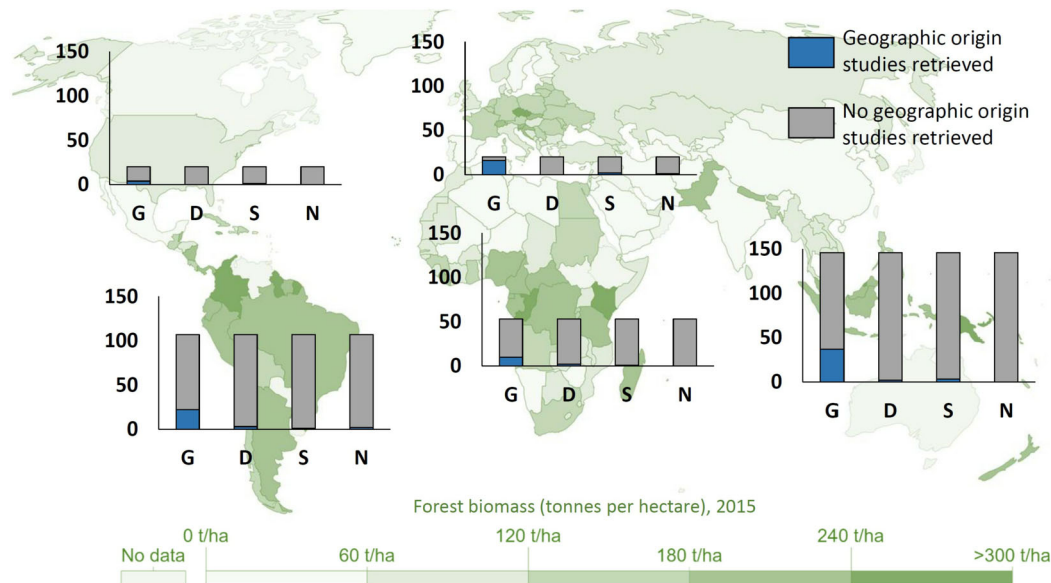
**Fig. 4.** The number of priority taxa in Africa; Asia, Pacific and Oceania, Central and South America, Europe, and North America for which genetic (G), DART TOFMS (D), NIRS (N), and/or stable isotope (S) studies relevant to the determination of geographic origin were retrieved in the literature search results. Forest biomass figure published online at OurWorldInData.org. Retrieved from https://ourworldindata.org/grapher/above-ground-biomass-in-forest-per-hectare.

*Studies using genetic methods*

Of the 75 priority taxa on the GTTN list that were the focus of genetic studies, 14 were subject to genetic assignment tests to determine the geographic region of origin with varying levels of success (*Cedrela ordorata, Dipteryx odorata, Dipteryx* spp., *Entandrophragma cylindricum, Erythrophleum ivorense, Gonystylus spp., Hymenaea courbaril, Intsia* spp., *Larix decidua, Pinus sylvestris, Shorea platyclados, Swietenia macrophylla, Quercus petraea* and *Quercus robur*) (See Appendix B at 10.6084/m9.figshare.20268018 for species-specific results).

In Africa, for the highly valuable timber *E. cylindricum*, nSSRs were used to successfully determine if timber samples came from within a particular forest concession in Eastern Cameroon or from outside the concession for six out of seven blind samples (Jolivet & Degen 2012). For *S. platyclados* in Southeast Asia, Ng *et al.* (2017) used nSSRs to self-assign samples to either eastern or western Malaysia with an average success rate of 99.11%. The assignment rate was lower when attempting to assign samples to populations within these regions (60.6% for populations within western Malaysia and 94.95% for populations in eastern Malaysia). The authors suggested the continuous topography in western Malaysia allowed for the dispersal of seeds and pollen of *S. platyclados* and contributed to weak genetic differentiation between populations. Ng *et al.* (2016) used nuclear SSRs and chloroplast DNA to correctly self-assign individuals of *G. bancanus* to populations, genetic clusters, and regions with average percentages of 55, 100 and 100%, respectively, where regions corresponded to Peninsular Malaysia and Malaysian Borneo.

In Central and South America, Chaves *et al.* (2018) used nuclear microsatellites (nSSRs; simple sequence repeats) to self-assign samples of *H. courbaril*, a high-value timber species from the neotropics, to locations within Bolivia, Brazil, French Guyana and Peru with success rates of ~88% depending on the assignment method used (nearest neighbour, Bayesian method or frequency method). Also using nSSRs, Degen *et al.* (2013) assigned blind test samples of *S. macrophylla* to their country of origin, either Guatemala or Brazil, with a success rate of 100%. For sites in Bolivia, assignment success rates were reported for *C. odorata* using nSSRs, 66.3% based on KDA, and 70% using blind test samples (Paredes-Villanueva *et al.* 2019). For the one site that corresponded to a genetic cluster in the PCA an assignment success rate of 91.8% was reported. Degen *et al.* (2017) used single nucleotide polymorphism markers

(SNPs) to assign individuals of *E. cylindricum* to five countries in Central Africa with success rates ranging from 66 to 74%, depending on the self-assignment methods used. Blanc-Jolivet *et al.* (2018) reported self-assignment success rates to the region of origin ranging from 74 to 88% using 253 SNP loci for *L. decidua* (larch) in Europe and Russia. Nowakowska (2011) used individualisation tests They reported individualisation assignment success rates of 97.45 to 98.89% using nSSRs and cpSSRs for the temperate species *Pinus sylvestris* (scots pine), *Quercus robur*, and *Quercus petraea* (white oaks).

A total of 61 of the priority taxa appeared in genetic studies that did not undertake assignment analyses, but the results indicated that genetic structure exists at some scale and corresponds to geographical locations (see Appendix B at 10.6084/m9.figshare.20268018). These studies were undertaken to investigate population structure, phylogeography, and conservation status, and not to determine geographic origin. The science for these species is still developing with regard to determining the region of origin, however, these studies prove potential exists.

*Studies using chemical methods: DART TOFMS*

Five priority taxa from studies retrieved in DART TOFMS literature search were subject to assignment analyses (*Aquilaria* spp., *Cedrela fissilis*, *Cedrela ordorata*, *Dalbergia* spp. and *Terminalia superba*). Paredes-Villanueva *et al.* (2018) attempted to identify sampling sites in Bolivia of *C. fissilis* and *C. odorata* with limited success using DART TOFMS. Success rates varied between 19.1 and 60.3% for *C. fissilis* and 51.5 and 61.6% for *C. odorata*, depending on the site and model. Paredes-Villanueva *et al.* (2018) suggested the influence of local conditions such as climate, soil characteristics, nutrient availability on the chemical composition of the trees may explain these classification errors. Espinoza *et al.* (2014) discerned wild from cultivated agarwood (*Aquilaria sinensis*, *Aquilaria crassna* and *Aquilaria beccariana*) with inference to country (Borneo, China, Thailand and Vietnam). Eleven of the 13 samples (85%) were correctly assigned to either cultivated or wild harvested for their respective geographic provenance. McClure *et al.* (2015) developed a method for determining whether *Dalbergia* specimens originated from Madagascar. The resulting model was tested using 10 specimens, not included in the model training, and each spectrum was correctly assigned to Madagascar. Deklerck *et al.* (2020) determined the country of origin (Democratic Republic of the Congo and Ivory Coast) of *T. superba* stem disc samples using DART TOFMS. The accuracy ranged from 43 to 100%.

