

Harnessing the potential of Precision Pest Management in plantation forests

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Abstract: There are numerous new and emerging technologies that allow for greater precision in forest pest management, from sequencing and chemical analyses, to data collection through smart technologies, and integration, analysis and sharing of data across fields. These technologies allow for the development of much more precise tools for pest management than has ever before been possible; an approach that we define as Precision Pest Management (PPM). They also allow for more rapid development of IPM tools, as well as the ability for early recognition and response to changes in pest population densities and distributions. We argue that there is an increasing need for a PPM approach and that we harness the opportunities these technologies offer to deal with the scale and complexity of pest management in the future.

Keywords: Precision Pest Management, Plantation forest pests, Integrated Pest Management, Invasive pests, Biological control, Forest entomology

Introduction

The number of emerging invasive pests of plantation forests is rising rapidly around the world (Wingfield et al. 2015, Hurley et al. 2016). While these numbers already cause alarm, they still represent only a fraction of the pool of potential future invasions from the native range of forest plantation species such as *Eucalyptus* (e.g. Dittrich et al. 2020, Makunde et al. 2020). Not only are the overall numbers and rate of introduction increasing rapidly, but the complexity of invasive populations is also increasing. This is evident from population genetic studies on invasive populations that commonly reveal patterns of multiple, large and recurrent introductions; hybridization or admixture creating unique gene pools; and cryptic species (Garnas et al. 2016, Mutitu et al. 2020). This diversity is expected to be reflected in life history traits that are relevant to pest management programs.

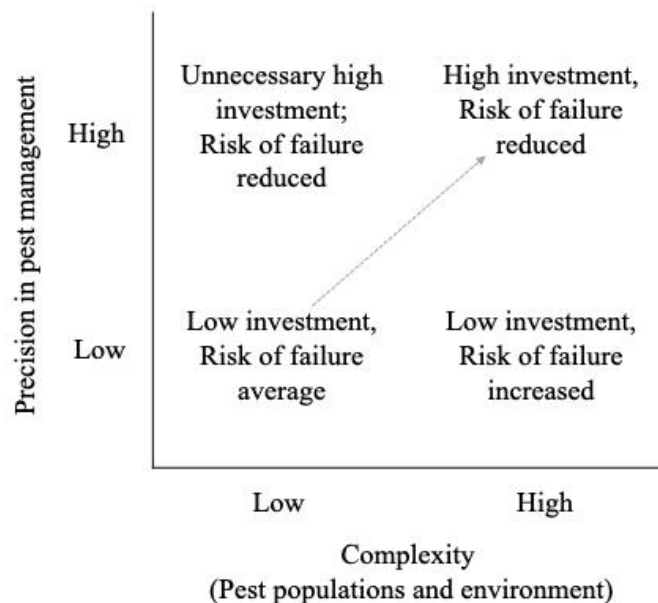


Figure 1. Invasive pests in plantations are often viewed as relatively uniform biological entities, even if they occur across a geographic range or continents. This might be true in some cases, but is often not. Genetic variation and phenotypic plasticity in the pest populations is expected to increase over time due to additional introductions or reproductive and evolutionary processes, or as a pest spreads across variable environments where expression of traits may vary. An increase in complexity in the pest population requires a shift in the focus on precision for control efforts to remain efficient, such as in the choice of a biological control agent or the timing and methods of application of control methods. A shift to greater precision is also expected to require more (interdisciplinary) expertise and resources, which are often only available in collaboration networks.

The scale and complexity of the threat of invasive and emerging pests requires precise management tools. The concept of precision agriculture is based on recognizing variability in cropping systems and accounting for it in management programs to increase yields and profitability (Bhakta et al. 2019). Application of this concept to pest management provides more precise tools required to address these threats, which can have a significant impact on the efficiency and cost-benefit analysis of the tools (Figure 1).

We define Precision Pest Management (PPM) as an approach to pest management that emphasizes characterizing variation and diversity in pest systems and developing Integrated Pest Management (IPM) programs that address this variation and diversity. We include in PPM consideration of both the inherent (genetic and phenotypic) variation of pest systems, as well as the variation in its expression in a landscape (due to variation in both abiotic and biotic interactions). This is an extension of past reference to precision in pest management as a concept that emphasized (remote) sensor measurements of the impact of pests on a landscape (Ahmed and Mahdi 2018, Iost et al. 2020).

