

abundance in a pixel and discusses its importance in hyperspectral image analysis with various algorithms. In the unsupervised case, the endmember estimation problem was well defined before introducing the search criteria. Supervised unmixing methods were described to derive abundance estimation with a linear mixing model. The importance of constrained unmixing has been brought out with an illustration of results from hyperspectral AVIRIS imagery. Recent advances in multiple spectral mixing and sparse regression models were described well with simulated spectral signatures.

The last three parts of the book deal with data assimilation and methodologies for integrating multiple high-level remotely sensed land variables as well as products. These highlight the benefits of integration of multiple high-level land surface products from various satellites capable of datasets with different spatial and temporal resolutions. Machine learning methods for calculations of vegetation cover variables are illustrated describing data assimilation framework in detail based on sequential and non-sequential methods for retrieval of land surface parameters with and without snow-covered surfaces. In particular, the dynamic model based on seasonal autoregression integrated moving average (ARIMA) model has been discussed in detail for developing the climatological data from multi-year MODIS LAI data and compared with field LAI values. The multi-resolution tree approach has been covered extensively for several land surface parameter retrieval including emissivity. A good treatment of combining low spatial resolution MODIS products with high-resolution Landsat after aggregation has been given with experimental illustrations. The merits of empirical orthogonal function-based integration are described with illustrations of filling data gaps of one satellite data with model-derived data. The authors have proposed in detail the Bayesian model averaging method for downward longwave radiation (DLR) and latent heat flux parameters and compared these with ground measured DLR data at 22 sites across the globe for assessing the accuracies of the estimation models. Similarly, for LAI products from five different models, ground measured data collected at 240-eddy covariance flux towers were used to evaluate their performance.

Machine learning and its variants with kernels, neural networks, manifold, ensemble learning, etc. including sufficient examples for each will attract the researchers. Of these, the kernel method has been dealt in considerable depth including more recent topics like sparse learning and active learning. An exhaustive introduction on neural networks and Markov Random field models is provided in the book. In ensemble decision making, the principles of boosting and bagging methods are very well explained with the help of flowcharts and explanations in detail. An interesting part of the discussion is the inclusion of a subsection after each technical description of methods on the applications of these in remote sensing fields with sufficient references on the current trend of research describing the applications of these methods in remote sensing.

Overall, this volume has covered a wide range of important topics from geometric processing and calibration of optical, LIDAR and SAR onboard sensors; advances in earth observation data analysis and feature extraction; machine learning and data assimilation and alike to address several aspects of data processing and analytical approaches in great detail. There are some overlapping topics across the chapters especially on multiresolution data analysis and fusion techniques; however, this is bound to happen with contributions from different authors. This book will find a place in the user community who is interested in gaining advanced knowledge involved in the processing of earth observation data to generate dependable geophysical and map products. This volume is a useful reading material for researchers from both academics, industries and decision-makers in administration.

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This volume with a collection of 23 articles representing important areas of plant pathology reviews not only the frontier fields but also racks up the traditional sub-disciplines bridging them with the genomics era. The lead article by Jeremy James Burdon, an eminent plant pathologist from CSIRO Agriculture and Food, Australia is a fascinating career biography written with an easy and absorbing style. His description demonstrates out-of-the-box approach that enabled him to move away in diverging directions involving a variety of aspects that has led to novel ideas and solutions associated with creativity. He has devoted his service in understanding the genetic basis of complexities in the role of pathogens in plant populations and in plant communities – deepening knowledge on co-evolution of plants and their pathogens, the conservation of plant genetic resources in addition to crop disease and weed management in agriculture. Burdon's contributions in plant pathology with a passion to be a field biologist emphasize 'the need for work in the field will never lessen' in the words of Webster (2005, cited in this chapter). Certainly, this essay reminds the Russian-born evolutionary biologist Theodosius Dobzhansky¹, who laid the foundation for the synthetic theory of evolution and, who advocated 'nothing in biology makes any sense except in the light of evolution' (Dobzhansky 1973, cited in this chapter) will lure the readers to this old science inextricably linked with the modern science and foster a desire to want to know more. Appropriate to this lead article, the editors have assembled a cascade of reviews which open up new opportunities fundamentally essential for burrowing deep into understanding plant health.

