

**Annual Review of Phytopathology, 2018.** Jan E. Leach and Steven E. Lindow (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, California 94303-0139, USA. Vol. 56. x + 677 pages. ISSN: 0066-4286 ISBN: 978-0-8243-1356-2. Price: US\$ 112.00.

The editors have crafted this volume with 28 reviews dealing with cutting edge research themes in plant pathology to mine the latest developments in the background of understanding reached in the past and project the outlook for future research. Themes presented range from emerging issues and new developments to a variety of questions in plant pathology with a bias on biochemical and physiological, molecular, genetic, immunological and cell biological aspects.

The insect vectored *Xylella fastidiosa*, a xylem-bound bacterial pathogen is capable of causing diseases on a number of economically important plants causing a variety of diseases. The early outbreaks of this pathogen on grapevine in the United States and in Brazil on citrus in epidemic proportions affected the grape wine and citrus-based industries. This has resulted in intensification of research and understanding of the pathogen–insect vector–plant interactions. The reemergence of this pathogen striking olive plantations in Italy and subsequently spreading to France and Spain has become a concern of this decade. Sicard *et al.* provide a comprehensive state-of-the-art report on diseases caused by *X. fastidiosa* that might help identify gaps in knowledge for further research towards effective disease management.

Ceresini *et al.* present a detailed account of the deadly devastating South America-originated wheat blast. The disease has already made inroads into Bangladesh through accident and inadvertent introduction of imported seeds with contaminations carrying the blast pathogen. These authors consider the pathogen as *Pyricularia graminis-tritici*, and is distinct from *P. oryzae*, causal agent of the globally important rice blast. Crucially important reassessment of the species status of wheat blast fungus based on genomic analysis has appeared in a parallel<sup>1</sup> and in a post-review<sup>2</sup> publications. These authors refute the species assignment of wheat blast pathogen as a new

phylogenetic species, *Pyricularia graminis-tritici* and consider wheat blast pathogen populations as an evolutionarily different lineage of *Pyricularia oryzae* other than the rice blast lineage. Based on this, it has become possible to speculate and warn<sup>2</sup> that the possible evolution of new threats arising in the form of emergence of aggressive strains of *P. oryzae* from the sexual recombination of *Triticum* strains with sexually fertile *Oryza* strains capable of infecting both these two vital crops, in regions where these two crops are grown in rotation, cannot be ruled out. Taxonomic error carried over in this review with the pathogen identification would block this realization of the anticipatory possible evolutionary changes in pathogen virulence stressing the need to take necessary precautions for avoiding future catastrophe in the cultivation of these two vital crops having major influence on global food security, particularly in the rice–wheat belt track of the Himalayan foothills presenting sexually fertile *Oryza* strains of this pathogen.

Beattie *et al.* probe the role of photosensing in the biology of plant-associated bacteria and fungi. Microbes access light both on the plant surface and within plant tissues. Light sensing through photoreceptor proteins in plant microbes is often coupled with sensing other environmental signals. Among the different forms of light, far-red-light influences the pathogenic ability and blue light influences the symbiotic properties of beneficial plant symbionts. However, studies on the molecular pathways involved in light sensing by microbes are in their early stages, while in the context of plant–microbe interactions they are very limited. Nevertheless, these projections could help stimulate new kinds of light-based research in the field of plant pathology. Soft-rots caused by several genera of Gram negative and Gram positive bacteria are common to vegetables and ornamental crops. These bacterial pathogens also cause blackleg of potato, foot rot of rice and bleeding canker of pear. Charkowski points out that despite the growth of knowledge regarding the etiology, ecology of the pathogen, epidemiology of the disease, molecular aspects of pathogen virulence generated with potato pathosystem, there has been no advancement in disease containing measures practiced by farmers. Further, in the absence of resistance genes, the

