



Contents lists available at ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Developing forensic tools for an African timber: Regional origin is revealed by genetic characteristics, but not by isotopic signature

Mart Vlam^{a,*}, G. Arjen de Groot^b, Arnoud Boom^c, Paul Copini^d, Ivo Laros^b, Katrui Veldhuijzen^a, David Zakamdi^e, Pieter A. Zuidema^a

^a Forest Ecology and Forest Management, Wageningen University & Research, P.O. Box 47, 6700AA, The Netherlands

^b Animal Ecology, Wageningen Environmental Research, Wageningen University & Research, P.O. Box 47, 6700AA, The Netherlands

^c Department of Geography, University of Leicester, University Road, Leicester LE1 7RH, UK

^d Vegetation, Forest and Landscape Ecology, Wageningen Environmental Research, Wageningen University & Research, P.O. Box 47, 6700AA, The Netherlands

^e Groupe Rougier, Cameroon

ARTICLE INFO

Keywords:

DNA
Geographic origin
Microsatellites
Stable isotopes
Timber forensics
Tropical timber

ABSTRACT

Combating illegal timber trade requires forensic tools that independently verify claimed geographic origin of timber. Chemical and genetic wood characteristics are potentially suitable tools, but their performance at small spatial scales is unknown. Here we test whether stable isotopes and microsatellites can differentiate Tali timber (*Erythrophloeum* spp.) at the level of forest concessions. We collected 394 wood samples from 134 individuals in five concessions in Cameroon and Congo Republic. The nearest neighbour concessions were 14 km apart and the furthest pair 836 km apart. We constructed genetic profiles using eight nuclear microsatellite markers and measured concentrations of $\delta^{18}\text{O}$, $\delta^{15}\text{N}$ and $\delta^{13}\text{C}$. We differentiated provenances using PCA (microsatellites), ANOVA and kernel discriminant analysis (isotopes). Next, we performed assignment tests using blind samples ($n = 12$, microsatellites) and leave one out cross validation (LOOCV, isotopes). Isotopic composition varied strongly within concessions and only $\delta^{13}\text{C}$ differed significantly between two concessions. As a result, LOOCV performed only marginally better than random. Genetic differentiation among provenances was also relatively low, but private alleles were commonly found. Bayesian clustering analysis correctly assigned 92% of the blind samples, including those of nearby concessions. Thus, Tali timber can be successfully assigned to the concession of origin using genetic markers, but not using isotopic composition. Isotopic differentiation may be possible at larger spatial scales or with stronger climatic or topographic variation. Our study shows that genetic analyses can differentiate the geographic origin of tropical timber at the scale of forest concessions, demonstrating their potential as forensic tools to enforce timber trade legislation.

1. Introduction

Despite numerous measures illegal logging is still a widespread phenomenon. It is estimated that 10–30% of the timber traded in the global market is illegally harvested (Nellemann, 2012). The problem of illegal timber trade is most predominant in the tropical forestry sector where an estimated 30–90% of the volume is illegally harvested (Hirschberger, 2008; Hoare, 2015). This illegal trade is detrimental to the economies of exporting countries, for example through tax evasion, and uncontrolled illegal logging poses a serious threat to rich and biodiverse tropical forests. To combat the illegal timber trade several legislative actions have been taken in key importing countries, including the EU timber regulation (EUTR) and amendment of the US Lacey Act (Lawson, 2015). In general these laws prohibit any illegally

sourced timber from entering the domestic markets. Their implementation has resulted in an increasing demand for means to independently verify the legal status of timber, including forensic techniques.

So far the primary focus of forensic timber studies has been on the identification of timber species based on wood anatomical features (Gasson, 2011). Though useful in the struggle against illegal trade, wood anatomy alone is rarely sufficient when fraudulent claims of timber origin are suspected. Such fraudulent claims of origin, including forged forest management plans (INTERPOL, 2016), false export permits (Tacconi et al., 2016) and mixing of timber from different origins, are predominant ways of ‘laundering’ illegally sourced timber. False claims of geographic origin of tropical timber are likely the most important form of illegal trade in tropical timber. Therefore development

* Corresponding author.

