

Photosynthesis. Regulation Under Varying Light Regimes. V. S. Rama Das. Science Publishers, Inc, Post Office Box 699, Enfield, New Hampshire 03748, USA. 2004. 175 pp. Price: US \$65.

Photosynthesis is one of the important metabolic components of plant systems. Despite the fact that quality and quantity of light are crucial, the process of photosynthesis adjusts quickly whenever the available light is either limiting or in excess of the optimal requirement. A concise and informative book on this topic authored by Rama Das, who has decades of experience in this field, is quite welcome. Rama Das has made a splendid effort in putting together extensive information on this topic into a handy small book.

Short- and long-term fluctuations in light pose a serious challenge to photosynthesis in higher plants. These fluctuations include not only supra-optimal or high light, but also sun-flecks, shaded environment under tree canopies and extended cloudy days in rainy season. This book provides a detailed, yet compact resource of information on 'photosynthesis in response to high light stress'. Thus, it forms an essential supplement to other popular textbooks on photosynthesis¹⁻³.

The first chapter of the book describes the requirement of light for photosynthetic processes, introducing the reader to the concept of antennae and the two photosystems of PSI and PSII. The next chapter discusses the phenomenon of photoinhibition, and its occurrence, on either acceptor or donor side of PSII. This chapter also gives a lucid view of molecular basis of photoinhibition and protective mechanisms. The focus mainly has been on the damage to D1 protein and attempts by chloroplasts to restore the functional PSII. The third chapter, one of the best in the book, presents how the plants avoid excess light and protect themselves. These protective mechanisms include xanthophyll cycle, production of reactive oxygen species (ROS) and relevant scavenging enzymes/compounds. All these phenomena contribute to minimize the oxidative stress on chloroplasts. The next three chapters are small and deal with leaf movements, acclimation of photosynthesis and biotechnological approaches respectively. The last chapter is a brief section with concluding remarks.

I find the book to be quite simple to read, clear in its presentation of the concept of photoinhibition and description of protective

mechanisms. The book would be useful for both beginners and experts in the area of photosynthesis. However, a few topics could have been covered in more detail, for example, the response of plants to limiting light, which occurs frequently in temperate regions. Even the injurious effect of excess light is amplified, when combined with low temperature. Since the title of the book refers to the regulation under varying light regions, description of the interactions of limiting or excess light with other factors such as temperature, UV light and nutrition deficiency would have been beneficial. The aspects of state transitions, and mobility of PSII could have been given more attention, because of the dynamic and dual role of PSII, being the target of photoinhibition as well as a protector of thylakoid membranes from excess light.

Indication should also have been made about the long- and short-term effects of excess light and the contrasting strategies of plants during such varying time periods. While changes occur in xanthophyll cycle or ROS scavenging enzymes occur during short-term adaptation of plants, long-term exposure to excess light invariably demands modulation of gene expression pattern. The importance of heliotropism in protecting plants against excess light is still debated. The description on transgenic and biotechnological approaches, mostly on modulation of light harvesting complexes, PSI and PSII in general, could have been extended to photoinhibition.

The importance of the topic of photoinhibition of photosynthesis to plant sciences is evident from the release of a Special Issue of *Journal of Experimental Botany* (2005, 56) on light stress in plants and a forthcoming book under the series of *Advances in Photosynthesis and Respiration*⁴. The present book on photoinhibition of photosynthesis is informative and is available at an attractive price of US\$ 65. I recommend the book to all educational institutions, teachers and research workers interested in the field.

1. Hall, D. O. and Rao, K. K., *Photosynthesis*, Cambridge University Press, Cambridge, UK, 1999, 6th edn.
2. Lawlor, D. W., *Photosynthesis: Molecular, Physiological and Environmental Processes*. BIOS Scientific Publishers, UK, 2001, 3rd edn.
3. Raghavendra, A. S., *Photosynthesis. A Comprehensive Treatise*, Paperback Edition, Cambridge University Press, Cambridge, UK, 2000.

