

BOOK REVIEWS

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.

1. Gladieux, P. *et al.*, *mBio*, 2018, **9**, e01219-17.
2. Valent, B. *et al.*, *Mol. Plant Pathol.*, 2019, **20**, 173–179.

3. Janeway Jr, C. A., *Cold Spring Harb. Symp. Quant. Biol.*, 1989, **54**(Pt 1), 1–13.
4. Matzinger, P., *Annu. Rev. Immunol.*, 1994, **12**, 991–1045.

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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

budding scholars to trace how a life time work has come to fruition.

The reviews in this volume have a good mix of basic science, topical issues related to microbes and diseases, and organism-specific topics. Four high quality reviews focus on mechanistic aspects of transcription and translation. Werner and colleagues review the evolutionary origins of two-barrel RNA polymerase and how they control transcriptional initiation at specific sequences. Transcription termination in bacteria employ two mechanisms – those involving terminator sequences, or that employs the RNA-dependent ATPase protein, the Rho factor. Ranjan Sen and colleagues provide an authoritative review of Rho-dependent transcription termination involving a wealth of structural, biochemical and genetic data. With coupled transcription and translation in bacteria, the integration of translation elongation on nascent mRNA is a challenge. Rajkovic and Ibba review how the translation elongation factor P coordinates this process involving a range of posttranslational modifications. The design of altered genetic codes and the technologies employed to stably express non-canonical amino acids has been of fundamental interest and this aspect has been well chronicled by Dieter Soll and colleagues.

Drug resistance is a huge biomedical problem and efforts to understand the mechanisms of drug resistance is a very vibrant field. In this volume, four reviews pertain to the evolution of bacterial and antifungal drug resistance, and environmental antibiotic resistance. *Neisseria gonorrhoeae* drug resistance is reviewed by Jerse and colleagues. As regards fungal drug resistance, Leah Cowen and colleagues describe the current knowledge about antifungal treatment, the mechanism of fungal drug resistance, and discovery platform using systematic screens using compound libraries to examine options for combination therapy.

Microbial pathogens and virulence mechanisms occupy a central stage in microbiology. *Clostridium difficile*, first reported in early 1960s, is an opportunis-

tic pathogen and is a major public health problem especially in the elderly people. *C. difficile* infection predominates during antibiotic intake and produces three protein toxins to cause serious bowels and diarrhoea, and their biology and the mechanism of action is described by Thomas Jank and colleagues.

In the area of fungal biology, there are five timely reviews. Fungi, as a kingdom of life, evolved independently among the eukaryotes and the time scale estimates range between 900 and 2400 million years ago. Here, Strullu-Derrien and colleagues review the diversity and impact of terrestrial life by the early fungi. Fungal cell wall has a complex structure and are linked to the host cell interactions. Chamilos *et al.* describe the *Aspergillus fumigatus* cell wall structure, immune cell interaction and virulence. Cell–cell mating is an essential attribute of several fungi belonging to Saccharomycotina. Wolffe and Butler review the current understanding of how mating system has evolved and diversified in the order Saccharomycotina. Trace metal ions such as copper and iron are essential for all living cells and more so for fungal pathogens as they survive under *in vivo* conditions of iron and copper limitation. Thiele and colleagues review the current understanding of copper acquisition and utilization in various fungi. RNAi and small RNAs are centre piece of cellular regulators. Torres-Martinez and Ruiz-Vazquez review the current knowledge of the RNAi universe in filamentous fungi and how these small RNAs have broad role in the biology of these fungi.

The bacterial membranes hold specific importance in terms of how bacteria interact with environment, and interaction with host tissues, in case of pathogenic bacteria such as *Bacillus anthracis*. The bacterial cytoplasmic membrane is composed of lipids and proteins. Strahl and Errington describe the recent advances in our understanding of membrane proteins and the role of membrane curvature for cell elongation and division. The surface layer (S-layer) proteins are key virulence factors for *B. anthracis* and has been reviewed by Missiakas and Schneewind.

Bacterial lipid bilayer outer membrane biogenesis occurs presumably by the budding model or by the bacterial outer membrane protein (Bam) complex. Silhavy and colleagues provide critical evaluation of the two models for outer membrane biogenesis.

Microbiota refers to the community of microbes that co-exist, and microbiome, a description of all genes of the microorganisms in a community has emerged as key aspects governing the human health including diseases of gut and life-style diseases. Lewis and Pamer describe microbiota-based therapies involving microbiota transplant in gut for treatment of *C. difficile* and antibiotic-resistant gut infections. In a related review in this area, Porter and Martens review the critical roles of dietary polysaccharides in shaping gut microbial ecology and physiology.

Given the current importance of microbiota and microbiome, it would have been appropriate to have a couple of more articles on the influence of microbiota and the field of microbiome in disease biology. Given the large number of reviews in this volume, it is difficult to navigate for a reader interested in a particular subject area and therefore, the reviews, could be arranged in a thematic manner in the future Annual Review volumes. Another aspect that the publishers could consider for future Annual Reviews is to include a consolidated keyword index to cross-reference reviews in the broad subject of microbiology. Notwithstanding these aspects, in closing, this volume of *Annual Review of Microbiology* has an impressive collection of articles carefully chosen by the volume editors that would enable active researchers to keep abreast of the respective fields of research. This volume is a worthy addition to a library.

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