REVIEW



Biosurveillance of forest insects: part II—adoption of genomic tools by end user communities and barriers to integration

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Abstract

Early intervention, effective management, and regulations are essential to mitigate the potential negative impacts of invasive forest insects. Biosurveillance provides the necessary knowledge to inform management, and regulatory practices. Genomic approaches can contribute valuable information to this process. Unfortunately, adoption and incorporation of genomic tools into biosurveillance frameworks is not straightforward. To realize the full potential of genomic knowledge, researchers must work together with end users to ensure full adoption, standardization, validation, and interpretation of genomic results.

Keywords Biological invasion · Invasive · HTS · Regulation · Policy · Surveillance

Key message

- We bring an end user perspective to the application of genomic tools for the management of invasive species.
- We highlight the benefit of genomics to invasive species management, as well as the potential barriers to its adoption, and policy considerations for implementing genomics within a management and regulatory framework.
- We present Biosurveillance of Alien Forest Enemies (bioSAFE) as a model for how to engage with the end user community at all stages of project development; from inception to adoption.

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Introduction

Invasive species are a continual threat to a country's economy, environment, and society. Some of these effects can potentially lead to negative impacts on a more global scale, via permanently altered forest landscapes and global trade disruptions. Forest invasive alien species (FIAS) are introduced primarily through global transport pathways and thus threaten the long-term sustainability of our forests. Invasive species have harmful impacts on human health, forest productivity, and native biodiversity (Mazza et al. 2013; Simberloff et al. 2013; Millar and Stephenson 2015; Porth et al. 2015; Pimentel et al. 2000; Firn et al. 2015). Forests dominate one-third of the world's terrestrial habitats, and forest losses due to invasive pests have serious ecological consequences (Perry et al. 2008). Invasive pests also cause economic losses by negatively impacting trade and market access, and increasing production costs (Surkov et al. 2009; Cook 2008; Soliman et al. 2010; Wittwer et al. 2005). FIAS introductions are projected to increase in number and frequency with continually increasing trade volume (Roy et al. 2014; Hulme 2009). In today's globalized economy, the likelihood of an accidental invasion event is high and the potential impacts of this invasion represent an important risk.

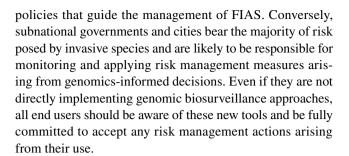


The International Plant Protection Convention (IPPC) is a multilateral treaty currently signed by 183 countries to protect cultivated and native plants, as well as plant products, from the introduction and spread of invasive species. Evidence-based decisions form the foundation of the IPPC and are paramount to an effective biosurveillance program supporting this convention. Effective biosurveillance, defined as the production, analysis, and circulation of information on biological invasions (Roe et al. 2018), is required to meet the international obligations of the IPPC (Taylor et al. 2013). Knowledge about invasive species comes from a wide variety of sources including species identifications in newly intercepted samples, historical records, risk assessments, spread mapping, cost-benefit analyses and, in recent years, genomics. Genomics-informed biosurveillance capitalizes on the knowledge that genome-wide data can bring to our understanding of the process of biological invasions by integrating it into the surveillance workflow, thereby reducing uncertainty in our risk assessments and responses (Roe et al. 2018).

Who are the end users?

Biosurveillance, FIAS management, and research are carried out by several end users: (1) National Plant Protection Organizations (NPPOs), (2) national and subnational governments, (3) post-secondary institutions, (4) private and not-for-profit organizations, (5) cities and communities. NPPOs are the official bodies established by governments to discharge the functions specified by the IPPC, such as regulate phytosanitary treatments, certify exports, regulate imports, cooperate with other NPPOs, share information, and develop and implement International Standards for Phytosanitary Measures (ISPM). Researchers, employees, and citizens within these end user groups collaborate with NPPOs to study the biology of FIAS and develop tools for detection, monitoring, or phytosanitary treatments. Post-secondary research institutions (colleges and universities) have significant roles to play in actively exploring fundamental and/or applied research questions in invasion biology. These institutions also train highly qualified personnel needed to develop and implement FIAS management programs. Often subnational governments (e.g., states or provinces) are the primary landowners and managers of forest resources, so they must be engaged in the decision-making process. The same is also true for cities and communities who are responsible for urban planning, tree management, and ultimately bearing the financial costs of removing trees killed by FIAS (Kovacs et al. 2014).

