IRSTI 68.37.13 https://doi.org/10.26577/bb1072202614

Z.T. Syeda Bukhari

Johannes Gutenberg University Mainz, Mainz 55122, Germany
e-mail: dr.syedazanira@gmail.com

INNOVATIVE TECHNOLOGIES FOR THE MONITORING AND PROTECTION OF PLANTS: FROM MOLECULAR DIAGNOSTICS TO ARTIFICIAL INTELLIGENCE

Pests and pathogens cause losses estimated at 20–40% of global crop production, and the threat is intensifying under climate change and the globalisation of trade. Meanwhile, traditional methods of plant health monitoring, such as visual symptom inspection and pathogen culturing, are time-consuming, dependent on specialised expertise, and often unable to detect harmful organisms before significant damage occurs. The aim of this review is to provide an integrated account of the innovative technologies transforming the monitoring and protection of plants across three converging domains. The methodology is a structured narrative review of the international literature, organising the technologies into molecular diagnostics, digital monitoring, and artificial intelligence, and analysing their principles, applications, advantages, and limitations. The molecular technologies (PCR and its real-time and isothermal variants, and next-generation sequencing) identify harmful organisms from their nucleic acids with high sensitivity and specificity, increasingly at the point of need; the digital technologies (satellite remote sensing, unmanned aerial vehicles, and the agricultural Internet of Things) observe crops across scales from the region to the individual plant; and artificial intelligence (computer vision, machine learning, and predictive modelling) interprets the resulting data, diagnosing disease, identifying pests, and forecasting phytosanitary risks. The principal finding is that these technologies are complementary rather than competing approaches. Their integration into decision-support systems and digital platforms, together with emerging technologies such as CRISPR-based diagnostics and big data analytics, enables a more proactive, precise, and sustainable approach to plant protection that surpasses conventional methods. The value of the review lies in uniting domains usually treated in isolation, and its practical significance is its contribution to the early detection of threats and the reduction of crop losses essential to food security.

Keywords: plant disease diagnosis, molecular diagnostics, remote sensing, deep learning, integrated pest management.

З.Т. Саида Бухари

Иоганн Гутенберг атындағы Майнц университеті, Майнц 55122, Германия
e-mail: dr.syedazanira@gmail.com

Өсімдіктерді мониторингтеу мен қорғаудың инновациялық технологиялары: молекулалық диагностикадан жасанды интеллектке дейін

Зиянкестер мен патогендер ауыл шаруашылығы дақылдарының әлемдік өндірісінің 20–40 %-ына дейінгі шығындарына себеп болады және бұл қауіп климаттың өзгеруі мен сауданың жаһандануы жағдайында күшейе түсуде. Сонымен қатар, өсімдіктердің денсаулық жағдайын бақылаудың дәстүрлі әдістері, атап айтқанда симптомдарды визуалды анықтау және патогендерді өсіру, көп уақытты қажет етеді, арнайы сараптамалық білімге тәуелді және көбінесе зиянды организмдерді елеулі залал туындағанға дейін анықтауға мүмкіндік бермейді. Осы шолудың мақсаты – өсімдіктерді мониторингтеу мен қорғауды түбегейлі өзгертетін инновациялық технологияларды өзара байланысқан үш бағыт аясында кешенді түрде сипаттау. Зерттеудің әдіснамалық негізі халықаралық ғылыми әдебиеттерге жасалған құрылымдалған шолу болып табылады, оның барысында технологиялар молекулалық диагностика, цифрлық мониторинг және жасанды интеллект бағыттары бойынша жүйеленіп, олардың жұмыс істеу қағидаттары, қолданылу салалары, артықшылықтары мен шектеулері талданды. Молекулалық технологиялар (ПТР, оның нақты уақыттағы және изотермиялық нұсқалары, сондай-ақ жаңа буын секвенирлеу әдістері) нуклеин қышқылдары негізінде зиянды организмдерді жоғары сезімталдықпен және нақтылықпен анықтауға мүмкіндік береді. Цифрлық технологиялар (спутниктік қашықтықтан зондтау, ұшқышсыз ұшу аппараттары және ауыл шаруашылығындағы заттар интернеті) егістіктерді өңірлік деңгейден бастап жекелеген өсімдіктерге дейінгі әртүрлі кеңістіктік ауқымда бақылауға мүмкіндік береді. Жасанды интеллект әдістері (компьютерлік тосанитарлық тәуекелдерді болжау) алынған деректерді талдап, ауруларды диагностикалауды, зиянкестерді анықтауды және фитосанитарлық тәуекелдерді болжауды қамтамасыз етеді. Негізгі қорытынды – бұл технологиялар бір-бірімен бәсекелеспейді, керісінше өзара толықтырады. Оларды шешім қабылдауды қолдау жүйелері мен цифрлық платформаларға біріктіру, сондай-ақ CRISPR негізіндегі диагностика және Big Data технологиялары сияқты жаңа бағыттарды қолдану өсімдіктерді қорғаудың анағұрлым проактивті, дәл және тұрақты тәсілін қалыптастырады. Шолудың ғылыми құндылығы – әдетте жеке қарастырылатын ғылыми бағыттарды біріктіруінде, ал практикалық маңыздылығы – азық-түлік қауіпсіздігін қамтамасыз ету үшін аса маңызды болып табылатын қауіптерді ерте анықтауға және өнім шығындарын азайтуға қосатын үлесінде.

Түйін сөздер: өсімдік ауруларын диагностикалау, молекулалық диагностика, қашықтықтан зондтау, терең оқыту, зиянкестермен кешенді күрес.

З.Т. Саида Бухари

Майнцский университет имени Иоганна Гутенберга, Майнц 55122, Германия
e-mail: dr.syedazanira@gmail.com

Инновационные технологии мониторинга и защиты растений: от молекулярной диагностики до искусственного интеллекта

Вредители и патогены вызывают потери, оцениваемые в 20–40% мирового производства сельскохозяйственных культур, причём данная угроза усиливается под воздействием изменения климата и глобализации торговли. В то же время традиционные методы мониторинга здоровья растений, основанные на визуальном выявлении симптомов и культивировании патогенов, являются медленными, зависят от наличия специализированных экспертных знаний и зачастую не позволяют обнаружить вредоносные организмы до возникновения значительного ущерба. Целью настоящего обзора является комплексное представление инновационных технологий, трансформирующих системы мониторинга и защиты растений в рамках трёх взаимосвязанных направлений. Методологической основой исследования послужил структурированный обзор международной научной литературы, предусматривающий классификацию технологий по трём направлениям: молекулярная диагностика, цифровой мониторинг и искусственный интеллект, а также анализ их принципов действия, областей применения, преимуществ и ограничений. Молекулярные технологии (ПЦР, её варианты в режиме реального времени и изотермические методы амплификации, а также секвенирование нового поколения) обеспечивают высокочувствительное и высокоспецифичное выявление вредоносных организмов по их нуклеиновым кислотам непосредственно в месте проведения диагностики. Цифровые технологии (спутниковое дистанционное зондирование, беспилотные летательные аппараты и сельскохозяйственный интернет вещей) позволяют осуществлять наблюдение за посевами на различных пространственных уровнях – от региональных территорий до отдельных растений. Методы искусственного интеллекта (компьютерное зрение, машинное обучение и методы прогнозирования) обеспечивают интерпретацию получаемых данных, диагностику заболеваний, идентификацию вредителей и прогнозирование фитосанитарных рисков. Основной вывод исследования заключается в том, что указанные технологии являются взаимодополняющими, а не конкурирующими подходами. Их интеграция в системы поддержки принятия решений и цифровые платформы в сочетании с перспективными направлениями, такими как диагностика на основе CRISPR и технологии больших данных, обеспечивает более проактивный, точный и устойчивый подход к защите растений, превосходящий традиционные методы. Научная ценность обзора заключается в объединении направлений, которые обычно рассматриваются изолированно друг от друга, а его практическая значимость состоит в содействии раннему выявлению угроз и снижению потерь урожая, что имеет ключевое значение для обеспечения продовольственной безопасности.

Ключевые слова: диагностика болезней растений, молекулярная диагностика, дистанционное зондирование, глубокое обучение, интегрированная защита растений.

Abbreviations

PCR – polymerase chain reaction; qPCR – quantitative real-time PCR; RT-PCR – reverse-transcription PCR; LAMP – loop-mediated isothermal amplification; RPA – recombinase polymerase amplification; NGS – next-generation sequencing; HTS – high-throughput sequencing; CNN – convolutional neural network; UAV – unmanned aerial vehicle; IoT – Internet of Things; NDVI – normalised difference vegetation index; AI – artificial intelligence; DSS – decision-support system; COI – cytochrome c oxidase subunit I.