4. Demmig-Adams, B., Adams, W. W. and Mattoo, A. K. (eds), *Photoprotection, Photoinhibition, Gene Regulation and Environment – Advances in Photosynthesis and Respiration*, 2005, vol. 21, Springer, in press.

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Microbial Genomes. C. M. Fraser, T. D. Read and K. E. Nelson (eds). Humana Press, Totowa, New Jersey, USA. 2004. 536 pp. Price: US\$ 150.

The sequencing of complete genomes of a number of free-living, pathogenic and obligatory intracellular microorganisms of late, has provided a plethora of information about microbial genomes. This has brought a radical change in our understanding of genome organization and function, mechanism of microbial pathogenicity, evolution and interactions of microbes in the environment. The foreword to the book under review has been written by J. Craig Venter, founder of The Institute of Genomic Research (TIGR, MD, USA). According to Venter, the great expanse and astounding possibilities of microbial genomics may be realized from the fact that ideas and concepts, which sounded like science fiction a few years ago, are being pursued vigorously today. And the pace of the microbial genome sequencing continues.

The book under review has been divided into six parts, each comprising many chapters. Part I comprising only one introductory chapter contributed by H. O. Smith, is devoted to the history of deve-

lopment of microbial genomics, which includes a description of the events and discoveries that set the stage for microbial genomics. Ample readable, this section brings out the visionary and leadership role of the US Department of Energy and National Institute of Allergy and Infectious Diseases in initiating the field of microbial genomics. Part II of the book entitled 'Bioinformatics as a tool in genomics', comprises four chapters. The common bioinformatics tools for bacterial genome analysis such as GlimmerM and MUMmer have been discussed. The former attempts to find all genes in a genome, whereas the latter is meant for whole genome comparisons. The use of bioinformatics for understanding microbial pathogenicity has been discussed at length. A major attraction of this section is the inclusion of several important websites and programs, which would be helpful to readers interested in knowing more about microbial genomics and related field, including bacteriophage bioinformatics.

Part III deals with genomics of core functions, viz. metabolism, membrane transport and cell cycle. Genomic data may be used to identify and study several novel, hitherto unknown or uncharacterized metabolic pathways. It is well known that only a small fraction of microorganisms extant in nature has been cultured *in vitro*, which constitutes a major limiting factor in studying the metabolic diversity of the microbes. The genome sequence data may be used to understand the nutritional requirements of such organisms, so that a greater number of microorganisms may be cultivated in the laboratory making these amenable to further studies. The induction and expression of housekeeping genes of a number of microorganisms have been compared to uncover the metabolic variability. The microbial sequence analysis for various membrane transporters, their phylogenies and genetic regulation has also been explored, as transportation of various molecules constitutes the very basis of life. The last chapter in this section discusses genomic-based analysis of the bacterial cell cycle. Despite identifying more than 550 genes involved in cell-cycle regulation, it has not been possible to resolve some of the major points even by the best of the methodologies available. The author has also raised certain questions, answers to which are still awaited. Prominent among these are – do bacteria use checkpoints and surveillance mechanisms to control cell cycle? And how are

the changes in cell morphologies coupled to mechanisms of cell cycle? This section has been particularly illustrated by the use of neatly drawn, high quality colour figures.

The study of microbial evolution has been revolutionized by the availability of DNA sequencing, and analysis tools. Section IV on the evolution of microbial genomes – a collection of four chapters – is an attempt to understand prokaryotic evolution and taxonomy in the light of genomic data. There is a comparative account of the classical and molecular taxonomy of microbes. The exchange of genetic material amongst different microbes occurring in the natural environments is now recognized as a major factor responsible for microbial evolution. The enormity and significance of horizontal gene transfer (HGT), also known as lateral gene transfer, has been realized only after the advent of comparative genomics of the microbial species. The occurrence of HGT across different domains has also been discussed. The concept of bacterial biodiversity has been correlated with microbial genomics. The role of horizontal gene transfer in the appearance of new bacterial species having capabilities to colonize distinctly new environmental niches has been described. Genetic exchange among bacterial populations has been considered as responsible for ecological divergence of microbes. The genomic co-evolution of host and the associated microbes, whether symbiont or pathogenic, has also been discussed. The microbial genomic information has been used to discern the complex relationships between pathogens and their hosts.