*Studies using chemical methods: NIRS*

For NIRS, few examples exist of its potential to determine the origin. Sandak *et al.* (2011) used Fourier transform near-infra-red spectroscopy (FT-NIR) to determine whether there were significant differences in provenance for *Picea abies*. They focused on the following provenances: Central Finland, Northern Poland, Southern Poland, and Northern Italy. In a second test, Sandak *et al.* (2011) focused on several locations in neighboring forest districts selected in a narrow area in Trentino (Italy). These sites varied in terms of altitude, soil structure, or silvicultural history. There were clear differences between samples coming from Central Finland, Northern Poland, Southern Poland and Northern Italy, and they were able to separate the samples based on their location. Differences were also found when looking at the narrower region within Italy, although these were less straightforward/distinctive. Ramalho *et al.* (2018) differentiated *Cedrela* sp., *Apuleia* sp., *Aspidosperma* sp. and *Jacaranda* sp. belonging to native forests (Brazil) from two commercial *Eucalyptus* clones (both hybrids from *Eucalyptus grandis* × *Eucalyptus urophylla*) from plantations (Brazil). In addition, within the native forest species group, they were able to differentiate the species with 86 to 100% accuracy via PLS-DA. The clones were more difficult to differentiate. Silva *et al.* (2018) investigated the use of handheld devices to determine the country of origin (either Brazil, Guatemala, Peru, Mexico, or Bolivia) of *Swietenia macrophylla* and had promising results. We want to make a special note here on the project NIRWOOD (http://nirwood.com/), which is funded by the EU Horizon 2020 Framework Program and focuses on the development of a NIR spectrometer to be able to distinguish wood species and their geographical origin.

*Studies using chemical methods: stable isotopes*

For stable isotopes, five priority species occurred in studies retrieved in the literature search (*Erythrophleum ivorense, Shorea leprosula, Shorea pauciflora, Picea abies* and *Quercus* spp.). Assignment tests are only done in two of the four retrieved studies. The studies use different combinations of stable isotopes, which may influence the origin determination success. As the variation of stable isotope ratios within the species range depends on natural variations of the underlying mechanisms (for example water availability or rainwater source; van der Sleen *et al.* 2017) some stable isotopes may be more or less discriminative for a certain species and area.

Using stable isotopes for two of the most traded African tree species, *Erythrophleum suaveolens* and *E. ivorense* (both traded as Tali and grouped as one species under *E. ivorense* in analysis as per the GTTN list), only 35% of the blind samples were correctly assigned to forest concessions in Cameroon and Congo Republic based on oxygen, nitrogen, and carbon stable isotopes (Vlam *et al.* 2018b). In comparison, 92% of blind samples were correctly assigned using nSSRs (Vlam *et al.* 2018b). The poor results for the stable isotope analysis were attributed to insufficient spatial variation in environmental conditions that determine isotopic signatures of wood. Several issues with the stable isotope analysis were identified in a response by Horacek *et al.* (2018) (and see the response by Vlam *et al.* (2018a). Watkinson *et al.* (2020) used isoscapes to test origin determination accuracy for *Quercus* spp. in the United States. Samples were not assigned to a specific location but maps of potential origin were created. Based on a combination of oxygen, hydrogen, carbon, and sulfur stable isotopes they were able to assign 14/18 test samples to an area that encompassed the correct origin.

For *S. leprosula* and *S. pauciflora*, Kagawa *et al.* (2007) did not undertake assignment tests but used principal coordinate analysis to conclude that stable oxygen, carbon, and nitrogen isotope ratios can differentiate timber from the Philippines and Borneo. Differentiation within Borneo was not possible. Gori *et al.* (2018) produced isoscapes for a 600 km² region in Italy with predicted yearly $\delta^2$H and $\delta^{18}$O values for *P. abies*. They did not do any subsequent assignment tests to validate the model other than Leave-One-Out Cross-Validation to establish the most accurate model.

One additional study was included after the literature search, as it is not published in a peer-reviewed journal. Förstel *et al.* (2011) is still considered relevant as they conducted an in-depth study on origin identification of *Tectona grandis* and *Swietenia* spp. They were able to successfully assign 10 out of 11 blind samples of *T. grandis* to the country of origin, as well as one out of two blind samples of *Swietenia* spp based on hydrogen, oxygen, carbon, nitrogen, sulphur and strontium stable isotopes.

## Discussion

### THE POTENTIAL OF SCIENTIFIC VERIFICATION TECHNIQUES FOR SPECIES IDENTIFICATION AND GEOGRAPHIC ORIGIN DETERMINATION

The successful implementation of logging laws, developed to combat the trade in illegal timber and to verify the legality of timber supply chains globally, is dependent upon accurate identification of species and the geographical origin of timber. In this review, we surveyed the research undertaken up until August 2021 to gain an understanding of the capability for identifying species and geographic origin considered by the GTTN to be at risk, or already impacted by, illegal logging. We compared the capacity to identify species with that for determining geographical origin. The results of the review demonstrate that a substantial body of work already exists. For wood anatomy, reference data exist for all taxa on the GTTN list. DNA barcoding loci exist for 277 taxa (86%), DART TOFMS spectra exist for 133 taxa (41%), and NIRS spectra for 18 taxa (6%) on the GTTN list. The review highlights the current potential for identifying species is greater than for geographic origin with only 24% of priority taxa the focus of research identifying geographic origin or studies creating a starting point from which to do so. More research focused on determining the geographical
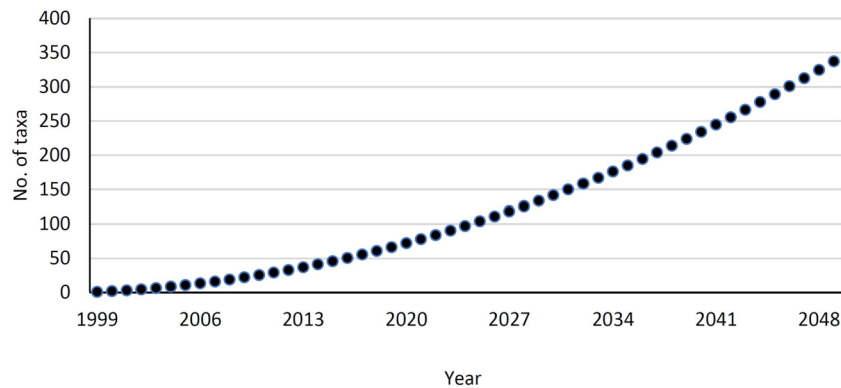
**Fig. 5.** The number of taxa that appeared in studies retrieved in the literature search results and published since 1999 and the predicted number of years it will take to capture all 322 priority taxa in research determining the geographic origin, determined using the relationship between the numbers of taxa studied between 1999 and 2021.

origin of timber is required. The greatest number of priority taxa from the GTTN list requiring attention are in the Asia, Pacific, and Oceania region, particularly Southeast Asia, in addition to Central and South America.

