

in daily-life, which the authors have introduced. This part is also involved with the issues of geometric optics, including their astrophysical and/or gravitational physics applications, e.g. gravitational lensing.

Many modern fields of research are involved with the knowledge of fluid/plasma physics, including magnetohydrodynamics. Origin of (experimentally) observed sub-critical transition to turbulence in laboratory shear flows, e.g. plane Couette flow, plane Poiseuille flow, is a long-standing puzzle. Similar problems lie in several astrophysical flows, which often are nothing but rotating shear flows. The related astrophysical issue is the origin of viscosity and transport in an accretion disk, which is known to have an insignificant molecular viscosity. Hence, any transport therein is argued as of turbulence origin, which is difficult to explain as the underlying flows are stable under (linear) perturbation. In order to resolve these outstanding issues, a solid foundational level knowledge of fluid/plasma physics is very important which this book offers.

After developing all the above topics, finally the authors have embarked on general relativity, including recapitulation of required special relativity and some cosmology. Perhaps, this is the only textbook, as of now, discussing general relativity, however brief it may be, which also contains chapters with in-depth discussion of statistical, optical (geometrical, physical and nonlinear), acoustical and fluid/plasma physics along with electrodynamics. Some modern ideas/topics are included in this part, e.g. Penrose and Blandford–Znajek (via exercise) processes, detection of gravitational waves. The former is employed for extracting energy from a rotating black

hole by means of electromagnetic effects, which often helps explaining the jet-power of magnetized accretion flows around a spinning black hole. This process was proposed by one of the authors of the book in late 1970s. However, a similar idea was also proposed by an Indian relativist N. Dadhich and his collaborators, who considered the magnetized version of Penrose process and showed that it is extremely efficient for as little as milli gauss order of magnetic field. The prediction of this process has now been verified by general relativistic magnetohydrodynamic simulations. Gravitational wave is perhaps going to be the topic of this century, which the authors have judiciously discussed concisely, when the first author himself is one of the pioneers in this field of research.

There are many excellent textbooks on general relativity including that by the first author of this book. Also, the theme of this book is not to elaborate upon general relativity, rather classical physics. Therefore, the authors have kept the part on general relativity reasonably concise and end the book by leaving three mysteries of the universe.

All the above discussions establish the book to be a very useful and unique one. However, in a lighter note, I feel the book to be quite heavy, weight-wise, and easily could be split into a few volumes, which perhaps could be more handy for the readers. Nevertheless, it is perhaps the style of the authors, in particular, the first author whose book titled *Gravitation* is equally heavy. More so, having all the materials in a single volume has its advantage too, so that one does not need to search around various volumes for a topic of interest. The book presents a timely set of chapters, as discussed above. It has separated track two from track one in such a way, that without going through more demanding track two, the readers can grasp the subject matter of their interest.

On the whole, this is definitely a special addition to the Princeton University Press and is expected to be a valuable asset for the library collecting advanced textbooks.

BANIBRATA MUKHOPADHYAY

*Department of Physics,  
Indian Institute of Science,  
Bengaluru 560 012, India  
e-mail: bm@iisc.ac.in*



Photograph of the two vortices emerging from the wingtips of an Airbus, made visible by light scattering off water droplets in the vortex cores. Photo © Danel Umaña.

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Development of novel plant disease management strategies requires knowledge of the co-evolution or arms race, affecting phenotypic variations of disease in nature. Advances in understanding genetics of disease resistance and its functional aspects, especially pathogen-secreted (elicitors/effectors) and host surveillance (effector targets) molecules, underpin the recognition and specificity in plant–pathogen interactions at the molecular level operating through cell-autonomous, multilayered immune system in plants. Seven of the 25 reviews in this volume connect to this theme, demonstrating the significance and expectations from it for better crop improvement. Two of these chapters (Hawes *et al.* and Deleris *et al.* – annotated below) even take a step closer in connecting plant and animal immunity systems.

