Genomic tools for traceability: Opportunities, challenges and perspectives for the Canadian forestry sector

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ABSTRACT

Consumers, retailers, investors, and governments want quality products that are both safe and obtained through legal and sustainable practices. The solution put into place to meet those challenges requires the implementation of a traceability system. In the context of forestry, traceability is the ability to inform about the identity or provenance of a wood product. The principle of traceability helps establish trust among the various stakeholders throughout the value chain. To this day, most traceability systems are based on paper permits, which are easier to falsify than systems that are based on genetic markers. In this manuscript, we define the elements of a traceability system based on genomic tools that could be useful for the Canadian forest sector. We also present several examples in which genomic tools are or could be used as traceability systems. Genomic tools and data happen to be available in quantity for several forest species and they could constitute the basis for the development of such traceability systems. Our aim is to demonstrate that there are actually great opportunities to develop such systems that could be applied to the Canadian forest sector.

Keywords: traceability, genomic, markets, certification, sustainability, urban forestry, quality control, value chain, taxonomy, origin, database

RÉSUMÉ:

Les consommateurs, les détaillants, les investisseurs et les gouvernements veulent des produits de qualité, sécuritaires et qui résultent de pratiques légales et durables. Les principes de la traçabilité permettent de répondre à ces différents enjeux. Dans le contexte forestier, la traçabilité est la capacité d'informer sur l'identité ou la provenance d'un produit du bois. Ce principe aide à établir la confiance entre les différents acteurs de la chaîne de valeur. À ce jour, la plupart des systèmes de traçabilité sont basés sur des permis en papier qui sont facilement falsifiables. Dans ce manuscrit, nous définissons les éléments d'un système de traçabilité basé sur des outils génomiques qui pourrait être utile pour le secteur forestier canadien. Nous présentons aussi plusieurs exemples de la façon dont les outils de la génomique sont ou pourraient être utilisés. Des données et des outils génomiques sont actuellement disponibles en grandes quantités pour plusieurs essences forestières et ceux-ci pourraient constituer la base du développement de tels systèmes de traçabilité. Notre objectif est de démontrer qu'il y a actuellement de grandes opportunités pour développer de tels systèmes qui pourraient s'appliquer au secteur forestier canadien.

Mots-clé: traçabilité, génomique, marchés, certification, développement durable, foresterie urbaine, contrôle de la qualité, chaîne de valeur, taxonomie, origine, base de données

Introduction

The concept of traceability dates back to the 1930s when it was used to promote the high quality of wines from France's Champagne region (CIVC 2011). In the wake of food supply chain scandals such as chicken dioxin contamination in Belgium (Bernard *et al.* 2002) and mad cow disease in the United Kingdom (Wales *et al.* 2006), traceability really began to draw large public attention by becoming a powerful tool proposed by authorities to protect consumers (European Parliament 2002). In addition, the endorsement of the traceability concept was certainly stimulated by the emergence and development of new markets relative to "fair trade" products. As a consequence, various goods (coffee, cacao, cotton, as well as wood) are now sold to consumers with the

promise that their production and distribution meet sustainable development criteria (UN Global Compact and BSR 2014). In response to public and world market demands, the forestry sector efficiently endorsed this "fair trade product" principle by adopting different forest certification systems (NRCan 2017). Forest certification is now accepted as a golden standard that largely guarantees sustainably-grown, responsibly-harvested and legally-traded forest products. The forest certification principle, since it informs about practices related to the harvesting of trees, is similar to a system of traceability. Indeed, it tells about the origin of a wood product which gives it an additional value that is extrinsic, that is to say it is not linked to observable attributes (such as wood appearance or durability).

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Whether the purpose is to comply with regulations, to guarantee sustainability or to secure market shares, the concept of traceability now helps to establish trust among the various stakeholders throughout the value chain. Two main criteria can be used to assess the quality of a traceability system: **independence** and **reproducibility**. Citing forest certification as an example, we could say that these systems meet the independence criterion as the certification processes are managed by an independent third party that checks the credibility of the label through verifications and audits. However, forest certification systems, albeit highly effective, are vulnerable to tampering as they mostly rely on a paper permit system which, by its nature, is non-reproducible. Forest certification systems currently in use have not been developed to ascertain the nature of a wood product. Consequently, prosecuting for illegal logging and associated trade, mislabelling of timber species or smuggling of wood products can only be supported by the development of robust tools and technologies that can infer the nature and origin of timber and wood products.

Technoscientific tools, such as genomic tools, provide reproducible results that are difficult to falsify. For example, genetic markers have uncovered cases of misidentification of fish and seafood in markets and restaurants (e.g., Logan *et al.* 2008; Khaksar *et al.* 2015). Such mislabelling cases may stem from human error or intentional deceit. Genomic tools therefore offer a reliable alternative to traditional identification, especially for processed products for which morphological criteria cannot be checked. These methods, of course, apply to all products in which the raw material is organic (living material).