To estimate how long it will take to capture all 322 priority taxa in research determining geographic origin we applied a trendline to the number of taxa researched per year between 1999 and 2021 (see Appendix C at 10.6084/m9. figshare.20268018). Using this relationship, we predict it will take until 2048, approx. 27 years, to capture all priority taxa on the GTTN list (Fig. 5). Approximately 27 years represents a best-case scenario given the number of species on the GTTN list is expected to increase with the increasing global demand for timber and further depletion of species. However, we are seeing an increase in the rate of reference database building, both for species identity and origin. See, for example, the efforts by World Forest ID, which aims at creating the world's largest georeferenced sample collection and associated analytical database.

### THE CHALLENGES ASSOCIATED WITH ORIGIN IDENTIFICATION

Our review revealed that tests for determining geographic origin have not yet been used for forensic purposes for any of the priority taxa on the GTTN list. With regards to the readiness of geographic origin tests for use in forensic cases, relevant preliminary research has been undertaken for 78 (24%) of the priority taxa, with assignment analyses only undertaken for 19 of these. The only mention of forensic validation for a geographic origin test for timber in the literature search results was in the study by Ng *et al.* (2016) who assigned individuals of *Gonystylus bancanus* to populations, genetic clusters, and regions and made reference to a full developmental validation study underway to address the reliability of the STRs being used. However, at the time of writing, this developmental validation study is yet to be published.

With such a paucity of validated studies, it begs the question; what are the barriers preventing the transition of tests for determining geographic origin from research to forensic tools? Tests for determining geographic origin pose unique challenges that may contribute to the differences in capacity when compared to species identification. One such challenge is that tests for geographic origin determination require extensive sample collections representing the range of populations within a species (Dormontt *et al.* 2015). For all methods, reference data are essential, and collecting samples across a species range is resource intensive. Especially where species span multiple states, countries, or continents obtaining samples will depend on collaborations.

Another challenge is the mismatch between phylogeographic and political boundaries, i.e., discrete genetic populations will not always comply with regulatory jurisdictions. The same can be said for the region of origin tests using DART TOFMS and stable isotopes, trees do not follow political borders, and the country delineation is an

artificial one (Deklerck *et al.* 2020). Thus, differences in genetic markers and chemical spectra may not exist between the regions in question.

Whilst these three barriers are reasonably well recognised and understood in the timber forensic literature (Dormontt *et al.* 2015), another issue less commonly addressed is the lack of clarity regarding the acceptable process for undertaking a robust forensic validation of a geographic origin determination test. Here we join Ogden and Linacre (2015) in calling for consensus within and between the wildlife forensic and timber tracing scientific communities to develop robust forensic validation guidelines for geographic origin determination tests.

### LIMITATIONS OF USING A PREDEFINED SPECIES LIST

The priority species list, developed by the GTTN, captures the majority of species susceptible to, or already impacted by, illegal logging and trade across the world. Nevertheless, restricting the review to a predefined list of species results has the potential to underestimate the extent of markers, spectra, or anatomical data that exist for species not on the GTTN list. Similarly, scientific literature demonstrating the use of genetic and chemical methods for determining geographic origin for other species can be excluded. Tnah (2010) reported the potential to assign individuals of *Neobalanocarpus heimii* to three subregions in Peninsular Malaysia using nSSRs and reported genetic structure in clumps at distances of 0 to 140 m. Stable isotope analyses of non-target species were similarly excluded from the review, such as Kagawa and Leavitt (2010) who revealed the geographic origin of pinyon pines (*Pinus edulis* and *Pinus monophylla*) from the southwestern United States based on stable carbon isotopes of tree rings, and sulphur isotopes from Christmas tree needles distinguished Austrian samples from other European countries (Horacek 2012). Horikawa *et al.* (2015) and Hwang *et al.* (2015) reached 100% accuracy in discriminating between *Pinus* species, *Pinus densiflora* versus *Pinus thunbergia* and *Pinus densiflora* Sieb. et Zucc. versus *Pinus densiflora* for. erecta Uyeki. In both studies, PLS-DA and PCA were performed and coefficient of determination for calibration ($R^2_c$) and the root mean square error of calibration (RMSEC) were used to assess the calibration performance.

### FUTURE DIRECTIONS

We believe four key opportunities exist to improve our capacity for tracing timber and bring us closer to having a usable system of timber identification for a range of species: (i) research into the barriers to the uptake of scientific verification tests of timber by law enforcement and the timber industry; (ii) research into the forensic validation of geographic assignment tests and agreeance among the scientific/forensic community, (iii) the intensification of sampling effort, across taxa and species distributions, and (iv) the integration of anatomical, genetic and chemical methods in a nuanced approach for species and origin identification.

Ultimately, the rate of research focusing on the geographic region of origin determination must increase collectively, in particular in the Asia, Pacific, and Oceania region, so that geographic assignment tests exist for all species considered highly vulnerable or already impacted by illegal trade. There is no point in investing in the further development of these tests, however, if we do not simultaneously increase uptake by law enforcement and/or industry. A lack of test availability is only one dimension; issues of forensic suitability, costs, awareness, infrastructure, and political will are all potentially impacting on disappointing utilisation of scientific timber verification. A robust qualitative exploration of the perspectives of a variety of stakeholders could help to unpick this complexity. Improved understanding of the barriers to scientific verification uptake will enable more targeted efforts to overcome them and provide greater assurance and return on research investment.

One major barrier to law enforcement uptake is likely to be the lack of forensically validated timber identification tests available. Our review revealed that no published literature on the priority species from the GTTN list had undertaken a forensic validation of their geographic origin assignment tests. Whilst publication of forensic validation studies is not strictly required for the application of tests to the law, developmental validation studies must be made available to the court if the results of a test are to be submitted as evidence. The publication of developmental

validation studies in the peer-reviewed literature has a range of benefits, however, the most important of which is that other laboratories are then able to utilise the tests without undertaking a full developmental validation (an internal validation is sufficient), thereby reducing some of the barriers to the broader application of developed forensic tests across different laboratories. In addition, commercial validation measurement tests are available to check whether measured values are correct across institutions, e.g., for isotopes ring tests are undertaken regularly to ensure results are correct and the process is validated. Research providing robust forensic developmental validation of geographic assignment tests for timber is therefore sorely needed but is reliant upon a consensus within the scientific/forensic community on what that entails.