author pins hopes on development of genetically modified crops capable of producing antimicrobial peptides as the only feasible way for managing this disease complex. The experience of myrtle rust and its impact on native ecosystems affecting native oil and food industries in Australia emphasizes the importance for involvement from environmental agencies in biosecurity, preparedness, response and resourcing in the management of already established invasive environmental pathogens (Carnegie and Pegg). Additionally, the need for preventing the establishment of such diseases through pre-border, border and post-border biosecurity strategies, of which quarantine is a subset, is emphasized. Strengthening the nematology-oriented pest management and the needed capacity building for research in this area along with favourable policy directions in the sub Saharan Africa for containing the crop losses due to nematode disorders is raised by Coyne *et al.* Oxalic acid production by *Sclerotinia sclerotiorum* through which the pathogen modulates the cellular environment in its favour has been considered to be the determinant of virulence. Xu *et al.* bring forth the gaps in oxalate-dependent concept to reveal that the creation of acidic level of the hydrogen ion concentration in the infected zone favours the disease development rather than the oxalic acid *per se*. Further, it is emphasized that there is a need to identify the pH sensing or regulation mechanism in this host–pathogen interaction is more important in the virulence of the pathogen. The use of the terms pathogenicity and virulence complementary to each other in this review some what intermingles both qualitative and quantitative pathogen traits. However, future studies might help understand the distinct differences between pathogenicity and virulence in this pathosystem.

The never ending molecular warfare or arms race between pathogens and their host is a natural phenomenon for the survival of the participants in the host–parasite relations. The exertion of strong selection pressures mutually by each other drive rapid and drastic changes in their genomes. In this tug-of-war, many of the staple crops developed for disease resistance become vulnerable to the emergence of new pathogen strains with modified virulence strategies. The genome-based approaches offer opportunities to

associate host genes with the pathogen genes for the development of sustainable crops. Keller *et al.* trace the developments in the largest and most complex genomics of wheat and its pathogens and discuss implications for practicing pathogen-informed wheat breeding strategies. The need for international collaboration to isolate all the resistance genes and the respective avirulence genes of the pathogen and to enhance the knowledge on pathogen diversity and evolution on a global scale are stressed. Both beneficial and pathogenic prokaryotic and eukaryotic microbes have evolved strategies to enter and colonize plants. Since the birth of two aspects of concept on immunity put forth by Janeway<sup>3</sup> and Matzinger<sup>4</sup>, a large volume of information on innate immunity has accumulated particularly in the last two decades. Plants, in the absence of animal adaptive immunity, have evolved multiple layers of pathogen sensing mechanisms through different classes of host-encoded proteins, referred to as pattern recognition molecules (PRMs) or the receptor proteins. To live or die, reprogramming the host physiology is a necessity for microbial symbionts. One of the layers of host immunity, operates on the cell surface based on the perception of the conserved microbial structures or their fragments (pathogen components) soon after initiation of infection process providing a basal and general defense (pattern triggered immunity, PTI). The other functions intracellularly in the cytosol and can also act as transcriptional regulators in the nucleus consequent to the recognition of pathogen-secreted effector molecules (polypeptides, small molecules and even small RNAs) presenting a strain-specific robust form of defense. These molecular interactions determine either disease or activation of immunity. Sanchez-Vallet *et al.* examine the evolution and biology of the virulence (effector) genes in filamentous pathogens and emphasize the need for their overall knowledge together with the pathogen's ability for adaptation for effective disease management. Certain differences exist in virus-plant interactions, though viruses release its own macromolecules (proteins and nucleic acids) during infection. Leisner and Schoelz connect the virus-host plant interactions with the effectoromics of bacterial, filamentous fungal and oomycete, and nematode pathogens, one of the most

intensely studied aspects to understand the causal features of disease or resistance manifestation modulated by the effectors. The subject has been dealt in light of the differences in life cycles between the viruses, being acellular and the other pathogen categories, and the fact that the virus proteins execute a range of functions from virus replication cycle to suppression of host defenses dictated by the smaller genome size. Plants have evolved cytoplasmic immune receptors to counter the virulence activity of pathogen effectors. A majority of these belong to NLR (nucleotide-binding oligomerization domain (NOD)-like receptors, also known as nucleotide binding-leucine rich repeat) protein family. These receptors intracellularly monitor directly or indirectly the pathogen-secreted virulence factors and effector proteins which have evolved primarily to aid pathogen to cause disease by modifying the host cellular functions. In contrast, a subset of them interact with NLRs to trigger immunity (effector-triggered immunity, ETI). Most of the cloned resistance genes encode NLR proteins. Selection of host resistance for diseases to our advantage exert pressure on the pathogen to enter into molecular arms race with the pathogen. Despite advancements in our understanding of the NLR biology, Monteiro and Nishimura point out the deficiency in knowledge on the basic mechanistic aspects of the NLR functions, essential for engineering disease resistance, remain limited. The authors examine the structural, functional and genomic diversity of plant NLR proteins exposing the prospects of *in situ* engineering of NLRs for enhancing the success of immunity engineering in plants. Cytoskeleton in eukaryotes is a dynamic filamentous network with a diverse cellular and developmental functions, besides their role in the structural architecture of cells. Microtubules (tubulin dimers, MTs) and actin filaments (actin monomers, AFs) are the building blocks of plant cell cytoskeleton as with yeast cells. In recent years, the involvement of cytoskeleton in host-pathogen recognition events as revealed by alterations of actin arrays for repurposing its functions during the initial and late events of the innate immune response has become clear (Li and Staiger). The review presents the critical role played by cytoskeleton in the perception of pathogen signals and in execution of downstream signal perception and

