BURLEIGH DODDS SERIES IN AGRICULTURAL SCIENCE

Integrated management of insect pests

Current and future developments

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Introduction

Since the second half of the 20th century integrated pest management (IPM) has been the alternative paradigm to chemically-intensive pest control systems. IPM seeks, in the foundations of the ecological sciences, the means to keep pest populations below the level at which they can cause economically significant crop losses. To achieve this goal IPM taps a rich array of physical, cultural, and biological control methods conceived on the basis of an understanding of the principles of species, population, community, and ecosystems ecology. Chemical controls, within an IPM system, are used strictly as needed and in a way that minimizes any adverse environmental effects, particularly any negative impact on those biological methods of control. This collection reviews the latest research on optimizing IPM with a focus on management of insect pests.

Part 1 Ecological foundations of IPM

Chapters in Part 1 review the foundations on which successful IPM programs need to be based. Chapter 1 reviews the continuing challenges and advances in identifying and quantifying pests. The chapter emphases the importance of taxonomic expertise and reference collections as well as the increasing role of bioinformatics. It discusses developments in quantifying pests and assessing their spatial distribution as a foundation for planning an IPM program.

Once pests are identified, it is critical then to understand their life cycle and the environmental factors determining their development. A key tool here is phenology modeling. Chapter 2 reviews steps in model construction, including the major sources of error in phenology model development and implementation, as well the use of linear and non-linear approaches to modeling temperature-driven development data. The chapter includes an exemplary life cycle systems model for the spotted wing drosophila, *Drosophila suzukii*, a major fruit crop pest in the US and Europe, which provides a foundation for the development of IPM programs.

Effective IPM programs depend not just on understanding particular pests but the broader environment in which they interact with their hosts. Agroecology analyses the different components that make up an ecosystem such as soils, climate, plants and animals, and their interactions within agricultural landscapes. Chapter 3 explores agroecology and pest management practices, using the example of a particular agroecosystem: rice paddies in Japan. It discusses how an understanding of agroecosystem dynamics explains the limitations of early attempts at chemical pest control. It also shows how this understanding has informed the development of IPM strategies based on the

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enhancement of biodiversity in paddy rice ecosystems. The chapter explores how agroecological concepts can help address challenges such as invasive species and climate change.

Complementing the previous chapter, Chapter 4 discusses the changes needed to achieve IPM programs based on agroecological principles. It highlights the need to shift focus from particular commodities to diversified landscapes and agroecosystems, from pest suppression to promotion of ecosystem services, from technological inputs to ecological knowledge and experience, and from management by individuals to management by organizations at the landscape scale. The chapter presents detailed case studies of effective IPM via agroecosystem management and looks ahead to future research trends in this area. Building on both Chapters 3 and 4, Chapter 5 focuses on the particular and growing problems of invasive species. As the chapter points out, all biological invasions progress through similar stages of arrival, establishment, spread, and impact. Understanding invasive species ecology makes it possible to improve preventative measures, develop rapid response systems as well as develop techniques for suppressing invasive pests and then rehabilitating agroecosystems.

The interactions between plants and the arthropod herbivores that feed on them are intricate and multifaceted. Plant resistance results when a plant expresses traits that disrupt one or more aspects of a plant-arthropod interaction. Chapter 6 defines what we know about the fundamentals of plant resistance, outlining processes of resistance including host-plant selection and host-plant utilization. The chapter examines phenotypic plasticity in plant resistance, the mechanistic bases of plant resistance and tolerance and insect counter-defenses, as well as the genetic basis of plant resistance and its use in IPM. The chapter looks ahead to future research trends in this area.

Part 2 Cultural and physical methods in IPM

Chapters in Part 2 review cultural and physical tools available for use in IPM programs. Over the last sixty years, research involving the development and deployment of insect-resistant crop cultivars has led to significant crop improvements in the major food producing areas of the world. Chapter 7 provides a comprehensive review of the history, status, latest methods and challenges of breeding insect-resistant varieties as an ecological approach to managing crop pests, using the example of rice. The chapter assesses types and mechanisms of plant resistance and the various methods of screening for resistance traits based on insect feeding behavior. It then looks at advances in molecular breeding techniques including emerging methods such as gene editing. The chapter also discusses potential constraints, interactions with other control methods such as cultural, biological and chemical controls.

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Complementing the previous chapter, Chapter 8 provides a broad review of the application of genetically-engineered (GE) host plant resistance within an IPM context. Focusing on Bt crops, the chapter explores the basis of GE-based host resistance, its integration into IPM, and methods of resistance management. The chapter looks ahead to the future of GE in such areas as RNAi and CRISPR/Cas-based crops.

Chapter 9 broadens the scope by reviewing the range of biotechnology applications in pest management including pest diagnostic and genetic characterization of pests, molecular breeding for insect and disease resistance, genetically-engineered crops as well as the use of emerging genome-editing approaches for pest management. These applications provide additional options in IPM programs and in turn help reduce pest damage and crop losses, decrease the use of toxic chemical pesticides, and enhance agricultural productivity, economic growth and global food security as well as improve environmental quality. The chapter also highlights policy issues including intellectual property rights, biosafety, regulatory, communication, and stewardship aspects surrounding the access, utilization, deployment and management of biotechnology tools in pest management programs.

