

repressor FMRP are implicated in ID, ASD and SCZ as discussed by Haganir and co-workers. On the other hand, each disease condition is mapped onto mutations at multiple sites. For SCZ, a recent genome-wide association study (GWAS) of ~35,000 patients and ~100,000 control subjects identified about 600 candidate genes. Similarly, FMRP interacts with about 800 different mRNAs and it will be a herculean task to understand how any given FMRP mutation affects translation levels of each of these target mRNAs. In many cases, these data are corroborated by mutations of specific genes in mice. For example, mice lacking neurexins or neuroligins show ASD-related abnormal behaviours and deficits in glutamatergic synaptic transmission. Genomic data implicate the activity-regulated gene *Arc* in SCZ, and mice lacking *Arc* suffer deficits in memory consolidation. Thus, animal models can be utilized to better understand the functional readouts of genetic mutations identified in patients. An alternative approach is to derive neurons from human-induced pluripotent stem cells (hiPSCs) from patients and control subjects to understand how the mutation affects neural function. However, caution needs to be exercised with this approach for several reasons. These are pointed out by Heinzen and co-workers in their review of the genetics of neuropsychiatric diseases, as well as Haganir and co-workers. First, the penetrance of genetic mutations in causing the disease goes in the order ID > ASD > SCZ, while the influence of environmental factors to disease presentation goes in the order SCZ > ASD > ID. Secondly, these disorders are associated with low fecundity and the mutations rarely spread to high levels in the population to be detected via GWAS linkages. NGS of exomes is more powerful at detecting these rare variations and is being utilized. Thirdly, frequently, the disease is brought about by *de novo* mutations in the patient and is not detected in the parents. Even in the patient, if the mutation occurs at a later stage in development, leukocytes from which hiPSCs are derived may not harbour the mutation, while nervous tissue might. In these cases, deriving iPSCs from ectodermal tissue such as skin might be more fruitful. Fourthly, genetic variation associated with these diseases might occur outside of protein-coding regions and sequencing the exome will not reveal these varia-

tions. Lastly, gene discovery using GWAS and exome sequencing will yield a long list of contributing genes. To understand why these result in ID, ASD or SCZ, ingenious high-throughput functional assays are to be devised. The latest optogenetic neural stimulation and inactivation techniques together with imaging technologies offer hope in this regard.

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The present volume of the *Annual Review of Phytopathology* critically examines the developments in different aspects of plant diseases in a holistic manner through 28 comprehensive, well-illustrated and appropriately referenced reviews.

The opening chapter deals with the lifetime achievements of Dennis Gonsalves, who has made an indelible mark in the annals of phytopathology through his contributions spanning detection and characterization of papaya ring spot virus, cross-protection strategy and entry into molecular virology, culminating in a team approach for genetic engineering using pathogen-derived resistance (coat protein gene) approach for the development of transgenic papaya resistant to ring spot. The outcome of this research has helped to save the Hawaiian papaya industry from devastation by ring spot virus, marking the beginning of development of similar papaya for other coun-

tries. Certainly, this review is a source of inspiration alongside the human touch in a truly Hawaiian spirit of 'aloha' to youngsters stepping into the field of plant pathology.