Pertinently, this volume opens up with an autobiographical reflection of a remarkable academic de Wit, who was engaged in understanding host–pathogen interactions in tomato – *Cladosporium fulvum* pathological system, with an urge to protect crop plants with their own immune system<sup>1</sup>. Passing through the critical stage of understanding recognition and specificity, more particularly in eukaryotic pathogen and plant relationship, his pioneering achievements include identification of the first fungal avirulence gene in addition to four more; isolation and purification of the *Avr* gene products from *in planta* interactions, now known as effectors, lead to cloning of these genes, and elucidating their functions. These credited de Wit to be the first to provide molecular proof for the pathogen race-cultivar specificity envisaged by gene-for-gene hypothesis. Cloning of the effector genes enabled the research group of Jonathan Jones to isolate all the cognate immune receptor genes that include the first fungal disease resistance gene to be isolated<sup>2</sup>. The products of these genes which are receptor-like proteins mediate recognition of matching effectors, directly or indirectly.

Entry into the genomics era with the sequencing of *C. fulvum* attracted others to delve into this pathosystem. This helped deepen our understanding on plant immunity to fungal pathogens. de Wit's narration demonstrates the perseverance, patience and creativity in tackling plant pathological problems in a holistic manner, leaving a lot for emulation, especially by younger generations.

The effector–receptor protein recognition in a single crop (soybean) to its diverse pathogen groups (viruses, bacteria, oomycetes, fungi and nematodes) dealt separately, shed light on our understanding of the molecular mechanisms of immunity and its suppression (Whitham *et al.*). Multiple disease resistance (MDR) trait in crop plants is of agricultural importance in enhancing the efficiency of crop management strategies. An eloquent coalescence of genetics, genetic epidemiology and ecological genetics, besides the molecular responses in plant–pathogen interactions towards gaining deeper insight on MDR is stressed by Wiesner-Hanks and Nelson. Dealing with effector biology, Toruño *et al.* examine the effector targets focusing on the cellular sites of action and function relative to the infection and pathogenesis process and specificity. Hemibiotrophic pathogens modulate the cellular environment through sets of effectors in a coordinated manner for switching over their lifestyle from biotrophy to necrotrophy. This chapter also illustrates how pathogens manipulate host gene expression through effectors. Expansion of knowledge on effector biology hopefully moves towards opportunities for exploitation in devising novel control strategies. Homogeneity in agroecosystems favours the appearance of pathogens with new virulence traits for their survival. A recent (post-review) discovery of the genetic mechanism of host jump in the case of wheat blast traces to past inadvertent compositional disturbance of the ecosystem by way of cultivar introduction lacking specific resistance genes resulting in the present homogenization of the ecosystem. Wheat blast has now emerged as a global threat to an important staple food crop<sup>1</sup>. Jacques *et al.* document ecological, physiological and molecular basis of pathogenicity related to the lifestyle alterations and possible pathogen adaptability with xanthomonads as an example to conclude molecular basis of host, specificity as the key issue that may

provide the answer for shifts in host range. The persistence and metabolic potential of sloughed-off root border cells (root cap cells) released into the rhizosphere for a longer time than originally thought open a new dimension in innate immunity of plants, particularly against the worst root-infecting bacterial and fungal pathogens. These cells provide an early extra-root defence layer forming DNA-based extracellular traps with functions similar to white blood cells (neutrophils) in mammalian immune system, and exDNase of the pathogens emerging as a virulence factor. Hawes *et al.* present an overview, a discussion of the fundamental science of root border cells with relevance to engineering rhizosphere for protecting plants against the root-invading pathogens and even bridging with human immune studies for deeper insights. Successive immune responses to pathogens, activate a cascade of gene expressions under tight regulation. Deleris *et al.* detail the current understanding of epigenetic mode of action in the extensive transcriptional reprogramming modulating immune responses in the model plant *Arabidopsis*. The epigenetic inheritance over generations points to the involvement of epigenetic alleles (epi-alleles) in the transgenerational immune priming, raising an issue that it could be an adaptive factor and attract future investigations.