In this article, we will first define the essential elements of a traceability system and present different theoretical approaches associated to the specific use of genomic tools in the forestry context. Second, we will demonstrate how a vast diversity of forestry-related questions, not exclusively related to illegal logging, could be answered with several examples where genomic tools are actually used to trace forest products. We will also discuss new areas where such tools could be applied in a near future to address traceability questions. Finally, we will highlight the perspectives and challenges associated with traceability in general as it is applied to the Canadian forest sector.

What exactly is a traceability system?

Traceability can be defined as “the ability to trace the history, application or location of an entity by means of recorded identifications” (ISO 1994). It thus implies tracing back a product or a few key ingredients at every stage of the supply chain (Fig. 1). In forestry, it refers more specifically to the 1) identity and/or 2) provenance of timber or wood products. By identity, we mean the taxonomical identification of the tree, which could present different degrees of precision corresponding to different genetic units: genera, species, subspecies, cultivars, varieties, or even a specific individual. By provenance, we generally refer to the geographic location where the tree would have grown, such as a country or a territory. In the latter case, and depending on the method used, this may also point to an ecological area such as a habitat rather than to a specific geographical region.

Practical framework of a traceability system

A traceability system should be developed in order to answer a specific and predefined question. Such an answer (identity and/or provenance, in the case of a tree as presented before) is obtained by using both mandatory elements that define the practical framework of a traceability system: a **technoscientific tool** and a **reference database** (Fig. 1). The context, in which the traceability system is thought to be applied, will determine the specific question and the degree of precision needed. Therefore, it is imperative that developers establish the capacity of the system to provide an answer (i.e., its resolution) before it can be used in a practical framework. Those limits will be dependent on the choice of tools, but also on the richness of the reference database. For each traceability system, equal importance should be given to the building of a complete database as to the validation of the tools. Their development should be conducted in parallel because the quality of the database will be dependent of the precision of the technoscientific tools.

The technoscientific tools

Different scientific or technical tools can be used to check the identity and/or the provenance of a living product. We can classify those tools into three categories based on the type of information they can provide: genomic, morphological and chemical (Table 1). Tools from these three different categories are not mutually exclusive, and they can be used in combination. Each category of tools has its own specific technical and practical characteristics that influence its ability to inform about the identity or the provenance of the products tested (for a complete review of the different techniques, see Dormontt *et al.* 2015).

Rationally, one of the first constraint in the establishment of a traceability system will be the cost for its development (tools and database) and its subsequent implementation (efficiency). In terms of development, genomic tools may have some advantages over chemical or morphological tools since a lot of resources are already available. In fact, the development of a traceability system could already benefit from the large-scale genome projects (e.g., Arborea, SmartForests, SpruceUp) that produced valuable genomic resources (DNA sequences and genetic markers) for several Canadian forest tree species (e.g., Pavy *et al.* 2013).

The reference database

For traceability purposes, genomic tools alone are inefficient. They have to come with an associated database that contains genomic data obtained from validated reference materials corresponding, for instance, to a particular tree species (i.e., its “identity”). A “good” reference database would thus include information relative to all potential species or individuals thought to be tested (e.g., species found in the same area, sister species).

These reference specimens are individuals for whom the identity and provenance are known and verified. Considering a database that could be applied to the forestry sector, they can be retrieved either from provenance trials, living collections of trees from different geographical origins (often repre-

Fig. 1. Representation of a traceability system and the information it can offer at different steps of the chain of custody as well as the taxonomical and/or geographical information it can provide at different resolution levels.

sentative of species' range and established in plantations, or from herbaria). In Canada many provenance trials for several commercial forest species have already been established by different forest departments (provincial and federal) for research and monitoring purposes since the 1950s.

To feed data into the database, the reference specimens must be analyzed with the genomic tools developed using a validated and standardized protocol; i.e., the same protocol that will be used at the time of using the traceability system

with unknown specimens. Such standardization of the protocol will result in standardized data that can be easily compared with those of the reference database in order to answer the question asked.

Three approaches when using genomic tools in a traceability system

Depending on the question to be resolved, three main approaches, which correspond to different levels of resolu-

Table 1. Different types of data that can be used to develop a forestry traceability system

Type of data	Information given	Expertise and knowledge required	Data examples
Genomic	Identity: species, subspecies, cultivar, varieties, clonal line	Low technical expertise is required if the process is automated. At small scale, moderate to great technical expertise is necessary to apply the method / Low to moderate knowledge is required to interpret the results	DNA sequences, genotypes from all types of markers (SNP, microsatellite, genotyping by sequencing)
Morphological	Identity: species, subspecies, cultivar, varieties, clonal line	Moderate technical expertise needed / Great knowledge necessary to interpret the results	Morphological characteristics of the harvested wood or the standing trees: colors, wood pattern, bark, bud, flower, leaf Dendrochronological data
Chemical	Provenance: geographical region, ecosystems & Identity: Species	Comparable to genomic data	Isotopes Metabolites (phenolic compounds, terpenoids, fatty acids, sugars, etc.)

tion, can be applied for traceability purposes (Fig. 2). They are: i) the fingerprinting approach, which differentiates individuals within the same species (refers to identity); ii) the taxonomic identification approach, which differentiates individuals belonging to different taxonomic units—genus, species or variety (also refers to identity); and, iii) the phylogeography approach, which identifies the geographic region of origin of an individual (refers to provenance).