Introduction

The plants that feed the world are under continuous assault from a taxonomically diverse assemblage of harmful organisms – fungi and oomycetes, bacteria, viruses and viroids, nematodes, and insect pests – whose cumulative effect upon agricultural production is immense. An expert-based global assessment estimated mean yield losses to pathogens and pests of 21.5% for wheat, 30.0% for rice, 22.5% for maize, 17.2% for potato, and 21.4% for soybean, with the heaviest burdens falling upon the food-deficit regions least able to absorb them (Savary et al., 2019). The Food and Agriculture Organization estimates that up to 40% of global crop production is lost annually to plant pests and diseases, at a cost exceeding 220 billion United States dollars for plant diseases alone (FAO, 2021). These losses are not static: the changing climate is reshaping the geography of plant disease, with pests and pathogens observed to have shifted polewards at a mean rate of approximately 2.7 kilometres per year since 1960 (Bebber et al., 2013), and modelling projects further substantial reorganisation of the global pattern of infection risk through the present century (Chaloner et al., 2021).

Against this background, the timely and accurate detection of harmful organisms is of the first importance, for the early identification of a threat – before symptoms appear, before an epidemic develops, before an invasive species becomes established – may determine whether it is contained or allowed to spread. Yet the traditional methods of monitoring plant health are poorly suited to this task. The visual inspection of plants for the symptoms of disease depends upon the appearance of those symptoms, which may lag the infection by days or weeks, and upon the scarce expertise required to interpret them; the culture and the microscopic examination of pathogens are slow, demanding of specialised skill, and inapplicable to the many organisms that cannot be cultured; and the serological methods, though valuable, are frequently insufficiently sensitive to detect organisms present in small numbers or at early stages, and unable to discriminate closely related strains. These limitations – of speed, of sensitivity, of specificity, of scalability, and of dependence upon scarce expertise – have motivated the development of the innovative technologies that this review surveys.

The object of this review is the body of innovative technologies for the monitoring and protection of plants; its subject is their principles, applications, and integration. The aim is to provide an integrated account spanning the molecular, the digital, and the artificial-intelligence domains, which have hitherto frequently been treated in isolation, and to show that their integration – rather than the isolated application of any one – is the distinguishing achievement and the principal promise of the contemporary science of plant protection. The scientific significance of the review lies in this synthesis; its practical significance lies in the contribution of these technologies to the early detection of threats and the reduction of the crop losses upon which the security of the world's food supply depends.

The literature on the innovative technologies of plant protection has grown rapidly across three largely separate communities. In molecular diagnostics, foundational work established the polymerase chain reaction and, subsequently, its real-time quantitative form as the standard for sensitive and specific pathogen detection, while the introduction of loop-mediated isothermal amplification opened the way to field-deployable, instrument-light diagnosis, and the advent of high-throughput sequencing extended detection to the untargeted discovery of novel and unexpected agents. In digital monitoring, the literature on precision agriculture and remote sensing has documented the observation of crop condition across scales from the satellite to the unmanned aerial vehicle and the in-field sensor network. In artificial intelligence, a large body of work has demonstrated the diagnosis of plant disease from images by deep convolutional networks, the identification of pests, and the forecasting of phytosanitary risk.

The scientific contribution of these bodies of work is considerable, yet they have for the most part developed independently, each community advancing its own technologies with limited reference to the others. The principal gap that the present review addresses is the absence of an integrated account that unites the molecular, the digital, and the artificial-intelligence domains and that emphasises their complementarity and their integration – the union of the molecular identification of a pathogen with the digital mapping of its spread, and the interpretation of both by artificial intelligence – as the distinguishing feature and the principal promise of the contemporary field. This review draws together more than forty international studies across the three domains, analyses their respective contributions, and synthesises them into a unified account directed at that integration.

Several strands of this literature bear directly upon the present synthesis. The foundational work on DNA barcoding established that a short, standardised gene sequence can serve as a universal identifier of species, furnishing the conceptual basis for the molecular identification of pests and pathogens alike (Hebert et al., 2003). The reviews of molecular diagnostics have charted the progression from the enzyme-linked immunosorbent assay to the polymerase chain reaction and, latterly, to next-generation sequencing, documenting at each step gains in sensitivity, specificity, and breadth of detection (Boonham et al., 2014; Hariharan & Prasannath, 2021). In parallel, the surveys of artificial intelligence in agriculture have catalogued the rapid displacement of hand-designed image features by learned representations, and the consequent transformation of automated disease diagnosis (Kamilaris & Prenafeta-Boldú, 2018). What unites these separate literatures, and what this review seeks to make explicit, is that each addresses a different facet of a single problem – the timely, accurate, and scalable detection of threats to the plant – and that their convergence is therefore not incidental but necessary.

Materials and methods

This work is a structured narrative review of the international scientific literature on innovative technologies for plant monitoring and protection. The research question guiding the review was how molecular, digital, and artificial intelligence technologies function in plant protection, what their respective strengths and limitations are, and how their integration may provide a more effective and sustainable approach to plant protection than the isolated application of any single technology.

The review was conducted by identifying, across the three domains, foundational studies, landmark methodological papers, principal application studies, and relevant recent publications from the international peer-reviewed literature. The technologies were organised into three groups – molecular diagnostics, digital monitoring, and artificial intelligence – and analysed according to their underlying principles, applications in the detection and management of phytopathogens and pests, demonstrated performance, and limitations. The analysis subsequently addressed the integration of these domains through decision-support systems, digital platforms, and emerging technological frontiers. Throughout the review, technologies were compared with one another and with the traditional methods they supplement or supersede, and their performance was evaluated according to sensitivity, specificity, speed, scalability, cost, and suitability for field deployment.

The literature search was conducted using the Scopus, Web of Science, and PubMed databases, supplemented by Google Scholar. Peer-reviewed publications published primarily between 2016 and 2025 were included, while earlier landmark studies (2000–2015) were selectively incorporated to provide the conceptual and methodological foundations of molecular diagnostics, digital monitoring, and artificial intelligence applications in plant protection. Publications were selected based on their scientific relevance, methodological quality, topical relevance, and practical applicability to plant monitoring and protection technologies.

The assessment criteria were defined as follows: sensitivity referred to the ability to detect an organism present in low abundance or at an early stage; specificity referred to the ability to distinguish target organisms from closely related non-target organisms; speed referred to the time interval between sampling and obtaining results; scalability referred to the ability to extend applications from individual samples to field and regional levels; cost referred to the requirements for equipment, reagents, and specialised expertise; and field-readiness referred to the suitability of technologies for deployment outside laboratory conditions by non-specialist users.

Results and discussion

The review distinguishes three converging domains of innovative technology – molecular diagnostics, digital monitoring, and artificial intelligence – and their integration. Each is considered in turn.

1. Molecular technologies for the diagnosis of harmful organisms

The polymerase chain reaction (PCR) remains a workhorse for pathogen diagnostics. PCR can amplify minute amounts of DNA or RNA from a plant sample with high sensitivity and specificity; in practice, primers are designed to match unique pathogen genes, yielding a diagnostic fragment. PCR-based assays have been developed for bacteria (e.g. *Xanthomonas*, *Ralstonia* spp.), fungi (e.g. *Magnaporthe oryzae*), and nematodes. However, PCR requires purified nucleic acids and laboratory thermocyclers and is sensitive to inhibitors in crude samples (Lievens & Thomma, 2005; Boonham et al., 2014). PCR also cannot distinguish live from dead organisms and, by itself, does not quantify pathogen load (Lievens &

Thomma, 2005); furthermore, opening tubes for gel electrophoresis raises the risk of contamination, and PCR must often be followed by post-PCR analysis to confirm results (Boonham et al., 2014).

To address speed and throughput, quantitative real-time PCR (qPCR) uses fluorescent probes or dyes to detect amplification as it happens (Boonham et al., 2014). qPCR removes the need for gel runs and provides enhanced speed and sensitivity relative to conventional PCR (Boonham et al., 2014). It can quantify pathogen DNA, allowing threshold-based decision-making, and typical plant-virus assays are now multiplexed to test several viruses in one tube (Boonham et al., 2014). The trade-offs are higher equipment and reagent cost and the need for skilled operators (Hariharan & Prasannath, 2021). Overall, PCR and qPCR assays remain the gold standard for pathogen confirmation in diagnostic laboratories and are widely used in regulatory testing.