Chapter 10 shifts the focus to developments in physical control methods in IPM. The evidence is mounting for pesticide failures on many fronts, including environmental contamination and pest resistance to chemical products. As an alternative, physical management methods are environmentally friendly, are not subject to the development of resistance, leave no residues, and require no complicated registration procedures. In this chapter, recent advances in physical control methods are reviewed, and how they are applied to both pre-harvest and post-harvest stages of production, notably for fresh fruits, vegetables and flowers. Pre-harvest techniques reviewed include soil solarization and mulches as well as barrier techniques such as screened greenhouses, floating row covers, insecticide-impregnated nets and leaf shredding. Post-harvest methods discussed include developments in pest exclusion, early detection, the use of thermal techniques and ionizing irradiation, as well as computer-assisted decision support tools. The chapter concludes by discussing the future of post-harvest phytosanitary measures, which includes the possibility of artificial intelligence coupled with affordable sensors.

The final chapter in Part 2, Chapter 11, focuses on the incorporation of robotics and automation in IPM programs. Echoing some of the challenges highlighted in Chapter 1, it reviews ways of automatically detecting and identifying pests based on inputs such as vision and odor, including pheromone-based insect detection systems. It also reviews the potential use of unmanned autonomous vehicles (UAVs) in such areas as soil sampling and delivery of insecticides or biocontrol agents.

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Part 3 Biological methods in IPM

Part 3 reviews the rich body of research on developing and enhancing biological methods of control in IPM programs. Chapter 12 reviews advances in classical biological control to support IPM in perennial crops. The chapter examines the key steps required in the development of a successful classical biological control program for managing invasive insect pests. These include identifying and sourcing natural enemies, evaluating host specificity and host range of natural enemies as well as planning release and establishment programs. The chapter includes a detailed case study of classical control of Asian citrus psyllid, *Diaphorina citri*, an invasive pest of California citrus

Chapter 13 reviews developments in conservation biological control and habitat management as key components of IPM programs. There have been substantial advances in such areas as understanding insect ecology and agroecosystem dynamics at the landscape and regional scale. It looks at the way this understanding has been used to improve habitat management at both the farm and landscape scale in such areas as banker plants for mite management and soil habitat management to control pests whilst supporting beneficial insect species.

Complementing the previous two chapters, Chapter 14 assesses advances in augmentative biological control in IPM. Augmentative biological control uses mass-reared natural enemies for releases in large numbers to reduce pest populations. The chapter describes the role of augmentative biological control in IPM, its advantages and disadvantages as well as when the technique is best deployed. It reviews the range of natural enemies commercially available and techniques for their mass production and release. It also includes examples of the successful use of augmentative control both to control sugarcane pests in Brazil and greenhouse pests in The Netherlands.

As Chapter 15 points out, production in greenhouses, high tunnels and other protected environments is expanding worldwide to allow for more intensive and continual cultivation to mitigate the effects of climate change. IPM practices in greenhouses and high tunnels are unique and specific to the target pest, geographical location and crop. This chapter describes the process of scouting for both pests and beneficials in the greenhouse environment, before discussing plant-mediated IPM systems, including the use of trap, banker, habitat and guardian plants. It also discusses the use of biocontrol agents. Entomopathogenic fungi and UV light. The chapter includes case studies on IPM for greenhouse ornamentals in both developed countries (USA) and developing countries (Lebanon).

Building on a theme in Chapter 15, Chapter 16 reviews the use of entomopathogenic fungi to control insect pests which has been expanding in recent years with improvements in formulation and more commercial

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applications. The chapter summarizes what we know about the way entomopathogenic fungi work and the range of products available. It reviews ways of integrating the use of entomopathogenic fungi with other control measures, including combinations with lower doses of pesticides, as well as use alongside predators and parasitoids. entomopathogenic bacteria and nematodes as well as botanical extracts. The chapter also looks at ways of optimizing environmental conditions to support fungal activity against pests, the use of attractants and vectors to promote pest contact with fungi, as well as the potential use of endophytic entomopathogenic fungi in suboptimal conditions. The chapter includes case studies on the use of entomopathogenic fungi such as *B. bassiana* to control coffee berry borer and cotton aphid as well in greenhouse cultivation.

Chapter 17 addresses the use of entomopathogenic viruses such as baculoviruses in IPM programs. These are highly target pest-specific, have no detrimental side effects, are often as effective as chemical alternatives, and leave no detectable residues. The chapter discusses ways of using entomopathogenic viruses alongside other biocontrol measures such as parasitoids and predators, as well as how to overcome the challenges associated with their usage including slow speed of kill, a narrow host range, limited shelf life, cost and the possibility of resistance development. Three baculovirus biopesticide case studies are included to show the practical benefits of using baculoviruses in IPM systems.

The final chapter in Part 3, Chapter 18, looks at advances in use of entomopathogenic nematodes in IPM. As the chapter points out, entomopathogenic nematodes in the genera *Heterorhabditis* and *Steinernema* are potent biological control agents that have been commercialized widely for control of economically important insect pests. This chapter describes the latest research on the foraging and infection behaviour of nematodes and the production, formulation, application technology and commercialization of entomopathogenic nematodes. The chapter considers the factors affecting the efficacy of nematodes in IPM and methods to improve their efficacy. Finally, the chapter looks ahead to future research trends in this area.

Part 4 Chemical methods in IPM

Part 4 explores the future of pesticides as part of IPM programs. Chapter 19 discusses advances in pesticide formulation and use including the development of more selective pesticides, the importance of dose selection, timing of chemical pesticide treatments, and changes in pesticide application technology to improve targeting. The chapter also offers an overview of biopesticides such as baculoviruses and bacterial biopesticides, as well as the application of entomopathogenic nematodes, release of predators and parasitoids and the use of pheromones to complement pesticide use.