Understanding the pathogens and the diseases together with the pathogen lifestyle in their natural ecology in more detail would unravel fresh avenues for further investigations and possible applications for their management. The modern theory of metaorganism has its origin

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to the concept of holobiont put forward by the German theoretical biologist Adolf Meyer-Abich in 1943 (ref. 2). Treating plant as a metaorganism which serves as a flexible habitat to microbes with diverse lifestyles comprising mutualists, commensals and pathogens engulfing them together as its microbiome, Hassani *et al.* elucidate the dual role of plant immunity defending against the pathogens on one side and accommodating the friendly microbes on the other to benefit from their functions using its recognition and specificity mechanism. The authors stress the inadequacy of knowledge on microbial interactions within the plant microbiota and explain the process of plant domestication might have had its influence in reshaping the constituent microbes ultimately impacting the plant fitness. The genetic compatibility of a parasite with a breadth of different host species (host range) is central to understanding pathogen epidemiology and pathogenicity for better crop protection and management and gaining knowledge on the ecological and evolutionary causes of specialization or generalization from an anthropocentric viewpoint. Morris and Moury enumerate the importance of studies that link host range and fitness, and genetic factors behind host jumps among others essential for novel disease management approaches.

Two reviews are devoted to smut pathogen–host interactions. One deals with assessing pathogen population using combined pathogen and comparative genomics and the other on pathogen virulence.

Knowledge on the evolutionary forces shaping the never ending coevolutionary arms race between the pathogen and its host is of fundamental importance for plant disease management. Hartman *et al.* base their review on knowledge gained with another smut fungus model pathosystem to discuss pathogen adaptation, diversification, host specialization in relation to climatic conditions, biodiversity and ecosystem dynamics. These will be useful for understanding emerging diseases including host jumps besides for development of disease control strategies. Pathogens secrete effector proteins (virulence factors) and inject them into the host tissues for successful colonization. Pointing to the fact that the mechanistic understanding of only a handful of effectors of fungi has been achieved, Zuo *et al.* critically portray the biology of

corn smut pathogen deciding the outcome of the host–pathogen interactions, and the genome evolution in the context of pathogen virulence in the biotrophic relations.

Based on the recent genomics and transcriptomic studies on sooty blotch and flyspeck fungal ectophytic pathogens, Gleason *et al.* suggest a transition, possibly through reductive evolution via genome contraction has resulted in the loss of pathogenicity-related genes from plant penetrating parasitism to non-invasive plant surface-dwelling ectoparasitic lifestyle of these economically important orchard pathogens which mainly affect fruits, thereby their marketability. Daughtrey writes about the basic pathology of boxwood blight, an aggressive ornamental disease that has got introduced in this decade into Western Asia and North America from the United Kingdom through nursery trade causing extensive damage to landscapes and gardens resulting in huge financial loss emphasizing the need for disease-resistant genotypes. Grunwald *et al.* dissect out the epidemiology, evolution and ecology of the pandemic of sudden oak death disease in the United States and in Europe causing bleeding cankers in tree trunks and dieback of foliage in devastating proportions in oak and larch forest plantations. They trace the origin of the causal oomycete pathogen, *Phytophthora ramorum*, in Vietnam. Thapa *et al.* report the present information on the differential lifestyles of Gram-positive bacteria which includes a major class of plant-associated beneficial and a lesser number of pathogens with an evolutionary perspective.

Two other reviews deal with *Fusarium*, a large genus of soil-borne filamentous fungi causing important plant diseases, and capable of producing many mycotoxins of major concern to plant, animal and human health. Summerell points to the confused taxonomy and systematics of this genus negatively impacting diagnosis, management and biosecurity legislations justifying the need for a stable taxonomy for this historically important fungal genera. Chen *et al.* comprehensively collate information on the biosynthesis of a group of sesquiterpene toxins produced by *Fusarium graminearum*, causing Fusarium head blight in cereals along with its possible management. Lack of host resistance and environmental issues for using chemicals

remain as the main hurdles for realizing toxin-free produce. One of the most time-tested efficient and successful management of two globally important quarantine pests of potato cyst nematodes that has been developed and implemented through regulatory and research efforts during the past nine decades in the United States is described by Dandurand *et al.* This plant-healthcare has relied on the strong network of the national plant protection agencies of the US and Canada, where also the pests have been occurring, involving state, federal, university and private industries. This dynamic operation centred around containment, management or eradication, and regulation sets an example for handling the disastrous biotic stresses in agriculture for the other nations to follow.