The three approaches differ in the type of genetic markers used. Genetic markers are variable genomic regions that provide information allowing a distinction between individuals, species or individuals from different geographic regions. In the **fingerprinting approach**, markers allow the generation of a unique fingerprint for each individual in the traceability system. This is used in forensic sciences when an unidentified sample found at a crime scene is matched to a known individual (Gill *et al.* 1985; Jeffreys *et al.* 1985, 1988) whose fingerprint may be found in a database or which could be tested using the same set of markers. Uniqueness is a critical factor to take into account in order to avoid false positives (i.e., in the case of a unique fingerprint attributed to two members of the same family). The **taxonomic identification approach** uses genetic markers that vary little between individuals of a same species but show differences between species. This is the type of approach used in the Barcode of Life project, which aims to identify all species using one or more genomic regions (Hajibabaei *et al.* 2007; Ratnasingham and Hebert 2007). For some taxonomic groups, the Barcode project differentiates species from a single genomic region (like birds, Kerr *et al.* 2007 or fish, Ward *et al.* 2005); but that is not the case for plants. In best case scenarios, it is necessary to target several regions (Pennisi 2007; Fazekas *et al.* 2008), while for taxonomical groups that notably included many tree species, there are still no marker sets available to differentiate species. Finally, the **phylogeographic approach** identifies the geographic origin of a specimen. It uses genetic markers that show variations between individuals of the same species as well as differences associated with various geographic areas. Major climatic changes, such as those that occurred during

the Quaternary glaciation periods, may explain regional differences found within the same species today (Hewitt 2000, 2004). During a glaciation period, species sought protection in places called glacial refugia (Fig. 2), where groups deviated and acquired differences that remain perceptible today, even after recolonization of the area. The ability to capture a phylogeographic signal for a species will depend on several factors: the territory of the species and the presence of physiographic barriers would promote the species' intraspecific differentiation or dispersal capacity, whereas a more mobile species would get distributed more evenly.

Present and potential applications of traceability systems in forestry

Traceability in forestry production: quality assurance control

In forestry, scientific research has benefited from major investments in genomic projects over the past few years. A recent study has evaluated that more than \$123 million have been allocated among research projects in forest genomics in Canada (Porth *et al.* 2015). A significant portion of these funds was used to develop ways, in combination with genomics or not, to increase Canadian forest productivity (e.g., Beaulieu *et al.* 2014; Park *et al.* 2016). Combining traditional selection methods with somatic embryogenesis was one of the strategies proposed to increase genetic gains (by more than 20%), and also to reduce the rotation age of a plantation (by more than 10 years) (Petrinovic *et al.* 2009; Gélinas and Bull 2013). With a clonal multiplication technique like somatic embryogenesis, it is now possible to channel 100% of field-measured gain and to reproduce the selected tree (clone) in as many copies as needed. Unfortunately, a human-made error can sometimes jeopardize the expected yield gain: one can easily imagine what could result from the massive propagation of a mislabelled tree that does not have the desired attributes. Therefore, the principle that the origin and identity of a tree can be established all along the production chain is particularly relevant in this modern forestry context where many steps (from the laboratory to the field) are necessary to produce the improved tree. Moreover, such a traceability system

Fig. 2. Representation of the three approaches using genomic tools in a traceability system.

can be seen as an insurance that the expected genetic gain will be obtained at the time of harvesting 35 years after planting.

The tree nursery of St-Modeste (Québec, Canada) has worked to implement a traceability system that uses genetic markers previously developed for white spruce (Pavy *et al.* 2013). This traceability system project has two objectives (Godbout *et al.* 2017): 1) to develop methods that make it possible to trace back the origin of the seedling produced (cross of origin); and, 2) to generate a unique genetic fingerprint that could be used to differentiate each embryogenic cell line from the cryobank to the field. Two criteria were also identified: a minimum number of low-cost DNA markers should be used (40 SNPs), and the traceability system (from DNA extraction to data interpretation) should be easy to use by non-specialists. The 40 SNPs corresponded to the capacity of a single Sequenom® genotyping array. Accordingly, this traceability system was developed using simulated data sets and classification methods currently available in the literature. After running computer simulations to generate crosses among elite parent plants for which genomic information was already available, the restricted set of markers was selected without the need to genotype thousands of specimens (i.e., laboratory-produced lines). With this set of markers (36 in total), the nursery of St-Modeste was able to identify the most common sources of error in its white spruce seedling production pipeline. The majority of errors occurred at the time of the controlled crosses, a result that reflects the technique's complexity. This is also in line with previous results from work in similar production systems (Corley 2005; Kumar *et al.* 2007; Doerksen and Herlinger 2008; Moriguchi *et al.* 2009; Padi *et al.* 2015). Most importantly, a unique fingerprint was generated for a majority of the embryogenic cell lines. Finally, although most errors originated at the controlled cross stage, about 25% of those detected had other and very diverse causes, such as material misidentification or plants

being mixed up in the fields or in the cryobanks. Therefore, the propagation of these errors throughout the production line supports the use of a traceability system before the deployment of a reforestation program derived from such production methods.