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Poorly-managed pesticide use can exacerbate pest problems by affecting the natural enemies that control pests. Chapter 20 reviews what we know about the ecological impacts of pesticides and the ways they can be mitigated, including a better understanding of pesticide resistance in natural enemies, mechanisms of pesticide toxicity and amounts of chemicals to apply. The chapter includes a detailed case study on optimising pesticide use as part of an overall IPM program to control the diamondback moth.

As well as ecological and environmental damage, inappropriate use of pesticides can have serious effects on human health. Chapter 21 looks at developments in monitoring exposure to pesticides, including ways to collect data, and how to minimize human health risks related to their use. The chapter includes a case study on health risks from pesticides amongst smallholder farmers in the Republic of Benin. It shows that pesticide poisoning remains a significant problem in many low- and middle-income countries (LMICs).

Building on the previous chapters, Chapter 22 explores new research to develop more environmentally-friendly, selective insecticides and biocides for use in the production of food crops. As insect hormone neuropeptides govern almost all aspects of insect physiology and survival, neuropeptide-based insecticides provide a promising solution. The chapter reviews the key steps in developing this new class of biopesticide, including neuropeptide profiling, neuropeptide families, peptide modifications, synthetic chemistry and validation, as well as the assessment of peptide effects on insects.

Part 5 Implementation

The final part of the book looks at ways of implementing IPM programs in practice. Chapter 23 reviews advances in integrated management of nematode pests of crops. As the chapter points out, there is still limited research on the long-term impact of IPM programs to combat nematodes. This particularly applies to major cereal (maize, wheat and rice) and leguminous (peanut, soybean and sunflower) crops on which this chapter focuses, and the economically most important nematode pests (root-knot, cyst and root-lesion nematodes) damaging such crops. The chapter summarizes what is known about the basic biology and morphology of nematodes as well as the effectiveness of the main control strategies (cultural, biological and chemical control and host plant resistance) used worldwide. A case study demonstrates ways of integrating multiple nematode control strategies. The chapter also discusses the novel use of transgenic crops with nematode resistance, challenges faced in terms of nematode management under changing environmental conditions and practices (focusing on minimal disturbance of soil and conservation of soil-fauna communities), and the challenge posed by weeds as hosts of major nematode pests.

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As Chapter 24 highlights, plant feeding mites are major pests of agricultural crops and ornamentals. They disrupt physiological processes, change the physical appearance of the plant and transmit diseases to crops. This chapter takes a holistic approach to integrated mite management (IMM) by reviewing the basics of mite taxonomy and morphology and then studying key plant mite families, focusing on major plant feeding mite pests as well as natural predators that regulate these mite populations.

A key aspect of implementing any pest management program is economic viability. Besides reducing health and ecological risks of pest control, IPM seeks to increase farm income. Economic constraints also act as barriers to adoption of IPM practices. An understanding of how IPM affects the farm 'bottom line' is crucial to efforts to encourage IPM. Chapter 25 discusses methods for estimating the economic impacts of IPM, devoting special attention to advances in statistical methods to account for sample selection bias in program evaluation. The chapter also discusses methods for estimating economic values of reduced environmental risks. Finally, the chapter examines the effectiveness of farmer field schools in promoting pest management knowledge, IPM adoption, and farm income and discusses ways to improve economic assessments of IPM programs.

The concluding chapter in the book reviews the future evolution of IPM. It identifies the ways modern agriculture has disrupted plant defences and the control of pests by their natural enemies. The chapter discusses ways of restoring and enhancing these controls both through breeding and the use of biological methods. It demonstrates how IPM can be taken to the next level of integration with a case study of a pome fruit IPM program in the Pacific Northwest of the United States.

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Part 1

Ecological foundations of IPM

Chapter 1

Foundations of an IPM program: detection, identification, and quantification

Michael E. Irwin, University of Illinois, USA; and Wendy Moore, University of Arizona, USA

1 Introduction
2 Detection and identification
3 Bioinformatics
4 The DNA transformation
5 Quantifying target organisms
6 Future trends and conclusion
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1 Introduction

The practice now termed 'integrated pest management' had its beginnings in the 1940s, during and just after the Second World War, when synthetic pesticides, particularly dichlorodiphenyltrichloroethane (DDT), first became commercially available. A miracle therapy, it countered the ravages of insect pests and before long was widely applied, among other places, to cotton fields in the Cañete Valley of southern Peru to control *Helicoverpa zea* (Boddie) (Lepidoptera: Noctuidae), referred to by various common names (e.g. the 'cotton bollworm' or 'corn earworm'), a devastating pest that soon became resistant to the synthetic pesticide. The resistant population of *H. zea* began to flourish in agroecosystems where the pest's natural enemies had been appreciably reduced and rendered ineffective by the synthetic chemical (Luckmann and Metcalf, 1994; Peshin et al., 2009). After a short time with drastically reduced harvests, a group of Peruvian entomologists, realizing the problem, convinced the government of Peru to pass legislation prohibiting the use of synthetic pesticides in the Cañete region. In fact, the only chemical control allowed there was the sparse and sporadic use of inorganic arsenic. Within a short period of time, the agroecosystem, particularly the natural enemies'

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component, rebounded, and cotton production again became economically viable. This was, as far as we are aware, the first instance of managing pests in an agricultural setting through the elimination of synthetic pesticides.