Section V entitled 'A survey of microbial genomes' and comprising nine chapters, by far the largest in the book, is devoted to detailed descriptions of characteristics and peculiarities of microbial genomes. These include plant pathogens, extremophiles, pathogenic enterobacteria, obligate intracellular pathogens, low G + C and high G + C Gram-positive organisms, anoxygenic phototrophic bacteria, protozoan parasites and an extremely halophilic archaeon. Relatively, only a few plant-pathogen genomes like *Agrobacterium*, *Ralstonia* and *Xanthomonas* have been sequenced. This area definitely needs further impetus. Comparative genomic studies reveal mechanisms which underlie the existence of microbes at extremely high temperature and the adaptations required for thermophily, especially pecu-

liarities of their cell metabolism. The genomes of intestinal inhabitant, i.e. members of the family Enterobacteriaceae have been described, highlighting investigations from well-studied genera like *Escherichia coli* and *Salmonella*. The success of these organisms as pathogens is attributed to the acquisition of large genomic fragments called pathogenicity islands and small-scale genetic changes such as excisions, deletions and mutations. The unique features of obligate intracellular pathogens such as *Rickettsia* and *Chlamydia* highlight the continuous retrograde evolution of their genomes, which is balanced to some extent by the influx of genes. Does it mean that reductive evolutionary processes in these microbes will eventually lead to their extinction? The genomes of Gram-positive bacteria having low G + C content such as *Bacillus*, *Clostridium*, *Listeria*, *Mycoplasma*, *Staphylococcus* and *Streptococcus* have been described because of their ability to cause diverse human diseases and unique physiologies. *Actinobacteria*, the Gram-positive bacteria with high G + C content are important in human and veterinary medicine, biotechnology and ecology. Comparative genomics of microbes under this group revealed that *Mycobacterium tuberculosis* probably originated from *M. bovis* approximately 15,000 years ago. Further studies on the comparative genomics of mycobacteria in general, may reveal insights into the transition of harmless soil bacteria into obligate intracellular pathogens. Besides the evolutionary cues, comparative genomics has uncovered several functional aspects too. The genetic regulation of energy-conversion pathways in phototrophs and non-phototrophs has been compared in order to understand comparative microbial metabolism (N₂ fixing capabilities, CO₂ fixation, H₂- and S-metabolism). Sequencing genomes of parasites is a different game – they have complex life cycles, are difficult or impossible to maintain in the laboratory and have relatively larger genomes. However, large investments are being made for sequencing genomes of many parasites, viz. *Entamoeba*, *Leishmania*, *Plasmodium*, *Toxoplasma* and *Trypanosoma*, which are sure to bear fruits in the near future. This section ends with genomic analysis of an extremely halophilic archaeon, *Halobacterium*. It illustrates how enormous amount of information about diverse aspects of microbes may be extracted from their genomic data.

The last part of the book (part VI) brings into focus applications of the genomic data. All areas of application of microbial genomics to human health, such as development of vaccines, drugs and diagnostics as also other areas like biocatalysis, discovery of new enzymes and biodegradation have been discussed in the six chapters included here. Besides, there is one chapter each on the use of microarray for expression analysis of microbial genomes and environmental microbial genomics (metagenomics). The last chapter aptly highlights the importance of proteomics, which is a prerequisite for studying gene expression.

This book is a treasure trove of state-of-the-art information on wide-ranging aspects of microbial genomes, written and edited by hard-core practitioners of the discipline. The language and presentation is simple, so that even postgraduate students may not find any difficulty in understanding the subject matter. Each chapter is supported by a list of carefully selected bibliography, which includes papers published in high-impact journals only. Thus, the book may also serve as a reference work on microbial genomes. It is strongly recommended for students of general microbiology, bacteriology, virology, molecular biology, biochemistry,

microbial population genetics, microbial ecology, microbial evolution, microbial proteomics, and those interested in the development of antimicrobials, drugs and vaccines for infectious agents.

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