Three reviews present the current available knowledge on various subjects that may arouse interest in certain areas of study, with the availability of advanced technologies. Singh *et al.* examine the status of globally important wheat diseases and weigh up the available opportunities for mitigating the problem. Alternate hosts play a significant role in disease epidemiology and pathogen diversity of small-grain cereal rusts. These may serve as tools for studying the genetics of rust pathogens (Zhao *et al.*). Working with tree diseases demands a long-term commitment. Taking bananas and cacao as examples, Drenth and Guest explore the challenges posed by filamentous pathogens in tropical fruit trees.

Several important milestones have been achieved with tobacco mosaic virus. However, morphological details of compartmentalized space where viral RNA multiplication takes place in the host cell and the replication machinery are yet to be known (Ishibashi and Ishikawa). Similarly, the molecular processes in-

involved in tobamovirus RNA multiplication reveal lack of information on enzymatic activation of replication proteins. The authors stress the need for advanced electron microscopy analyses together with cell biological studies for eliminating these knowledge gaps. Arthropod-borne negative-strand RNA (NSR) viruses infecting plants through transmission by phytophagous thrips are relatively few in contrast to those infecting animals and humans. Turina *et al.* dealing with tospoviruses belonging to NSR viruses that cause havoc in vegetables, provide updated information on virus taxonomy, biology and plant–virus interactions, with attention to infection cycle and host resistance. Reverse genetics analyses facilitated understanding of the interactions of these viruses with the host at genetic and molecular level in animal systems, while the non-availability of these genetic tools had hampered advancements in plant system (Jackson and Li). Recent advancements in the development of the first reverse genetics system for a Nucleorhabdovirus along with alternative approaches available for furthering knowledge on infection cycle and pathogenesis in plants are discussed. Stable expression of foreign proteins by these viruses has been pointed out to be of high value for biotechnological and medical applications. Outbreaks of leafhopper and planthopper-vector reoviral diseases, transmitted in a persistent propagative manner, is a concern for rice production in Asian countries. Knowledge of virus–vector relationships would facilitate possibilities of disrupting viral transmission. The transmission barriers within insect vectors, molecular aspects of viral persistent infection and vector competence in reoviral diseases of rice are elegantly portrayed by Wei and Li. The authors emphasize the need to direct future studies on multiple interaction systems among the virus, insect vectors, insect obligate bacterial endosymbiont and plant.

Despite the agricultural importance of root lesion nematodes as a potential yield-limiting factor, especially in cereal, sugarcane and horticultural crops, the nematode–host interactions are not well understood. Fosu-Nyarko and Jones lay the ground with the present knowledge on the molecular and genomic information regarding these obligate migratory endoparasites for furthering research on host defence and on how the nematodes

safeguard themselves amidst the rhizosphere microbiome. The amenability of manipulating endophytic microbes harboured inside plant root tissues in contrast to complex microbiomes of the soil or rhizosphere regions, make them preferable for harnessing their potential in improving plant health. Schouten describes the possible direct antagonism and indirect protection through modulation of host defence by the fungal endophytes against nematodes involving multifold interactions. This necessitates discrete modulation of plant defence by the microbial endophytes to protect themselves and to fight the parasitic nematodes.