During the 1950s, entomologists, led by the late Ray F. Smith (Adkisson et al., 2001) of the University of California, Berkeley, laid the foundation for a new approach to pest control (Smith, 1969) by focusing theory, experimentation, and outreach on four components: (1) insects become resistant to synthetic pesticides (Kogan et al., 1999), (2) chemicals eliminate natural control agents (Newsom, 1967), (3) the environment and human health must be protected (President's Science Advisory Committee, 1965), and (4) harvestable products must be profitable (Stern et al., 1959; Stern, 1965). Over the next several years, entomologists, in addition to the team led by Smith (including Rabb (1972), Newsom (1967, 1980), Adkisson (1969), Glass (Glass and Hoyte, 1972), and others), were instrumental in pushing the boundaries of the emerging concept. Since then, integration of management efforts based on advanced technologies and multiple pest assessments in multi-field and areawide venues (Koul et al., 2008) has led to a host of sophisticated approaches that will shape the discipline in the future. From the initial efforts in Cañete to the present, the concept of pest control has evolved into the ecological, economic, and sociological paradigm known as integrated pest management (IPM).

IPM has two primary audiences: the largest and most obvious encompasses those who implement IPM packages by following previously developed and accepted management guidelines–farmers, growers, producers, ranchers, nursery personnel, and pest management practitioners, scouts, and consultants, to name a few. The second comprises the team or teams of researchers, technocrats, modelers, engineers, and others who, individually and collectively, design, develop, assemble, and test the reliance of and confidence in IPM packages. It is the second audience that develops and constructs appropriate algorithms and provides critical background for validating IPM packages. This chapter is written for both audiences, although more space is devoted to supporting the latter.

Conceptually, an IPM program consists of three tiers of information: fundamental (perhaps more appropriately termed foundational), tactical, and operational (Irwin, 1999). This chapter, the first in a book focused on advances in IPM, explores two of the most foundational components of the IPM paradigm: (1) accurate identification of the pivotal species impacting the biological, economic, and social dynamics of the ecosystem under assessment and (2) measurement and evaluation of these influential species through time and space. The chapter emphasizes evolving principles of these two bedrock components of IPM, both pertinent to managing annual and perennial fruit, grain, vegetable, and greenhouse crops, and ornamentals. Even though the emphasis is placed on recently formulated and emerging

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technologies and their current and future impacts on the two foundational IPM components covered here, a glimpse into the status quo is also provided as are insights into constraints imposed by the state of technology and by society at large.

2 Detection and identification

Imagine a grower who has just inspected the family farm and found some strange-looking organisms that appear to be methodically devouring the crop. His/her initial instinct might be, 'How do I rid the crop of this infestation?' However, that first question should be, 'What organism is it?' That grower's next concern should be, 'Is it having a negative impact on the harvest and therefore on my earnings potential?' Only after that the grower ought to decide if the target organism needs to be controlled and at what cost, both economically and environmentally. Addressing the question 'What is it?' is the subject of this section.

2.1 Common names versus scientific names

The act of identifying a target organism, that is, determining the species name, is critical and is discussed below. Vernacular or 'common' names, often used in local settings, are easy to recall and can, to a limited degree, help in searching the internet, the literature, pamphlets, and other sources for the organism's life history traits and its potential to do harm. A common name, however, is often far from unique to a species and a single species can have more than one common name. Information about a different organism with the same common name can lead to spurious, even misleading information and referring to only one of a number of common names for a species limits the information that can be uncovered.

According to the Linnaean system of binomial nomenclature (herein termed 'Latin binomial'), a species name is composed of two components, both italicized: (1) a genus name, capitalized, followed by (2) a specific epithet, not capitalized. For example, *Helicoverpa zea* is the scientific name of the species commonly known as the cotton bollworm or the corn earworm *(Helicoverpa* is the genus name and *zea* is the specific epithet). In formal writing, scientific names are often followed by the last name of the person who originally described the species and, occasionally, the year the original description was published. This system, used throughout the world, provides species with a truly unique identity.[1]

1 Cases arise when the same name is ascribed to a different species, but when this happens, the two names are termed the senior (first named) and junior (last named) homonyms; this occurs rarely and the species bearing the junior homonym must be given a different binomial so that both species have unique names.

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The scientific name (genus + species) affords two lines of evidence for revealing information about the target organism: it provides the link to (1) all published knowledge of that species, which is often extensive, including its life history traits, distribution, and its natural enemies; and (2) all published knowledge of the species' closest relatives, that is, all other species classified in the same genus or closely related genera. If little information is discovered through literature searches of the species' binomial itself, a further search of its close relatives can reveal noteworthy, commonly held life history traits to help inform an effective IPM implementation plan. In contrast, common names are not unique and lack the nested hierarchy needed to place organisms into an evolutionary framework. Therefore, when at all possible, search out and utilize scientific names (Latin binomials).

Beyond the close kinship of species nested in the same genus, the entire evolutionary hierarchy can provide valuable information. This hierarchy involves populations nested within races, varieties, subspecies, or other subspecific categories, which are in turn nested within species, and those are nested within genera, families, orders, and even higher levels of classification. To which level of these various nested groupings, one might ask, should the organism be identified? The answer is not clear-cut; it takes more effort to identify a population than a subspecies, more to identify the subspecies than the species, and, similarly, more to identify a species than a genus. In most cases, identifications to the species level are adequate, but in some cases, realizing that a specific population, race, or subspecies has gained resistance to some crop variety or some pesticide, or has adapted to feeding on a different crop may be essential knowledge.