The financial cost is another barrier for both species and origin identification and the need for a forensic test needs to be balanced against cost. The process of forensic validation is expensive, and the cost is often prohibitive to tests being validated and the results being available for use in a court of law. This is particularly true for geographic assignment techniques, which are specific to the species, resulting in a resource-intensive validation process (Ogden & Linacre 2015). Financial costs associated with scientific verification techniques for identifying timber have been addressed by Dormontt *et al.* (2015) and Schmitz (2019).

The collection of more reference samples is considered one of the greatest obstacles to implementing genetic and chemical methods for species identification and determining the geographic region of origin (Dormontt *et al.* 2015; Jiao *et al.* 2020). The World Forest ID consortium aims to tackle the lack of well-documented reference data by building the world's largest collection of forest samples (Gasson *et al.* (2021). Collecting more samples from across a species range will enable researchers to establish if genetic and/or chemical structure exists and where geographic assignment might be applied. Not having samples spanning the species range has been reported as a limitation in several studies (Degen *et al.* 2017; Vlam *et al.* 2018b). In the absence of genetic and chemical data spanning the species range, it may not be possible to identify the actual geographical origin of timber but rather to demonstrate timber does not come from a certain location (Lowe & Cross 2011). There may be much gained from revisiting species where some relevant preliminary work has identified genetic structure and then assessing assignment capabilities. By utilising existing reference sample collections in this way, or through the utilisation of herbaria and xylaria resources, researchers can avoid some of the major costs and complexities associated with timber research, namely collecting samples. Existing reference data can be similarly augmented with additional sample information to expand the scope and power of identification tests. This re-purposing however presents its own challenges in terms of standardisation of laboratory and analysis methods, and collaborative agreements to share samples and benefits arising from research.

The potential of scientific verification methods for timber may be enhanced through the nuanced integration of methodologies (Dormontt *et al.* 2015; Jiao *et al.* 2020; Schmitz *et al.* 2020). As our results have revealed, there is much disparity with regard to the scientific verification tests available for timber species. In any given situation, the most appropriate test will depend on the question to be answered and the availability of scientific verification for that species. Integration of methods may mean the serial application of different available tests in order to accurately identify the timber, for example, wood anatomy identification to genus followed by DNA barcoding or DART TOFMS to determine exact species. In other cases, where reference data exists, it may be preferable to use only DART TOFMS for both species and geographic origin identification. As was shown by Vlam *et al.* (2018), genetic and chemical methods are based on different principles and rely on different biological processes making each technique more or less applicable in different circumstances. When an individual method cannot provide high enough assignment accuracies to trace timber origin, another method may improve the accuracy. However, the cost of forensic validation needs to be taken into account, especially where multiple methods are employed. Most stakeholders needing to verify the identity or geographic origin of timber cannot afford one, let alone multiple tests. The development of cheaper versions of tests that are fit-for-purpose in producer country laboratories would help to overcome this limitation. In addition, the GTTN has shown that, although varying in capacity, there is a large network of researchers and institutes capable of undertaking wood identification services alleviating the need for all countries to have their own service (globaltimbertrackingnetwork.org). As our analyses suggest that at the current rate, it will be approx. 27 years before

all priority taxa on the GTTN list are the subject of research on geographic origin identification, the need to be strategic in research priorities is evident. Species for which robust verification tests (spanning highly technical tests through to methods requiring less equipment e.g., wood anatomy, phone apps) already exist should not be a priority for further research with different methodologies; resources would be better directed towards priority species for which no fit-for-purpose test exists.

## Conclusions

Here we reviewed the current state-of-the-art for timber tracing using the scientific verification methodologies of wood anatomy, chemical analysis (stable isotopes, DART TOFMS and NIRS), and genetic analysis (DNA barcoding and population genetics/phylogeography) for species and geographic origin identification.

Our results indicate that all priority taxa from the GTTN list can be identified at least to genus with wood anatomy but that finer scale species identification with anatomical, genetic or chemical methods is much more variable. Studies exploring the capacity to trace timber back to geographic origin have only been completed for 24% of the priority species and none have been demonstrated as suitable for forensic purposes through developmental validation.

Based on our findings, we make recommendations for future research directions to help ensure science is best positioned to support the implementation of logging laws around the world.

Species and origin identification tests are essential to verify claims made in compliance documentation and for demonstrating legality in timber supply chains. Increasing the investment in scientific verification techniques for timber is needed to combat the illegal timber trade and protect the world's forests.

## Acknowledgements

## Glossary

### Illegal logging

"All practices related to the harvesting, processing, and trading of timber inconsistent with national and sub-national law," as defined by Kleinschmit *et al.* (2016).

### Species identification

Species-level identification of a timber sample. Species-level identification depends upon differences in genetic markers, chemical fingerprints, or wood anatomical structure among species.

GEOGRAPHIC ORIGIN DETERMINATION

Within a species, the identification of the geographic region of origin of a timber sample. Geographic origin determination depends upon the existence of spatial genetic structure or differences in chemical fingerprints, or stable isotopes among the regions in question. Regions may be populations, concessions, or countries and do not necessarily conform to political boundaries.

CERTIFICATION

A voluntary process whereby an independent third party assesses forest management, production, and the chain of custody of forest products against a set of principles, criteria, and indicators as defined by a certification scheme, e.g., Forest Stewardship Council (FSC); Program for the Endorsement of Forest Certification (PEFC). Certification is a way that forest managers can inform consumers about their product and may attract better prices, maintain or increase access to markets, improve public image and achieve social and environmental goals.

VERIFICATION

The demonstration that timber products at any point along the timber supply chain (e.g., log yard, sawmill, processing, export, import, point of sale) match origin claims made on the chain of custody documentation presented at customs inspections, audits, or required by certification schemes. Whereas certification schemes provide a framework for addressing illegal trade, verification is a practical tool used to assess compliance and can be used to support certification and/or claims of legality (Lowe *et al.* 2016).

FORENSIC VALIDATION

The process by which a particular test (e.g., species identification or geographic origin determination) is subject to extensive studies to verify it is fit for purpose. Validation can be "developmental", where examination of the precision, accuracy, and sensitivity (which relate to the reliability, reproducibility, and robustness) of the test is initially assessed. Validation can also be "internal", where a laboratory demonstrates that a test already developmentally validated, performs as expected (UNODC 2016).

FORENSIC TOOL

Scientific method or technique that has undergone the process of forensic validation and may be used to support the claims of the prosecution or defense in a court of law.

## References

Bergo MCJ, Pastore TCM, Coradin VTR, Wiedenhoeft AC, Braga JWB. 2016. NIRS identification of *Swietenia macrophylla* is robust across specimens from 27 countries. *IAWA J.* 37(3): 420–430. DOI: 10.1163/22941932-20160144.