Prominent examples that illustrate the need for PPM include some of the most damaging *Eucalyptus* pests. For example, *Leptocybe* and *Gonipterus* both contain more than one species or lineage that have been confused in the past (Dittrich-Schröder et al. 2018, Mapondera et al. 2012, Schröder et al. 2020). Invasive populations of *Gonipterus* were known as *G. scutellatus* for decades, and its management relied heavily on the egg parasitoid *Anaphes nitens*, collected from a single site in South Australia. Today we know that at least three *Gonipterus* species are invasive, none of which are *G. scutellatus*. This has major consequences for understanding the potential origin of invasive populations and optimal sites and species to select for biological control. Similarly, invasive populations of *Leptocybe invasa* were recently shown to contain at least two distinct lineages, with admixture in some populations. A lack of recognition of this diversity can have major consequences for biological control, as well as efforts to select resistant *Eucalyptus* varieties (Dittrich-Schröder et al. 2012).

Fortunately, there are numerous new and emerging technologies that allow for greater precision in forest pest management, from sequencing and chemical analyses, to data collection through smart technologies, and integration, analysis and sharing of data across fields (Naidoo et al. 2019). These technologies allow for the development of much more precise tools for pest management than has ever before been possible. They also allow for more rapid development

of IPM tools, as well as the ability for early recognition and response to changes in pest population densities and distributions. We highlight a few of these technologies and argue that it is essential that we harness the opportunities they offer to deal with the scale and complexity of pest management in the future.

A first obvious advantage that new technologies provide is greater precision in the identification of pests. This is aptly illustrated by the examples of *Leptocybe* and *Gonipterus* mentioned earlier (Dittrich-Schröder et al. 2020, Schröder et al. 2020). In these examples it has taken many years, and even decades, to recognize the diversity in these invasive pest populations using traditional approaches. Sequence data not only facilitated the taxonomic resolution of the invasive species but clarified invasion routes and identified populations where admixture occurs (Dittrich-Schröder et al. 2018). It also provided the data necessary for the development of rapid diagnostic tools (species specific PCR and PCR Restriction Fragment Length Polymorphism) with which spread of the genotypes across landscapes could be monitored (Gevers 2019).

Molecular diagnostics such as that described above are readily developed for any organism (Estoup and Guillemaud 2010, Madden et al. 2019). However, the capacity to handle even the simplest of these tools, such as barcoding, is still unequally distributed around the world and often not used (Hurley et al. 2017); let alone more powerful population genetics or various ‘omics’ tools. To address this problem, governments, industries and the science community need to connect and share capacity across borders. Invasive species are by their nature an international problem, requiring international solutions (Wingfield et al. 2015). Thus, the current unequal distribution in capacity for molecular diagnostics, to facilitate targeted management options, threatens all regions of the world, irrespective of local capacity.

The development and implementation of PPM using molecular data can be hampered by the speed at which this data becomes available. Unfortunately, few databases reflect up to date information, with a lag of many years from the generation of data to its global availability (at the time of publication). While large databases such as GenBank and Barcode of Life Database (BOLD) are invaluable global tools for storing and sharing data (Ratnasingham and Hebert, 2007, Leray et al. 2019), there is also a need for more specialized tools for collaboration and management. One example relevant to forest pest management is the online curated Forest

Insects Mitochondrial Barcode Database (www.fabnet.up.ac.za/fimt), which allows real time comparison of data in a manner that protects the data rights of the generator prior to publication.

Biological control is the main tool for control of many forest pests and stands to gain much from the adoption of a precision management approach. While biological control is important for the management of many forestry pests, developing biological control programs is time consuming and frequently fails to result in control of the pest (Cock et al. 2016, Kenis et al. 2017). There are many factors that influence program success, but a failure to recognize variation in genotypes or ecotypes and its consequences for interactions between species is thought to contribute substantially (Roderick and Navajas 2003, Yek and Slippers 2014). Understanding species and population diversity and the geographic distribution of diversity for both the pest and its biological control agents is thus important (Garnas et al. 2016, Mlonyeni et al. 2018, Hurley et al. 2020). It is also important to recognize that these populations will evolve, including evolving resistance (Roderick et al. 2012, Szűcs et al. 2019, Tomasetto et al. 2017). The monitoring and management of diversity below the species level is thus necessary for sustained success in biological control programs.