Even at the higher classification categories of tribe, family, order, superorder, and subclass, some vital information can be gained. For instance, knowing the target organism belongs to the order Hemiptera (true bugs) immediately confirms that the adult developed from a nymph rather than, like members of the Superorder Holometabola, through larval and pupal stages. That classification placement suggests that true bugs probably spent their entire lives (egg, nymph, adult) feeding on the same species of host plant, probably within the same field. Even more specifically, if, as suggested above, it proved to belong to the order Hemiptera, it will have piercing-sucking mouthparts, and that provides an important clue to its life history traits and, thus, how it might be managed. If, on the other hand, the target organisms were classified within the order Lepidoptera (moths and butterflies), it would belong to the Holometabola and adults would have spent most of their feeding lives as caterpillars (larvae), often in a very different habitat than the adult. And the larvae too would have chewing mouthparts and the type of injury to the crop would differ from that of the piercing-sucking habit of true bugs.

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2.2 Detecting the pest

Let's inspect the grower's field mentioned above. Assuming the field is not drenched in organic pesticides, several dozens to hundreds of arthropod species are likely present. (At the upper extreme, alfalfa, grown for its seed in parts of southern California, is known to harbor up to 1200 species (Schlinger, pers. comm.)). Some of these species will be more difficult to detect than others. The only sign of an infestation might be the wilting of scattered or clustered plants within the field. The cause of wilting could be difficult to detect and thus determine. It might be root-feeding beetle grubs or the larvae of stem-boring moths. Indeed, it might not be an insect at all, but rather an organism outside the scope of this book, such as a fungus or bacterium. Some observed problems might have been caused by nonbiological phenomena, such as the lack of fertilizers—or their excess—or even overly wet or dry field conditions. The grower or IPM practitioner must examine plants showing symptoms, looking closely at the underside of leaves along the entire architecture of the plant, digging the plant up and dissecting the stems and roots to expose the causal agent. Once the target species is detected and in hand, it can be identified. That will provide the evidence needed to give it a Latin binomial, opening a gateway into baseline data needed to pursue a course of action regarding the organism's presence in the field.

Plants in a field that are notably different (i.e. stunted; have elongated, spindly stems; or pitted or blotchy, often yellow, leaves) might be infected by a plant virus or a phytoplasma, most of which are transmitted by specific insect groups (e.g. thrips, beetles, aphids, leafhoppers, psyllids, mealybugs, planthoppers) and other organisms (e.g. mites, nematodes, fungi). The pathogen has likely entered the field with the vector and, as the vector probes or feeds, is transmitted to the plant. (A few viruses, however, are seed borne and are present in a field as soon as plants emerge, while others are mechanically transmitted by humans, livestock, and human-operated machinery). Some vectors are able to spread viruses rapidly and are transitory within a field. Therefore, not all agents or their vectors contributing to the proliferation of malformed, low-yielding plants can be easily detected or are confined to pest species that take up residence in the crop ecosystem itself.

2.3 Identification: providing critical Latin binomials

Even assuming all of the species in a field could be tracked down (an extremely difficult task), it would take an herculean effort for that grower or a pest management specialist, or, for that matter, anyone else, to identify all of the species, providing each with an accurate Latin binomial. Fortunately, for an IPM program, the identity of only a small portion of these organisms is required.

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The grower or IPM practitioner ought to know the identity of those organisms germane to the well-being of the crop (i.e. those species that could directly or indirectly cause stress to the crop), and, ultimately, to the economic impact they could have on the crop's harvestable products. Not surprisingly, experienced growers, IPM practitioners, and regional IPM extension agents will be well aware of these key species.

2.3.1 Accuracy of determinations

Many factors are influenced by the accuracy of identifications. Closely related species are one such concern because they can easily be mistaken for one another. A target species, if incorrectly identified as belonging to a closely or even distantly related 'cryptic' species, is likely the host of a parasitoid that differs from the parasitoid that attacks the target pest. Misidentifying cryptic pest species can lead to the release of the wrong species of host-specific parasitoid, resulting in a complete classical biological control failure (Rosen, 1978). Similarly, an exotic, invasive species can rapidly gain pest status in a region well before its identity is widely recognized. Determinations of these pests by all but taxonomic experts can miss the mark, providing yet another source of spurious information. This is also true when an undetermined or incorrectly determined pest has a high degree of resistance to specific pesticides or is highly tolerant of specific cultivars, varieties, or isolates of a given host plant. Initiating management tactics for a species not properly identified can lead to utter control failure. When a pest appears a bit unusual or behaves a bit differently than those normally observed, having an expert taxonomist identify it is prudent and well worth the effort.

2.3.2 Literature and digital searches

Literature that will help identify a pest organism is abundant and rich. The concept of identification has been honed over generations and is summarized in a book edited by Hawksworth (1994), which includes information on biosystematic services, information, and methodologies. If both the crop species and the region are known, a search of the literature and internet will, in most instances, provide valuable information concerning the major pest species. As an example, the University of California, Division of Agricultural Sciences, has, through the years, published a number of pest management guides for various crops in California. Its publication No. 4105 (Flaherty et al., 1981) not only lays out the pests (diseases, arthropods, nematodes, and others) of grapes in California, it also furnishes Latin binomials for them and their most effective natural enemies and provides photographs of the pests and the injury they cause to the vines and fruit. It also provides information on how to best manage

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each of the pests. Similar guides take on landscape or areawide perspectives of IPM (Krischik and Davidson, 2004), which provide clear illustrations of the pests and their natural enemies. Detailed accounts can be found about most pest species by searching the internet. Thus, using digital and printed resources, Latin binomials can be obtained for most pest species, providing most growers and IPM practitioners a means to unlock the countless windows into the written knowledge banks of those organisms.

