

in biological systems are discussed in detail. While patterns observed in biological systems are due to complex processes of molecular sorting, flux and segregation, the authors outline how these can be described by principles of physics. Illustrations convey the essence of the review.

Bagnat *et al.* describe how generated hydrostatic pressure can act as a morphogenetic force in 'Morphogenetic roles of hydrostatic pressure in animal development'. Physical principles of fluid transport in epithelial tubes and control of fluid secretion are discussed. Mathematical models of lumen formation with figures explaining the models should help cell biologists appreciate the approach. Clearly, there is an increasing interest in explaining events in cell and developmental biology using principles of physics.

Tissue homeostasis is the subject of two reviews but with different emphases. In 'Tissue homeostasis and non-homeostasis: from cell lifecycles to organ states', O'Brien, with an emphasis on epithelial organs, covers different aspects of cell cycle life. While the sub-headings in sections are informative, only two figures appear in the introduction. More illustrations would have benefitted the readers, considering the complexity of the topic. The review by Scott-Solomon and Hsu entitled 'Neurobiology, stem cell biology and immunology: an emerging triad or understanding tissue homeostasis and repair' is on understanding tissue homeostasis and repair via neurobiology, stem cell biology and immunology. Figure 1 and table 1 give excellent overviews of the crosstalk between components of the 'triad'. The illustrations essentially summarize the contents of the review.

Two reviews discuss how imaging techniques are used to essentially 'see' development. In 'Organoid imaging: seeing development and function', Keshara *et al.* outline how organoids are generated, followed by a section describing imaging methods used in organoid research. However, there is only one figure that shows examples of images from different techniques and, in the end, a figure that shows how different types of microscopes can be used for various organoid studies. Since the area is relatively new, more illustrations in the various sections, at least one in each section, would have helped in appreciating the power of imaging techniques in organoid research. Mihlan *et al.* discuss in 'Surprises from intravital imaging of the innate immune response' dynamic immune cell behaviour obtained from modern intravital

microscopy (IVT). The techniques described encompass two-photon laser scanning and spin-disc confocal microscopy combined with fluorescent reporter animals. The authors focus on the innate immune cell types: macrophages, microglia, neutrophils, dendritic and mast cells in mice. The overview of cellular dynamics revealed by IVT is summarized for each of the five cell types with schematic illustrations. Some images obtained by IVT would have helped non-specialists appreciate the power of IVT.

In summary, while the reviews give a wealth of information, some have very few figures or summary tables, particularly as one of the objectives of ARDCB is to cater to non-specialists, students and teachers.

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This year's *Annual Review of Phytopathology (ARP)* provides a comprehensive overview of the latest research and developments in the field of plant pathology, including nematodes, covering a wide range of topics that are critical to understanding and managing plant diseases. It consists of 17 articles, and each one maintains the pace with constantly evolving technology and stays up-to-date with the latest research. This *ARP* consists of research and developments in the field of host-pathogen interactions, genetic resistance, climate change and integrated pest management. The review is essential for researchers and students in plant pathology, plant science, agriculture and related disciplines. It provides a broad overview of the state of the art in phytopathology and highlights the latest advances in understanding plant diseases and their control.

It is believed that in the absence of a resistance host, early pathogen detection and

disease diagnosis in the field could be an invaluable asset for disease management programmes, which will help reduce crop losses worldwide. Although several diagnostic approaches are developed and handed over to the public, it is imperative to consider that any laboratory protocol would be performed in the field by non-scientists who have to perform nucleic acid extraction and amplification together.

The review by Botella encompasses a detailed coverage of the latest research on plant disease diagnostics, including the development of new molecular techniques for detecting and identifying plant pathogens. The review also covers some challenges and opportunities for deploying these diagnostic tools in the field, including the need for effective training and capacity building. The review suggests a hand-held DC-powered loop-mediated isothermal amplification (LAMP) protocol in which dipsticks-based purification of the nucleic acid and Arduino-based platform 'Diagnostic droid' are used to incubate and monitor LAMP amplification reactions.

Studying history enables us to develop a better understanding of the world in which we live, and it is always fascinating to know about the plant-microbe interactions, as plants are deeply connected not only to rich microbial environments in the soil but also to endophytic microbes within their tissues and epiphytic microbial community. The insight into this area unravels the impact of agriculture development mainly due to changes in agricultural practices and other environmental shifts, including climate change, on the spread of plant diseases. Malmstrom *et al.* thoroughly discuss the methodology for examining past plant-pathogen interactions using herbarium samples and indicate that a potential solution can be designed for reducing pathogen impact in agriculture. The information also improves our ability to predict and prevent plant diseases and enhances our knowledge of the photodiode and its importance in plant-microbe interactions.