The impacts of genomic-based decisions may vary among end users. NPPOs are the most likely to use genomicsinformed biosurveillance as they develop regulations and



How can genomic tools contribute to biosurveillance?

Biosurveillance and knowledge of FIAS invasions is needed throughout the end user community to help inform evidence-based decision-making. Genomic-informed biosurveillance provides access to knowledge of biological invasions that can significantly benefit end users (Roe et al. 2018). We provide three examples of how genomics-derived knowledge can help improve risk assessments. Then, we demonstrate how genomics can effectively diagnose potential invasive pests, enabling and improving both early intervention and monitoring systems. Ultimately, this can translate into effective and timely responses to invasive species and allow for proactive responses to this threat.

Risk assessments

Pest risk assessments are a starting point for regulations and quarantine response measures aimed at eradicating or controlling biological invasions (Fuentealba et al. 2013; ISPM 2 2007; ISPM 11 2013). Risk is the probability that an undesired event will occur with some information about the consequences of the event (Kaplan and Garrick 1981). For biological invasions, the undesirable event typically means introduction, establishment, or spread of the invader into previously uninvaded areas, combined with the associated negative economic, ecological, or social impacts of invasion (IPPC 2016). Risk assessments take into account these different aspects within a cohesive framework. Risk assessments can be generalized in terms of estimating hazard, exposure, vulnerability, communication, and mitigation (Fuentealba et al. 2013). Estimating hazards involves identifying conditions that may promote the colonization and spread of a FIAS in new areas. This could include identifying pathways of spread, points of entry, impact of climate change, biotic interactions, or modes of dispersal. Vulnerability and suitability of new hosts is also of interest, but can be challenging to assess (Fuentealba et al. 2013).

Tracing the pathways of invasion is one step in assessing risk. The heterogeneous nature of imported commodities and multiple supply chains creates uncertainty about the origins



and pathways of invasive species introductions. Import volumes correlate well with the number of biological invasions, but knowledge of the origin, destination, frequency of imports, and shipping modes can better define these risks. Risk of entry can be modeled with a variety of data (Costello et al. 2007; Magarey et al. 2007; Koch et al. 2009), but greater resolution is needed (Hulme 2009). For example, in the 2000s, satellite populations of the pine processionary moth (PPM, Thaumetopoea pityocampa) were detected well beyond the main population (Robinet et al. 2012). Humanassisted long-distance dispersal was suspected, but not confirmed. If long-distance dispersal was the case, then where did these satellite populations originate from and what was the most probable pathway? Using molecular markers, Robinet et al. (2012) demonstrated that at least three satellite populations originated from distant populations, most likely due to human-mediated dispersal during the pupal stage. Human-assisted translocations may play a greater role in the movement of this species; therefore, it must be included in spread models (Robinet et al. 2014) to more accurately quantify the risk PPM poses to European forests. Genomic biosurveillance provided key evidence needed to inform spread models, guide pathway management, and reduce the movement of this invasive pest.