Literature focused on the systematics of biological control agents in IPM exists as well. Schlinger and Doutt (1964) explore theoretical aspects of systematics of biological control agents and provide a number of dichotomous keys for identifying families of natural enemies—both predators and parasitoids—within the class Insecta. A digital or literature search of the crop and its pests can lead to pertinent information on most other relevant species that inhabit an agroecosystem under assessment, specifically those that directly impact the biological, economic, and social dynamics of that system; their determinations can lead to sounder and more comprehensive approaches to managing the crop and its pests.

2.3.3 Taxonomic expertise

Recognizing when a pest cannot accurately be identified through various means available to the grower and pest management practitioner is critical. When the identity of a pest or its various natural enemies is in doubt, or prior determinations need confirmation, it is prudent to seek advice from an expert taxonomist. However, few taxonomists are able to identify species across the insect realm. Most specialize on taxonomic groups consisting of hundreds to thousands of species in related genera or even related families, for which they build mental databases of diagnostic features and their linked Latin binomials. Taxonomists require years of study to learn and hone their identification skills. So, just getting the material in question to an insect taxonomist is insufficient; you must get your organisms to the appropriate taxonomist. In other words, it helps to know a bit about the taxonomy of the target organism so that it can be directed to the appropriate authority. Although this might seem daunting to a grower or lay person, most practitioners and extension agents specializing in entomology or IPM are aware of who studies which groups of insects and from whom to seek further advice.

2.3.4 Collections and taxonomists: vital resources

Hundreds of insect collections are situated across the United States and, indeed, the world, each housing many hundreds of thousands to millions of arthropod specimens, for the most part each specimen associated with its

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unique Latin binomial and arranged in a fashion that allows curators, collection managers, and expert identifiers (i.e. arthropod taxonomists) to critically and efficiently compare specimens they are charged with identifying with those in their respective collections. These collections not only contain accurately identified specimens, they also house extensive literature devoted to the taxonomy and identification of a vast array of arthropod taxa; these literature sources feature dichotomous keys, more flexible multi-entry key formats such as LUCID and Delta, species descriptions, and other aids to assist taxonomic experts in tracking down and verifying binomials.

The US Department of Agriculture's Agricultural Research Services has, nestled within the Smithsonian Institution in Washington, DC, with a component in Beltsville, MD, the Systematic Entomology Laboratory, a unit employing numerous taxonomic specialists, each assigned to identify specific groups of organisms sent to the laboratory for determination. They are particularly aware of the importance of timely IDs for insects sent to them from border entry checkpoints because the freshness of fruit or other perishable commodities entering our markets is dependent on a rapid turnaround of the specimens being identified. A task taken very seriously, all other work is set aside until those specimens are properly identified, provided Latin binomials, and the port authority alerted and given permission to proceed by either allowing the cargo to enter the country, demanding that the cargo undergo fumigation to eliminate the pest, or prohibiting its entry entirely.

A few states (e.g. California, Florida, Massachusetts, Illinois) also have identification services staffed with several expert taxonomists, and they too provide accurate Latin binomials for specimens sent to them, particularly those insects found in agricultural settings and those that are found at state-operated border agricultural checkpoints. Many other states (e.g. Oregon, Arizona) employ one or two insect taxonomists charged with the identification of insects sent to them from state agricultural extension specialists, quarantine facilities, and others within their respective states. They are attached to state institutions, each with an extensive insect collection and associated literature, including taxon descriptions, dichotomous and multi-entry keys, to aid in the determination of target insect species they are sent and charged with identifying. Moreover, many universities around the country (especially those that are designated as Land Grant Institutions), and indeed the world, maintain insect collections; their curators and collection managers are often responsible for identifying (i.e. placing binomials on) specimens sent to them. If state and university taxonomists lack the ability to provide accurate Latin binomials for organisms in question, they solicit help from other taxonomists, and those are often the state and national resources for species determination and confirmation, the most noteworthy being the Systematic Entomology Laboratory in Washington, DC. Thus, a nested network of tiered taxonomically focused identification services

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exists within the United States and elsewhere around the globe, each with its curated arthropod collection and appropriate literature, and is responsible, among other things, for the identification of pest and beneficial arthropods (Foote, 1977). The taxonomists staffing these institutions work in harmony to assure that organisms sent to them are identified accurately and in a timely manner.

Most local extension entomologists and IPM practitioners are aware of the identification services offered locally and nationally. They rightly acknowledge the critical importance, timeliness, and monitory worth of the arthropod collection-based, identification-oriented institutional resources, including the dedication of the expert taxonomists who staff these institutions.

