

**Annual Review of Phytopathology, 2020.** 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. 58. xii + 406 pages. Price (personal copy): US\$ 118.00. ISSN: 0066-4286; ISBN: 978-0-8243-1358-6.

If there is one source for plant pathologists for digging out the past discoveries, refresh and update knowledge, and for forward thinking, it is the *Annual Review of Plant Pathology* series. The present 17-review packed volume is well balanced in covering the major areas of plant pathological research. This collection is indeed a welcome addition to the literature.

The catastrophic destruction of coffee plantations by coffee leaf rust (coffee rust) during 1860s in erstwhile British Crown colony Ceylon (now Sri Lanka), considered as the original focus of the disease, changed the Britisher's preference from coffee to tea. Subsequently, coffee leaf rust was realized as a determinant factor of the economies of many United States allies in Latin America which produced most world's coffee during the Cold War era following the World War II due to simmering rivalry between the United States–Great Britain front, and the Soviets. McCook and Peterson revealingly trace the history of this dangerously devastating commodity disease to show how the anticipatory moves taken in the form of regional followed by global networking of coffee research for sharing knowledge, expertise and resources generated by the participating centres, steered through by the notable American Plant Pathologist, Fredrick Wellman has remarkably prevented any further major threat to coffee production.

False smut of rice, a pre-semidwarf era disease has now become a concern in food security hotspots limiting the realizable yield significantly<sup>1</sup>. Presently, progress in managing this disease through the preferred host resistance is hampered due to difficulties of mass scale phenotyping of germplasm for resistance evaluation. A review exclusively devoted to rice false smut as an emergent threat to rice production (Sun *et al.*) identifies the areas that need further exploration for handling the disease effectively. Invasions of ecosystems by non-

native species disrupt the key ecosystem functions leading to significant economic damage. Goss *et al.* compare the ecological impact of pathogen emergence and accumulation in non-native invasive plants and cultivated plants, and elucidate the long-term outcomes of biological invasions in light of the pathogen colonization and disease epidemics in relation to evolutionary processes. Besides the pathogens serving as a biocontrol tool in proven cases, the authors point out that the invasive plants form bridges among urban, agricultural, and natural, both disturbed and undisturbed, environments facilitating pathogen movement among host and environments. The complexity of biological functions increases with each of the organizational levels (individual, population, community and ecosystem) in the ecosystem when dealt at species level. Applying the principles of functional ecology in which the pathogen communities of the forest ecosystem can be grouped on the basis of their functional traits for reducing the complexity is discussed by Oliva *et al.* This serves as a measurable factor influencing the fitness of an organism in the ecosystem, besides allowing the interpretation of evolutionary relationships between diseases and trees using the functional phenotypic and genotypic traits in addition to assessing the invasiveness of pathogens at species level.

The availability of digital sensors has widened the feasibility for use of sensor technology in remote sensing of plant diseases. Its application for non-destructive assessment of epidemiological components and parameters through spectral signatures or volatile organic compounds (VOC) emitted by diseased plants and the infecting pathogens in relation to decision making for undertaking disease control measures, crop loss assessments, and phenomic evaluations is dealt by Oerke. The review also raises the challenges involved in dealing with latent infections and early stages of infection before the symptoms appear, and the suitability of the sensors for use in unmanned aerial vehicles. Relevance of employing artificial intelligence for processing the information acquired by hyperspectral sensors with deep learning architectures to solve specific tasks for select applications like disease detection requiring more precision is also indicated.

The origin of viruses is considered to be of polyphyletic in nature. However, this tenet continues to be under debate. Dolja *et al.* in their treatise trace the evolutionary ancestry of plant virus lineages to primordial mobile genetic elements using phylogenetic approach and consider frequent horizontal virus transfer between divergent hosts to have played a significant role in shaping plant virome. Besides, the evolutionary processes involved and their interplay influencing virome evolution are elucidated. This insightful knowledge has contributed for reconstructing the evolutionary pathway and for framing the present megataxonomy of viruses. As the viruses form ubiquitous associations with cellular life making them the most abundant biological entities on earth, the authors point out to the availability of limited information arising only from harmful viruses, and the need for representative analysis including all components of the complete earth virome for enhancing the robustness of the megataxonomic schemes.