Blanc-Jolivet C, Yanbaev Y, Degen B. 2018. Genetic timber tracking of *Larix* sp. in Eurasia. Paper presented at German Russian Conference on Forest Genetics — Proceedings; 21-23 November 2017, Ahrensburg, Germany.

Bolson M, Smidt EdC, Brotto ML, Silva-Pereira V. 2015. ITS and trnH-psbA as efficient DNA barcodes to identify threatened commercial woody angiosperms from Southern Brazilian Atlantic Rainforests. *PLoS ONE* 10(12): e0143049. DOI: 10.1371/journal.pone.0143049.

Braga JWB, Pastore TCM, Coradin VTR, Camargos JAA, da Silva AR. 2011. The use of near infrared spectroscopy to identify solid wood specimens of *Swietenia macrophylla* (Cites Appendix II). *IAWA J.* 32(2): 285–296. DOI: 10.1163/22941932-90000058.

Bremer LL, Farley KA. 2010. Does plantation forestry restore biodiversity or create green deserts? A synthesis of the effects of land-use transitions on plant species richness. *Biodivers. Conserv.* 19(14): 3893–3915. DOI: 10.1007/s10531-010-9936-4.

Brunner M, Eugster R, Trenka E, Bergamin-Strotz L. 1996. FT-NIR spectroscopy and wood identification. *Holzforschung* 50(2): 130–134. DOI: 10.1515/hfsg.1996.50.2.130.

Chaves CL, Degen B, Pakull B, Mader M, Honorio E, Ruas P, Tysklind N, Sebbenn AM. 2018. Assessing the ability of chloroplast and nuclear DNA gene markers to verify the geographic origin of Jatoba (*Hymenaea courbaril* L.) timber. *J. Hered.* 109(5): 543–552. DOI: 10.1093/jhered/esy017.

Clark WM. 2017. Scientists are using this collection of wood samples to combat illegal logging. Smithsonian Magazine. Smithsonian Associates, Washington, DC. Available online at https://www.smithsonianmag.com/smithsonian-institution/scientists-are-using-collection-wood-samples-combat-illegal-logging-180964305/.

Cody RB, Dane AJ, Dawson-Andoh B, Adedipe EO, Nkansah K. 2012. Rapid classification of White Oak (*Quercus alba*) and Northern Red Oak (*Quercus rubra*) by using pyrolysis direct analysis in real time (DART (TM)) and time-of-flight mass spectrometry. *J. Anal. Appl. Pyrolysis* 95: 134–137. DOI: 10.1016/j.jaap.2012.01.018.

Cramm M, Van Brusselen J. 2019. List of priority tree species for the development of reference data for determination of tree species and their geographic origin. Update of the GTTN priority tree species list of 2013. Global Timber Tracking Network, European Forest Institute, Joensuu. Available online at https://globaltimbertrackingnetwork.org/portfolios/priority-tree-species/.

Cronn R, Finch KN, Hauck LL, Parker-Forney M, Milligan BG, Dowling J, Scientists A. 2021. Range-wide assessment of a SNP panel for individualization and geolocalization of bigleaf maple (*Acer macrophyllum* Pursh). *For. Sci. Int.: Anim. Environ.*: 100033. DOI: 10.1016/j.fsiae.2021.100033.

Degen B, Ward SE, Lemes MR, Navarro C, Cavers S, Sebbenn AM. 2013. Verifying the geographic origin of Mahogany (*Swietenia macrophylla* King) with DNA-fingerprints. *Forensic Sci. Int. Genet.* 7(1): 55–62. DOI: 10.1016/j.fsigen.2012.06.003.

Degen B, Blanc-Jolivet C, Stierand K, Gillet E. 2017. A nearest neighbour approach by genetic distance to the assignment of individual trees to geographic origin. *Forensic Sci. Int. Genet.* 27: 132–141. DOI: 10.1016/j.fsigen.2016.12.011.

Deklerck V, Finch KN, Gasson PE, Van den Bulcke J, Van Acker J, Beeckman H, Espinoza EO. 2017. Comparison of species classification models of mass spectrometry data: kernel discriminant analysis vs random forest; a case study of Afrormosia (*Pericopsis elata* (Harms) Meeuwen). *Rapid Commun. Mass Spectrometr.* 31(19): 1582–1588. DOI: 10.1002/rcm.7939.

Deklerck V, Mortier T, Goeders N, Cody RB, Waegeman W, Espinoza E, Van Acker J, Van den Bulcke J, Beeckman H. 2019. A protocol for automated timber species identification using metabolome profiling. *Wood Sci. Technol.* 53(4): 953–965. DOI: 10.1007/s00226-019-01111-1.

Deklerck V, Lancaster CA, Van Acker J, Espinoza EO, Van den Bulcke J, Beeckman H. 2020. Chemical fingerprinting of wood sampled along a pith-to-bark gradient for individual comparison and provenance identification. *Forests* 11(1): 107. DOI: 10.3390/f11010107.

Deklerck V, Price E, Vanden Abeele S, Lievens K, Espinoza E, Beeckman H. 2021. Timber identification of *Autranella*, *Baillonella* and *Tieghemella* in the taxonomically challenging Sapotaceae family. *Plant Methods* 17(1): 64. DOI: 10.1186/s13007-021-00766-x.

Dormontt EE, Boner M, Braun B, Breulmann G, Degen B, Espinoza E, Gardner S, Guillery P, Hermanson JC, Koch G, *et al.* 2015. Forensic timber identification: it's time to integrate disciplines to combat illegal logging. *Biol. Conserv.* 191: 790–798. DOI: 10.1016/j.biocon.2015.06.038.

Dormontt EE, Jardine DI, van Dijk KJ, Dunker BF, Dixon RRM, Hipkins VD, Tobe S, Linacre A, Lowe AJ. 2020. Forensic validation of a SNP and INDEL panel for individualisation of timber from bigleaf maple (*Acer macrophyllum* Pursch). *Forensic Sci. Int. Genet.* 46: 102252. DOI: 10.1016/j.fsigen.2020.102252.

Edwards DP, Laurance WF. 2013. Biodiversity despite selective logging. *Science* 339(6120): 646–647. DOI: 10.1126/science.339.6120.646-b.

Espinoza EO, Lancaster CA, Kreitals NM, Hata M, Cody RB, Blanchette RA. 2014. Distinguishing wild from cultivated agarwood (*Aquilaria* spp.) using direct analysis in real time and time of-flight mass spectrometry. *Rapid Commun. Mass Spectrometr.* 28(3): 281–289. DOI: 10.1002/rcm.6779.

Evans PD, Mundo IA, Wiemann MC, Chavarria GD, McClure PJ, Voin D, Espinoza EO. 2017. Identification of selected CITES-protected Araucariaceae using DART TOFMS. *IAWA J.* 38(2): 266. DOI: 10.1163/22941932-20170171.