Hydathodes serve as natural openings on the leaf surfaces providing a direct entry for bacterial pathogens especially xylem-limited ones. However, infection of many of these pathogens occur through fresh wounds such as growth cracks in the roots and wind-caused injuries on the leaves in field grown plants. Cerutti *et al.* compiled the information on the anatomy and physiology of hydathodes and relate them to the early host responses to infection process. It is also suggested that relating the early events of infection processes with plant immunity in these cases would be more relevant with true hydathode-specific pathogens. The general notion that the quantitative resistance (QR) to crop diseases is more



Colonies of a *Peltaster* sp. on apple cultivar Dalinbel associated with an overwintered fruit mummy in an organically managed orchard in northern Germany.

stronger and lasts long compared to major gene (qualitative) resistance is well established, although the molecular nature of this is unclear. Cowger and Brown critically assess the durability of QR in relation to pathogen adaptation and evolution with an eye on the differential vulnerability of QR sources for pathogens to overcome and the man-made underestimation of QR introduced by publication bias to provide a futuristic view for exploiting QR in crop breeding for sustainable disease resistance, particularly in the changing environments.

The process of immunity against microbial infections begins at the plasma membrane (PM) forming the borderline interface between the interior of plant cell and the external environment including the pathogens. The early immune responses of the host cell use vesicular trafficking to initiate and modulate the movement of various immune proteins and carbohydrates to and from the PM for remodelling the cell surface as per the need (Ekanayake *et al.*). Recent information on vesicular trafficking involving clathrin-coated vesicles (CCVs), as they are not only well studied, but the CCV components have emerged to play a key role in plant defense against a variety of pathogens, particularly influencing defense signalling are explicitly discussed. Plants recognizing a microbe (bacteria, oomycetes and fungi) as a pathogen through its structural components (pathogen/microbe-associated molecular patterns, PAMP/DAMPs), initiate the first level of resistance (PAMP/MAMP-triggered immunity, PTI/MTI). Seidl and Van den Ackerveken deal with necrosis and ethylene-inducing protein 1 (NEP1)-like proteins (NLPs), a distinctly different class of these molecular patterns, termed immunogenic patterns³, produced by all three taxonomic groups. These patterns are classed into two: extracellular and intracellular immunogenic patterns based on their location of activity⁴, and NLPs are placed under extracellular immunogenic patterns. The perception of NLPs by the host immune receptor RLP23 triggers immune response. The authors comprehensively document the biology and genomics of NLPs, especially as virulence factors, their role in microbial lifestyles and plant immunity.

Tospoviruses vectored by thrips in a propagative and persistent manner are a group of important plant viruses globally. Zhu *et al.* enumerate plant immunity

against these viruses. Resembling the plant innate immunity against non-viral pathogens, plants also execute a multi-layer antiviral innate immunity process. Mutual recognition of viruses by the plant and host detection by the viruses impact the immunity response, and the activation of virulence strategies respectively. In the absence of detection of any virus-derived PAMPs/DAMPs and a cognate receptor at the host cell surface to signal the initial layer of basal immunity, Zhu *et al.* present the RNA silencing or RNA interference (RNAi) pathway, a natural antiviral defence mechanism as the first layer of immunity in plants in which the viruses are both inducers and targets of RNA silencing. Adapted plant viruses encode silencing-suppressor proteins to counteract the host RNA silencing-based antiviral process. Further, the effector-triggered immunity is presented as the second layer of defence along with opportunities for manipulating viral immunity to control tospovirus diseases.

