2 gives the English version of CR's explanation of the simple technique of measuring the Sun's parallax, during the transit of Venus, and thus estimating the Earth–Sun distance. Shylaja has also taken lot of pains in providing the corrected versions of the Sanskrit *shlokas* quoted by CR, often misspelt, from several original Sanskrit texts. Thus Shyjala's contribution to our understanding CR's eminence as a dedicated astronomer, an effective communicator and also an achiever in contemporary Indian astronomy in his time, can hardly be exaggerated. She richly deserves our gratitude and congratulations.

S. BALACHANDRA RAO

Bhavan's Gandhi Centre of Science and Human Values,
#43/1, Race Course Road,
Bangalore 560 001, India
e-mail: balachandra1944@gmail.com

Annual Review of Phytopathology, 2012. Neal Van Alfen *et al.* (eds). Annual Reviews, 4139 El Camino Way, P.O. Box 10139, Palo Alto, California 94303-0139, USA. 2012. Vol. 50. 494 pp. Price: US$ 89.

This volume contains 23 review chapters covering diverse aspects and recent advancement in plant pathology. The remarkable progress in molecular methods and genomics has greatly contributed to our understanding of plant diseases. This knowledge has led to innovative methods of disease control. The volume provides updated in-depth analysis on various fascinating topics of plant–pathogen interactions, including biology of plant pathogens and their mechanism of pathogenesis, molecular basis of plant–microbe interactions, signalling involved in plant immunity, microbial ecology and epidemiology, plant disease management and other important topics.

The prefatory chapter opens with personal history Kurt J. Leonard (University of Minnesota, St Paul, USA) reflecting his outstanding career as an eminent plant pathologist and his important work on epidemiology and genetics of disease resistance in plants. This article is a treat to read for budding scientists and science graduates as it describes how dedication, right decision, timely advice, hard work and suggestions from colleagues can help develop a fruitful career. The following chapter is a tribute to a distinguished plant pathologist Kelman, intelligently complied by Luis Sequeira. Kelman was one of the influential scientists and an extraordinary leader of his era, who made significant contributions in the areas of bacterial plant pathogenesis and ecology.

The recent rapid development of genomics has significantly helped in understanding of plant diseases by providing new information about the virulence mechanisms employed by successful pathogens. In this context, the chapter by Lindeberg elaborates that genome sequence data have revealed several novel and critical molecular determinants of pathogenicity, not only in the better characterized bacterial pathogens such as *Xylella*, *Xanthomonas* spp., *Ralstonia solanacearum*, *Pectobacterium*, *Pseudomonas syringae*, etc. but also from less characterized pathogens such as phytoplasmas and *Candidattus* spp. Genomic comparisons provide further insights into the evolution of pathogens and their adaptation to various niches. Moreover, information generated from genome-scale sequencing will be useful in devising new methods in disease control.

In a separate chapter, Genin and Denny describe the molecular determinants responsible for virulence and host-range species of *R. solanacearum*. A detailed account on the regulatory networks important for pathogenesis has been presented. The authors discuss that genome sequencing of several strains of *R. solanacearum* has provided insight into speciation and evolution of this pathogen, and recent progress in identifying new virulence factors. The article by Malnoy *et al.* focuses on another bacterial phytopathogen *Erwinia amylovora*, a causal agent of fire blight in members of Rosaceae family, such as apple, pear, etc. This chapter offers insights on current understanding of fire blight host–pathogen interactions; recent advances in the genomics of *E. amylovora* and one of the its hosts (apple), and improving management of fire blight disease using genomics approaches. Chorkowski *et al.* have comprehensively reviewed the role of protein secretion systems (types I–VI) and multiple types of small molecules in pathogenesis of soft-rot Enterobacteriaceae (SRE), including genera *Pectobacterium* and *Dickeya*, the causal agents of wilt, rot and blackleg disease on a wide range of plants.

Barak and Schroeder have reviewed the emerging discipline of plant pathology aiming at detailed study of association between human enteric bacterial pathogens and plants. The authors have covered various modes of contamination of agricultural produce with bacterial food borne food borne human pathogens such as *Salmonella*, pathogenic *Escherichia coli*, etc. Recent research progress revealing plant colonization mechanism used by human pathogens has been complied. Presence of other phytopathogens increases the risk of contamination of agricultural produce with these pathogens. The authors have summarized few applications that could decrease the risk of human illness via reducing contamination of fresh agriculture produce by human pathogens.

The comparative genomics of obligate, nonobligate fungal pathogens (ascomycetes and basidiomycetes) and oomycetes has been described by Spanu. Comparative genome analysis of sequenced biotrophic pathogens has indicated loss of genes that encode proteins participating in inorganic nitrogen and sulphur metabolic pathways, thiamine metabolism, carbohydrate active enzymes and secondary metabolic enzymes. Additionally, these studies highlight that in some biotrophs, overall genome size has increased due to active proliferation of retrotransposon. Overall, the mechanisms underpinning obligate biotrophy have been well presented in this chapter. Jiang and Tyler focus on virulence mechanisms, pathogenicity factors, genomic properties and genomics led insights into evolution and host specificity of plant oomycetes group of pathogens. Oliver *et al.* provide a well-complied review on a wheat pathogen *Stagonospora nodorum*, a model for necrotrophic pleosporales group of pathogens. The authors have emphasized that various tools such as functional genomics, genome sequencing, proteomics, metabolomics and source of large number of isolates have helped in identifying the key pathways important for its pathogenesis.