Förstel H, Boner M, Höltken A, Flandung M, Degen B, Zahnen J. 2011. Fighting illegal logging through the introduction of a combination of the isotope method for identifying the origins of timber and DNA analysis for differentiation of tree species. Deutsche Bundesstiftung Umwelt (German Federal Foundation for the Environment). Report no. AZ 26452/31. Deutsche Bundesstiftung Umwelt, Osnabrück.

Freyman WA, Thornhill AH. 2016. Matrix Maker. Available online at https://github.com/wf8/matrixmaker.

Gasson PE, Lancaster CA, Young R, Redstone S, Miles-Bunch IA, Rees G, Guillery RP, Parker-Forney M, Lebow ET. 2021. World-ForestID: addressing the need for standardized wood reference collections to support authentication analysis technologies; a way forward for checking the origin and identity of traded timber. *Plants People Planet* 3(2): 130–141. DOI: 10.1002/ppp3.10164.

Gori Y, Stradiotti A, Camin F. 2018. Timber isoscapes. A case study in a mountain area in the Italian Alps. *PLoS ONE* 13(2): e0192970. DOI: 10.1371/journal.pone.0192970.

Hartvig I, Czako M, Kjaer ED, Nielsen LR, Theilade I. 2015. The use of DNA barcoding in identification and conservation of rosewood (*Dalbergia* spp.). *PLoS ONE* 10(9): e0138231. DOI: 10.1371/journal.pone.0138231.

He T, Jiao L, Wiedenhoeft AC, Yin Y. 2019. Machine learning approaches outperform distance- and tree-based methods for DNA barcoding of *Pterocarpus* wood. *Planta* 249(5): 1617–1625. DOI: 10.1007/s00425-019-03116-3.

He T, Lu Y, Jiao L, Zhang Y, Jiang X, Yin Y. 2020. Developing deep learning models to automate rosewood tree species identification for CITES designation and implementation. *Holzforschung* 74: 1123–1133. DOI: 10.1515/hf-2020-0006.

Helmling S, Olbrich A, Heinz I, Koch G. 2018. Atlas of vessel elements: identification of Asian timbers. *IAWA J.* 39(3): 249–352. DOI: 10.1163/22941932-20180202.

Helmling S, Olbrich A, Tepe L, Koch G. 2016. Qualitative and quantitative characteristics of macerated vessels of 23 mixed tropical hardwood (MTH) species: a data collection for the identification of wood species in pulp and paper. *Holzforschung* 70(9): 839–844. DOI: 10.1515/hf-2015-0195.

Hoare A. 2015. Tackling illegal logging and the related trade, what progress and where next? Chatham House Report, Chatham House, The Royal Institute of International Affairs, London.

Hollingsworth PM, Graham SW, Little DP. 2011. Choosing and using a plant DNA barcode. *PLoS ONE* 6(5): e19254. DOI: 10.1371/journal.pone.0019254.

Horacek M. 2012. Christmas tree production in Europe: control of declared geographical origin by stable isotope analysis – a pilot study. *Bodenkultur* 63: 35–41.

Horacek M, Rees G, Boner M, Zahnen J. 2018. Comment on: developing forensic tools for an African timber: [. . . ], by Vlam *et al.*, 2018. *Biol. Conserv.* 226: 333–334. DOI: 10.1016/j.biocon.2018.06.037.

Horikawa Y, Mizuno-Tazuru S, Sugiyama J. 2015. Near-infrared spectroscopy as a potential method for identification of anatomically similar Japanese diploxylons. *J. Wood Sci.* 61(3): 251–261. DOI: 10.1007/s10086-015-1462-2.

Hwang S-W, Lee W-H, Horikawa Y, Sugiyama J. 2015. Chemometrics approach for species identification of *Pinus densiflora* Sieb. Et Zucc. and *Pinus densiflora* for. *Erecta Uyeki* — species classification using Near-Infrared Spectroscopy in combination with multivariate analysis. *J. Korean Wood Sci. Technol.* 43(6): 701–713. DOI: 10.5658/wood.2015.43.6.701.

INTERPOL. 2016. Uncovering the risks of corruption in the forestry sector. International Criminal Police Organization (ICPO) – INTERPOL. Interpol, Lyon.

Jianbang G. 2016. Quantifying illegal logging and related timber trade. In: Kleinschmit D, Mansourian S, Wildburger C, Purret A (eds.), *Illegal logging and related timber trade – dimensions, drivers, impacts and responses. A global scientific rapid response assessment report. IUFRO world series 35*: 37–59. International Union of Forest Research Organizations (IUFRO), Vienna.

Jiao L, Lu Y, He T, Guo J, Yin Y. 2020. DNA barcoding for wood identification: global review of the last decade and future perspective. *IAWA J.* 41(4): 620–643. DOI: 10.1163/22941932-bja10041.

Jiao LC, Yin YF, Cheng YM, Jiang XM. 2014. DNA barcoding for identification of the endangered species *Aquilaria sinensis*: comparison of data from heated or aged wood samples. *Holzforschung* 68(4): 487–494. DOI: 10.1515/hf-2013-0129.

Jiao LC, He T, Dormontt EE, Zhang YG, Lowe AJ, Yin YF. 2019. Applicability of chloroplast DNA barcodes for wood identification between *Santalum album* and its adulterants. *Holzforschung* 73(2): 209–218. DOI: 10.1515/hf-2018-0047.

Jolivet C, Degen B. 2012. Use of DNA fingerprints to control the origin of Sapelli timber (*Entandrophragma cylindricum*) at the forest concession level in Cameroon. *Forensic Sci. Int. Genet.* 6(4): 487–493. DOI: 10.1016/j.fsigen.2011.11.002.

Kagawa A, Kuroda K, Hisashi A, Tomoyyuki F. 2007. Stable isotopes and inorganic elements as potential indicators of geographic origin of Southeast Asian timber. In: *International symposium on development of improved methods to identify shorea species wood and its origin, September 25-26, 2007. Tokyo, Japan.*

Kagawa A, Leavitt SW. 2010. Stable carbon isotopes of tree rings as a tool to pinpoint the geographic origin of timber. *J. Wood Sci.* 56(3): 175–183. DOI: 10.1007/s10086-009-1085-6.

Kitin P, Espinoza E, Beeckman H, Abe H, McClure PJ. 2021. Direct analysis in real-time (DART) time-of-flight mass spectrometry (TOFMS) of wood reveals distinct chemical signatures of two species of *Afzelia*. *Ann. For. Sci.* 78(2): 31. DOI: 10.1007/s13595-020-01024-1.

Kleinschmit D, Mansourian S, Wildburger C, Purret A. 2016. *Illegal logging and related timber trade – dimensions, drivers, impacts and responses. A global scientific rapid response assessment report. IUFRO world series 35.* International Union of Forest Research Organizations (IUFRO), Vienna.