Precise identity of the pathogens is a basic requirement equally important for research, inspection, quarantine services and for sustainable disease management. Bacterial taxonomy has met with frequent changes due to insufficient knowledge of the pathogens, gained at diagnostic levels. Bull and Koike point out the dependability of molecular tools, over the phenotypic characteristics, particularly for diagnosing bacterial diseases. They stress that it is crucial to have accessibility to the use of modern molecular tools, including technologies based on multi-locus and whole-genome sequence analysis accompanied by hands-on-training to diagnostic technicians and pathologists directly in contact with extension workers and farmers at the diagnostic centres. However, these are applied now for already known pathogens and not for pathogen discovery. While pointing out the accelerated developments in fungal systematics in the recent decade and a half, which now incorporates genomics, web-based systems and DNA data enabling global collaborations for rapid identification of species to metadata, Crows *et al.* suggest linking names to type specimens, cultures and reference sequences. Use of DNA barcoding, progress made in attempts to merge sexual and asexual generic and species names for implementing one fungus-one name system and sequence-based classification of fungi, which will shed more light on fungal diversity are critically discussed. Presently, use of meta genomic approach employing the next-generation sequencing technologies aided by bioinformatics tools for the detection and identification of both known and new viruses and viroids infecting plants has gained momentum. Wu *et al.* bring to light the need for development of new computational algorithms capable of discovering novel viruses from next-generation sequencing datasets in a homology-independent manner, easily accessible user-friendly software interfaces and fulfilling Koch's postulates for the viruses and viroids.

Ever since Janeway's¹ concept of innate immunity was adopted to plant science², there has been an explosion in studies related to it during the past

couple of decades. The defence response of the plant gets primed as a consequence of recognition of molecular patterns of biological origin and injury, effectors and chemical compounds of non-self agents activating immunity or abiotic stress tolerance. Conrath *et al.* update the molecular mechanisms of priming, focusing on chemical signals of natural or synthetic origin associated with the host sensitization and examine the similarity in mammals. Though the screen is opening wide, the review points out that a lot more is to be learnt for translating our knowledge into crop improvement and human medicine.

Among the two-layer plant immunity systems, cell surface-mediated immunity offers a localized defence against the invading pathogens at the infection portal. Khaled *et al.* highlight the sub-cellular trafficking processes involved in the delivery of pattern recognition receptors at the plasma membrane and subsequent removal of the activated receptors by endocytic trafficking route for vacuolar degradation. Recognition of the molecular patterns of non-self origin by these receptors sets forth the initial phase of response in the host-microbe interaction, known as pattern-triggered immunity. Pathogens reprogramme the membrane trafficking through their effector molecules released at the site. The need for studies oriented towards understanding of the pattern recognition receptor-mediated immune response at the cell-specific and sub-cellular level is emphasized, for unravelling the mechanistic part of the initial layer of immunity.

Different conceptual models of innate immunity in plants exist. Cooke *et al.*, presenting an improvised model, declare that models are not the end, but serve as a benchmark, from which new hypotheses are generated for scientific discoveries. In their new model termed 'invasion model', the immunogenic ligands produced by the invader during invasion, considered as invasion patterns (IPs) are introduced as the interactive principles in place of the molecular patterns and effectors of the invader. This facilitates bringing in a more diverse form of plant-invader interactions covering a wider range of interactions, including those with endophytic and mutualistic types, apart from pathogenic symbionts, which also involve plant immune system. The authors make one leap forward to suggest that an understanding of the process

involved in the formation of IP may throw light on its variability and may open up the way to approach durable resistance at the molecular level.

Larkin updates the progress in relation to management of soil-borne and a few foliar diseases, and emphasizes the need for production system-oriented research on soil health. Rhizosphere characterizes many contrasting plant-microbe and microbe-microbe interactions in relation to plant health and nutrient uptake. Comprehensive understanding of community-level interactions of these microbes is woefully limited. Considering it as a global hotspot and an arena for boosting horizontal gene transfer, Reinhold-Hurek *et al.* focus on bacterial communities to stress the need for establishing the causal relationships of how plants shape their root microbiome.

The importance of signalling event that mediates a beneficial plant-microbe interaction involving symbiotic nitrogen fixing rhizobium and arbuscular mycorrhizal fungi, simultaneously modulating the innate-immune responses is discussed by Limpens *et al.* Although the lipochitooligosaccharide signals from these symbionts are perceived by the host plant through specific receptor-like kinases, closely related to chitin innate immune receptors, the mechanistic part of repression of defence responses is not clear. This would remain as a major objective for future studies on symbiotic signalling.