A traceability system, as described above, is designed to provide information at the time of forest seedling production, but can also be used for the complementary tracing of trees a few years after planting. The ability to trace trees on the ground could alleviate some community concerns about the use of clones in forestry and its impact on genetic diversity in natural forests (Gélinas and Bull 2013; Nilausen *et al.* 2014).

In France, a traceability system was designed to guarantee the authenticity of the oak used to make wine barrels. The OAKTRACK project developed two sets of genomic tools that could be used independently or together. The first kit was for the identification of oak species (taxonomic approach), while the second confirmed the oak's geographic origin by performing a conformity test to match it with a predicted origin (phylogeographic approach) (Deguilloux *et al.* 2003; Guichoux *et al.* 2011; Guichoux and Petit 2014). The OAKTRACK project's objectives were to develop antifraud tools and to improve the quality of the wood being used by optimizing procurement controls. By using the method upstream, managers were able to guarantee the conformity of the species and/or the geographic origin of the logs being sold. Downstream, oenologists can value the information obtained from the identification of the oak species to select for the aromatic potential of the wood being used for the maturation of the wine and other alcohol products. Actually, this service is offered to the community of oenologists. Specialists respond on a case by case basis according to identification needs. Currently, the limitations of the method relate to the state and age of barrel timbers that do not always allow quality DNA extraction.

Tracking exotic alleles from plantations to natural populations for forest certification

In Canada, the use of exotic species has quickly become an element of forest management and production (Derbowka *et al.* 2012). Fast-growing trees, such as interspecific hybrid poplar or larch varieties containing exotic components, are integrated in short-term rotation plantations for intensive production purposes. Their use into this context responds to economic, social and environmental demands. Moreover, such intensive silvicultural techniques on small tracts of land may help to reduce the impact of harvesting pressure on the larger areas under ecosystemic management.

Forest certification organizations in Canada (FSC, SFI or CSA) point to a particular concern with the use and planting of exotic species (Morissette 2002). For example, the Forest Stewardship Council (FSC) standard, which dictates a set of sustainable forest management criteria, states that: “the Organization shall only use alien species when knowledge and/or experience have shown that any invasive impacts can be controlled and that effective mitigation measures are in place” (Principle 10.3 in FSC 2015). To be certified, companies must demonstrate that any exotic species of interest when established in plantations is not invasive in order to limit its ecological impact. Forestry companies have limited means (e.g., technical tools and expertise) to measure the risk of potential “invasiveness” of exotic species posed to the environment. In the case of exotic poplars or larches, invasiveness may be observed through the off-plantation establishment of new individuals caused by clonal propagation (cuttings or suckers) or seed dispersion. Invasiveness can also be the result of hybridization between compatible exotic and indigenous species, which will result in new individuals presenting some exotic components.

The use of genomic tools for traceability purposes makes it possible to identify and monitor selected varieties deployed in commercial plantations and to measure putative gene exchange (referred to as genetic pollution) between the so-called exotic species and the indigenous species (Meirmans *et al.* 2007; Talbot *et al.* 2011). Recently, molecular tools were developed to characterize trees that would either result from the dispersion of exotic species or their hybridization with native species in surrounding environments (Isabel *et al.* 2013). These tools consist of a limited set of genetic markers that identify the different species used as well as their hybrids. Hundreds of reference samples from provenance trials, herbaria or directly collected in the field were tested to develop this assay. A sampling and laboratory protocol was also developed to quantify and localize exotic individuals or components resulting from hybridization (e.g., Talbot *et al.* 2012; Roe *et al.* 2014). Such a method becomes an efficient way for companies to comply with forest certification standards by providing a precise measure of the invasiveness of the exotic species introduced into their plantations. Moreover, the localization and quantification of exotic gene dispersion improve the targeting and effectiveness of potential mitigation initiatives (Talbot *et al.* 2012; Meirmans *et al.* 2014). In poplars, the use of these molecular tools showed that the extent of exotic gene dispersion from plantations with exotic components depends on the recipient native species, the gender of novel varieties used for plantations, the size of natural surrounding native populations, and the environment in

which they are found. For instance, disturbed habitats (e.g., near-urban locations) appear more prone to exotics establishment than natural ones (Meirmans *et al.* 2010; Thompson *et al.* 2010). Moreover, male poplar varieties should be preferred to female trees since the exotic pollen coming from plantations is diluted in the native pollen cloud (Talbot *et al.* 2012; LeBoldus *et al.* 2013). Indeed these tools have helped demonstrate that effective monitoring and risk assessment is imperative to ensure that plantations with exotics do not threaten the genetic integrity of native forest trees or Canada’s forest certification.

Urban forestry: resilient and well-adapted trees

From the time the term “urban forestry” was first introduced in 1974 (Jorgensen 1974), this specialized field of forestry has taken on increasing importance. In Canada, more than 80% of the population lives in urban areas (Statistics Canada 2011). Over the past few decades, research in urban forestry has shown the many benefits of trees in urban settings, for aesthetic, ecological, economic, social, and public health reasons (Tyrväinen *et al.* 2005). Moreover, and in a somewhat broader context, urban planners now integrate the concepts of green infrastructure, and valuation of ecological goods and services provide by trees in urban areas. Several Canadian cities have recently adopted urban forestry plans that set standards and management strategies to be applied in their territories (Ordóñez and Duinker 2013).