E-mail address: mart.vlam@wur.nl (M. Vlam).

of effective forensic techniques to verify claims of geographic origin are much needed (Dormontt et al., 2015). Such techniques would be particularly useful if their spatial resolution allows verifying timber sourced at the level of logging concessions, i.e., at the scale of 10–100 km (Jolivet and Degen, 2012).

Here we evaluate the potential suitability of two promising forensic techniques – stable isotopes and DNA microsatellites – to differentiate tropical timber sourced from different regions. Stable carbon, nitrogen and oxygen isotopes have been widely used for forensic tracing of various goods and products (Ehleringer et al., 2000; West et al., 2007), including trade in endangered species (Retief et al., 2014). Examples of isotope tracing from the forestry sector are scarce (but see: Horacek, 2012; Kagawa and Leavitt, 2010) and completely absent for the tropical forestry sector. The feasibility of DNA microsatellite tracing of tropical timber has been shown for a very limited number of tropical trees, e.g. *Swietenia* spp. (Mahogany) in South America (Degen et al., 2013), *Etandrophragma cylindricum* (Sapelli) in West Africa (Jolivet and Degen, 2012) and *Neobalanocarpus heimii* (Chengal) in Southeast Asia (Tnah et al., 2010). The study by Degen et al. (2013) focused on the assignment of country of origin, representing relatively large spatial scales, i.e. 100 s to 1000 s of kms. The study by Jolivet and Degen (2012) is the only known study at which origin was traced at the highly relevant concession level.

Forensic techniques to verify geographic origin likely have a minimal spatial scale of operation, because of limited spatial differentiation. For instance, genetic differentiation may be limited between nearby stands due to regular exchange of genetic material via seed or pollen (Bizoux et al., 2009). Likewise, low spatial variation in environmental conditions may cause limitations in spatial differentiation of isotopic composition (Wunder and Norris, 2008). Thus, an analysis of the spatial resolution at which the method can be applied is essential for any timber tracing method. Our study is the first to verify the potential of both genetic and isotopic timber tracing techniques to operate at the forest concession level.

We evaluate the potential of isotopic and genetic forensic approaches for one of the most traded African timbers, Tali, which is sourced from two species: *Erythrophloeum suaveolens* and *E. ivorense*. Specifically, we addressed the following research questions: (1) Do wood isotopic and genetic signatures differ among provenances? (2) What is the spatial resolution at which these two methods can differentiate timber samples? (3) What is the success rate of assigning blind timber samples to their respective regions of origin? To this end we collected wood samples from four provenances in Cameroon and Congo (nearest neighbour concessions were 14 km apart and furthest pair were 836 km apart), measured genetic (microsatellites; (Duminil et al., 2011)) and isotopic characteristics ($\delta^{13}\text{C}$, $\delta^{15}\text{N}$ and $\delta^{18}\text{O}$) of these samples and performed discriminant analyses to differentiate samples from different origins. We then used blind sample tests to evaluate the success of provenancing samples from unknown origin.

2. Material and methods

2.1. Study species

This study focuses on the timber sold under the trade name Tali, which is sourced from two botanically distinct species: *Erythrophloeum suaveolens* (Guill. et Perr.) Brenan and *Erythrophloeum ivorense* A.Chev. (for convenience we will from here on abbreviate the genus name when referring to the two species). These two closely related species are naturally occurring in West and Central Africa (Fig. 1). They are monoecious and likely insect-pollinated (Anaïs-Pasiphaé Gorel, 2015). *E. suaveolens* and *E. ivorense* diverged ~600 K years BP and within *E. suaveolens* two sub-populations can be distinguished that diverged 120 K and 60 K years BP (Duminil et al., 2015). While *E. ivorense* has a more coastal distribution and *E. suaveolens* a more inland distribution (see Fig. 1), they do occur in sympatry in a large part of their

distribution (Duminil et al., 2010), including in the areas sampled in this study. Where the two species occur in sympatry, hybridization cannot be excluded (Duminil et al., 2010).