Assessing the hazards posed by an insect pest can help identify key knowledge gaps. In 2014, the Canadian Council of Forest Ministers requested an assessment of the threats posed by the mountain pine beetle (MPB). MPB (Dendroctonus ponderosae Hopkins) is a highly destructive native forest pest whose range has expanded outside its historical distribution (Safranyik et al. 2010). MPB populations east of the Rocky Mountains are considered invasive and pose considerable risk to naïve jack pine forests of eastern Canada. Detailed risk assessments were limited by the lack of knowledge of beetle biology. Which tree species would MPB successfully attack? What was the source of the invasion? What will be the rate of spread? Would MPB be capable of adapting to this novel environment? These knowledge gaps introduced uncertainty to the understanding of the risk MPB posed to eastern boreal forests (Nealis and Cooke 2014), but genomic approaches were able to close some of these knowledge gaps. Using microsatellite genotypes and Bayesian cluster analyses (i.e., NEWHYBRIDS and STRUCTURE), Cullingham et al. (2011) showed that MPB was capable of attacking and surviving in both hybrid pines (lodgepole pine x jack pine) and pure jack pine. Confirmation of successful attacks in jack pine demonstrated that the MPB can survive in a novel host tree and that the risk of spread to eastern jack pine forests was high. Molecular data further demonstrated that the invasive populations of MPB were a result of recent expansions into the northern boreal forest and were originally derived from multiple populations in northern British Columbia (James et al. 2011; Janes et al.

2014). During this expansion and dispersal across the Rocky Mountains, the invasive MPB population became mixed and developed a unique genomic composition (Janes et al. 2014). Janes et al. (2014) further demonstrated that this unique invasive population of MPB shows signs of selection, which suggests that it is adapting to new climatic conditions or host associations. These genomic data show that the MPB poses high risks to the eastern boreal forest and supports its continued biosurveillance and management in its invasive range.

Risk maps are an efficient visual communication tool to show areas at risk of establishment by an invasive species, illustrate potential spread patterns, and define priority areas for FIAS surveillance (e.g., guide field inventories for FIAS detection) or mitigation actions (Fuentealba et al. 2013). Yet, such maps are simple spatial representations of observation data or model predictions, and strongly rely on the quality and quantity of underlying data, modeling choices (i.e., methods used and assumptions made), and mapping techniques (Venette et al. 2010). Risk maps document key climatic and ecological variables that may limit the survival of an invasive pest population in a novel landscape. Typically, assessments estimate the range of environmental and climatic variables that could support the survival of a pest population through ecological niche modeling (Jiménez-Valverde et al. 2011; Thuiller et al. 2005), thus providing an assessment of a species' invasion potential (De Meyer et al. 2010; Kumar et al. 2016; Peterson et al. 2007).

Incomplete knowledge of biological and ecological traits of FIAS in novel landscapes leads to coarse representations of risk and preferential use of simple analytical approaches (Andersen et al. 2004; Landis 2003; Landis and Wiegers 1997), which have limited utility for decision-makers. Furthermore, models often do not explicitly consider the different processes of invasion dynamics, (i.e., species arrival, establishment, and spread), leading to partial estimates of invasion probability (Venette 2015). For example, dispersal is a key process in range dynamics (Davis et al. 1998; Engler and Guisan 2009; Murray et al. 2011), but its impact on risk modeling using species distribution maps (SDM) has received little attention, been ignored (e.g., Ikegami and Jenkins 2018), or oversimplified. Genomics can help reduce these uncertainties by expanding our knowledge of FIAS physiological requirements (e.g., cold tolerance) and functional traits (e.g., dispersal capacity), either through identification of candidate genes, or through its insights into the history, source, or pathway of biological invasion (Roe et al. 2018). Such specific traits are highly relevant for both habitat suitability and spread modeling and can lead to more reliable FIAS risk maps. Linking such genomics-based assessments to SDM and the related decision support system (DSS) in an integrative framework should significantly improve pest risk assessment.