Virus-based biological control agents (BCAs) offer a safer and more sustainable disease management strategy by lowering the virulence of fungal pathogens and also enhancing the hosts' resistance to fungal diseases. In this review, Wagemans *et al.* have detailed the use of virus-based BCAs against the population of major pests like fungi, bacteria, viruses and insects. The classic example of the success and failure of mycovirus-based management of chestnut blight in Europe and the United States

through hypovirulent strains of *Cryphonectria parasitica* is well known. Utilization of baculovirus, densovirus, etc. as BCAs against insect pests, are also reviewed comprehensively. This review discussed regulatory hurdles for the use of viruses as host-specific BCAs. The cost of registering such BCAs is not affordable compared to the small potential market. As a result, viruses are underutilized for managing the host population. They also suggest new approaches to virus-based BCAs that rely not only on the direct biocidal virus component but also on the complex ecological interactions between viruses and their hosts. In another review on mycovirus, Kondo *et al.* describe the diversity of mycovirus in terms of genome organization, lifestyles and replication cycles, which will help develop new antiviral strategies against fungal diseases. The discovery of new virus lifestyles and genome organizations can also aid in developing new biotechnological tools for manipulating fungi. Additionally, recent studies on virome analyses and Next Generation Sequencing (NGS) of mycovirus can also be utilized in other fields of virology and microbiology.

Climate change is another critical factor influencing the distribution and severity of plant diseases. The review explores the latest research on the impacts of changing weather patterns on plant pathogens, as well as the potential implications for crop productivity, food security and ecosystem services. The review also highlights some of the opportunities for managing plant diseases through artificial intelligence in the context of climate change. Artificial intelligence is expected to play a crucial role in mitigating the challenges posed by emerging diseases. Artificial Intelligence (AI) can help in the prediction and prevention of pathogen outbreaks by analysing large amounts of data and identifying patterns that humans may overlook. Moreover, it is also believed that AI can support research translation into products useful for stakeholders, with feedback from stakeholder testing going back to research programs. Garrett *et al.* have discussed the effects of climate change on pathogen emergence and how artificial intelligence can help to mitigate it. The authors explain that climate change affects the interactions between pathogens, hosts and the environment, leading to new disease outbreaks. However, the article does not delve into specific case studies or examples of successful implementation. The challenges associated with using AI are also not dis-

cussed. Nonetheless, it provides a useful starting point for further research and discussion on this important topic.

Xylem-limited pathogens are evolved to live in the xylem, which has mostly dead plant cells with low nutrient availability and high water flow. Once established, they change the conditions in the xylem to multiply and cause disease. Fuente *et al.* explained the mechanism of pathogen survival by adapting to the specific and restrictive environment by reducing the genome size by getting rid of genes that are not necessary for their survival in the xylem. These pathogens are difficult to control because conventional control methods, such as fungicides or bactericides, do not reach the specific niche of the pathogen. The review of xylem-limited pathogens helps us to understand the nature of these microorganisms, their adaptation to life, and mechanisms to cause disease in the plants. This knowledge can be used to develop new strategies to manage plant diseases caused by xylem-limited pathogens. Additionally, understanding the genetic changes in these pathogens as they adapt to the xylem environment can provide insights into the evolution of microorganisms in general.

Lewis *et al.* present a comprehensive overview of the anatomy, physiology and biochemistry of phloem, indicating that the phloem provides a protected environment for plant pathogens to live and multiply, away from the plant's defense mechanisms. Additionally, the authors also throw light on the role of phloem-specific proteins, such as P-proteins and phloem lectins, in phloem/pathogen interactions. Pathogens like *Candidatus Liberibacter* spp., phytoplasmas and spiroplasmas cause damage to the crop by inhibiting the flow of nutrients, which leads to a decline in plant health. These pathogens form aggregates or biofilms or produce callose, a type of carbohydrate which gets accumulated inside the phloem tissue and impedes normal nutrient transport. Since most phloem pathogens are vectored, they are not exposed to any applied chemicals and are therefore difficult to control. By understanding the mechanisms by which these pathogens interact with the phloem, researchers may be able to develop new strategies for controlling their spread and mitigating their impact on agriculture. Nevertheless, the authors also suggest that the mechanisms by which phloem pathogens interact with the host plant are poorly understood, and more research is needed to develop effective control strategies.

Four critical topics are covered in this series of annual reviews on plant–nematode interactions. These interactions can significantly impact plant growth, development, and disease resistance. For instance, the interactions between root–knot nematodes (RKN) and plants have been studied for over a century. Rutter *et al.* highlight the complex parasitic interactions of RKN and the host in which nematode alters the patterns of plant gene expression to form a feeding site. Additionally, the review also explores the role of new molecular tools in understanding the biological mechanisms during infection of RKN and the manipulation of host mechanisms by pests. In another review, Mitchum and Liu explain the role of the diverse array of peptide effectors in mediating pathogenic and symbiotic interactions between the host and nematode. To counter the nematode attack, the host develops several resistance mechanisms depending upon the timing and localization of the resistance response associated with a particular resistance gene. Researchers have utilized host plant resistance to manage nematodes because of their long persistence as unhatched eggs encased in cysts in the soil and resistant to chemical treatments. Bent highlights the mechanisms underlying soybean cyst nematode (SCN) resistance in soybean. The success of the *rhg1-b* locus against resistance to SCN has been well documented and deployed on millions of hectares of farmlands. However, the SCN population evolves gradually to single gene resistance and compels the breeders to hunt for other SCN resistances like quantitative trait loci (QTL) to develop new resistant varieties. The author suggests integrated methods like quarantine, crop rotation, and host resistance to control cyst nematodes. Siddique *et al.* explain the interaction between the host and two groups of plant-parasitic nematodes: root–knot nematodes and cyst nematodes. The study deals with the cascade of defence response against the pest and the counteraction of nematodes against the host defences. The paper also indicates promising avenues to develop novel management tools against plant-parasitic nematodes.