Genetics and genomics based tools hold the promise to unlock even further PPM possibilities in biological control (Gurr and You 2015). This could include selection or even breeding of traits that influence the efficiency of a biocontrol agent (Le Hesran et al. 2019, Lirakis and Magalhaes 2019, Lu et al. 2016). For example, if the genetic basis of desirable traits such as virulence can be characterized, they could be selected for, or maintained in biological control populations (Lirakis and Magalhaes 2019). These and other traits have been selected in entomopathogenic nematodes (EPNs) for a long time, but genome assisted selection now promises to significantly enhance this possibility (Lu et al. 2016). Biological control programs will, however, require a more systematic approach to collection and storage of population samples to harness this potential (Yek and Slippers 2014). While large numbers of strains of the parasitic nematode *D. siricidicola* have been collected since the 1970's, only one strain was ever stored for longer term study, and then deployed across various continents and populations of its host, the woodwasp *Sirex noctilio* (Bedding and Akhurst 1978, Mlonyeni et al. 2011, Slippers et al. 2015). Only in recent years, and at great expense, could a larger number of strains of this nematode be collected for use in studies to select strains for different populations of *S. noctilio* and environments (Fitza et al. 2019).

Unlocking the potential of molecular tools and populating global databases requires access to global collections of pests and their biological control agents. Such collections can be exceedingly difficult and expensive to develop. In this regard structures such as the global BiCEP alliance (Biological Control of Eucalypt Pests; <https://bicep.net.au/>) can serve as an example of an international networking structure that can address many of the challenges of developing biological control programmes. The program is based at the University of the Sunshine Coast in Brisbane, Australia, but is funded jointly by partners in Australia, South Africa, South America and Europe. Apart from leveraged funding, the network partners share information, capacity and collections or cultures.

Semiochemicals are chemical signals and cues that influence the behavior of insects and can be integral components of forest plantation pest management programs. They are used as indirect management tools (e.g., survey and detection) to inform management decisions (e.g., the need for and timing of insecticide applications) and as direct management tools (e.g., mass trapping, mating disruption, lure-and-kill/infect) (Nadel et al. 2012, Noeth et al. 2020). The high level of specificity of how semiochemicals influence behavior necessitates precision in studying individual pest species (Scheepers et al. 2020). Understanding cryptic diversity is therefore important. For example, a potential pheromone has recently been discovered for *G. platensis* in Portugal (Branco et al. 2019), but its effectiveness for *Gonipterus* sp. 2 in South Africa and southern Europe (within the same species complex as *G. platensis*, but now known to be a different species) remains to be tested. Beyond species diversity, the potential variation in semiochemical signals amongst populations of a species across its range should also be considered (Allison and Carde 2016). For the discovery and screening of semiochemicals, ‘omics’ tools provide the opportunity for both scaling and increasing precision through a ‘reverse chemical ecology’ approach, in which potential ligands can be screened against *in vitro* expressed receptors and binding proteins (Choo et al. 2018).

A particularly exciting potential precision management tool for forest pests that has recently emerged is CRISPR-Cas9 guided gene editing (Champer et al. 2016, Harvey-Samuel et al. 2017, McFarlane et al. 2018). There are a host of potential applications of this technology for pest management, including targeting genes that control sexual dimorphism for sterile male production and targeting genes critical for fitness, survival or virulence (Kandul et al. 2019). CRISPR-Cas9 based gene editing systems also provide options to engineer gene drives, in which an edited gene is spread through a population at super-Mendelian inheritance rates. Gene

drives have the potential to change whole populations, or even eradicate them by targeting sex determination genes that affect female development (Adelman and Tu 2016). Such approaches can be done at unprecedented levels of precision, targeting specific populations or genotypes in a population if sufficient population genomics information is available. However, the technology is in its infancy and faced with significant barriers in terms of addressing potential negative effects in food webs in native areas, ensuring efficacy in wild populations and countering the emergence of resistance (Harvey-Samuel et al. 2017).

The (remote) sensing technologies that are typically associated with the term ‘precision’ in agriculture or pest management is covered in numerous other reviews and we will not discuss them in detail here. The integration of these technologies with knowledge of biological variation is at early stages but offer powerful opportunities to contribute precise information for decision making and implementation of PPM. For example, chemical detection by insect antennae are being integrated with autonomous robots and nanodrones and could support very specific pest detection (Martinez et al. 2014, Anderson et al. 2019). Increasing accuracy in remote sensing equipment and analysis also offer the opportunity to map fine scale biological variation in pests in interaction with their hosts and environment (Nansen and Elliott 2016, Iost et al. 2020).

In conclusion, a PPM approach offers opportunities to facilitate and accelerate the response to the serious threats posed globally by emerging invasive pests. In order to realize the potential of new technologies for pest management, there is an equally urgent need to develop stronger international collaborations. PPM requires a more structured collaborative approach than is currently practiced, where tools, capacity, collections and data can be exchanged more efficiently than what the publication process typically allows. For this, collaboration on short term projects will not be sufficient. Rather, the global problem of complex invasive pest populations requires long term and stable structures that optimally leverage funding and capacity across the barriers between sectors, institutions and national borders.

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