Intraspecific variability among FIAS populations can manifest as a range of environmental tolerances or physiological responses (Des Roches et al. 2018). Different populations of an FIAS could differ in cold tolerance or dispersal capacity or represent hybrids with unknown characteristics. Moreover, local adaptation or post-invasion evolution of a population can also lead to significant changes in traits, which are usually not considered in pest risk analyses (Whitney and Gabler 2008). For example, Lymantria dispar is composed of three subspecies: 1) L. dispar dispar (European gypsy moth—EGM), 2) L. dispar asiatica (Asian gypsy moth—AGM), and 3) L. dispar japonica (Japanese gypsy moth—also referred to as the AGM). The EGM has been established in North America since the last century; its spread, however, has been relatively slow, in part because its females are flightless. The two Asian subspecies represent a more serious threat because of their broader host range and higher flight capacity. Mated EGM females (Lymantria dispar dispar) have little to no flight capacity, while the mated AGM females (Lymantria dispar asiatica or L. dispar japonica) can fly long distances, thus dramatically increasing its dispersal capacity. Keena et al. (2008) demonstrated that flight capacity was partially correlated with geographic origin, but an accurate molecular assay for flight would require better understanding of the functional basis for flight and substantially more genetic markers. Inability to predict flight capacity directly increases the uncertainty associated with predicting gypsy moth dispersal, which translates to uncertainty in the spread model and the resulting risk maps. Opportunities exist to develop a more detailed genomic assay to screen for flight capacity in gypsy moths. The use of genomics can once more be valuable, as it allows us to analyze actual FIAS populations, identify important markers, and refine the value of essential traits to be included in up-to-date populationspecific SDM and risk maps.

Diagnostics

Regulatory agencies need fast, reliable tools to support their biosurveillance efforts. Precise diagnostics and accurate identification of potential invasives is the cornerstone of successful biosurveillance programs. Management and regulatory responses are tightly linked to species identity (Boykin et al. 2012), so it is essential that identifications are accurate and reliable. Traditional morphological approaches are often limited by available expertise, time, specimen quality, morphological similarity, or life stage (Thomas et al. 2016). DNA-based detection and identification of invasive species is one aspect of genomic biosurveillance. In this respect, DNA sequencing technology has been used to successfully identify species from all Kingdoms of life (Darling

and Blum 2007). Environmental DNA (eDNA), defined as genetic material obtained directly from environmental samples, has provided evidence of species in a variety of ecosystems (Ficetola et al. 2008; Thomsen et al. 2009; Chariton et al. 2010; Taberlet et al. 2012), even without specimens in hand.

When developing molecular assays, tools must be designed that can fit within the time and budgetary constraints of the end user. This requires an open dialogue between the front-end research and the downstream users. Gypsy moth identification in North America presents a good example of the translation of genomic resources into a functional tool that provides rapid, reliable identifications of unknown samples. Immature stages of EGM and members of the AGM complex (Fig. 1) cannot be differentiated morphologically. Several other Lymantria species are also considered a biosecurity concern to North America and require biosurveillance and regulation. In North America, AGM and its allied species are currently monitored in two different ways: (1) visual inspections of Asian ships entering ports, and (2) a network of pheromone traps. From a diagnostic perspective, these two survey methods pose different technical challenges. Port inspections typically intercept small numbers of specimens, usually immature stages, so they can be screened using a molecular assay designed for individual samples. Conversely, pheromone traps can contain hundreds of moths and require bulk processing, so a diagnostic assay must be sensitive enough to detect a single AGM among a large number of EGM.

A technology called real-time or quantitative polymerase chain reaction (qPCR) is a technique with high detection sensitivity. It relies on genetic differences between species to change the efficiency of the PCR reactions, and these reactions are monitored in real time with fluorescent markers. Targeted species will show a distinct fluorescent profile when they are present in a sample. PCR-based approaches have been developed for many applications in human health diagnostics (Shafiee et al. 2015; Jorgensen 2015). This qPCR approach was well suited for AGM surveillance due to its sensitivity and short processing time (i.e., within a few hours). Two qPCR assays have been developed to meet the requirements of the different AGM surveillance methods (i.e., port inspections and pheromone trapping) (Stewart et al. 2016; Stewart unpublished, see also Islam et al. 2015). First, Stewart et al. (2016) designed an assay based on species-specific variation in a mitochondrial gene (Hebert et al. 2003). This region could discriminate all species and subspecies of the "AGM complex," as well as EGM and five additional Lymantria species (Stewart et al. 2016). This assay was structured as a molecular identification key, analogous to a standard dichotomous taxonomic key, with a series of nested assays (Fig. 1). The molecular signatures (in this case, amplification or no amplification) substitute for