Disruption of relationships between the wild relatives of the present-day cultivated crops and their associated pathogens by modern agricultural practices, involving newer plant genotypes with high yield potential, possessing favoured quality traits and associated resource inputs, has triggered the co-evolution or arm's race between plants and pathogens favouring disease outbreaks. Zhan *et al.* point out that for achieving sustainable disease management, it is desirable to retard the evolutionary potential of plant pathogens by manipulating the agricultural practices.

The molecular and cellular nature of quantitative resistance (QR), also referred to as basal resistance, has not been fully understood due to the absence of defined models for the study or its utility in crop improvement. Two reviews deal with durable resistance to diseases. Brown views durable resistance in an evolutionary sense. Recalling the gain of

satisfactory level of resistance by barley and wheat, which were once highly susceptible to powdery mildew over a period of time in the United Kingdom, he points out that the durability of disease resistance has been achieved by different routes in these two important crop species. Understanding the co-evolution of both the partners – the host and the parasites – in the light of the concept on gene-for-gene resistance, influence of agro-ecosystems on the durability of resistance and consciousness of the similarity between natural and forced thematic selections would aid in devising methods for managing durable resistance. The review critically examines different approaches for incorporating durable resistance. One among them is by stacking resistance genes *not previously exposed to the pathogen population* in a cultivar, especially in the case of asexual parasites, that would aid in prolonging the durability of resistance genes. The review analysing the various ways in which durable resistance operates, stresses the importance of handling the agro-ecosystem in a manner suitable for making resistance durable.

Niks *et al.*, in a critical treatment of QR with reference to biotrophic filamentous plant pathogens, describe durable resistance as a poor suppression of pathogen- or microbe-associated molecular pattern-triggered defence by pathogen effectors, or improving access of the pathogen to nutrients. The mechanistic nature of durable resistance, which might vary with the participating genes, will be fully understood only when the biochemical and physiological events associated with it are unravelled. The review provides certain indications in that direction. It is attractively hypothetical in nature based on well-founded evidences and opens up new avenues for future studies in understanding the response of the plant mediated by newer genes, governing basal defence and the ability of the pathogen to tackle them at the molecular level.

The pathology of perennial trees and vines differs from the models applicable to small annual plants in which the present-day understanding of genetic, molecular and cellular information on plant-pathogen interactions has accumulated. With tristeza virus disease of citrus, the need for concerted research, involving perennial host models has been emphasized (Dawson *et al.*). The chapter

dealing with the most complex and economically important grapevine leaf roll complex of viral nature, presents information on viral biology and plant–virus interactions, generated with molecular biology, -omics, and cell biology investigative approaches (Naidu *et al.*). The major stumbling block is the lack of available natural resistance in grapevines. A similar situation has also been pointed out by Ploetz *et al.* with banana, an export-oriented fruit crop, against black leaf streak and tropical race 4 of *Fusarium* wilt. Both the reviews (Naidu *et al.* and Ploetz *et al.*) suggest independently the possibility of using the remarkable genome editing technology of the 21st century (CRISPR/Cas9) in place of classical breeding and transgenic approaches for targeted genome modification of grapevine and banana cultivars with resistance to the respective pathogens. The review on Torrado viruses described initially on tomato and later shown to have a much wider host range, exposes opportunities for discovering new plant viruses of this group, affecting crop plants and excitement in understanding their biology (van der Vlugt).

Comparative genomic analyses of *Verticillium* wilt pathogens have led to understanding the evolutionary mechanisms that shaped the pathogen genomes (Klimes *et al.*). However, studies on nutrient and oxidative stress on colonization of the vascular region which might lead to identification of novel genes related to virulence and host defence are stressed. Finally, the article on leaf rust of barley documents the gaps in the achievable targets for disease management (Park *et al.*).