Tree selection in urban areas is based on several practical criteria (e.g., appearance, seed or pollen production, available space, soil conditions, native species) that differ among the various stakeholders (architects, managers, foresters, citizens, and nursery operators) (Conway and Vander Vecht 2015). Nevertheless, in spite of these differences, one may observe great redundancy in the species/varieties chosen for planting (Bourne and Conway 2014). This can be explained by the stringency of selection criteria related to urban stresses and constraints as well as by the lack of research or breeding programs aimed at developing new tree varieties. As an example of these constraints, we can mention the requirements for contractors to guarantee the survival of planted stock for some stipulated period of time (e.g., two years), which results in extremely conservative approaches when it comes to species choices. With diseases decimating and currently killing thousands of trees in urban forests, experts are calling for the selection of more diversified species (at both the taxonomical and functional levels; Paquette 2016).

Another criterion that can be identified in urban development plans is the prioritization of indigenous species (Ordóñez and Duinker 2013). This common preference reflects the desire to preserve local biodiversity (Almas and Conway 2016). It can also be explained by the fact that local species use local resources more efficiently and are more likely to support the biodiversity of native animal species (McKinney 2002; Burghardt *et al.* 2009). However, to ensure that the expected benefits of indigenous trees translate into real benefits, they need to be well-adapted to the environment where they are planted; for instance, they have to come from the appropriate hardiness zone. Still, the native character of a species does not guarantee these benefits as tree species distributions often encompass large territories. For example, in a recent study, professionals in the City of Toronto’s urban

Box 1. Valorising the available data for Canadian forest tree species

Several types of data, in addition to genomic data, are currently available for economically important forest tree species in Canada. These data could be used to create a traceability system based on mixed data that could produce a “Protected Designation of Origin (PDO-like) certification system” to achieve rapid and efficient identification of timber and wood products in Canada. In comparison to conventional forest certification, the focus is put on the origin of the product rather than wood harvesting processes. In addition, such a controlled designation of origin implies a close link between the product, the terroir and the know-how of the artisan. By doing so, not only could a PDO-like label hamper illegal logging, it could also significantly help the expansion of new markets, especially with highly-valuable products. Indeed, very prestigious brands of highly-valuable products have addressed this issue by providing consumers a high-quality standard designation (e.g., for wines, cheese but also oils, and even meat: in the province of Québec, the “Agneau de Charlevoix” was the first meat product to receive a reserved designation (BNQ 8015-900). In the case of wood products, this could be applied to particular attributes that confer significant value to wood, e.g., acoustic (for the manufacture of musical instruments), mechanical or aesthetic qualities.

The establishment of a close relationship between the environment in which a tree has grown and its wood quality could be achieved by drawing on the various data that have been gathered over decades of forestry research. We can hypothesize that the juxtaposition of many types of data would significantly increase the power of resolution necessary to identify the specific signature of a wood sample that would be representative of its environment of origin. Such resolution could be reached through the connection of several databases and the power of algorithms that could identify the right combination to obtain the most informative data (e.g., artificial neural network).

White spruce could constitute the first candidate to test the possibility of identifying such a PDO-like signature; first, because it is of major economic importance in Canada, and second, because incidentally, very large quantity of data is already available. When considering all the potentially useful types of data available from diverse databases and projects for Canadian forest tree species (Fig. 3), we can roughly estimate that more than 50% of the data concern white spruce.

Fig. 3. Representation of different families of data potentially useful to constitute a PDO-like label for a Canadian forest species (non-exhaustive). Bold numbers correspond to the number of items when available for each category found in TREESOURCE (Canada's national database on wood and tree quality developed by NRCAN and available to the forest sector: governments, university and industry) for all data, with the exception of genomic data which are available in GenBank (publicly available and managed by NCBI) and also from previous large-scale genomic Canadian projects in the field of forestry. Datasets joined by full lines are from same categories, and dashed lines represent potential connections that could be made in order to constitute a significant signature of environment or provenance. DBH: Diameter at breast height; MFA: Microfibril angle; MOE: Modulus of elasticity; SNPs: Single nucleotide polymorphisms.

forestry unit mention that they do not have the means to verify that the trees they bought come from the right climatic zones (Conway and Vander Vecht 2015). They explain that if local nurseries cannot meet the demand, plants are sometimes procured from U.S. nurseries located farther south which provide plants that are ill-adapted to northern climatic conditions. As a result, while indigenous, these plants will be planted outside of their hardiness zone, so they will be more sensitive to various urban stresses (dry conditions, pathogens,

wind, salt, soil compaction) and their survival rate will be reduced. Such maladaptation could therefore translate into significant costs for cities.