Both disease severity and the efficiency of its management strategies are largely influenced by environmental heterogeneity. The diverse microbial communities of nonpathogenic organisms and coinfecting pathogens and the interactions among themselves and the host cells shape the disease ecology. Borer *et al.* apply the meta-community theory to probe pathogen dynamics at multi-scale level that would also facilitate gaining knowledge on plant microbiome on the whole. In the recent decade, there has been growing attention to examine evolutionary relatedness among interacting species and the phylogenetic diversity in a community resulting in the emergence of the concept known as phylogenetic signal. This is a tendency of related species to be more similar in their traits to each other. Gilbert and Parker project the conceptually new approach along with the available tools for use in research on plant disease ecology spreading over co-evolutionary dynamics of plants and pathogens, disease severity, host range, emerging disease threats, biological control and phytosanitary risk analysis. The advent of whole-genome sequencing would power population genomics for gaining deeper insights into the biology, genetics and pathogen evolution. Grünwald *et al.* visualize its application in plant pathogenic fungi, and oomycetes might lead to molecular phenotyping in place of traditional ways of pathotyping and in the evaluation of fungicide sensitivity furthering into molecular epidemiology (as is being used in human medicine) and also in the creation of virtual pathogen collection complementing the existing

live pathogen collections required as a biological resource. The metabolic activities of aboveground and belowground plant compartments function in a tightly coordinated manner. Addressing the molecular dialogue between the compartments, Biere and Govere show that plant-associated diverse groups of phytophages (pathogens, arthropod herbivores and nematodes) facilitate each other between the same or different kingdoms, both within and cross-compartments. This plant-mediated function influences not only host resistance, but also the resource dynamics as with sugar signalling in defence and defence hormones in source-sink relationships.

Molecular breeding for improving disease resistance either with single resistance gene or by stacking multiple major resistance genes, using marker-assisted selection (MAS) strategy has been successful, when the need is driven by market demand for an improved elite cultivar that is otherwise vulnerable to diseases. Quantitative resistance conferred by many minor genes is preferable for durability of this trait. Combining disease phenotyping for quantitative resistance, with yield assessment and other agronomic traits results in genetic constraints. This necessitates diversion of molecular breeding approach from MAS to genomic selection and using whole-genome prediction models. Poland and Rutkoski justify the practicality of genomic selection for disease resistance in breeding programmes. Emmer wheat is considered as one of the base eight founder crops of the origin of agriculture. The value of its descendants existing as natural populations in the Near East that have emerged through exposure to high selection pressures exerted by different biotic and abiotic factors resulting in primitive progenies with diverse preferred agronomic traits, has been projected by Huang *et al.* Their compatibility with durum and bread wheat makes them centrally important in wheat breeding. Conventional genetic approaches together with advanced molecular technologies would facilitate mechanistic understanding of various stress-tolerances ushering into function-based molecular breeding of wheat.

The depiction by Fry of how efficiency of late blight management has

improved by clubbing new and modern information with the old knowledge is insightful. It stands out as an example for the integration of epidemiological understanding, computational skill, population genetics, pathogen biology and molecular plant-pathogen interactions that led to the success of late blight management. However, the author points out that the occasional, but continued more severe incidence than the predicted level is of concern. This would stimulate further improvement in late blight management. The analysis by van Bruggen and Finckh on disease situation in organic farming reveals that the severity of root diseases is less in organic, compared to conventional farming systems, while the aerial diseases fluctuate in both. Higher potential yield accompanies greater risk of losses due to biotic stresses in conventional farming systems. However, comprehensive information on disease severity and crop losses from large-scale experimentation is still lacking. The arguments suggest that disease management strategies for organic farming systems are yet to be evolved. Global movement of plant and plant products has been on the rise to new heights. Martin *et al.* critically examine the powerful tools offered by metagenomics for their utility in plant quarantine testing.

The varied presentations in this volume accurately depict current information with perspectives for filling up the lacunae and project emerging concepts for future research. These appropriately illustrated and well-referenced reviews deserve to be widely read by phytopathologists and plant biologists in general.

1. de Wit, P. J. G. M., Farewell address, Wageningen University, 5 June 2014; ISBN 978-94-6173-976-6
2. Jones, D. A., Thomas, C. M., Hammond-Kosack, K. E., Balint-Kurti, P. J. and Jones, J. D. G., *Science*, 1994, **266**, 789–793.
3. Inoue *et al.*, *Science*, 2017, **357**, 80–83.

R. SRIDHAR

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