transduction in plant innate immunity responses.

Plant microbiome is subjected to the ecological selection pressures offered by both the abiotic and biotic factors. The latter includes the influence of plants themselves and the components of the microbial community and their response to the biotrophic and multitrophic interactions. Under this umbrella, Koskella and Taylor place the bacteriophages in the centre for critically upraising their impact in altering the bacterial phenotypes, their populations and the community at large. The virulent phages replicate in host cells and lyse the bacterium which provides opportunities for coevolution leading to the development of resistant bacterium. On the other hand, temperate, quiescent lysogenic forms integrate their DNA into the host genome by recombination to become prophages, thereby facilitating horizontal gene transfer among bacteria. The consequences of interactions have been pointed out to impact basically on the constitution of plant microbiome itself and extend to plant's response to bacterial infections either beneficial or pathogenic and possible use of phages as biocontrol agents against plant pathogens. The authors however, do not fail to raise that most of the information on this are based on *in vitro* studies in microcosm, and how these are translated to natural environment is an issue for future investigations. The early divergent fungi belonging to the phylum Mucoromycota display an ancient form of heritable bacterial symbiosis and is an evolutionary novelty (Pawlowska *et al.*). This involves the vertical transmission of endosymbiotic bacteria between host generations, and matches with the endosymbiotic origin of bacterial organelles (mitochondria and chloroplasts) in the eukaryotic cells. Three plant-related lifestyles in which members of Mucoromycota clade associations with bacterial symbionts known for decomposing of plant materials, mutualists (mycorrhiza) and plant pathogens are projected to highlight this dormant field of host biology for stimulating future research. This may allow development of conceptual models for investigation on the origin of mutualism. Arbuscular mycorrhizal symbiosis found in nearly 80 per cent of land plant families offers opportunities for manipulating plant growth and productivity. This mutualistic relationship reflects a well-balanced molecular

crosstalk between both the symbionts elegantly modifying the plant's defense responses and benefiting the nutritional requirements of both the host and the endophyte. Choi *et al.* dissect the molecular aspects of signalling right from the presymbiotic communication in the rhizosphere through different stages of the establishment of plant–fungal intimacy to reveal the existence of gaps in our understanding for further research. Bacterial endosymbionts, though are less common and rare in plant parasitic nematodes, Brown drawing inferences from the genomic data describes the distinct physiological roles of these symbionts with three major examples. These include partnership between cyst and lesion nematodes and *Cardinium*, dagger nematode and *Xipjinematobacter* (obligate mutualism), and root lesion and burrowing nematodes and *Wolbachia*. The symbiotic effect dealt in these systems includes modification of host reproduction through parthenogenesis induction, metabolic integration especially for essential amino acid synthesis, and nutrient accessibility by way of aiding the host for iron (heme) uptake and iron homeostasis, in that order. It has been emphasized that future understanding on the effect of agricultural practices on the nematode endosymbionts towards virulence or the development of nematode-resistance in nematodes would help better management of nematode disorders.

The Australian-originated *Nicotiana benthamiana* initially projected as a model plant by the virology community has become a universal cell biology model plant for investigations on plant–pathogen interactions concerning innate immunity and defense signaling. Bally *et al.* point out the role played by this plant species in many plant biology discoveries and biotechnology applications. The review also unveils the initiation of joint venture initiatives on genome engineering for molecular farming employing new plant breeding techniques and web-based access for community input and gene annotation besides provisions for global access to *N. benthamiana* research materials for increased exploitation of its full potential.