The strengths of the amplification methods rest upon the specificity with which a primer binds only its intended target and the sensitivity with which a single starting molecule may be multiplied into a detectable quantity. These properties allow the detection of a pathogen present in numbers far too small to produce a visible symptom or to be cultured, and the discrimination of closely related organisms – of one species of *Phytophthora* from another, or of a virulent strain from an avirulent one – that the older serological and microbiological methods could not achieve (Lievens & Thomma, 2005). Against these strengths must be set the requirement, in the conventional laboratory format, for extracted and purified nucleic acid, for a thermocycler, and for skilled operators, and the inability of a test designed for one organism to detect any other; the molecular methods are powerful precisely where the target is known and the question is its presence, less so where the task is the discovery of an unknown agent (Lievens & Thomma, 2005; Boonham et al., 2014).

Isothermal methods have emerged to bring PCR-like sensitivity to the field. Loop-mediated isothermal amplification (LAMP) is especially popular in plant pathology, using four or more primers and a strand-displacing polymerase to amplify DNA at a constant temperature of about 60–65 °C (Notomi et al., 2000). Ivanov et al. (2021) describe LAMP as more robust and sensitive than PCR, since it avoids thermocycling and tolerates simpler sample preparation. Reaction times are short (often 10–30 minutes), and amplification can be read by simple visual cues such as turbidity or colorimetric dyes (Ivanov et al., 2021). LAMP can be run on a simple heat block (Ivanov et al., 2021) and read by eye. Tomlinson et al. (2007) demonstrated early LAMP tests for the oomycete *Phytophthora ramorum* that worked without specialized instruments and allowed naked-eye detection, and Niessen and Vogel (2010) showed that placing a piece of infected barley seed directly into a LAMP mix could reliably detect the fungus *Fusarium graminearum*.

The practical benefits of LAMP are well documented: assays are usually faster than PCR, require a single temperature step, and tolerate inhibitors, so that they can amplify targets from crude plant sap, soil, or tissue without extensive DNA purification. For example, a LAMP test for *Phytophthora capsici* (pepper blight) could detect the pathogen from leaf samples using a simple 5–10 minute crude extraction (Ivanov et al., 2021), and portable LAMP devices now allow DNA-based diagnosis directly in the field (Ivanov et al., 2021). LAMP also has challenges: primer design is complex and error-prone (Ivanov et al., 2021), and the high amplification efficiency makes contamination control critical (Ivanov et al., 2021). Despite these issues, recent surveys list hundreds of LAMP assays targeting fungi, oomycetes, bacteria, viruses, and even pest insects (Ivanov et al., 2021; Hariharan & Prasannath, 2021).

LAMP is not the only isothermal method of importance. Recombinase polymerase amplification (RPA) amplifies DNA at a still lower and gentler temperature, of about 37 to 42 °C – close to body heat, so that in some implementations the warmth of the hand suffices – using a recombinase enzyme to drive the binding of primers in place of the heat of thermocycling (Babu et al., 2018). RPA is rapid, frequently yielding a result within twenty to forty minutes, tolerant of the inhibitors present in crude plant extracts, and readily coupled to a lateral-flow strip for a visual read-out, and it has been applied to the detection of a range of plant viruses, bacteria, and fungi in field-deployable formats (Babu et al., 2018; Ivanov et al., 2021). Its chief limitations are the comparative complexity and cost of its proprietary reagents and the care its primer and probe design demands; nonetheless, together with LAMP it constitutes the foundation of the field-deployable molecular diagnosis of plant disease, and the coupling of either method to a CRISPR-based read-out, considered below, is among the most promising recent developments (Babu et al., 2018; Ivanov et al., 2021).

High-throughput sequencing, often called next-generation sequencing (NGS), has revolutionized pathogen detection and surveillance. Unlike targeted assays, sequencing can survey all nucleic acids in a sample, identifying both known and novel agents and several pathogens simultaneously (Boonham et al., 2014). NGS technologies (Illumina, Oxford Nanopore, PacBio, and others) produce millions of reads in parallel, enabling comprehensive analysis of plant-associated microbiomes and pathogen populations; entire viral genomes are routinely assembled from infected plant samples, facilitating the surveillance of emerging variants. Metagenomic sequencing is especially powerful, for it can detect any pathogen – virus, bacterium, fungus, or nematode – present in a sample without prior knowledge, and Boonham et al. (2014) cite studies in which NGS was used to monitor pathogen evolution and disease spread. The data load and complexity are challenges, but the power of the technology is undisputed.

The power of sequencing for the discovery of the unknown deserves emphasis, for it marks a genuine departure from the targeted methods. A metagenomic analysis, sequencing the total nucleic acid of a sample without prior selection, can in principle detect any organism present – a virus never before described, a bacterium unexpected in the host, a mixed infection of several agents – and so serves not only to confirm a suspected diagnosis but to discover the cause of a disease whose agent is unknown (Boonham et al., 2014). This capacity has transformed plant virology in particular, where the sequencing of total RNA from a symptomatic plant routinely reveals the full complement of viruses it carries, and has been applied to the investigation of disease outbreaks, the certification of planting material, and the surveillance of quarantine pathogens. The obstacles are no longer chiefly those of generating the sequence, which has become rapid and inexpensive, but those of interpreting it: the assembly of the reads, their comparison against reference databases, and the distinction of the pathogen from the innocuous background demand bioinformatic skill and computational resource, and the very sensitivity of the method raises the question of how to interpret the detection of an organism whose role in disease is uncertain (Boonham et al., 2014).

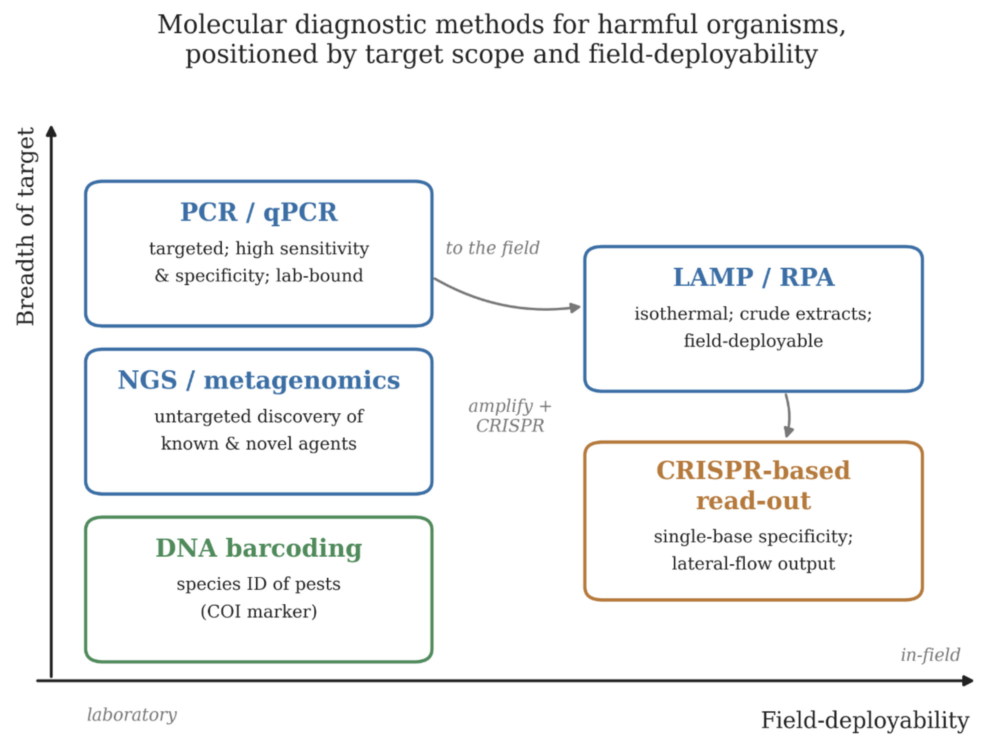
These tools have been applied broadly across pathogen types. In plant virology, multiplex RT-PCR and qPCR assays routinely detect viruses such as *Citrus tristeza virus*, and the methods of virus diagnostics have progressed from serological tests such as ELISA through PCR to next-generation sequencing (Boonham et al., 2014); bacterial pathogens such as *Ralstonia solanacearum* and *Xanthomonas oryzae* are detected by qPCR with high accuracy (Hariharan & Prasannath, 2021). In fungal and oomycete disease, numerous LAMP assays exist for pathogens such as *Phytophthora* spp., *Fusarium* spp., and *Puccinia* spp. (Tomlinson et al., 2007; Hariharan & Prasannath, 2021), and LAMP can detect wheat rust pathogens such as *Puccinia striiformis* one to two days after infection, before symptoms are visible (Ivanov et al., 2021). Insect pests are also diagnosed molecularly: Agarwal et al. (2020) designed a LAMP assay targeting the mitochondrial COI gene of the grape phylloxera (*Daktulosphaira vitifoliae*), and Agarwal et al. (2023) developed a LAMP test for the Asian citrus psyllid (*Diaphorina citri*). Emerging metabarcoding and metagenomic approaches can screen leaf, soil, or insect-trap samples for pathogens and pests at once, informing integrated pest management (Hebert et al., 2003; Boonham et al., 2014). In sum, molecular diagnostics now cover the full spectrum of plant pathogens and extend into insect-pest monitoring, enabling earlier and more specific detection than visual scouting.