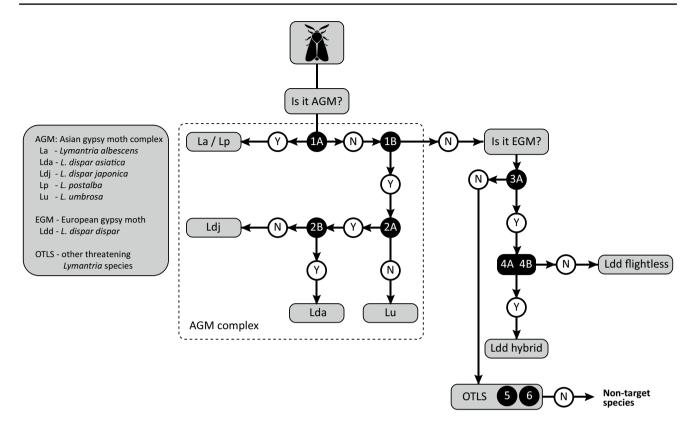


Fig. 1 A "molecular key" to regulated *Lymantria*. This flowchart demonstrates a series of molecular assays (black circles) designed to identify *Lymantria dispar* subspecies and eight additional *Lymantria* species of regulatory concern. The assays answer a series of nested questions. Is the specimen: (1) a member of the AGM complex, and if

so which one (1A, 1B, 2A, 2B)?; (2) an EGM, and if so does it show signs of AGM hybridization (3A, 4A, 4B)?; (3) neither AGM nor EGM, but instead is it one of five other threatening *Lymantria* species (OTLS, assays 5, 6), or none of the above (non-target species)? [Adapted from Stewart et al. (2016)]

morphological characters and guide the user through a series of yes/no questions to an identification. To detect AGM in pheromone traps, a different assay was needed. Surveillance of bulk samples, like those from pheromone traps, requires detecting rare events. The DNA barcode region alone could not provide adequate genetic variation for this type of diagnostic assay. Djournad et al. (2017) scanned whole mitochondrial genomes of gypsy moth populations to identify additional markers that could improve AGM detection in this context. A qPCR assay using three mitochondrial markers in triplex enabled the identification of a single AGM sample in bulk samples containing up to 1000 EGM specimens (D Stewart, unpublished). These tools have become relatively easy to use in operational diagnostic laboratories, and there is potential for applications in situ using portable instruments that can deliver even faster results (Thomas et al. 2018).

Biosurveillance requires high-quality data from a broad range of sources to support invasive species management. We demonstrated how genomics can provide increased resolution and insight into many key questions about biological invasions (Roe et al. 2018, Fig. 1), including routes and sources of invasion, adaptation to novel environments,

and refined diagnostics. BioSurveillance of Alien Forest Enemies (http://www.biosafegenomics.com/?dev=1) is a genomic biosurveillance pipeline that will harness the informative power of genomic data to develop biosurveillance tools that will inform FIAS mitigation and management (Fig. 2). To ensure that the benefits of this project are realized and deployed operationally, there must be adoption and integration within the end user community. This is not straightforward. There are barriers to implementation, and they range from adoption of genomic technologies to integration into policy frameworks and to acceptance by the wider international community. We discuss these barriers below and outline a potential path forward.

Barriers to adoption and integration

Despite significant advancements in genomic research and genomic tool development, there are few examples of their successful integration into operational biosurveillance. A number of factors may be influencing adoption and integration of these new tools and slowing their real-world



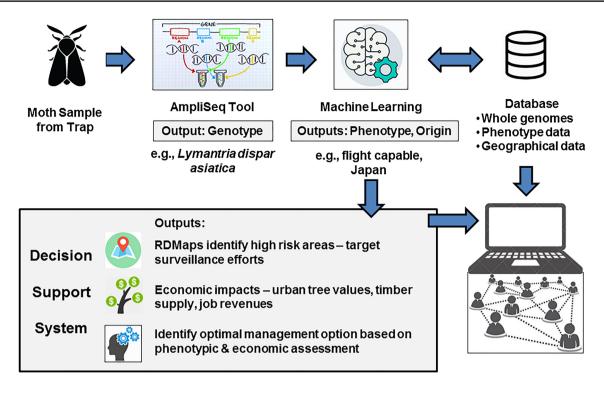


Fig. 2 Flowchart describing the movement of sample information from acquisition to the end user community for one of four key FIAS species under development in the bioSAFE research project