The plant hosts and their parasites have evolved specialized, complex regulating systems for controlling their interactions reflecting long periods of coevolution. While the hosts resist parasitic attack, all classes of adapted parasites modulate their relationships for avoiding this resistance, traits essential for each of their survival. Holistic understanding of these recognition specificities at gene and their functional aspect levels in case of *Arabidopsis–Pseudomonas syringae* pv. *tomato* pathosystem reveals the mechanistic intricacies of immunity specific to this model (Pottinger and Innes). These proof-of-concept studies bring to light a new paradigm of indirect pathogen recognition (guard, decoy, integrated decoy models with intrinsic variations) in plant disease resistance, subsequent to the famous gene-for-gene relationships involving direct pathogen recognition hypothesis. The indirect pathogen recognition operates through a distinctly different host protein (without any other function, termed as decoy) other than the resistance protein. These insights have already begun to trickle out opportunities for novel eco-friendly strategies for disease management. Convincingly, the authors highlight the translation of the 'decoy approach' to diverse crop species possessing native endogenous orthologs of this *Arabidopsis* decoy protein, PBS1. This opens up new

approaches of engineering disease resistance in plants through protein engineering (specifically 'decoy engineering' in this context) allowing the modification of recognition specificity to suit different pathosystems. Opportunities for the development of GMO-free genetic resistance for diverse pathogens and parasites like nematodes and sap-sucking insects involving protease activity for their infection cycle or replication machinery are now available.

The downstream cellular responses following the pathogen recognition involving the host receptors and the conserved molecular patterns or the pathogen-secreted virulence factors is executed by a complex nucleotide-binding-leucine-rich-repeat (NLR) network. In this, lipase-like proteins belonging to EDS1 (Enhanced Disease Susceptibility 1) family constitute a regulatory hub controlling basal and effector-triggered immunity. Lapin *et al.* examine the phylogenetic, structural and mechanistic understanding gained so far that expands the knowledge on the immune regulatory hub. For increasing their fitness, microbes exploit the host and become cheaters without being a mutualist partner, a phenomenon discovered with uncooperative non-nodulating and non-N<sub>2</sub> fixing rhizobial strains capable of proliferating in host without offering any benefit<sup>2</sup>. Such strains arise as products of eco-evolutionary processes. Pathogens form an inevitable component of plant microbiome. Placing the pathogen virulence and plant disease progression at the centre stage of plant microbiome, Friesen conceptually analyses the social cooperative interactions and cheating among the members of microbiome community supported by available evidence pertaining to plant-pathogen interactions at molecular level. This understanding might pave the way for using the microbes exploiting pathogens through microbiome engineering aimed towards effective bio-control disease management practices.

Parasitic nematodes establish on their host plants by creating feeding site inside the root. Feeding site is a form of tissue modification called syncytium or symplasm (giant cells) formed by fusion of several cells around the primary invaded cell that receives the nematode-secreted effectors through nematode stylet. This interface in the process of infection is characterized by modulation of gene expressions coordinated by epigenetic

events. Small noncoding RNA sequences (sRNAs) generated by epigenetic mechanism alter the gene expression or silencing. Exchange of sRNAs between the host plants and parasites/pathogens is also evident. The epigenetic influence mediated by small noncoding RNAs reflecting the host responses to cyst and root-knot nematodes is dealt by Hewezi. A comparative treatise on gall formation in plants as a response to interaction with sedentary herbivorous insects and parasitic nematodes is presented by Favery *et al.* The similarities in the process of manipulating the plant tissue development by these agents, presumably arising from convergent evolutionary strategies, reflect in their lifestyles. The review focuses on the secreted parasite factors (effectors) in inducing galling effect. The projection of the role of symbiotic microbes associated with these gall inducers gain significance in influencing the lifestyles and ultimately their evolution as potential plant tissue reprogrammers.