The molecular identification of pests rests upon a foundation laid by DNA barcoding, the proposal that a short, standardised gene sequence – for animals, a region of the mitochondrial cytochrome c oxidase I gene – can serve as a universal marker for the identification of species (Hebert et al., 2003). Because this sequence varies little within a species but appreciably between species, it permits the assignment of an unknown specimen to its species by comparison against a reference library, and so the identification of a pest from a fragment, an egg, or an immature stage that morphology could not resolve. Upon this foundation the field-deployable assays for insect pests have been built, the LAMP tests for the grape phylloxera and the Asian citrus psyllid among them, which target conserved genes and return a species-level identification in minutes without the expertise of a taxonomist (Hebert et al., 2003; Agarwal et al., 2020). The same principle underlies the metabarcoding of environmental samples, in which the barcode regions amplified from the total DNA of a soil, water, or trap sample reveal the assemblage of species present, extending the molecular identification of pests from the individual specimen to the community (figure 1).

2. Digital technologies for the monitoring of plants

Whereas the molecular technologies diagnose harmful organisms from individual samples, the digital technologies of monitoring observe crops continuously and across large areas, detecting the signs of stress, disease, and infestation and mapping their spatial pattern. They rest upon the principle that the radiation reflected and emitted by vegetation carries information about its physiological condition – healthy vegetation absorbing strongly in the red, where chlorophyll captures light, and reflecting strongly in the near-infrared, with an abrupt transition, the "red edge," between them – so that the alterations of the spectral signature that accompany stress may be detected, frequently before symptoms are visible to the eye.

Figure 1
Molecular diagnostic methods for the detection of harmful organisms, positioned by the breadth of their target and their field-deployability



The detection of plant disease by imaging sensors has become a discipline in its own right, drawing together precision agriculture and plant phenotyping, and resting upon the careful study of how the optical properties of a leaf change as infection alters its pigments, its cell structure, and its water content (Mahlein, 2016). These changes are not uniform across the spectrum but concentrated in particular regions, and their pattern differs from one disease to another: the pigments that absorb in the visible region decline as chlorosis and necrosis develop; the internal structure of the leaf, which governs reflectance in the near-infrared, is disrupted as tissue is destroyed; and the water content, which governs absorption in the shortwave infrared, falls as the plant's water relations are disturbed. Because each pathogen produces its own characteristic progression of these effects, a sufficiently detailed measurement of the spectral signature can not only detect that a plant is stressed but begin to identify the cause, distinguishing, for example, the net blotch, the rust, and the powdery mildew of barley by the differing shapes of their reflectance curves (Mahlein, 2016; Terentev et al., 2022).

Satellites carrying remote-sensing instruments observe the crops of the entire world from orbit, providing a synoptic view across regions that no other platform can match. Several systems are of particular importance for agriculture: the Landsat programme, continued by Landsat 9 (launched in 2021), provides imagery at 30-metre resolution with a half-century unbroken record; the Sentinel-2 mission of the European Copernicus programme provides imagery at 10- to 20-metre resolution across thirteen spectral bands – including several red-edge bands – with a five-day revisit interval and free availability; and commercial constellations of small satellites provide imagery at a few metres' resolution with near-daily revisit. The information in reflected radiation is commonly distilled into vegetation indices, of which the normalised difference vegetation index (NDVI) is the most widely used; it rises with the density and vigour of healthy vegetation and falls as vegetation becomes stressed, and its variation across a field or its change over time reveals the spatial and temporal pattern of crop condition (Drusch et al., 2012; Sishodia et al., 2020). The principal contribution of satellites lies in the detection and mapping of stress over large areas; their limitations – a spatial resolution that may be too coarse to resolve the early, patchy onset of disease, a revisit interval that cloud may extend, and the difficulty of distinguishing the specific cause of a detected stress – are addressed, in part, by the aerial and ground-based methods (Sishodia et al., 2020).

The applications of satellite remote sensing in precision agriculture are correspondingly broad, encompassing the assessment of crop biomass and vigour, the estimation of yield, the mapping of soil and water status, the guidance of variable-rate application of inputs, and the detection of the stress imposed by disease, drought, and nutrient deficiency (Sishodia et al., 2020). The limitations of the satellite are, however, equally real. The spatial resolution of the freely available systems may be too coarse to resolve the early, patchy onset of disease within a field; the revisit interval, though short, may be extended by cloud, which obscures the optical view of the surface; and the vegetation indices, while sensitive to the presence of stress, are frequently unable to distinguish its specific cause, since drought, disease, and nutrient deficiency may depress the same index in similar ways. NDVI in particular saturates over dense canopies, losing sensitivity where the vegetation is most vigorous, and declines only after the reduction of chlorophyll is already advanced, so that it may register a problem only once it is well established. These limitations are addressed, in part, by the finer resolution and the richer spectral and thermal information of the aerial and ground-based methods (Sishodia et al., 2020; Mahlein, 2016).

Considered together, the platforms of remote sensing form a continuum of scale, each suited to a different grain of observation, and the art of their application lies in their combination. The satellite surveys the region and the season, detecting the broad patterns of stress and furnishing the long record against which change may be judged; the drone surveys the field and the day, resolving the patch and the plant and responding to the immediate question; the in-field sensor surveys the point in continuous time, recording the microclimate within the canopy where infection begins. No one of these displaces the others, and the most complete picture of the state of a crop is assembled by drawing upon all three – the satellite to direct attention, the drone to localise and characterise, the sensor to monitor the conditions that govern the course of disease (Drusch et al., 2012; Sishodia et al., 2020; Farooq et al., 2019). The integration of these complementary scales of observation, and of the optical, spectral, and thermal information they gather, is among the principal achievements of digital crop monitoring and a foundation of the integrated protection considered later in this review.

Between the satellite and the in-field sensor lies the unmanned aerial vehicle (UAV), or drone, which observes the crop from low altitude with a detail and a flexibility that neither satellite nor ground sensor can provide, resolving features of the order of centimetres and so detecting the early, localised onset of disease that the coarser resolution of a satellite would miss. Drones carry payloads of multispectral, hyperspectral, and thermal sensors, and the images they capture are commonly assembled by photogrammetry into a single high-resolution map of the field. Multispectral imaging measures reflectance in a few broad bands, sufficient to compute the principal vegetation indices; hyperspectral imaging measures reflectance in hundreds of narrow, contiguous bands, permitting the detection of subtle and specific spectral features that distinguish one cause of stress from another and that may reveal disease at an early stage, the red-edge region being of particular value; and thermal imaging detects the canopy temperature governed chiefly by transpiration, serving as a sensitive indicator of the water stress and disturbances of water relations that accompany many diseases, frequently before visible symptoms appear. Studies of the cereal rusts and of many other diseases have shown that hyperspectral data, combined with machine learning, can distinguish diseased from healthy plants before symptoms are visible to the eye (Terentev et al., 2022).

The hyperspectral approach has been developed into a sophisticated body of technique, in which the hundreds of measured wavebands are reduced, by the methods of statistics and machine learning, to the few that best discriminate a given disease, and combined into spectral disease indices tailored to particular pathogens (Mahlein et al., 2018). By these means, studies of the cereal rusts and of many other diseases have shown that hyperspectral data can detect infection at an early stage, identify which disease is present, and quantify its severity. The transfer of these methods from the controlled conditions of the laboratory and the glasshouse to the variable conditions of the field remains, however, a substantial challenge, for the changing illumination, the mixed background, and the natural variability of the crop all complicate the spectral signal; the bridging of this gap between laboratory and field is among the central practical problems of sensor-based phytopathology (Mahlein et al., 2018; Terentev et al., 2022).