3 Bioinformatics

Bioinformatics is increasingly becoming an important tool for acquiring and organizing large datasets, including data obtained from millions of curated insect specimens (Graham et al., 2004; Kampmeier and Irwin, 2009). Recent efforts in digitization and deep extraction of data from individual specimens from arthropod collections, coincidentally, are generating data that provide broad historical insights into the dynamic shifts of geographic ranges, host-plant expansions, and much more for target pests, their natural enemies and other beneficials, information that can improve our ability to devise and execute anticipatory components of IPM programs (see Section 5.4, Anticipatory responses and IPM). As an example, examining, determining, and recording pollen grain adhering to archived insect specimens offers important ecological clues about which plants were visited over a long timeline (Roderick and Navajas, 2017). Geographic range expansions of various species, including those that are alien and invasive (see Section 5.2, Invasive species and early detection), can be mapped out from collection-associated data and online databases when coupled with appropriate algorithms and modeling efforts (Roderick and Navajas, 2017). Mass digitization and deep extraction (Schuettpelz et al., 2017) will, using informatics tools, afford vastly enhanced information that can be a powerful means for fine-tuning identification, sampling protocols, and a host of other aspects of IPM. Bioinformatics is the discipline that can bring many parts of the puzzle together to inform appropriate IPM decision-making.

4 The DNA transformation

Imagine a world where the complex task of identifying a specimen to the species level was as simple as inserting a probe into a target organism and having an associated display report the organism's correct species name, along with all information known about that species and, when appropriate, how

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best to manage it. Soon, the days of routinely sending specimens to expert taxonomists around the world for identification will be a thing of the past. Such specialists will be sought out only for the most obscure and least known species under scrutiny. It may sound like science fiction, but this scenario could become a reality, thanks to technological advances associated with acquiring and curating DNA sequence data from select regions of the genome of specimens identified by taxonomic experts.

In 2003, scientists at the University of Guelph, Canada, introduced the concept of 'DNA barcoding' (i.e. identifying organisms to the species level using specific regions of the genome) (Hebert et al., 2003a,b). For each region of the genome, the patterns of the four DNA building blocks (the nucleotides A, C, T, and G) evolve, or change, over time, resulting in taxon-specific templates. In the first (and current) phase of DNA barcoding, a region of the mitochondrial genome, the cytochrome oxidase 1 gene (COI), was selected as the species-specific sequence for use across the entire animal kingdom (the Metazoa).[2] The concept relies on having a reference library or database of authority-verified species names attached to DNA sequence data from the COI gene. For example, barcode-based identifications of insects rely upon an extensive library of COI sequences with correct species names attached to each, providing a template, in effect, upon which all unknowns are compared and identified.

The reference library for the barcode effort is termed the Barcode of Life Database (BOLD), which currently contains 6.7 million sequences representing 287 000 species of animals, plants, and microbes (Ratnasingham and Hebert, 2007).[3] The BOLD database has rigorous data quality standards that set it apart from other DNA sequence aggregators, such as GenBank. For example, to publish a barcoding sequence in BOLD, the following documentation must be provided: a photo of the specimen, label data including georeferences, the trace files from the DNA sequencing run, an accession number for the specimen in a natural history collection, and the name of the identifier. The very high-quality data standards demanded by the BOLD reduce the risk of species misidentifications.

While the resolving power of a single segment of the genome has so far been found insufficient to definitively reveal the identity of all species, DNA barcoding has proven exceptionally efficient at detecting and delimitating closely related species of various groups of insects and mites (Blaxter, 2004; Hebert et al., 2003b; Savolainen et al., 2005; Dasmahapatra and Mallet, 2006; Hajibabaei et al., 2007; Janzen et al., 2009; Ratnasingham and Hebert, 2013;

2 Non-metazoan barcode sequences (e.g., barcodes used to identify plants, fungi, and microbes) are found on other regions of the mitochondrial genome. Two segments of the chloroplast genome, rbcL and matK, were selected for land plants, a segment of the 16S ribosomal gene was selected for Bacteria and Archaea, and ITS was selected for Fungi.

3 There are currently about 2,000,000 described and an estimated 10–100 million still undiscovered species.

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Hubert and Hanner, 2015; Kress et al., 2015; Miller et al., 2016; Chroni et al., 2017; Pešić et al., 2017; Tyagi et al., 2017; Wilson et al., 2017; Gebiola et al., 2017; Kim and Jung, 2018).

The DNA barcode was conceptually developed using Sanger sequencing technology (Hebert et al., 2003a,b). In that technology, DNA is first extracted from an individual specimen, then the barcode sequence is amplified using PCR, and, ultimately, the PCR product is sequenced. Using Sanger sequencing, one barcode sequence is obtained per individual. Recent advances in DNA sequencing technology have increased the usefulness of molecular barcoding at an exponential rate. An emerging technology, next-generation sequencing (NGS), in contrast, utilizes parallel, simultaneous sequencing of DNA to obtain many sequences from one individual or even barcodes from multiple species in multiple-species samples. After the sequencing step, the species-level barcodes are separated from one another using bioinformatics. NGS thus generates multiple barcodes at the same time, keeping the costs down. This technology opens many exciting avenues for research, including diet and gut content analyses (Leray et al., 2013; Krehenwinkel et al., 2017) and host–parasitoid relationships (Lefort et al., 2017; Sigut et al., 2017; Kitson et al., 2019).

Importantly, NGS technologies also allow the sequencing of barcodes from archived museum specimens, something that was impossible to accomplish before NGS became available. The most complete resource of expertly identified arthropod specimens is found in natural history collections. Dried, preserved specimens in these collections have not heretofore been used to generate barcode sequences because their DNA breaks down into smaller fragments over time, limiting its utility when using the more antiquated Sanger sequencing technology. However, the NGS methodology relies on small fragments or regions of DNA prior to sequencing, making even old, pinned museum specimens suitable candidates for DNA extraction and sequencing (Haran et al., 2018; Sproul and Maddison, 2017). Because historical specimens contain low amounts of total DNA, extractions are highly susceptible to contamination. Facilities established to safely extract DNA from older specimens are often called 'Ancient DNA Laboratories,' and through them, NGS technology has opened the door for this new development to rapidly expand and enhance the COI reference library. This large increase in barcoding of specialist-identified specimens will provide a foundation for both identification and quantification of pests and beneficial insects in agriculture, ornamental horticulture, and the natural world in general.