Genetic resistance is also a critical tool in managing plant diseases. The annual review provides an overview of the latest advances in breeding for disease-resistant plant varieties, including identifying resistant genes and developing new breeding techniques. The review also explores some of the challenges and limitations of genetic resistance, such as the potential for pathogen

adaptation and the need for effective deployment strategies. With the recent improvement in the mechanism behind host resistance and pathogen virulence, *Brassica napus*–*Leptosphaeria maculans* are on the verge of becoming a model organism for studying plant–pathogen associations. Borhan *et al.* have highlighted the importance of resistance genes in response to pathogen elicitors and discuss the recent advances in genomic technologies for a clear understanding of this host–pathogen interaction. The information could serve as a torch bearer for other researchers working on this crop to develop new strategies for managing blackleg disease in canola, thereby improving crop yields.

Bacterial diseases are a constant threat to crop production globally. Bacteria use an array of effectors for their survival on the host. These effector molecules are responsible for disease manifestation. For instance, *Pseudomonas syringae* employs suites of type III secreted effector proteins (T3SE), which play an important role in pathogenesis. In this Annual Review, Bundalovic-Torma *et al.* have covered the diversity of *P. syringae* effectorome, which has evolved over the years to avoid the host immune detection mechanism. However, effectors like T3SE proteins can also serve as avirulent factors when detected by host-resistant mechanisms. Researchers harness these mechanisms in the form of resistant varieties, which are used in integrated disease management, including crop rotation, selection of pathogen-free seeds and transplants, sanitation practices, biological control, and chemical control. Sharma *et al.* provide an overview of the durable, sustainable, accessible and environmentally friendly technology for bacterial disease management. The latest developments in cultural, chemical, biological and plant activators are reviewed in detail. The review also explores the shortcomings of existing

practices and dissects recent advances in bacterial management, including disease resistance through genome modification. The authors highlight the importance of developing novel bacterial disease management tactics to meet the food demand for the growing global population.

One of the key topics covered in this year's Annual Review is facilitating reforestation through plant microbiomes. The multitude of tree-associated microbes (fungi, bacteria, and archaea) play an important role in the survival of planted and naturally regenerating seedlings, long-term forest carbon capture and conserving forest biodiversity. The review also explores the significance of mycorrhizal fungi in the tree microbiome, their importance in plant nutrition and the structure and function of forest soils. Busby *et al.* suggest studying the variation in new forests ranging from monoclonal plantations to highly diverse forests and naturally regenerated or surviving old forests to understand how greater initial diversity can shorten the period new plantings spend as carbon sources before becoming carbon sinks.

Cereals are a high source of food energy and have served as the principal component of the human diet for thousands of years. Among the cereals, wheat, maize, rice, and, to a lesser extent, sorghum and millets have played a major role in shaping human civilization. Globally, the human population derives daily caloric intake directly from cereal grain consumption. The crops are challenged by the attack of yellow dwarf disease, causing significant yield losses in wheat, barley, rice, maize, oat, rye-grass, etc. The ubiquitous nature of associated viruses is also found in grassland ecosystems, which influence community dynamics. Peters *et al.* highlight the extent and impact of yellow dwarf viruses in diverse plant communities along with the vector behaviour of virus transmission. The

review also explores the epidemiology of yellow dwarf viruses with reference to climate change, including rising temperatures, drought, elevated CO₂ concentration, etc. This disease is caused by two types of yellow dwarf viruses (barley yellow dwarf virus and cereal yellow dwarf virus), which share common biological properties like phloem limitation, replication machinery, *cis*-acting signals and obligate aphid transmission. Miller and Lozier explain the reclassification of both viruses based on their different genomes. Besides, they also review in detail the viral protein functions and their interactions with the host and vector, replication mechanisms of viral and satellite RNAs, and complex gene expression strategies. This review will help in designing viral disease management in the field.

Finally, the annual review of phytopathology provides a comprehensive overview of the most recent research and developments in crop protection. It focuses on the challenges and opportunities for managing plant diseases in the context of global food security and environmental sustainability, as well as critical insights into plant–pathogen biology, epidemiology and control. The authors, reviewers, and editors who helped to make this publication deserve great appreciation. Their dedication and hard work attest to the significance of this field of study and its contribution to global sustainability.

We hope this annual review will be useful to anyone interested in plant pathology and its contributions to food security and environmental sustainability.

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