The unmanned aerial vehicle has, in the space of a decade, passed from a research curiosity to a practical instrument of crop monitoring, and the reasons for its rise are instructive. It occupies a niche of resolution and flexibility that neither the satellite nor the ground sensor can fill: flying below the cloud that obscures the satellite, it is unconstrained by the revisit schedule of an orbit and may be dispatched whenever and wherever it is needed; flying above the crop, it surveys in a single flight an area that would take a person days to walk; and resolving features of the order of centimetres, it discerns the early and localised onset of disease that the coarser satellite would average away. Its payload may be chosen to the task – a multispectral camera for the routine computation of vegetation indices, a hyperspectral sensor for the discrimination of specific diseases, a thermal camera for the detection of water stress – and the imagery it gathers is assembled by photogrammetry into a map of the whole field, within which the distribution of stress may be read at a glance (Mahlein et al., 2018; Terentev et al., 2022). Its limitations are those of endurance, of payload, of the regulation of airspace, and of the labour of flying and of processing the imagery, but within these bounds it has become a central instrument of precision crop protection.

Thermal imaging deserves particular notice, for it exploits a different physical principle from the optical methods and so furnishes information complementary to theirs. The temperature of a leaf is governed largely by transpiration, the evaporation of water from its surface, which cools it as perspiration cools the skin; when a plant closes its stomata in response to water stress, or when disease disrupts its water relations, transpiration falls and the leaf warms. Because this response frequently precedes any visible symptom and any change in the optical reflectance, a thermal camera can in principle reveal stress at a very early stage, and the canopy temperature, measured against the temperature of the air, has been used as an indicator of water status and of the disturbances that accompany many diseases (Mahlein, 2016). The interpretation of thermal imagery is complicated, however, by the many factors other than disease that influence leaf temperature – the ambient temperature, the humidity, the wind, the radiation of the sun – so that thermal data are most powerful when combined with the optical and the spectral, each sensor compensating for the blind spots of the others (Mahlein et al., 2018).

The continuous acquisition of data from the field is accomplished increasingly through the agricultural Internet of Things (IoT) – the extension of network connectivity to the sensors and devices distributed throughout the agricultural environment. An IoT system comprises a perception layer of sensors measuring temperature, humidity, leaf wetness, soil moisture, and other variables; a communication layer, frequently a low-power wide-area network such as LoRaWAN that transmits small quantities of data over several kilometres at very low power; and an application layer that stores, processes, and acts upon the data. Networks of microclimate sensors supply the data required by the disease-forecasting models that predict the risk of infection and guide the timing of protective measures, while automated monitoring systems – among them the camera-equipped "smart traps" that capture images of the insects they catch and transmit them for automatic identification and counting – replace the laborious manual inspection by which pest populations have traditionally been monitored, providing a continuous and timely picture of pest abundance and distribution (Liakos et al., 2018; Wolfert et al., 2017; Soussi et al., 2024).

The architecture of such systems is commonly described in terms of layers: a perception layer of sensors measuring temperature, humidity, leaf wetness, soil moisture, light, and other variables; a network layer that conveys the measurements, frequently by a low-power wide-area network such as LoRaWAN that transmits small quantities of data over several kilometres at very low power, suiting the dispersed and power-constrained conditions of the farm; and an application layer that stores, processes, and acts upon the data, increasingly with the support of cloud computing and data analytics (Farooq et al., 2019). The connection of this architecture to cloud computing and big-data analytics is what converts a scattering of measurements into a coherent picture of the state of the crop, and its integration supports the broader enterprise of precision agriculture, in which inputs are applied not uniformly but in proportion to local need, reducing both cost and environmental burden (Farooq et al., 2019; Soussi et al., 2024).

The choice among the imaging methods involves a characteristic trade-off between the richness of the spectral information and the practicality of its acquisition and analysis. Multispectral imaging, measuring a few broad bands, yields data that are compact, readily processed, and sufficient for the computation of the principal vegetation indices, and it is for these reasons the most widely deployed; its limitation is that the few broad bands cannot resolve the fine spectral features by which one cause of stress is distinguished from another. Hyperspectral imaging, measuring hundreds of narrow and contiguous bands, captures the full shape of the reflectance curve and so permits the detection and identification of specific diseases, but at the cost of instruments more expensive and delicate, data far larger and more complex, and analyses that demand the methods of machine learning to extract the few informative bands from the many (Mahlein et al., 2018; Terentev et al., 2022). The history of sensor-based phytopathology may be read, in part, as the search for the point of balance between these competing virtues, and as the gradual descent of hyperspectral capability from the laboratory toward the affordable field instrument (Mahlein, 2016; Mahlein et al., 2018).

The normalised difference vegetation index, for all its ubiquity, is but one of a family of vegetation indices, and its limitations have driven the development of others suited to particular purposes. The index saturates over dense canopies, losing its sensitivity precisely where the vegetation is most vigorous, and it responds to a fall in chlorophyll only once that fall is well advanced, so that it may register a disease only after the damage is done; it cannot, moreover, distinguish the cause of a depression in greenness, which drought, disease, and nutrient deficiency may all produce (Sishodia et al., 2020). The remedies are indices tuned to other features of the reflectance: those exploiting the red edge, the steep transition between the red and the near-infrared, which respond to chlorophyll content with greater sensitivity and at an earlier stage; those exploiting the shortwave infrared, which respond to the water content of the canopy and so to the water stress that accompanies many diseases; and the spectral disease indices, derived from hyperspectral data, which combine the particular wavebands that best distinguish a given pathogen (Mahlein et al., 2018; Sishodia et al., 2020). The proliferation of these indices reflects the central lesson of the field, that no single measure captures the whole of a plant's condition, and that the detection and identification of disease are best served by the combination of complementary measures (Mahlein, 2016; Mahlein et al., 2018).

A recurring consequence of all these technologies is the generation of data in quantities that exceed by far the capacity of any person to examine, and the resulting deluge is at once the great opportunity and the great challenge of digital monitoring (Singh et al., 2016). A single drone flight may yield thousands of images; a network of in-field sensors may report continuously through a growing season; a satellite constellation may revisit a field every few days for years. The value latent in such data is realised only through the methods of data assimilation, feature extraction, and machine learning that turn raw measurement into useful knowledge, and the development of these methods has therefore advanced in step with the sensors themselves, the one without the other being of little use (Singh et al., 2016; Liakos et al., 2018). It is at this junction – where the data of the digital sensors meet the methods of artificial intelligence – that the monitoring of plants passes into their intelligent interpretation, the subject of the section that follows.

3. Artificial intelligence in plant protection

The digital technologies generate data far exceeding the capacity of any person to examine, and the conversion of this data into useful knowledge – the detection of disease, the identification of pests, the prediction of outbreaks – is accomplished increasingly by artificial intelligence (AI), and above all by the methods of machine learning, which learn from data to perform tasks formerly requiring human expertise. The visual diagnosis of plant disease by computer has been among the most successful applications, transformed over the past decade by deep learning, which dispenses with the manual design of image features, learning instead, directly from labelled images, both the features relevant to the task and the rule for classifying them. The networks best suited to this task are the convolutional neural networks (CNNs), whose design exploits the spatial structure of images, building from the raw image a hierarchy of features of increasing abstraction (Kamilaris & Prenafeta-Boldú, 2018).

The training of such networks from scratch demands very large collections of labelled images and great computational resources, and the dominant practical technique is therefore transfer learning, in which a network already trained upon a vast general collection of images is adapted, by further training upon a smaller collection of plant images, to the particular task of disease diagnosis (Kamilaris & Prenafeta-Boldú, 2018). The application of machine learning across agriculture has, more broadly, grown rapidly and now encompasses not only the diagnosis of disease but the prediction of yield, the detection of weeds, the management of soil and water, and the recognition of animal and plant stress, drawing upon the full range of learning methods, from the support-vector machine and the random forest to the deep neural network (Kamilaris & Prenafeta-Boldú, 2018; Liakos et al., 2018).