Precision biotechnology techniques constitute new plant breeding techniques (NBTs). Genome editing using CRISPR-Cas technology enable direct generation and selection of plants (cisgenic plants) with desirable agronomic traits in a short

span of time. This allows to work with native DNA without involving transfer of DNA between species. Langner *et al.* provide a comprehensive description of different types of CRISPR systems in comparison with earlier gene modifying techniques and the alternatives. The review traces the progress made in CRISPR-Cas-mediated genome editing along with applications to plant science, particularly for enhancing disease resistance against pathogens. Another review deals with RNA interference. Small non-protein-coding RNAs (sRNAs also termed micro RNA, miRNA) are abundant in plants and animals and are involved in gene regulation. The mechanism of miRNA-mediated gene regulatory systems known as RNA interference (RNAi) inhibits gene expression at the stage of translation or transcription of specific genes. This has become a powerful tool for studies on gene function and also for plant protection. Rosa *et al.* give an account of this emergent technology projecting through the history, biogenesis and the initial use in plant–virus disease management and its utility for other diseases caused by microbial and nematode pathogens and insect pests particularly those vectoring plant pathogens. Its ability to make targeted changes to a genome has opened up additional opportunities for engineering pest resistance with the use of second generation genome editing CRISPR-Cas technology for crop improvement. The authors also point out the need for considering to examine the possible off-target effects of this technology for which possibilities exist to avoid or minimizing them. These new technologies forming part of the new plant breeding techniques would facilitate the development of transgene-free gene-edited crops that can invite lower regulatory procedures and can be of use with lesser acceptability issues.

Minimizing stem rust of wheat in the United States and reducing the risk of pathogen diversity facilitating effective breeding for stem rust resistance has been credited to the eradication of the alternate host (barberry which also hosts the sexual reproduction phase) of the rust pathogen, *Puccinia graminis* f. sp. *tritici*. Peterson enumerates the public participation and policies together with the leadership behind this successful Barberry Eradication Programme that has become a model disease management strategy. The need to focus on integrated use of

organic amendments and beneficial microbes with disease suppressing activity as a part and parcel of soil and root microbiome is projected for the management of soil-borne pathogens (Bonanomi *et al.*). Fungicide resistance posing a threat to crop protection has been handled with a cross-disciplinary approach (Hawkins and Fraaije). This biological phenomenon develops fitness penalties resulting in an evolutionary trade-off. The review raises the fact that much work need to be done for its effective management in a field-realistic manner. The very limited knowledge on plant surface and soil microbiome prevents the understanding of the acquisition of the antibiotic resistance by bacterial pathogens which defeats the use of antibiotics for the management of bacterial diseases particularly in high-value fruit crops. Sundin and Wang propose that antibiotic selection impacts ecosystems leading to collective evolution of antibiotic resistance through horizontal gene transfer in commonsal bacterial communities precipitating to individual pathogens. Drawing parallels from animal agricultural systems, the concept of antibiotic resistance (assemblage of antibiotic-resistance genes) is introduced to plant agricultural systems for further elaboration of the effect of commonsal microbiome on the plant pathogens for the evolution of antibiotic resistance. This also paves the way to examine the possible impact of antibiotic use for plant disease management on human health. Being the largest family of plant viruses with a great deal of diversity, the widespread geminiviruses cause economically important diseases of food, feed and fibre crops with the aid of phloem feeding insect vectors of whiteflies and leafhoppers in tropical and subtropical regions. Rojas *et al.* reaffirm that these diseases can be managed effectively only with the integrated pest management (IPM) strategy. The need for the modern technologies like GMO and genome modification and the regulatory policies related to long-distance movement of infectious materials in containing the diseases are stressed. Effective disease management depends upon the extraction of knowledge scooped out from the complexity of plant pathological information.