Koch G, Haag V, Heinz I, Richter HG, Schmitt U. 2015. Control of internationally traded timber — the role of macroscopic and microscopic wood identification against illegal logging. *J. Forensic Res.* 6(6). DOI: 10.4172/2157-7145.1000317.

Lancaster C, Espinoza E. 2012. Analysis of select *Dalbergia* and trade timber using direct analysis in real time and time-of-flight mass spectrometry for CITES enforcement. *Rapid Commun. Mass Spectrometr.* 26(9): 1147–1156. DOI: 10.1002/rcm.6215.

Lee SY, Lamasudin DU, Mohamed R. 2019. Rapid detection of several endangered agarwood-producing *Aquilaria* species and their potential adulterants using plant DNA barcodes coupled with high-resolution melting (Bar-HRM) analysis. *Holzforschung* 73(5): 435–444. DOI: 10.1515/hf-2018-0149.

Lens F, Liang C, Guo Y, Tang X, Jahanbanifard M. 2020. Computer-assisted timber identification based on features extracted from microscopic wood sections. *IAWA J.* 41(4): 660–680. DOI: 10.1163/22941932-bja10029.

Lowe AJ, Cross HB. 2011. The application of DNA methods to timber tracking and origin verification. *IAWA J.* 32(2): 251–262. DOI: 10.1163/22941932-90000055.

Lowe AJ, Dormontt EE, Bowie MJ, Degen B, Gardner S, Thomas D, Clarke C, Rimbawanto A, Wiedenhoeft A, Yin Y, *et al.* 2016. Opportunities for improved transparency in the timber trade through scientific verification. *Bioscience* 66(11): 990–998. DOI: 10.1093/biosci/biw129.

Ma L, Peng Y, Pei Y, Zeng J, Shen H, Cao J, Qiao Y, Wu Z. 2019. Systematic discovery about NIR spectral assignment from chemical structural property to natural chemical compounds. *Sci. Rep.* 9(1): 9503. DOI: 10.1038/s41598-019-45945-y.

May C. 2017. *Transnational crime and the developing world.* Global Financial Integrity, Washington, DC.

McClure PJ, Chavarria GD, Espinoza E. 2015. Metabolic chemotypes of CITES protected *Dalbergia* timbers from Africa, Madagascar, and Asia. *Rapid Commun. Mass Spectrometr.* 29(9): 783–788. DOI: 10.1002/rcm.7163.

Muellner AN, Schaefer H, Lahaye R. 2011. Evaluation of candidate DNA barcoding loci for economically important timber species of the Mahogany family (Meliaceae). *Mol. Ecol. Resourc.* 11(3): 450–460. DOI: 10.1111/j.1755-0998.2011.02984.x.

Musah RA, Espinoza EO, Cody RB, Lesiak AD, Christensen ED, Moore HE, Maleknia S, Drijfhout FP. 2015. A high throughput ambient mass spectrometric approach to species identification and classification from chemical fingerprint signatures. *Sci. Rep.* 5: 11520. DOI: 10.1038/srep11520.

Nellemann C, INTERPOL. 2012. Green carbon, black trade: illegal logging, tax fraud, and laundering in the world's tropical forests: a rapid response assessment. United Nations Environment Programme, GRID, Arendal.

Ng CH, Lee SL, Tnah LH, Ng KKS, Lee CT, Madon M. 2016. Genome size variation and evolution in Dipterocarpaceae. *Plant Ecol. Divers.* 9(5-6): 437–446. DOI: 10.1080/17550874.2016.1267274.

Ng CH, Lee SL, Tnah LH, Ng KKS, Lee CT, Diway B, Khoo E. 2017. Geographic origin and individual assignment of *Shorea platyclados* (Dipterocarpaceae) for forensic identification. *PLoS ONE* 12(4): e0176158. DOI: 10.1371/journal.pone.0176158.

Nithaniyal S, Newmaster SG, Ragupathy S, Krishnamoorthy D, Vassou SL, Parani M. 2014. DNA barcode authentication of wood samples of threatened and commercial timber trees within the tropical dry evergreen forest of India. *PLoS ONE* 9(9): e107669. DOI: 10.1371/journal.pone.0107669.

Norman M, Saunders J. 2017. Regulating the trade in illegal timber: asian approaches compared — state of play June 2017. *Forest Trends.* Available online at https://www.forest-trends.org/publications/regulating-trade-illegal-timber/.

Nowakowska JA. 2011. Application of DNA markers against illegal logging as a new tool for the Forest Guard Service. *Fol. For. Polon. A: Forestry* 53(2): 142–149. DOI: 10.5281/zenodo.30813.

Ogden R, Linacre A. 2015. Wildlife forensic science: a review of genetic geographic origin assignment. *Forensic Sci. Int. Genet.* 18: 152–159. DOI: 10.1016/j.fsigen.2015.02.008.

Paredes-Villanueva K, Espinoza E, Ottenburghs J, Sterken MG, Bongers F, Zuidema PA. 2018. Chemical differentiation of Bolivian *Cedrela* species as a tool to trace illegal timber trade. *Forestry* 91(5): 603–613. DOI: 10.1093/forestry/cpy019.

Paredes-Villanueva K, de Groot GA, Laros I, Bovenschen J, Bongers F, Zuidema PA. 2019. Genetic differences among *Cedrela odorata* sites in Bolivia provide limited potential for fine-scale timber tracing. *Tree Genet. Genomes* 15(3): 1454. DOI: 10.1007/s11295-019-1339-4.

Pastore TCM, Braga JWB, Coradin VTR, Magalhães WLE, Okino EYA, Camargos JAA, Muñiz GIBd, Bressan OA, Davrieux F. 2011. Near infrared spectroscopy (NIRS) as a potential tool for monitoring trade of similar woods: discrimination of true mahogany, cedar, andiroba, and curupixá. *Holzforschung* 65(1): 73–80. DOI: 10.1515/hf.2011.010.

Price ER, Miles-Bunch IA, Gasson PE, Lancaster CA. 2021. *Pterocarpus* wood identification by independent and complementary analysis of DART-TOFMS, microscopic anatomy, and fluorescence spectrometry. *IAWA J.* 42(4): 397–418. DOI: 10.1163/22941932-bja10064.

Ramalho AB, Andrade J, Hein PRG. 2018. Rapid discrimination of wood species from native forest and plantations using near infrared spectroscopy. *For. Syst.* 27(2): e008. DOI: 10.5424/fs/2018272-12075.

Ravindran P, Costa A, Soares R, Wiedenhoeft AC. 2018. Classification of CITES-listed and other Neotropical Meliaceae wood images using convolutional neural networks. *Plant Methods* 14(1): 25. DOI: 10.1186/s13007-018-0292-9.

Ravindran P, Thompson BJ, Soares RK, Wiedenhoeft AC. 2020. The XyloTron: flexible, open-source, image-based macroscopic field identification of wood products. *Front. Plant Sci.* 11(1015). DOI: 10.3389/fpls.2020.01015.