Linking these issues and traceability principles indicates that these last ones could potentially serve the different actors and users of urban forestry. Indeed, it highlights the fact that there is a need to a greater taxonomic and functional diversity in urban forestry and that there is a cost to plant the wrong tree at the wrong place. Here we suggest that the different

approaches using genomic tools presented in this article could help to address some of those issues in urban forestry. For example, the use of genomic tools may appear useful when cities purchase large quantities of plants for large-scale urban developments, i.e., in particular situations when young trees may be difficult to be identified using classical morphology. A taxonomic identification approach could then be used to verify the species, varieties or cultivars. Application of the principle of traceability to urban forestry could also be used to assess provenances in order to ensure that the specimens being planted are of local origin and are therefore adapted to local climatic conditions. To our knowledge, such a phylogeographic approach does not exist in practice and it could certainly be applied to horticultural tree species, but it would need to be preceded by a phase of research and development. Nonetheless, the development of a system for horticultural tree species would require the same methodology as for forest tree species traded on international markets (see below).

Taxonomic identification tools could also be used to monitor pests and diseases in urban areas in order to identify the most (and least) susceptible trees to better inform management and future developments. A better understanding of the genetic diversity of trees (i.e., the hosts) affected by biotic and abiotic stresses could also lead to a better understanding of the evolution of new diseases as soon as the first symptoms appear. Indeed, a better characterization of the host would complement the traditional phytopathological approach that focuses mainly on the pathogen. This could facilitate the identification of species, cultivars, and specimens with higher tolerance or even, in some cases, resistance.

Other evidence emerging from the scientific literature in urban forestry is that such traceability systems should be developed and applied in close collaboration with nurseries that supply trees for urban purposes. Ultimately, the selection of trees for planting often depends on their availability in the nurseries. At present, the needs of cities when selecting trees to fulfil their management plans do not necessarily match the nurseries' available stocks (Sydnor *et al.* 2010). It is also worth mentioning that nursery stock management is based on client demand, while client choice will also depend on the species available in nurseries (Conway and Vander Vecht 2015). These dynamics, which are not conducive to stock diversification, should be broken by nursery involvement in projects related to the origin or taxonomic identification of trees for urban forestry. It should also be proposed that governmental forest science research departments, which are currently mainly focused on boreal tree species, could take part in the research associated with the development of new varieties that are better adapted to urban environments.

Illegal timber: market and imports

The need for traceability in the case of wood products arises most commonly in the context of international trade. Canada is a signatory to the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES). Under the terms of this agreement, Canada adopted in 1992 its own domestic legislation, the Wild Animal and Plant Protection and Regulation of International and Interprovincial Trade Act (WAPPIITA). According to this act, it is illegal to possess, distribute or transport wild plants or animals (or products derived from them) that are threatened with extinction (as

per CITES lists), that were obtained illegally in their country of origin, or that threaten Canadian ecosystems. Legislation of somewhat similar purpose was adopted elsewhere in the world: the Lacey Act (amended in 2008) in the U.S., the EU Timber Regulation (2010) in Europe and the Illegal Logging Prohibition Act (2012) in Australia. However, while legislative frameworks have been established to identify specific illegal actions, having access to additional scientific tools would help enforce these laws on the ground.

At present, Canadian customs services are on the front line to intercept these products. The identification of suspicious products starts with the examination of the CITES permit that is required for imported products and on which the name of the forest species must be stated. Environment and Climate Change Canada (ECCC) has produced a guide for customs personnel tasked with wood inspection to help with the quick identification of tropical woods listed by CITES. In the same vein, a guide (CD-ROM) dedicated to timber regulated by CITES has also been developed by the Kew Botanical Gardens (Garrett *et al.* 2010). This guide contains essential information about permits or international trade patterns. Moreover, the CD-ROM contains a database of photographs of macroscopic characteristics with descriptions and a classification method to identify timber. These guides (mainly for morphological inspections) help with the taxonomic identification of the genus (rarely the species) and, in doubt, customs officers are required to call in ECCC specialists for a more extensive analysis. The anatomical analysis of imported woods may be used in some cases to identify prohibited products. However, this work demands a high degree of scientific expertise and time. Again, having access to genomic-based tools would help customs agents do their job.

Presently, countries and organizations do not use systematically large-scale genomic traceability systems to counter illegal wood trading. There are, however, various small-scale or *ad hoc* initiatives for the inspection and certification of wood products: DoubleHelix (<https://www.doublehelixtracking.com>) is a pioneer in the field. Founded in 2008 in Singapore, the company provides chain-of-custody (supply chain) auditing of wood species from regions where illegal harvesting is a major problem. Through this scientific process, producers can qualify for the Certisource certification, which guarantees the legality of the products to Australian importers. One of DoubleHelix's auditing methods is genomic fingerprinting, where products are sampled at harvest (before export) in plantations or forests where harvesting is legal. Genetic markers are then used to confirm that the trees are the same at the other end of the chain, and that no substitution was observed for these genetically-checked batches. This method of fingerprinting using microsatellite markers is now available for merbau (*Intsia* spp.), a commercially important wood in Indonesia (Lowe *et al.* 2010). Another method using SNP markers is presently being developed for Indonesian teak (*Tectona grandis* L. f.) destined to the Australian market (Lowe *et al.* 2015). According to a group of experts, this method of individual genomic identification is more suitable for species of very high economic value where the volumes harvested are rather low (Lowe *et al.* 2016). In a legal context, genomic fingerprint methods have also been used to identify: 1) stolen bigleaf maple (*Acer macrophyllum* Pursh.) wood from the protected Gifford Pin-

chot National Forest in the State of Washington (U.S.); and, 2) red cedar (*Thuja plicata* D. Don) wood from Carmanah Walbran Provincial Park on Vancouver Island (Canada). In these two cases, genomic markers previously developed for those species (White *et al.* 2000, Jardine *et al.* 2015) were used as forensic tools to verify the origin of the wood. Concerning the bigleaf maple wood, it allowed for the prosecution of the poachers (Goldfarb 2017).