applications in forestry. Two recent qualitative studies analyzed end user's understanding of the role and benefits of genomic technologies and identified potential barriers to adoption. In Crann et al. (2015), interviews with forest stakeholders revealed three distinct elements that practitioners should consider to ensure successful translation and adoption of genomic technologies: end user knowledge of genomics, efficiency of genomic tools, and their cost-effectiveness. Similarly, Nilausen et al. (2016) identified end user knowledge, economic feasibility, and a defined policy framework as the main elements to facilitate genomic tool adoption.

End user knowledge and understanding of genomics and biotechnology

Engagement with end users throughout the process of technology integration can be particularly important in the forest sector (Moeller and Shafer 1981). Upstream engagement with end users must be a strategic process to ensure the successful adoption of new technologies (Parwada et al. 2012). When an individual understands the methods, risks, and benefits of using new technology, then their perceptions and attitudes toward those tools tend to be more favorable (Crann et al. 2015; Hallman et al. 2004; Nilausen et al. 2016; Pardo et al. 2002). Pardo et al. (2002) found that being a member of the informed public was a significant predictor of an individual's perception of the benefits of biotechnology.

The informed public in this case are those with a basic understanding of biology and genetics and have an interest in biotechnological issues. This segment of the population harbored attitudes for technological optimism and believed in the promise of biotechnology.

According to Rogers' Diffusion of Innovations Theory (DIT, Box 1), compatibility is one of five essential attributes needed for successful diffusion of an innovation (Straub 2009). Compatibility means that the innovation aligns and builds upon existing knowledge and previous experiences. Surveys of members of the forestry sector in British Columbia noted that many end users lacked knowledge and experience with genomics, thereby lowering compatibility for new genomic innovations (Crann et al. 2015; Nilausen et al. 2016). However, understanding and knowledge can be improved in several ways: Effective scientific communication, opportunities for observation, and/or involvement with field trials were all identified as useful strategies to improve adoption of new technologies (Crann et al. 2015). This links back to DIT, which argued that opportunities for involvement in field trials can facilitate adoption of new innovations (Straub 2009). Nilausen et al. (2016) suggested that a non-biased, educational package could complement trials or demonstrations. This educational package would highlight the process, benefits, costs, and limitations of using genomic tools in common language, and its development should involve a range of stakeholders. An educational



Box 1 Summary of selected technological adoption and diffusion theories

Diffusion of innovations theory (DIT)

Rogers (1962) published *The Diffusion of Innovations*, which was foundational in our current understanding of how an innovation diffuses through a specific population over time. This theory describes diffusion as the result of individual adoptions over time. Rogers' identifies five distinct stages that an individual experiences when evaluating an innovation (awareness of innovation, persuasion (knowledge of innovation+personal judgment), decision, implementation, and confirmation (reflection+reevaluation)). He also describes the four elements of diffusion theory: (1) the innovation, (2) communication channels, (3) social system, and (4) time. Within the "innovation" element, he further identifies key attributes that can impact the adoption of an innovation (relative advantage, compatibility, complexity, testability, and observability)

Technology acceptance model (TAM)

Davis (1989) developed the TAM which models how an individual goes through the process of accepting and using a technology. He argued that there are two main characteristics that predict the eventual adoption of a technology: (a) perceived ease of use (PEOU), and (b) perceived usefulness (PU). Davis defined PEOU as "the degree to which a person believes that using a particular system would be free from effort," and PU as "the degree to which a person believes that using a particular system would enhance his or her job performance"

Unified theory of acceptance and use of theory (UTAUT)

The UTAUT was developed by Venkatesh et al. (2003) who tested and compared eight of the most common theories around individual adoption and use of technology. The intent of the UTAUT is to explain an individual's intention to use an information system, as well as subsequent usage behavior. Drawing on the findings of this study, a model was developed that includes four determinants of use (performance expectancy, effort expectancy, social influence, and facilitating conditions) and four moderators of individual use behaviors (gender, age, experience, and voluntariness of use)

approach aims to support compatibility by informing end users of the relative advantage of the innovation, thereby facilitating downstream adoption.