The use of the term 'tolerance' in the context of plant diseases continues to pose a confusing picture, and its impact when used in resistance evaluation both at field and laboratory/greenhouse experiments results in erroneous assessment as a level of resistance attributed as partial resistance. Rather, the term need to be approached in a phenomenological sense. Pagan *et al.* reinforce the principles of tolerance to diseases in plants characterized by 'enduring infection/disease' that has been clearly laid down in a pioneering and classical review by Schafer (1971, cited in the text) published five decades ago in the *Annual Review of Phytopathology*. Challenges involved in demonstrating and quantifying tolerance together with the current understanding of its mechanistic basis and role in plant-pathogen coevolution portrayed in this review might help to use the phenomenon of tolerance with proper perspective in future studies.

Despite numerous studies under laboratory and greenhouse conditions, availability of bioherbicides involving live microorganisms for the control and management of weedy plants is woefully limited (Morin). Even some of the claims of their success is untenable for want of critical evaluation of post-introduction effectiveness and safety aspects including the possibility of host jumps in farm environments. More in-depth knowledge on weed pathosystems including the

omics-derived information might help the weed-pathogen selection, and guide genetic modifications, if required, together with the development of suitable methodologies for application besides framing up of proper regulatory issues are stressed.

Three reviews deal with pest and disease management, and another one related to reachability of technologies and material to the end users, the farmers, by linking private and not for profit agencies. The current perception of plants and their microbiome especially of rhizospheric microflora anchors around the concept of coevolution based on selections for beneficial attributes to each other<sup>3</sup>. This originates from studies on naturally occurring disease suppressive soils emphasizing the need to understand molecular cross-talk between the two partners at genetic level. The immediate prospects of creating disease suppressive environment by manipulating the microbiome composition through organic amendments to soil for lessening the impact of soil-borne diseases and parasitic nematode damage in annual fruit and vegetable cropping systems are examined with existing experimental data by Roszkopff *et al.* Soil moisture is one of the important epidemiological factors in predisposing plants to diseases. The impact of measures taken to mitigate the insufficiency of water to the farming sector has not been critically examined in relation to crop diseases. Swett in his review deals with managing crop diseases under water scarcity highlighting the significance for a comprehensive understanding of the intricacies of the pathosystem together with soil and plant water status as affected by the adaptive water use practices. Knowledge on crop losses due to plant diseases is essential for prioritising research directions for augmenting food production to meet the demand synchronizing with shifts in global food system required for accommodating diet improvement and climate change together. Savary and Willocquet stress modelling for crop loss assessment due to diseases with a system-analytical perspective. Placing disease together with crop growth and yield losses pertinent to global food security and considering the principles of damage analysis<sup>4</sup>, the modelling framework at the agrosystem scale suggests the need for a built-in dynamic diversity of deployed disease resistance genes, of plants differing in their genetic

makeups and of crops within landscapes facilitating agrosystem reengineering. This can be achieved through the combined use of both traditional cultural practice of crop rotation and the modern gene transfer technologies for gene rotation.

Essentially meant for effective and economic delivery of services to the citizens through contractual agreement, public-private partnership (PPP) is being defined variably by the involved entities, and more so by different countries. Hence, the performance efficiency of this system has been mixed. Markell *et al.* futuristically outline the utility of PPPs related to plant pathology in the agricultural community, based on analysis of several case studies from the United

States of America. These authors, besides identifying a set of key areas in which PPPs can make positive impacts, underpin the importance of trustworthiness of the partnering scientists, and understanding the needs, challenges and weaknesses of other's organizations for successful PPPs.

For every plant pathologist, this volume is a must to read and consult. The manner in which the subjects are treated is stimulating for enriching knowledge, and the important feature of it is that it would force the reader's mind along new paths.

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