Phylogeographic approaches using genomic tools were also punctually developed and used to identify the geographic origin of timber, such as in the case of merbau (DoubleHelix 2011) or for the Malaysian *Neobalanocarpus heimii* King P. Ashton (Tnah *et al.* 2010). Likewise, similar studies, for which the first objective was not to track illegal logging, could serve as a starting point to develop traceability systems, as for the economically important tropical wood of Kapok (*Ceiba pentandra* (L.) Gaertn.) (Dick *et al.* 2007) or Carapa (*Carapa guianensis* Aubl.) (Cloutier *et al.* 2005). Most of those ongoing projects concern tropical species, but the same methods and approaches could potentially be applied to Canadian native species for which the geographical structure has been previously studied, such as black spruce (Jaramillo-Correa *et al.* 2004; Gérardi *et al.* 2010), jack pine (Godbout *et al.* 2005, 2010, 2012) or lodgepole pine (Godbout *et al.* 2008). Indeed, the application of traceability systems to counter the import of illegal exotic wood is currently the subject of most of the studies and development efforts because the needs are great. That being said, the challenges are also significant, notably because the species and territories targeted may be difficult to access and little is actually known about most of those exotic species.

While there is currently no requirement for Canada to guarantee a “local” origin for its export-oriented wood products, such tools may become necessary in future as it would increase the ability to legally guarantee the Canadian origin of our products to our trading partners. Indeed, the absence of a traceability system could eventually lead importing countries to suspect extraterritorial origins for our wood products; they could also suspect that Canada is acting as a mere transit point in order to “launder” illegal goods. Furthermore, a traceability system that authenticates the wood’s local origins could pave the way for the implementation of a “Made in Canada” label for wood products sold on domestic markets. According to a recent study, consumers see value in local origins when they shop for wood products, particularly for value-added products (Chamberland *et al.* 2016).

Perspectives and Challenges

All the examples presented in this report face the same two major challenges: applicability and databases. In both cases, these challenges involve technical (or technological) aspects as well as socioeconomic aspects.

The applicability challenge

The primary and obvious first question that may challenge the development and the use of a genomic-based traceability system is certainly: “How much does it cost?” Our aim here was not to discuss in depth this complex aspect since it is context dependent. In fact, multiple factors should be examined. Among them the choice of markers technology, which in turn depends on i) the material (solid wood products, 2nd trans-

formation products) to be tested; ii) where and by whom the analyses will be conducted; iii) how fast the results will be required (minutes vs hours vs days); and, iv) for which purposes (legality and prosecution or sustainability and principles). It is also worth to take into account the risk that the chosen technology will become obsolete after a certain period of time. Indeed, we observe a rapid turnover of these technologies. Depending on the scale at which the traceability system will be applied, the question of dealing with an external genomic platform or to develop in-house genomic resources (i.e., equipment and expertise) should also be evaluated. Over the last decade, the cost of sequencing and genotyping have considerably decreased, and we can expect that this trend will continue. New technologies are still to come in this area. Following these complex considerations, it clearly appears that the decision to develop a traceability system or not will likely be made on a case-by-case basis. Still, economic scenarios to help decision makers should consider and include the cost of doing nothing. Hence, pilot studies based on the use of different tools should be developed to help answer these socio-economic considerations.

Any traceability system using genomic-based tools necessarily involves DNA extraction. The quality and quantity of DNA extracted will depend on the source material and on the method used. Furthermore, for trees it is easier to extract DNA from fresh material (e.g., leaves, cambium or phloem) than from wood. Compared with other plant tissues, DNA extraction from wood is more arduous because 1) it must be mechanically treated first; 2) it contains chemical compounds that could compromise the quality of the sample extracted; 3) the DNA may be degraded by decomposers like fungi or microorganisms; and finally, 4) the DNA may be degraded if it comes from cells that have been dead for some time, depending on how much time has passed since the wood was harvested (Rachmayanti *et al.* 2009). However, it is possible to adapt extraction protocols to wood, even in the case of processed products such as dried or heat-treated wood (e.g., Deguilloux *et al.* 2003; Asif and Cannon 2005; Rachmayanti *et al.* 2006). The choice of protocol must also be adapted to the method of DNA analysis used, since the different techniques will require specific quantities and qualities of DNA. Hence the material to be tested and the quality of DNA that can be expected will limit the choice of genomic technologies and should also be considered in designing the traceability system. The combination of different protocols and analyses should be in line with the degree of uncertainty that will be tolerated by the users. Indeed, this uncertainty will have to be reduced and strictly controlled in cases where the results will be used as legal evidence and must meet forensic identification standards (e.g., ISO 18385 used for human evidence; see Ogden *et al.* 2009, Ogden 2010 for further details on these important aspects).