Effectiveness and efficiency of innovation

A number of technological and diffusion models (Box 1) demonstrate that innovations are more likely to be adopted if they are effective and require equal or less effort than the current method or system (Straub 2009). We define effectiveness as perceived usefulness or performance expectancy. The end user must perceive the tool as something that will enhance his/her job performance and provide a relative advantage over the status quo and available alternative options (Davis 1989). Moreover, delivering results in a timely fashion is another important component of effectiveness, acknowledging that "timeliness" can differ among contexts and applications (Crann et al. 2015). Delayed results may impede the overall goal of genomic biosurveillance and undermine the benefits of using these tools. Efficiency, on the other hand, refers to ease of tool use. If the new innovation is complex and difficult to understand, end users may be less willing to learn how to use it, or discontinue use over time. A tool must be simple (or at least not overly complex) for an end user to readily adopt it. Innovations that are perceived to be effective without requiring a burdensome amount of effort are more likely to be adopted (Straub 2009).

Complexity was also identified by DIT as an attribute that could negatively impact adoption (Straub 2009). Practitioners that struggle to understand how to operate a new tool (whether literal or perceived) are less likely to adopt the technology. Crann et al. (2015) further argued that practitioners must be able to understand at least some of the

underlying science behind the technology, as well as how the technology works, for adoption to be successful.

Cost-effectiveness

Cost-effectiveness is a key to the adoption of new innovations. FIAS management has limited resources and will only adopt innovations that fit within existing financial frameworks. Participants in the studies by both Nilausen et al. (2016) and Crann et al. (2015) identified costs as a substantial barrier. The costs associated with developing genomic tools were perceived as burdensome or restrictive. These concerns extended to the costs of implementation, training, trials, etc. Therefore, any gain achieved by the technology must not be drowned by the costs of development and application. In 2015, it was estimated that over \$120 million had been invested in forest genomic research in Canada since 2001, with very little of these monies spent on economic analysis (Porth et al. 2015). Future genomic tool development should incorporate an economic aspect that models the economic benefits of using genomic tools against the costs of developing and applying the technology. Nevertheless, the costs of genomics are continually falling (Roe et al. 2018), with cost-effectiveness improving every year.

Defined policy framework

Because genomic biosurveillance is still in its infancy, it would be beneficial to consider whether implementation should coincide with an appropriate, well-defined policy that details its usage and limitations. It has been argued that some genomic tools harbor unknown impacts, in which case a defined policy that sets limitations and/or defined usage



prior to implementation would provide due-diligence assurance to end users. However, genomic biosurveillance does not present the same risks as genetically modified organisms (GMOs) and regulatory policies may harm the process rather than support implementation (see "Integration into Policy" section below).

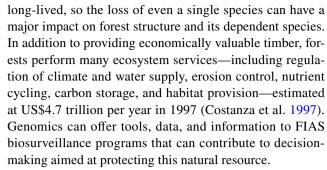
Integration into policy

The "omics" technologies, (e.g., genomics, transcriptomics, proteomics, and metabolomics) offer potential for biosurveillance of invasive species, among many other applications. Early detection can be improved with innovative tools, such as monitoring for environmental DNA (Ficetola et al. 2008) and genomics-informed risk management (Roe et al. 2018). The new BioSAFE project integrates a number of new genomic tools into a unified platform that can be used to rapidly assess the identity, source, and potential risk a set of invasive pests pose to the native environment (Fig. 2).