Understanding the variability of pathogens belonging to order Uredinales (commonly known as rust fungi) has provided ways of development of new plant cultivars with genetic resistance against rust pathogens. Park and Wellings describe the mechanisms that are responsible for genetic diversity in rust fungi. The single-step mutation, somatic hybridization and periodic introduction of exotic isolates are the major ways that have led to genetic diversity. The mechanisms involved in somatic hybridization have been discussed in detail. The authors have concluded the chapter by discussing resistance breeding in controlling rust. Hansen *et al.* point out that the number of described *Phytopthera* spp. has increased rapidly in the past decade because of exploration of new habitats such as forest ecosystem, in which *Phytopthera* spp. are widespread and diverse.

Stuart *et al.* have illustrated well the biology of hessian fly (HF)–wheat interaction, a model plant–parasitic insect pathosystem. In this chapter, the biology of HF as well as information on its genome have been highlighted. Several putative effector proteins are expressed in the salivary gland and these are recognized by wheat in the gene-for-gene manner, in which wheat *R*-genes provide resistance against HF. Overall, these indicate evidence for the presence of effector triggered immunity against HF in wheat. The role of nematode peptides and small molecules in plant pathogenesis has been reviewed by Mitchum *et al.* Nematodes are able to secrete mimics of plant peptide hormones, a kind of sophisticated strategy promoting nematode parasitism. Nematode genome encodes a number of secreted peptide family members, some of which are essential for parasitism. The best-studied class of nematode-secreted peptides is the CLE-like class, which is the main focus of this chapter. The authors have emphasized on the fact that this information would be useful in generating new strategies to achieve resistance against nematodes.

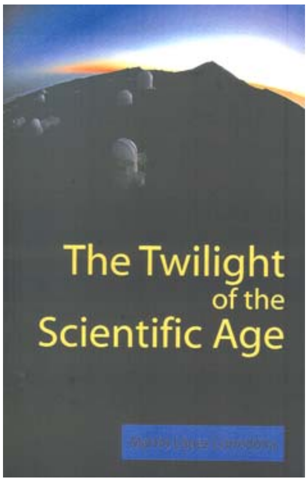
Plants have the ability to recognize and provide appropriate responses in the form of elaborate signalling events, against either pathogens or symbionts. This is achieved via cell surface plant pattern recognition receptors (PRRs) comprising receptor-like kinases (RLKs) and receptor-like proteins (RLPs). Antolin-Llovera *et al.* provide a comprehensive review about RLK-mediated signal transduction pathways in plant–microbe interactions. Plant PRRs-typically contain either leucine-rich repeats or lysine motif domain, through which they recognize various microbes and in turn induce immune or symbiotic responses. Components participating in the signalling pathways of RLKs leading to symbiotic or defensive responses are largely distinct. Similarity in early signalling events and differences in late signalling events lead to either defence or symbiosis. A biotechnological transfer of PRRs into economically important crops has been shown providing broad spectrum disease resistance. In a related area, Mengiste has given detailed account on plant immune responses against necrotrophs and has elaborated how these responses are different when plants encounter biotrophs.

Few chapters in this volume are dedicated to plant pathogen monitoring and disease control. Diagnosis of plant diseases as well as rapid detection and identification of plant pathogens are essential steps towards controlling plant diseases. De Boer and Lopez have highlighted the technology advancement and plant pathogen monitoring systems, while Mazzola and Manici describe the etiology of apple replant disease and its management. Various approaches that may suppress this disease in effective ways have been discussed. Hadar and Popadopoulou have reviewed the mechanism involved in plant disease reduction using compost. Suppressive compost provides a kind of environment in which plant disease is reduced. Plant disease suppression takes place because of action of antagonistic microbial consortia which naturally recolonize the compost.

Other topics included in this volume are: variation and selection of quantitative traits of pathogenesis in plant pathogens; landscape epidemiology of emerging infectious diseases in ecosystem; natural functions of antibiotics produced by beneficial and plant pathogenic bacteria and their diversification, and use of system biology in the study of plant defence compounds. Overall, this volume is highly informative and is a must read for all those interested in molecular plant pathology, microbiology, molecular biology and applied plant pathology.

ALOK PANDEY

CSIR-Centre for Cellular and Molecular Biology,
Uppal Road,
Hyderabad 500 007, India
e-mail: alok@ccmb.res.in



The Twilight of the Scientific Age. M. L. Corredoira. Brown Walker Press, Boca Raton, Florida, USA. 2013. 208 pp. Price not mentioned.

The basic premise of the book under review is wrong. Science is well and kicking and all the modern-day inventions are a direct result of scientific discoveries that are happening almost every day. As long as human beings are on this planet, science will continue to grow, because it is driven by curiosity. And human beings are inherently curious!

The book contains many clichés, half truths and unsupported statements, that one does not know where to start. For example, in the first paragraph itself, the author writes that the central theme of the book is, ‘Our era of science is declining because our society is becoming saturated with knowledge which does not offer people any sense of their lives.’ How the author came to such a conclusion is anybody’s guess. The book is full of such half-baked ideas which are without any foundation.

In my opinion a book, especially one based on the author’s belief rather than hard facts does not find a place in the library of scientists.

ANIL K. RAJVANSHI

Nimbkar Agricultural Research Institute,
P.O. Box 44,
Phaltan 415 523, India
e-mail: anilrajvanshi@gmail.com