Parasitic plants connect intimately with crop plants and deplete water and mineral nutrients resulting in devastating consequences for the host. Sensing the host root-exuded strigolactone, an endogenous hormone, the seeds of these noxious weeds germinate leading these seedlings to locate their host in a suicidal manner to the host. Clarke *et al.* deliberate considering parasitic plants as pathogens. Their documented evidences related to molecular basis of their interaction with the host plant highlight the similarities in host immune responses between parasitic plant infestation and microbial pathogenesis including immunity suppression are in support of the latter thinking. The need to translate the knowledge gained in this direction towards developing control strategies is pointed out.

Advances in understanding of plant immunity pave the way to view it in an ecological perspective. One of the reviews in this volume considers the process of immunity as applicable to tree/forest plantations. Defending against microbial pathogens and insect pests is a basic nature of plants for their survival. Wilkinson *et al.* partition the plant defence potential into two distinct entities. The cellular defense expressing through the process of innate immunity as an internal strategy and the ecological factors comprising soil and rhizosphere micro-

biome inducing the defence as the external strategy. Also, the involvement of plant volatiles produced at the site of pest ingestion attracting its natural enemies in a manner of tritrophic interaction forms an indirectly induced defence belonging to the second category. The authors stress the need for a comparative examination of these strategies in view of the changing scenario of global agriculture and forestry.

Plant transformation by *Agrobacterium* is a highly complex phenomenon. Lacroix and Citovsky bring together information on DNA transfer from crown gall bacterial pathogen, *Agrobacterium tumefaciens*, considered as a natural genetic engineer possessing the ability for horizontal gene transfer. This multi-step process exhibits a wide diversity involving interactions between the bacterial and host genetic factors. These variations, presumably, enable this bacterium to be pathogenic to a broad range of host plants. The authors point out that the mechanism of DNA and its associated protein transport is not very well known. Deciphering this would facilitate use of *Agrobacterium*-mediated transformation for improvement of the recalcitrant plant species and non-plant eukaryotic cells. Members of plant pathogenic bacteria of *Xanthomonas* genus inject proteinaceous transcription activator-like effectors (TALEs) into the host cells to modulate them in their favour. In the host cells nucleus, this effector protein binds with base-specific matching DNA sequence (effector binding elements), and activates the downstream susceptibility genes that aid bacterial infection to cause the disease. Perez-Quintero and Szurek lucidly trace the sustained research efforts on TALE biology leading to the discovery of the right combination of amino acids in the effector protein that would bind to the right DNA sequence in the promoter, what is known as the TALE code. This has become one of the unprecedented tools for engineering immunity to bacterial pathogens. Plant viruses has offered a fascinating set of tools that have expanded our genome biology knowledge and the creation of novel products. Cody and Scholth explore the present advancements coded as version 3.0 in the utility of plant virus gene vectors in association with CRISPR system as gene-editing tools. Background information on the use of viral tool

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technology for gene expression and virus-induced gene silencing (RNA silencing) employed using the gene expression knockout for protein production and plant functional genomic studies are appropriately presented for a holistic grasp of this chapter with optimistic expression for viruses to become biological software in the future.

Advanced genomic technologies offer a wide range of opportunities for crop improvement. However, only a few of them have been realized. Pixley *et al.* identify the hurdles posed to these proven concepts looking at them from the angle of engineering disease resistance in crop plants and in socioeconomic context with emphasis on benefits reaching the poor, especially those in net food-importing countries. There exists only a very limited number of genetically engineered disease resistant crop plants especially in

the US while they are prohibited in Europe. These authors attribute this to the non-scientific challenges in the context of prevailing political and economic scenario. They also add that the institutional forces significantly influence the choice of agronomic traits for genetic engineering which requires the backing of investments and policies besides concerns of stricter intellectual property protections and regulatory frameworks, critical societal concerns about their risks and benefits of genetic engineering, agroecological sustainability and social equality for accessing their benefits.

This volume is an outstanding collection of reviews in some of the most exciting frontiers of plant pathology covering a wide range of field and greenhouse pathology which link to the laboratory studies of modern molecular plant pathology. These appropriately

illustrated and well-referenced reviews will be of great use for reference and study to all plant pathologists.

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