The application of a traceability method using genomics-based tools will also require special expertise from the professionals processing the samples; this varies in importance depending on the technique chosen. In some cases, given the scope of the results, it may be recommended that certified teams apply the protocols. Generally, the need for expertise (in genomics) will be inversely proportional to the possibility of automating the method. Total automatization of the process is, to our knowledge, not actually possible, although promising

technology research has been performed in the fields of medical diagnostic and forensic science that could be adapted to forestry (Montpetit *et al.* 2005; Bissonnette and Bergeron 2016). Conservation-based initiatives are also currently being implemented by some organizations (e.g., Conservation X Labs), in collaboration with governments, universities, corporations and NGOs (e.g., WWF), with the goal of developing rapid identification technologies for living material.

A final and essential element to consider for the implementation and development of a traceability system in forestry is the relationship to be established between end-users and scientists. This link is a prerequisite to the creation of a system that will meet the needs of the former while using the technical and scientific skills of the latter. To this end, the development of a project, i.e., determining its objectives, the methods tested and the material to be used, should ideally be done through discussions between both parties. Hence, traceability systems should benefit from the contribution of technical knowledge (the scientists) and practical knowledge (end-users); this “knowledge co-production” (Callon 1999; Pouliot and Godbout 2014) can facilitate the deployment of applications in the field and also encourage their adoption by users.

The database challenge

The resolving power of a system is intimately linked to the quality of its database. The construction of a database and validation of the data it contains with reference samples form the cornerstone of any traceability project. Not only is it necessary to make sure that the database is rich in information, the information must also be of quality. This means that new data must be inspected before being integrated into the system (Butler 2006; Moore and Kornfield 2011). In certain cases, for instance when the data feed comes from various sources, a curator should ensure that new entries meet a set of predetermined criteria, as it actually is the case for big genomics databases, such as the NCBI's GenBank.

A large amount of data is presently available to constitute forest-traceability databases. They have been mostly generated by forestry science research and also by continuous field monitoring activities (see Box 1 for an example of how these diverse data could be used in a traceability context). Therefore, a preliminary step in the establishment of a traceability system would require an exhaustive inventory of already existing databases (GenBank, TREESOURCE, TreeGenes) to identify and structure the available data that could be useful to develop the genomic tools (i.e., genetic markers) and to identify validated reference specimens. Analysis of this abundant information and its diverse sources calls for expertise from the field of data science which involves the analysis and highlighting of trends in big data. These analyses could also identify the as-yet-unknown or unpresumed capacities of such data to inform on various issues, whether in the field of traceability or other topics.

One other challenge, and not the least in database management, is the notion of open data and ownership. At present, data that were generated by governmental agencies, universities or private enterprises either belong to the public or private domain. This means that before developing a traceability system based on existing data, agreements have to be reached

between the various parties to clarify data ownership and access issues. Similarly, the legal framework in which the traceability system will be used must also be established (i.e., cases of patenting or business disputes). Consequently, technical and scientific development will need to be carried out in parallel with the development of a legal framework that will set out the capabilities and limitations of its application.

Conclusions

Several parameters require consideration in the development and application of a genomics-based traceability system for the Canadian forestry sector, which faces numerous challenges today. Regulations within international markets are currently becoming tougher which could lead to demands for new proofs of identity, safety and/or origin of products destined for export. Domestically, consumers have expanded their purchasing criteria, particularly in relation to sustainability issues (Boivin and Durif 2012). At the same time, the Canadian forest, due to its northern location, is expected to be especially affected by climate change (Price *et al.* 2013). This will lead to certain practices being modified, such as the use of assisted migration (in natural and urban forests; Aubin *et al.* 2011), or to the application of new forest management practices to mitigate climate change effects (fire, pathogens, wind; Gauthier *et al.* 2015).

In Canada, some of these important questions are presently being addressed through regulatory and forest certification systems. However, we think there is still place for the development of complementary tools, such as those presented here, that would assist with mechanisms currently being implemented. One of the easiest ways to implement a traceability method for application to the Canadian forest sector would be to include it within forest certification systems. On the one hand, the new traceability system would benefit from the well-developed framework of the forest certification process. On the other hand, forest certification systems would gain strength and rigour as they would benefit from reproducible technoscientific tools, such as genomic tools.

Whether it is included into forest certification or not, we have demonstrated in this article that the opportunities to develop traceability methods are abundant. Internationally, the community is currently considering technical and conceptual means of answering traceability issues (e.g., via the *Society for wildlife forensic science*, which brings together international scientists whose interests include issues related to forestry or Forest Legality Initiative that gathers together partners and stakeholders to advance dialogue and initiatives related to the international trade in timber). In Canada, materials, data and expertise in forest genomics are currently available. All that remains to be done is to capitalize on them.

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