Richter HG, Dallwitz MJ. 2000 onwards. Commercial timbers: descriptions, illustrations, identification, and information retrieval. In English, French, German, Portuguese, and Spanish. Available online at https://www.delta-intkey.com/wood/index.htm.

Richter HG, Dallwitz MJ. 2016 onwards. Commercial timbers: descriptions illustrations, identification, and information retrieval. In English, French, German, Portuguese, and Spanish. Available online at http://delta-intkey.com.

Richter HG, Grosser D, Heinz I, Gasson P. 2004. IAWA list of microscopic features for softwood identification. *IAWA J.* 25: 1–70. DOI: 10.1163/22941932-90000349.

Sandak A, Modzelewska I, Sandak J. 2011. Fourier transform near infrared analysis of waste paper with the addition of cereal bran biodegraded by *Ascomycetes fungi*. *J. Near Infrared Spectrosc.* 19(5): 369–379. DOI: 10.1255/jnirs.951.

Sayers EW, *et al.* 2020. Database resources of the National Center for Biotechnology Information. *Nucleic Acids Res.* 48(D1): D9–D16. DOI: 10.1093/nar/gkz899.

Schmitz N (ed.) 2019. The timber tracking tool infogram. Overview of wood identification methods' capacity. Global Timber Tracking Network, GTTN Secretariat, European Forest Institute, Joensuu and Thünen Institute, Hamburg. DOI: 10.13140/RG.2.2.27920.25603.

Schmitz N (ed.) 2020. Scientific methods for taxonomic and origin identification of timber. Global Timber Tracking Network, GTTN Secretariat, European Forest Institute, Joensuu and Thünen Institute, Hamburg. DOI: 10.13140/RG.2.2.28416.46087.

Schmitz N, Beeckman H, Blanc-Jolivet C, Boeschoten L, Braga JWB, Cabezas JA, Chaix G, Crameri S, Degen B, Deklerck V, *et al.* 2020. Overview of current practices in data analysis for wood identification. A guide for the different timber tracking methods. Global Timber Tracking Network, GTTN secretariat, European Forest Institute, Joensuu and Thünen Institute, Hamburg. DOI: 10.13140/RG.2.2.21518.79689.

Silva DC, Pastore TCM, Soares LF, de Barros FAS, Bergo MCJ, Coradin VTH, Gontijo AB, Sosa MH, Chacon CB, Braga JWB. 2018. Determination of the country of origin of true Mahogany (*Swietenia macrophylla* King) wood in five Latin American countries using handheld NIR devices and multivariate data analysis. *Holzforschung* 72(7): 521–530. DOI: 10.1515/hf-2017-0160.

Snel FA, Braga JWB, da Silva D, Wiedenhoeft AC, Costa A, Soares R, Coradin VTR, Pastore TCM. 2018. Potential field-deployable NIRS identification of seven *Dalbergia* species listed by CITES. *Wood Sci. Technol.* 52(5): 1411–1427. DOI: 10.1007/s00226-018-1027-9.

Soares LF, da Silva JR, Bergo MCJ, Coradin VTH, Braga JWB, Pastore TCM. 2017. Evaluation of a NIR handheld device and PLS-DA for discrimination of six similar Amazonian wood species. *Quim. Nova* 40(4): 418–426. DOI: 10.21577/0100-4042.20170014.

Sun YH, Lin Q, He X, Zhao YH, Dai F, Qiu J, Cao Y. 2021. Wood species recognition with small data: a deep learning approach. *Int. J. Comput. Intell.* 14(1): 1451–1460. DOI: 10.2991/ijcis.d.210423.001.

Tnah LH, Lee SL, Ng KKS, Faridah Q-Z, Faridah-Hanum I. 2010. Forensic DNA profiling of tropical timber species in Peninsular Malaysia. *For. Ecol. Manage.* 259(8): 1436–1446. DOI: 10.1016/j.foreco.2010.01.017.

Tsuchikawa S, Inoue K, Noma J, Hayashi K. 2003. Application of near-infrared spectroscopy to wood discrimination. *J. Wood. Sci.* 49(1): 0029–0035. DOI: 10.1007/s100860300005.

UNODC. 2016. *Best practice guide for forensic timber identification*. United Nations Office on Drugs and Crime, Vienna.

van der Sleen P, Zuidema PA, Pons TL. 2017. Stable isotopes in tropical tree rings: theory, methods and applications. *Funct. Ecol.* 31(9): 1674–1689. DOI: 10.1111/1365-2435.12889.

Vijay V, Pimm SL, Jenkins CN, Smith SJ. 2016. The impacts of oil palm on recent deforestation and biodiversity loss. *PLoS ONE* 11(7). DOI: 10.1371/journal.pone.0159668.

Vlam M, Boom A, de Groot GA, Zuidema PA. 2018a. Tropical timber tracing and stable isotopes: a response to Horacek et al. *Biol. Conserv.* 226: 335–336. DOI: 10.1016/j.biocon.2018.06.036.

Vlam M, de Groot GA, Boom A, Copini P, Laros I, Veldhuijzen K, Zakamdi D, Zuidema PA. 2018b. Developing forensic tools for an African timber: regional origin is revealed by genetic characteristics, but not by isotopic signature. *Biol. Conserv.* 220: 262–271. DOI: 10.1016/j.biocon.2018.01.031.

Watkinson CJ, Gasson P, Rees GO, Boner M. 2020. The development and use of isoscapes to determine the geographical origin of *Quercus* spp. in the United States. *Forests* 11(8): 862. DOI: 10.3390/f11080862.

Waycott M, van Dijk K-j, Biffin E. 2021. A hybrid capture RNA bait set for resolving genetic and evolutionary relationships in angiosperms from deep phylogeny to intraspecific lineage hybridization. *bioRxiv*: 2021.2009.2006.456727. DOI: 10.1101/2021.09.06.456727.

Wheeler E, Gasson P. 1989. IAWA list of microscopic features for hardwood identification. *IAWA Bull, n.s.* 10: 219–332.

Wheeler EA. 2011. InsideWood — a web resource for hardwood anatomy. *IAWA J.* 32(2): 199–211. DOI: 10.1163/22941932-90000051.

Wheeler EA, Baas P, Gasson PE. 1989. IAWA list of microscopic features for hardwood identification. *IAWA J.* 10: 219–332.

Wyatt T. 2014. The Russian Far East's illegal timber trade: an organized crime? *Crime Law Soc. Change* 61: 15–35. DOI: 10.1007/s10611-013-9461-y.

Zhang MM, Zhao GJ, Guo J, Liu B, Jiang XM, Yin YF. 2019. A GC-MS protocol for separating endangered and non-endangered *Pterocarpus* wood species. *Molecules* 24(4). DOI: 10.3390/molecules24040799.

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