New technologies will need to be integrated into the standards, directives, and guidance documents that deal with invasive species. Amplification of DNA by PCR represents the only DNA-based technology currently approved by IPPC (ISPM 27 2016). New technological standards must be accessible and economical to ensure acceptance by all member nations. Developing nations may lack the resources or technological infrastructure to implement very costly technologies. Genomic biosurveillance tools must also be standardized and benchmarked prior to their use with survey samples. Validated reference libraries are also needed to accurately diagnose new samples. The need for validated libraries will grow as organizations approve molecular tools as a diagnostic standard (EPPO 2016), but can be challenging to develop (Carew et al. 2013). Once the empirical data have been validated for invasive species monitoring, detection, and identification, then new standards will be needed. Some have called for inclusion of these technologies into regulatory policies and law (Thomas et al. 2016), but care must be taken not to be too prescriptive in a legal framework. Including a specific methodology into a law might not ultimately be beneficial, given the rapid advancement of genomic technologies versus the time needed to develop governing laws and then amend them once enacted.

Conclusions

According to the World Resources Institute (2005), invasive alien species are one of the most important direct drivers of change in ecosystems, particularly in economically developing regions (Early et al. 2016). Trees are relatively large and



Despite potential benefits offered by genomic approaches, incorporation of genomic data into a biosurveillance framework lags behind similar advancements in infectious disease surveillance (Gardy and Loman 2017). For FIAS genomic biosurveillance to reach its full potential, we must answer a number of questions. Who are the end users of genomic biosurveillance data? Who will have access to the resulting data? How do we integrate genomic data into existing surveillance frameworks? How do we ensure effective standardization across different jurisdictions? What if an unknown species is detected, without any evidence of symptoms, a pathway, or negative impacts on the host? What are the legal implications of a genomics-based detection and is genomic surveillance alone (i.e., DNA) sufficient to justify legal actions against the suspected perpetrator?

Improvement in FIAS management resides in the efficient integration of information from various sources into a suitable DSS (Fig. 2). Such systems should enable comparisons and cross-analysis of information from pest risk assessment, entry pathways, most likely points of entry, species spread modeling based on climate and key physiological traits (Roe et al. 2018), impact modeling based on wood supply models and socioeconomic indicators, as well as cost-benefit analyses of possible FIAS mitigation strategies. This is precisely what the bioSAFE project is aiming to develop by harnessing the power of genome sequencing and bioinformatics analysis to develop a new suite of tools to rapidly and accurately characterize four key FIAS (Fig. 2), including Asian gypsy moth, Asian long-horned beetle, as well as two invasive pathogens. These species serve as "proof of concepts" for a genomic biosurveillance pipeline that could be readily applied to future invasive species. For example, the technologies developed to screen bulk trap catches for AGM could readily be developed for other high risk invasives. The active engagement of end users in the bioSAFE project should ensure that the resulting prototype model-based DSS is well adapted to effectively project the potential impacts of FIAS and the outcomes of different forest management and FIAS mitigation strategies.

This paper identified several directions that should be pursued to improve FIAS biosurveillance including: the need for increased collaboration to support more effective



prevention, the technical challenge of cost-effective monitoring of large forest areas, the constant need for innovative diagnostic tools, and the importance of having access to effective predictive models and DSS. As noted by Lodge et al. (2016), improved surveillance programs for early detection of incipient invasions rely on citizen science and emerging genomic technologies that are poised for rapid progress with additional investments. As most of these new developments require significant research capacity, there are unique opportunities for the academic research community to actively engage in biosurveillance with other stakeholders. This collaboration is needed to effectively train the next generation of highly qualified people (undergraduates, graduates, and postdoctoral fellows) who will be ready to transition from academia into any of the end user organizations described earlier. Finally, predictive models, risk maps, and other decision support tools are all instruments that must be developed and field-tested to ensure validity and effective integration of genomic information with other risk management information. As new pests are detected, predictive tools will be tested and updated. At the same time, genomic data on potential new FIAS will need to be integrated into existing DSS. While these different future directions require individuals with different skills/expertise, one common area they share is the need to work collaboratively across organizational and jurisdictional boundaries to maximize the efficacy and effectiveness of FIAS management.

Author contributions

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Compliance with ethical standards

Human and animal rights This article does not contain any studies with animals performed by any of the authors.

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