Tali wood is mostly shipped to Europe where it is applied in heavy construction works, such as sheet piling. In 2010, Cameroon exported an estimated 143,000 m³ of Tali logs and sawnwood at an average price of 102 € per m³ (ITTO, 2012). Tali is in the top-5 most valuable timbers for export in Cameroon. Neither of the two species yielding Tali has been classified as endangered, nor are they listed under CITES (the Convention on International Trade in Endangered Species of Wild Fauna and Flora). Yet, the distribution region of these species in West and Central Africa is known for high incidence of illegal logging (Hirschberger, 2008; Hoare, 2015).

In two of our study sites (concessions 2 and 3) possibly only one of the species (*E. suaveolens*) occurs based on the distribution data (Fig. 1), while at another site (Concession 1) a mix of the two species may occur. Yet, the high degree of species mixing, the difficulty of separating these species (both in the field based on bark and leaf characteristics and in the lab based on wood anatomical characteristics) and the occurrence of identification errors in distribution data do not allow us to state with certainty which of our sampled trees belong to which species. Nevertheless, the fact that our samples are taken from two botanical species and that these species can possibly hybridize does not provide limitations to our study. We evaluate the potential for tracing of geographic origin of a tropical timber that is derived from multiple species (this is often the case in tropical timbers), and we do not conduct a population genetic study in a species conservation context. In addition, in terms of isotope signature, differences in isotope values between species may be smaller than those across sites (van der Sleen et al., 2015b). Clearly, the results of our study should not be used to derive conclusions about species-specific patterns.

2.2. Sample collection

We collected samples in five logging concessions (Fig. 1). In three concessions (1–3) we sampled more intensively and samples from these concessions were included in both the isotopic and genetic analyses. Samples from concessions 4 and 5 were included in the genetic analyses only. In July and August 2015, a total of 381 sapwood samples (triplicates) of 127 individual Tali trees were collected in Cameroon, in three concessions of Groupe Rougier Cameroon (concessions 1–3; Fig. 1; Table A.1). Fresh wood samples of three Tali trees (triplicates) were taken in the Danzer-Interholco IFO concession (concession 4) in Congo-Brazzaville in July 2016. All samples were collected following a standardized protocol, specifically designed to allow sample collection by non-scientific personnel. Sampling took place at multiple spatial scales (14–836 km; Table A.2) using a tiered approach. Samples were collected from stumps of large (> 60 cm diameter at breast height, dbh) trees, < 33 days after logging. Wood samples were solely collected from those trees identified as ‘Tali’ (so either *E. suaveolens* or *E. ivorense*) by the botanist or prospector of the logging company. Per tree, three samples were taken at different locations along the circumference of the stem. These samples consisted of either ~1 cm³ of fresh bark/sapwood samples stored in silica gel (concession 1–3) or ~10 cm³ air-dried sap-/heartwood samples (concession 4). GPS-coordinates of the trees were taken and information, including dbh and estimated time since logging (days), were recorded on the provided field forms. Samples were sent to the Dendrolab at Wageningen University & Research, The Netherlands. Upon arrival of the samples superficial moulding was observed in ~50% of the samples stored in silica gel, any further decay of the wood was immediately stopped by adding extra silica gel to the bags. Finally, four single Tali heartwood samples previously collected in the northeast of Cameroon, were included (concession 5). These samples were collected in June 2011 in concession 11.001 of Transformation REEF Cameroon (TRC).

Download English Version:

<https://daneshyari.com/en/article/8847405>

Download Persian Version:

<https://daneshyari.com/article/8847405>

[Daneshyari.com](https://daneshyari.com)