The accuracy attained by convolutional networks under controlled conditions has been remarkable. A landmark study applied convolutional networks to the PlantVillage dataset – over 54,000 images of leaves spanning 38 classes of crop and disease – and reported, for the best network trained by transfer learning, an accuracy exceeding 99% in assigning an image to the correct class (Mohanty et al., 2016). Subsequent studies have repeatedly reported accuracies of comparable magnitude across larger collections and a succession of architectures (Ferentinos, 2018), and systematic comparisons of the principal network architectures have found the deeper and more modern of them, such as the densely connected networks, to attain accuracies approaching the ceiling of the benchmark datasets, in one careful comparison reaching 99.75% (Too et al., 2019). These results require an important caution, however: the high accuracies were attained largely upon images captured under controlled and uniform conditions, and the same networks, applied to images captured under the variable conditions of the field, have frequently performed far less well – the landmark study itself found accuracy falling to around a third upon images from different sources (Mohanty et al., 2016). The narrowing of this gap, through the assembly of representative collections of field images, through transfer learning and data augmentation, and through the retention of human oversight, is the central practical challenge of the field. The opacity of the deep network, which cannot of itself explain its judgements, is a further limitation that the methods of explainable artificial intelligence seek to address.

The distinction among the principal types of task that these networks perform is worth drawing, for it bears upon their application. Classification networks assign a whole image to a category, answering the question of which disease, if any, a leaf displays; detection networks locate and delimit the objects of interest within a larger image, drawing a box about each diseased region or each insect; and segmentation networks classify the image pixel by pixel, delineating exactly the diseased area and so permitting the quantification of severity. Each type has its place in plant protection, and the literature documents the rapid development of all three, with a clear trend toward models that are at once more accurate, smaller, and faster, and so better suited to deployment upon the modest hardware of a field device (Liu & Wang, 2021). These tasks may be situated within a broader scheme of the decision cycle of plant stress phenotyping, which distinguishes the identification of a stress, its classification by type, the quantification of its severity, and the prediction of its development – a framework that has helped to organise the application of machine learning across the whole of crop research and breeding, not the diagnosis of disease alone (Singh et al., 2016).

The forecasting of disease repays a closer look, for it brings together the data of monitoring and the understanding of biology in a manner that exemplifies the integration this review commends. The process-based models, grounded in the biology of the pathogen, compute from the recorded course of temperature, humidity, and leaf wetness the progress of infection through its stages – the germination of a spore, the penetration of the host, the development of the lesion, the production of the next generation of spores – and so predict, from the weather alone, the periods of greatest risk (González-Domínguez et al., 2023). The empirical models, by contrast, learn the relationship between conditions and disease from historical records, and the methods of machine learning have enlarged the scope and the accuracy of this approach, integrating the many variables that bear upon risk and discerning patterns too complex for a person to formulate (González-Domínguez et al., 2023; Liakos et al., 2018). The two traditions are complementary, the mechanistic understanding lending interpretability and generality to the data-driven model, the data correcting and refining the mechanistic one, and their combination, fed by the real-time data of the agricultural Internet of Things, promises forecasts grounded at once in biology and in the conditions actually obtaining within a particular crop (González-Domínguez et al., 2023; Farooq et al., 2019).

A recurring theme across all these applications is the gap between performance under controlled conditions and performance in the field, and the recognition of this gap has reshaped the priorities of the field (Barbedo, 2016). The difficulty is not chiefly the design of the network but the data upon which it is trained: a model trained upon clean images of detached leaves against a uniform background learns features that do not transfer to the cluttered, variably lit, multiply infected scenes of the real crop. The remedies are several – the assembly of large datasets of genuine field images, the augmentation of training data to embrace the variability of real conditions, the use of transfer learning to make the most of limited labelled data, and the careful validation of models upon images genuinely independent of those used in training – but the gap has not been closed, and the prudent deployment of these systems retains a place for human judgement (Barbedo, 2016; Mohanty et al., 2016).

The opacity of the deep network – its tendency to deliver a judgement without disclosing the grounds upon which it rests – is a limitation of particular consequence in a domain where the cost of error is a misdirected or omitted treatment. A network may attain high accuracy upon a benchmark yet rest its decisions upon features irrelevant to the disease, such as the lighting or the background of the training images, and so fail unpredictably upon new data. The methods of explainable artificial intelligence seek to open this black box, among them the techniques that highlight the regions of an image upon which a classification turns, allowing a human expert to judge whether the network attends to the symptom or to some artefact; such visualisation both builds the trust necessary for adoption and exposes the failures of reasoning that bare accuracy conceals (Singh et al., 2016; Barbedo, 2016). The retention of human oversight, informed by these methods, is widely held to be the prudent course in the present state of the art.

Underlying all these considerations is the question of data, which has come to be seen as more decisive than the choice of network architecture. The training of a deep network demands a large collection of images, each labelled with the correct diagnosis, and the quality of the resulting model is bounded by the quality and representativeness of this collection. The early successes of the field rested upon collections of images captured under controlled conditions, which proved a frail foundation for application in the variable field; the present effort is therefore directed at the assembly of large datasets of genuine field images, embracing the diversity of crop, of disease stage, of lighting, and of background that the real world presents, and at the techniques – data augmentation, transfer learning, and the generation of synthetic images – by which the most may be made of the labelled data available (Liu & Wang, 2021; Singh et al., 2016). The labelling of these images, which requires expert knowledge and great labour, remains a principal bottleneck, and the sharing of curated datasets among researchers is accordingly of considerable value to the field (Mohanty et al., 2016; Liu & Wang, 2021).

The same methods serve for the recognition of insect and other animal pests, though the task is more demanding, since pests are often small, diverse, variable through their life cycle, and set against a complex and cluttered background (Barbedo, 2016). For the location and counting of pests within an image, the object-detection networks are employed, and among them the single-stage detectors of the YOLO family are favoured for their speed, which permits detection in real time and so suits the processing of the continuous stream of images from a camera trap (Liu & Wang, 2021). The camera-equipped smart trap, which captures and transmits images for automatic identification and counting, provides a continuous monitoring of pest populations far less laborious than the manual inspection of traps, and a particular value lies in the early detection of invasive and quarantine pests, whose interception before establishment is the foremost object of phytosanitary security (Kamilaris & Prenafeta-Boldú, 2018; Liu & Wang, 2021).

The automatic monitoring of insect pests illustrates with particular clarity the convergence of the digital sensor and the artificial intelligence that interprets its output. The traditional monitoring of pest populations rests upon traps that must be visited, emptied, and their catch identified and counted by a person – a labour so demanding that it is performed infrequently and over few sites, yielding a picture of pest abundance that is coarse in both space and time. The camera-equipped smart trap replaces this labour with automation: it photographs the insects it catches, transmits the images for analysis, and applies an object-detection network to identify and count them, returning a continuous and spatially detailed record of pest abundance without the visit of a person (Liu & Wang, 2021). The value of such monitoring is greatest for the invasive and quarantine pests whose early interception is the object of phytosanitary security, for a network of smart traps may detect the first arrival of a threat in time for its containment, and the same network, reporting continuously, may track the progress of an established pest and inform the timing of its control (Kamilaris & Prenafeta-Boldú, 2018; Liu & Wang, 2021). The challenges are those of the reliable identification of small and similar species under field conditions, and of the power and connectivity that a remote trap requires, but the principle is established and its adoption is spreading.

The broader application of machine learning across agriculture, surveyed in the recent literature, encompasses not only the diagnosis of disease but the prediction of yield, the detection of weeds, the management of soil and water, and the recognition of animal and plant stress, and it draws upon the full range of learning methods, from the support-vector machine and the random forest to the deep neural network (Liakos et al., 2018). The value of these methods grows with the volume and variety of the data available to them, and the convergence of machine learning with the data streams of precision agriculture – the imagery of satellites and drones, the measurements of in-field sensors, the records of weather and management – is therefore mutually reinforcing: the data give the models something to learn from, and the models give the data their meaning (Wolfert et al., 2017; Liakos et al., 2018). It is in this convergence that the forecasting of phytosanitary risk finds its firmest foundation.

Beyond the detection of organisms already present, artificial intelligence supports the forecasting of phytosanitary risk – the prediction of where and when disease and pests will appear. The forecasting of disease rests upon the principle that its development depends upon the conjunction of a susceptible host, a virulent pathogen, and a favourable environment, the favourable conditions being specifiable and monitorable. Two broad traditions of modelling have developed over the past half-century. The process-based, or mechanistic, models embody the biology of the pathogen in mathematical descriptions of its life cycle, computing from the course of weather the progress of infection; the data-driven, or empirical, models, including those of machine learning, learn the relationship between conditions and disease from historical records without explicit representation of the underlying biology (González-Domínguez et al., 2023).