Cucurbit downy mildew is a model downy mildew system, and its epidemiology and disease management are well studied. However, Ojiambo *et al.* raise the need for further studies on genetic determinants of pathogenicity and host range of the oomycete pathogen, and to explore avenues for how they could be utilized for breeding approaches. Additionally, knowledge on locally produced inoculum to epidemic development, relative to inoculum introduced by long-distance dispersal, and the meaningful limited use of host resistance on an area-wide basis is essential for developing sustainable disease management practices.

Yuen and Mila present a paradigm shift in the epidemiological studies from

the traditionally focused individual field unit system to a landscape scale (range of pathogen dispersal distances) enabling the disease risk quantification and predictions on a much wider area. Though presently, the landscape epidemiology considers only the conditions for infections and movement of pathogen propagules, inclusion of all the parameters of disease triangle has been suggested to improve the system. Schmale and Ross discuss a transport continuum partitioned into pathogen scale, farm scale, regional scale and continental scale, wherein, the scale can be influenced by abiotic and biotic factors, for studying the transport models for risk predictions. However, these may further strengthen forecasting disease spread and quarantine measures, besides understanding the impact of climate change on plant diseases.

Thawing out the information on latitudinal shift in a range of crop pests and pathogens, Bebber points out that while the increased distribution of crop pests and pathogens is a reality, it can be attributed to human activities, and linking it to global warming appears to be largely speculative due to incomplete and biased datasets available at present. Even the model-based predictions of bioclimatic variables in the coming century would be limited, as they do not include host ranges of the pest, adaptation and dispersal patterns. The biotic–abiotic–migration framework might remove these limitations in future approaches for improved predictions of geographical range of the species.

The involvement of host factors in plant–virus interactions reviewed by Wang, presents how small genome of viruses with limited coding facility use the host cellular system and components for infection, multiplication and transport within the host plant for its spread. The present understanding has been unearthed through the use of genomic, proteomics and bioinformatics tools during the past decade. The availability of genome-editing technology would further accelerate research to know the mechanistic roles of these host factors, which remain elusive. Hopefully, this would facilitate development of antiviral strategies and beneficial biotechnological uses of viruses. Future research in gaining knowledge on the contribution for the disassembly and assembly of virus particles, the translation, replication and

viral particle assembly, intercellular and long-distance movement of virus particles facilitating viral spread and utility of green mutants of the host plants as modules, which lack the ability to support viral infection, while maintaining the regular cellular functions, for studying the role of host factors emerge from this review.

Globalization of agriculture and world trade resulting in transnational export of agricultural commodities, and international collaborative research, necessitating increased exchange of germplasm, require monitoring of pathogen migration for determining the ancestry populations with genome-wide markers for the purpose of disease management, including quarantine measures. Goss shows its feasibility for the clonal pathogens, while it still remains a challenge in the case of pathogens with mixed mating systems, raising the need for further studies.

Appreciating the fact that plant disease epidemics cannot be controlled by pesticides, Rimbaud *et al.* consider, that variations in the basic disease management principles (eradication, suppression, containment, resilience), lead to contrasting outcomes considering the experience with sharka disease in prune trees, caused by plum pox virus (genus *Potyvirus*). The lacunae still circles around insufficient basic knowledge on the presence, prevalence and diagnostic tools for the detection of latent infection, strain diversity, epidemiology and vector transmission, which need further studies.

Nematode–plant and nematode–nematophagous microbe interactions are dealt in two separate reviews. Quist *et al.* point out that the stylet, needle-like puncturing injection device hither to considered as the unique character to parasitic nematodes may not be valid, while the cell wall-degrading enzymes could be. The hypothesis that this trait might have been acquired through horizontal gene transfer events from pathogenic soil bacteria to nematode in the evolutionary pathways in transition of bacterivores into oomycetophagous nematodes, suggesting the origin of parasitic nematode from fungivorous ancestors, however needs to be substantiated by genome and transcriptome characterization. Li *et al.* consider that molecular clues from nematode–nematophagous microbe would facilitate development of novel biocontrol agents for nematode management.