Crop loss estimates derived through experiments, surveys and modelling are vital for the management of sustainable agriculture. It is a complex, time con-

suming and difficult task that too when dealing with multiple pests and diseases together with perennial crops. Avelino *et al.* conceptually synthesize a systems- and process-based approach and a model structure based on generic agrophysiological model for coffee agrosystem. Garrett *et al.* emphasize the utility of network analysis for integrating sub-disciplines of plant pathology and external disciplines like social sciences for effective analyses to derive appropriate disease management strategies. These include plant microbiome networks and their resilience capacity in the ecosystem, epidemiological factors including host-centred bipartite and tripartite networks of involved species for predicting disease emergence and linking epidemic and social network analyses along with evaluation of networks with proper statistical tools. New initiatives in the form of development networks for combining individuals and institutions, trade networks encompassing crop breeding and seed networks for deployment of disease resistance, and multilayer networks across disciplines for tracking the progress in science and database development for better informed disease management are also stressed. Actual assessments of disease-caused damage to crop plants including occurrence, severity and spread along with the associated epidemiological parameters are essential for timely decisions on plant protection measures for precision agriculture. Automation in evaluation of crop responses to diseases beyond the accuracy level achievable by human effort is a necessity. Mahleim *et al.* critically analyse the utility of the advancements in the field of hyperspectral (captures the spectrum with enhanced resolution for each pixel in the displayed image) sensors and imaging techniques. This is facilitated by machine learning and deep learning together with data acquisition,



Necrotic xylem in a potato plant infected with *Dickeya dianthicola*.

management and interpretation for feeding the phenomics benefiting better applications and generation of cues to related research areas. Yet the authors point out the uncertainty of replacing visual evaluations by humans due to challenges and limitations prevailing in field sensing with high potential processes. The solution lies how best the trait extraction from images obtained under challenging conditions via machine learning approaches can be achieved. The use of nanotechnology in agriculture would enable an efficient supply of nutrients, biocides (pesticides and weedicides) and target-specific delivery of active ingredients. Plant–nanoparticles interactions impact the functions related to uptake, translocation, localisation and activity. These could have positive impacts on crop growth, protection and production. Elmer and White collate the information on the utility of phyto-nanotechnology for plant protection-related field, which is in its infancy and elegantly define the nanoparticles, their types, mode of syntheses and their usefulness in different domains of plant disease systems. The applicability of the technology for disease management covering diagnostics, induction of resistance and as delivery vehicle for genetic material, probes, and agrochemicals is well presented. Further, the possible health hazards of utilizing nanomaterials, their fate in the environment and in human/animal food chain, and the need for plant physiology-guided crop-disease specific safety assessments have also been rightly pointed out.

Many of these reviews presented in this volume transcend the boundaries of plant pathology and encompass biology as a whole drawing supportive links from physical, chemical and social sciences, and computer applications. However, the absence of the usual autobiographic narration of research by pioneering phytopathologists, valuable for inspiring early-career researchers to shape their careers has been felt. The production of the book is good with appropriate illustrations and up-to-date references, and is of great interest and value to pathologists in particular and to plant biologists as a whole.

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R. SRIDHAR

Plot 54, Padmavathy Street,  
Santosh Nagar Extn,  
Madanandapuram-Porur,  
Chennai 600 125, India  
e-mail: rangsridhar@yahoo.com

### Annual Review of Microbiology, 2017.

Susan Gottesman, Caroline S. Harwood and Olaf Schneewind (eds). Annual Reviews, 4139 El Camino Way, PO Box 10139, Palo Alto, California 94303-0139, USA. xiii + 780 pages. Price: US\$ 107.

The *Annual Review of Microbiology*, like its sister volumes of Annual Reviews, is eagerly awaited almost like an annual tradition to welcome a new student into the laboratory. These volumes are multi-chapter edited volumes known for the breadth of topics with elaborate details. This volume too is large (~780 pages) and has 37 state-of-the-art reviews. The word cloud (page vii of the volume) generated from the review titles shows that bacteria and fungi are both represented in almost equal measure, and a range of topics spanning these and other microbes as model systems.

The Annual Reviews have undergone distinct format and layout changes in the recent years including use of colour for section headers, plenty of surrounding white space, as well as colour illustrations. The layout and format in this volume too should make it very endearing for a reader, rather than being intimidating, and in particular make it easy for young readers.

The first article is a personal account by James Hoch, who elegantly chronicled his life-time work in the area of two-component signal transduction in *Bacillus subtilis* in the context of the whole field. His work, starting off in France and then onto the US, employed the awesome power of genetics to unravel the signal transduction pathway and the molecular components in *B. subtilis* signal transduction. This review, written in a simple style, should inspire all