The evolution of these models over the last fifty years has been driven, as a recent and authoritative review observes, by three advances: in the sensors and automatic data-collection technology that supply the environmental inputs, in the instruments and methods of botanical epidemiology that furnish the biological understanding, and in the data analytics and computer science that turn data into prediction (González-Domínguez et al., 2023). The wheat rusts and apple scab serve as the classic case studies of this progress, the former illustrating the development of empirical models from weather data, the latter the refinement of process-based models grounded in the biology of the pathogen. The two traditions are increasingly combined, the mechanistic understanding constraining and informing the data-driven model, and the whole is increasingly fed by the real-time data of the agricultural Internet of Things, so that a forecast may rest upon the conditions actually obtaining within a particular crop rather than upon the average conditions of a region (González-Domínguez et al., 2023; Farooq et al., 2019).

The forecasting of disease and pests attains its fullest expression in the early-warning systems operated at regional, national, and international scales, which unite the data of monitoring with the models of prediction and deliver their conclusions to those who must act upon them. A novel and powerful source of data for such systems is furnished by the aggregation of the diagnoses gathered by mobile applications: when many growers photograph and identify the diseases of their crops through a shared application, the accumulated reports constitute a continuously renewed map of the occurrence of pests and diseases, from which their spread may be tracked in near real time and the regions of emerging risk identified. In this way the same artificial intelligence that diagnoses a disease from a photograph contributes, through the aggregation of its diagnoses, to the surveillance of disease across a whole region – an instance of the convergence of the individual and the collective, the local and the global, that characterises the contemporary science of plant protection (Kamilaris & Prenafeta-Boldú, 2018; González-Domínguez et al., 2023).

4. Integration of technologies and emerging frontiers

The three domains surveyed above are powerful in themselves, but their fullest power is realised in their integration – the union of the molecular and the digital, of the laboratory and the field. The molecular technologies furnish the identification of a pathogen by its sequence and the characterisation of its population; the digital technologies furnish the detection and mapping of disease across a region and the prediction of its spread; and their integration yields a management more powerful than either alone – the deployment of the resistance that molecular analysis identifies in the places that digital analysis shows to be at risk, and the anticipation of the breakdown of resistance from molecular monitoring combined with digital monitoring of spread. This integration depends upon cloud platforms that provide storage and computation as a service, upon the bioinformatic systems and reference databases that analyse molecular data, and upon the interoperability of data from different sources, whose achievement through common standards is among the principal challenges.

The most complete expression of this integration is the digital twin – a virtual replica of a physical crop or farm, continuously updated from the data of sensors, imagery, and weather, within which the state of the crop may be monitored, its future simulated, and the consequences of an intervention explored before it is undertaken (Pylianidis et al., 2021). Constructed from the same elements as the broader smart farm – the sensors and devices of the agricultural Internet of Things, coordinated through cloud computing – the digital twin draws these elements together into a single dynamic model, and so offers, in principle, a means of integrating the molecular, the digital, and the predictive into one coherent representation. Its realisation in agriculture is at an early stage, and the challenges are considerable: the complexity of the living system to be modelled, the volume and heterogeneity of the data to be assimilated, and the questions of data ownership and privacy that the gathering of so much information raises (Pylianidis et al., 2021; Wolfert et al., 2017). The broader integration of agricultural data rests, in turn, upon the big-data infrastructure of smart farming – the cloud platforms, the analytics, and the data standards through which the streams from many sources are combined – and upon the resolution of the attendant questions of governance, interoperability, and the distribution of the value that the data create (Wolfert et al., 2017).

The digital twin merits closer consideration, for it represents the most ambitious form of the integration of agricultural data. In its fullest conception, a digital twin is not merely a static model of a crop but a living virtual counterpart, continuously updated from the streams of sensor, image, and weather data, so that its state tracks the state of the real crop and may be interrogated in its stead. Within such a model the consequences of an action – the application of a treatment, the alteration of an irrigation schedule – may be simulated before the action is taken, and the future of the crop projected from its present condition, so that management becomes anticipatory rather than reactive (Pylianidis et al., 2021). The construction of a digital twin draws upon every technology surveyed in this review: the sensors and devices of the agricultural Internet of Things to supply its data, the cloud computing to coordinate them, the machine learning to interpret them, and, in principle, the molecular diagnostics to ground its representation of the crop's health in the identity of the organisms present (Pylianidis et al., 2021; Farooq et al., 2019). Its realisation in agriculture remains at an early stage, impeded by the complexity of the living system to be modelled and by the volume and heterogeneity of the data to be assimilated, but it offers a vision of the fully integrated, anticipatory protection of plants toward which the field is tending.

The integration of agricultural data acquires its value, for the protection of plants, only in the decisions it informs, and the systems that convert integrated data into guidance are the decision-support systems (DSS). A DSS gathers the data of monitoring, applies the relevant forecasting models and analyses, and presents to the grower not raw data but actionable guidance – a warning that conditions favour a disease, an assessment of the risk a pest presents, or a recommendation for intervention – thereby embodying the anticipatory, knowledge-based management that integrated pest management commends. Such systems are delivered increasingly through the smartphones and digital platforms that growers already command; the mobile application for disease diagnosis exemplifies this delivery, diagnosing disease from a photograph and returning advice within seconds, and, through the aggregation of its users' observations, generating maps of disease occurrence.

The value of the decision-support system rests upon the quality and timeliness of the data that feed it, and it is here that the convergence of the technologies surveyed in this review is most directly useful. The microclimate data of the agricultural Internet of Things furnish the forecasting models with measurements made within the crop itself; the imagery of satellites and drones, interpreted by artificial intelligence, furnishes the spatial pattern of stress; and the molecular diagnostics furnish the specific identification of the pathogen present. A decision-support system that draws upon all three can offer guidance more precise, more timely, and more reliable than any single source could support, and the delivery of such guidance through the smartphone places it within reach of growers who command no other computing resource (Farooq et al., 2019; Wolfert et al., 2017; Liakos et al., 2018). The realisation of this promise, however, depends upon the interoperability of the several data streams and upon the trust of the grower in the guidance offered, neither of which can be taken for granted.

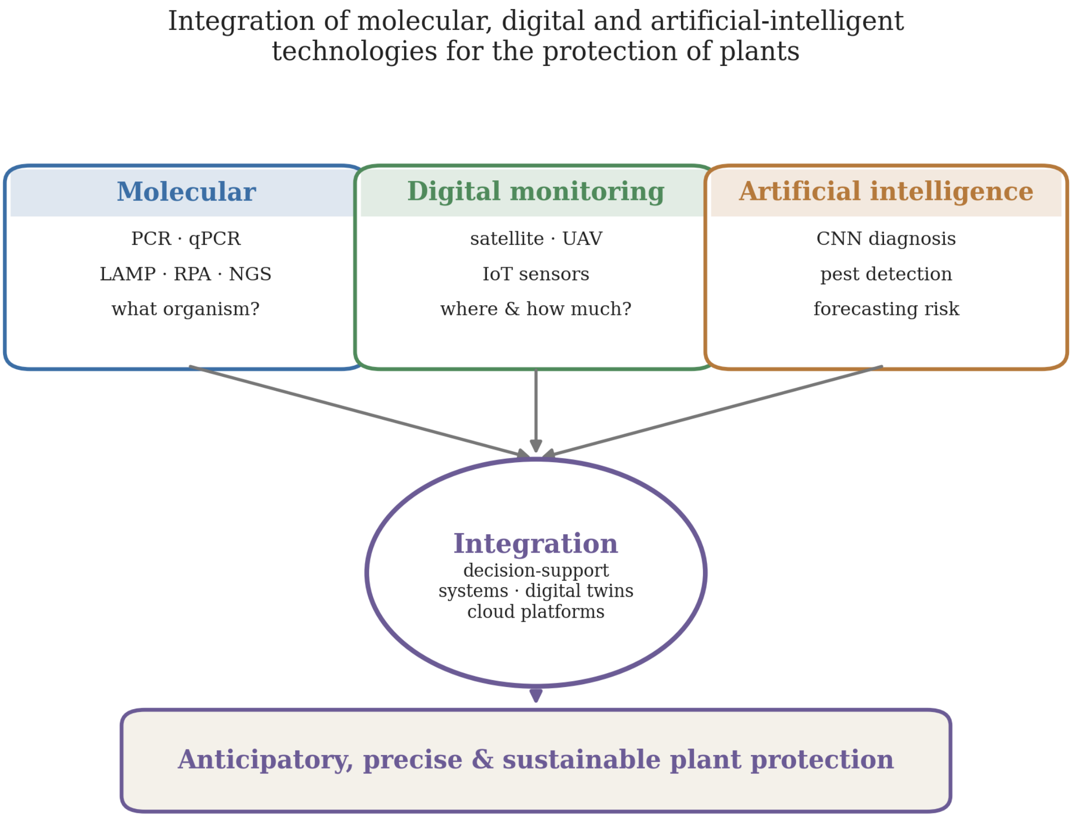
Among the most promising emerging frontiers is the application of CRISPR/Cas systems to diagnosis. Certain CRISPR-associated enzymes, when programmed to recognise a target sequence, exhibit upon binding a "collateral" cleavage of reporter molecules that may be coupled to a fluorescent or visual read-out; this principle underlies the SHERLOCK platform, based on the RNA-targeting enzyme Cas13 (Gootenberg et al., 2017), and the DETECTR platform, based on the DNA-targeting enzyme Cas12a (Chen et al., 2018). Combined with an isothermal amplification step, these methods attain a sensitivity reaching a few molecules, a specificity fine enough to discriminate a single-nucleotide difference, and a read-out simple enough to be read on a lateral-flow strip, uniting sensitivity, specificity, speed, and simplicity to a degree few other methods attain (Pozharskiy et al., 2025). Further frontiers include the analysis of the big data generated by monitoring and molecular technologies, whose aggregation across many farms and seasons reveals patterns invisible in any single dataset, and the digital platforms – increasingly augmented by conversational assistants founded upon recent advances in language models – that carry the power of these technologies into the hands of the world's growers.