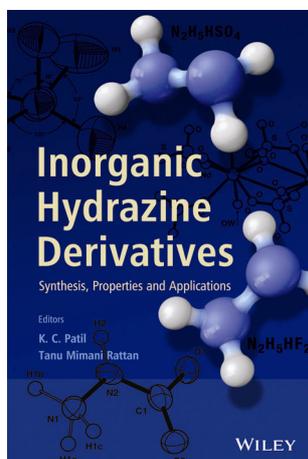
BOOK REVIEWS

This volume will certainly help the reader to gain knowledge and will have a tremendous impact on the science of plant pathology.

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Inorganic Hydrazine Derivatives: Synthesis, Properties and Applications.

K. C. Patil and Tanu Mimani Rattan (eds). John Wiley & Sons Ltd, The Atrium, Southern Gate, Chichester, West Sussex, PO198SQ, UK. 2014. 284 pages. Price: US\$ 155.

The chemistry of hydrazine and its derivatives has attracted a lot of attention since the 1950's. The importance of these compounds stems from a variety of factors, which include high energy density, reactivity and their ready availabi-

lity. So it is not surprising that hydrazine and their derivatives find use as fuels, reducing agents, additives and specialty chemicals. Entrants to this research field have to acquire a quick birds-eye view of the chemistry. Because applications of these compounds range from space research to laboratory-scale organic synthesis, it is difficult to get all the information readily in one place. In spite of its relevance, not many books are available on this specialized topic. The most authoritative source of information, apart from the primary literature, became available in 1984 when Eckart Walter Schmidt brought out an excellent treatise. This massive tome on *Hydrazine and its Derivatives: Preparation, Properties, Applications* came out in a second edition in 2001 by the same author with almost double the number of pages (2200). Fourteen years have passed without any authoritative book in this area, although the chemistry surrounding hydrazine has grown by leaps and bounds. So this book is a welcome addition. It is not surprising that the book is dedicated to Schmidt, who has been an inspiration to the editors.

This is probably the only book on this important molecule, which gives the researcher an accelerated start to the chemistry of hydrazine in about 250 pages. The book is a compendium of six chapters edited and authored by scientists with extensive experience in the area of hydrazine chemistry. In a nutshell, it is an excellent introduction to this unique molecule and their inorganic derivatives.

The book is organized in a logical and convenient way, according to the type of compounds formed by hydrazine. If you are not sure about the type of compound, then reading the first chapter is a must which gives you a clear idea of what each chapter is talking about. But if, for example, you know that you are interested in metal hydrazine complexes, you can go directly to the relevant chapter.

This makes it a handy reference tool. Apart from summarizing a large body of data on hydrazine compounds, the book quickly brings the reader up-to-date with the current state of affairs. A special feature of this book is that the authors deal with methods to generate inorganic nanomaterials using hydrazine derivatives.

The strength of the book lies in the fact that it deals not only with synthesis and properties of the inorganic derivatives of hydrazine, but also with several characterization techniques. Since these molecules are often used as propellants and explosives, it is appropriate that the book includes the thermal characterization of key molecules. For those dealing with these molecules in the industry, ready access to these details would be important, especially if they are working in quality control and trouble-shooting. As the authors have characterized several of these molecules using spectroscopy and single crystal X-ray crystallography, they also provide molecular structures of these species. This provides an insight into the chemistry of these molecules.

In conclusion, this book is meant for those who want a quick summary of hydrazine and the new developments in its use. It will be invaluable for those who plan to start research work in this area. For those who are in the industry and chemical plants where hydrazine derivatives are used, the book is a must because in a brief form, a large number of compounds are described. Interestingly, this book is now available on iTunes, Kindle and in the traditional hardback paper format. Also, the price for all of them is the same.

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