At the same time, NGS technology is also transforming what we think of as a 'barcode sequence.' Because many copies of the mitochondrial genome exist in each cell, the entire mitochondrial genome, and often the entire ribosomal gene complex, is sequenced when using NGS methods. One of the

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limitations of modern molecular barcoding is that the relatively small fragment of COI that was selected as the animal barcode is not entirely unique to each species and, therefore, is unable to resolve the identity of every species. In the future, perhaps the entire mitochondrial genome and the entire ribosomal gene complex will serve as 'barcode regions' for animals, thereby increasing the resolving power of the diagnostic procedure.

DNA barcoding techniques have also been employed for survey work to estimate species richness of a particular sample (e.g. a sweep net sample or malaise trap sample). In an approach known as community metabarcoding, the barcode gene is simultaneously sequenced for all the specimens in the sample (Taberlet et al., 2012; Yu et al., 2012). Metabarcoding makes it possible to rapidly assess the species composition of a given locality (Dejean et al., 2012) and quantify the turnover of species through time and space (Giguet-Covex et al., 2014; Yu et al., 2012). Thus, a sweep net sample, when subjected to metabarcoding, will reveal which species are present in that sample and which are different from those identified from the previously taken samples.

Metabarcoding projects have sometimes attempted to estimate species abundance (Elbrecht and Leese, 2015; Tang et al., 2015; Thomas et al., 2016). Abundance estimations are complicated; they are limited by inherent biases in each step of the barcode sequence acquisition process. Although the science and technology remain unsettled, researchers are attempting to resolve these biases in the datasets and to develop algorithms needed to verify abundance using NGS technology.

5 Quantifying target organisms

Once detected and the identity (Latin binomial) assured, the grower must determine whether the pest is at a density high enough to severely stress the plants to the extent that the crop's earnings potential is negatively impacted.[4] This subject addresses one of the most fundamental underpinnings of the IPM paradigm: the concept of economic injury. The economic injury level (EIL) is a finite value for economically acceptable pest population levels (Stern et al., 1959). Ideally an EIL is a flexible figure, taking into account the amount of stress exerted on the crop by the pest, the crop's physiological growth stage, the physical conditions of the field, including weather factors and forecasts, the pest's developmental stage, the presence or absence of other pests and diseases that may exert additional stress on the crop, and economic and cultural factors such as the price the grower will receive when the harvest is sold and the quality and appeal of the harvested product (is the fruit blemished or somewhat misshapen and therefore will sell for less?).

4 That is the essence of question-based monitoring (Lindenmayer and Likens, 2010).

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As suggested above, not only is the population density of a pest pertinent to establishing an appropriate EIL, of significant importance is the growth stage of the crop and of the target pest represented in that density count. As an example, the velvetbean caterpillar, *Anticarsia gemmatalis* (Hubner) (Lepidoptera: Noctuidae), is a recognized key defoliator of soybeans in the central and eastern parts of the United States. When young, during its first instar, each caterpillar consumes very little (about 1 cm^2 over 3.6 days), but as it grows larger and more mature, it progressively consumes much more (about 72 cm^2 over 5 days during its sixth and last larval instar) (Herzog and Todd, 1980). The EIL, therefore, needs to account not only for the growth stage of the crop when the sampling occurs (leaf surface available over time and amount of leaf surface needed to grow efficiently during that life stage), but also the physiological growth stage of the pest under scrutiny.

Establishing a reliable EIL is not something a grower can easily do; researchers, working with population dynamic, stochastic, and simulation modelers, can best establish them by applying data derived from carefully designed, replicated field and laboratory experiments to algorithms that integrate the various components mentioned above. That population level deemed sufficient to appreciably reduce yields, the EIL, can then be adjusted to accommodate the cost of implementing a tactic to reduce the population below that level, along with the potential delay in implementation timing, providing a slightly altered population density based on a 'recommendation algorithm' (Ruesink and Onstad, 1994), often referred to as an action threshold, that is, that population level at which some pest population-damping action should be initiated. These concepts, as central as they are to developing or carrying out an IPM implementation plan, are not discussed further in this chapter; instead we refer you to Ruesink (1976, 1980), Ruesink and Onstad (1994), and Higley and Pedigo (1996) for background theoretical, mathematic, and recommendation algorithm formulations, and definitions backstopping arthropod sampling in IPM programs. Here, we consider the background causes of pest buildup and decline and how those factors might impact sampling theory and, consequently, appropriate algorithms; we also discuss how to determine if an established EIL or one of its derivatives (e.g., the action threshold) has been met.

Supervised control, an early and ongoing, practical, field-oriented component of the IPM effort, requires the grower, IPM practitioner, or 'scout' to take timely, measured samples of the arthropods in a confined cropping unit (i.e. the field or orchard) to determine the pest species present and assess if population levels are high enough to cause economic injury to the crop (IPM Level I of Kogan, 1998, 2013). Supervised control often targets specific pest species and, far too frequently, fails to take into account multiple pest species that are simultaneously present in the samples (i.e. their collective stress on the crop) (IPM Level II of Kogan, 1998, 2013; Peterson et al., 2018) and the

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