The application of the CRISPR/Cas systems to plant diagnostics is itself a rapidly developing field, and recent reviews catalogue a growing number of assays directed at the viruses, bacteria, and fungi of crops, frequently coupled to an isothermal amplification step and read out upon a lateral-flow strip in the manner of a pregnancy test, so that a molecular diagnosis of laboratory sensitivity may be obtained in the field without laboratory equipment (Pozharskiy et al., 2025). The principal remaining obstacles are the need, in most current assays, for a separate amplification step that complicates the workflow, and the requirement that an assay be designed and validated anew for each target; the development of amplification-free assays and of multiplexed assays able to detect several pathogens at once is an active direction of research (Pozharskiy et al., 2025). Together with these molecular advances, the maturing of the digital platforms – the cloud services, the analytics, and the conversational interfaces through which the power of these technologies is delivered – promises to lower further the barrier between the laboratory and the field, and to place the means of precise diagnosis and timely decision in the hands of those who work the land.

The integration of these technologies is nowhere more consequential than in the surveillance of disease and the management of invasive and quarantine threats, where the union of the molecular and the digital yields a capability neither could supply alone. The molecular methods identify, with certainty and at the level of the strain, the organism present in a sample; the digital methods map, across a region, the distribution of the symptoms that organism produces and predict, from the conditions, the course of its spread; and artificial intelligence, drawing the diagnoses of many growers into a single picture, tracks in near real time the advance of a threat across a landscape (Boonham et al., 2014; González-Domínguez et al., 2023; Liu & Wang, 2021). The early detection that this integration affords – the interception of an invasive pest before it establishes, the recognition of a new disease before it spreads – is the foremost object of phytosanitary security, and the contribution of the technologies surveyed here to that object is among the strongest arguments for their adoption (Hebert et al., 2003; Boonham et al., 2014).

The realisation of this integrated capability is, however, attended by challenges that are as much organisational and economic as they are technical. The data of the several technologies are generated in different formats, by different instruments, under different standards, and their combination into a single coherent picture demands an interoperability that common standards alone can secure (Wolfert et al., 2017). The infrastructure of storage, computation, and analysis that the integration requires represents a cost that not every grower can bear, and there is a real risk that the benefits of these technologies accrue disproportionately to the large and well-resourced, widening rather than narrowing the inequalities of agriculture (Wolfert et al., 2017; Soussi et al., 2024). The questions of who owns the data that the sensors gather, who may use them, and who captures the value they create are unresolved, and bear directly upon the trust without which growers will not adopt the systems offered them (Wolfert et al., 2017; Pylianidis et al., 2021). The imperative that the benefits of these technologies be made accessible to all the world's growers, and not the smallholders who stand to gain the most, is therefore not a peripheral concern but central to the realisation of their promise (Farooq et al., 2019; Soussi et al., 2024) (figure 2).

Figure 2
Integration of the three domains of technology into an anticipatory protection of plants



The frontier of these technologies continues to advance, and several directions of development promise to extend their reach. The analysis of the big data accumulated by monitoring and molecular technologies, aggregated across many farms and many seasons, reveals patterns of disease and pest occurrence invisible in any single dataset, and so supports a surveillance and a prediction of phytosanitary risk at scales hitherto unattainable (Wolfert et al., 2017). The maturing of the molecular methods – the coupling of isothermal amplification to CRISPR-based read-outs, the development of amplification-free and multiplexed assays – promises to bring the sensitivity and specificity of the laboratory to the field in ever simpler and cheaper formats (Pozharskiy et al., 2025; Babu et al., 2018). And the digital platforms through which these technologies are delivered grow steadily more capable and more accessible, so that the diagnosis, the forecast, and the recommendation may be placed within reach of growers who command no specialist resource. The cumulative effect of these advances is to lower the barrier between the laboratory and the field, and to distribute the means of precise and timely protection more widely than before – a trajectory that, if its attendant challenges of cost, access, and trust can be met, promises a protection of the world's crops at once more effective and more sustainable than the methods it supersedes (Wolfert et al., 2017; Soussi et al., 2024).

Taken together, the results of this review indicate that the molecular, digital, and artificial-intelligent technologies are complementary rather than competing, each addressing limitations of the others: molecular diagnostics supplies the specific identification that imaging cannot, imaging supplies the spatial coverage that point sampling cannot, and artificial intelligence supplies the interpretation that the volume of data demands. Their integration, compared with the isolated application of any one, yields an anticipatory and precise protection of plants that is at once more effective, more economical, and more sustainable than the traditional methods it supersedes – a conclusion consistent with the trajectory of the field reported across the international literature.

Conclusion

This review set out to provide an integrated account of the innovative technologies transforming the monitoring and protection of plants, examining their principles, applications, and limitations by a structured review of the international literature. Its principal results may be summarised as follows. The molecular technologies of diagnosis – PCR and its real-time and isothermal variants, and next-generation sequencing – identify harmful organisms from their nucleic acids with a sensitivity, specificity, and speed beyond the reach of traditional methods, and increasingly at the point of need. The digital technologies of monitoring – satellite remote sensing, unmanned aerial vehicles, and the agricultural Internet of Things – observe crops across scales from the region to the individual plant, detecting the signs of stress frequently before they are visible. Artificial intelligence interprets the resulting data, diagnosing disease and identifying pests with an accuracy approaching that of the human expert and forecasting phytosanitary risk. And the integration of these technologies, in decision-support systems and digital platforms, converts their combined knowledge into actionable guidance.

The principal conclusion is that these technologies are complementary rather than competing, and that their integration – the union of the molecular and the digital, of deep understanding and powerful instrument – yields an anticipatory, precise, and sustainable protection of plants superior to the methods it supersedes. This integrated protection contributes to the early detection of threats and the reduction of crop losses, and so to the development of scientific knowledge in plant protection and to the security of the world's food supply under a changing climate. Its realisation depends, however, upon the resolution of real challenges: the narrowing of the gap between performance under controlled conditions and in the field; the improvement of the reliability, robustness, and affordability of the technologies; the resolution of questions of data governance and cybersecurity; and, above all, the imperative that the benefits be made accessible to all the world's growers, including the smallholders who stand to gain the most. The prospects for the practical implementation of these technologies are bright, and the principal direction for further research is the deepening of their integration –the development of the standards, the interoperability, and the unified systems through which the molecular, the digital, and the artificial-intelligent may be brought together into a single, intelligent enterprise of plant protection.

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Information about the author:

Syeda Bukhari Zanira Tahir – researcher at Johannes Gutenberg University Mainz (Mainz 55122, Germany, e-mail: dr.syedazanira@gmail.com).

Автор туралы мәлімет:

Саида Бухари Занира Тахир – Иоганн Гутенберг атындағы Майнц университетінің зерттеушісі (Майнц 55122, Германия, e-mail: dr.syedazanira@gmail.com).

Сведения об авторе:

Саида Бухари Занира Тахир – исследователь Майнцского университета имени Иоганна Гутенберга (Майнц 55122, Германия, e-mail: dr.syedazanira@gmail.com).