PREFACE

Genomics is the comprehensive study of genetic information of a cell or organism including gene sequences in living organisms, the function of specific genes, the interactions among different genes, and the control and regulation of gene expression through activation and suppression of target genes. The human genome has been the biggest project undertaken to date but there are many research projects around the world trying to map the gene sequences of other organisms. Many diseases due to single gene defects have already been identified. New data obtained by human genome sequencing will help scientists better understand multifactorial diseases such as asthma, diabetes, heart disease and cancer. Genomic mapping enables us to develop new preventative and therapeutic approaches to the treatment of disease and understand the mechanics of cell biology. Genomics is generating a lot of excitement not only in the scientific research institutes and pharmaceutical companies but also in the financial and insurance worlds. Proteomics is the large-scale study of proteins, particularly their structures and functions. It describes the qualitative and quantitative comparison of proteomes under different conditions to further unravel biological processes.

Genomics and proteomics are promising scientific fields of current society. In this book, different gene products with a similar role in neuronal defense against oxidative stress were discussed by Zhi-Gang Jiang and Hossein A. Ghanbari in Chapter 1. Gene-gene and gene-environment interactions in genetic epidemiology were discussed by Alison A. Motsinger and David M. Reif in Chapter 2. Jenny F. L. Chau and Baojie Li describe the elucidation of proto-oncogene c-Abl function with the use of mouse models and the disease model of chronic myeloid leukemia in Chapter 3. Francisco Prosdocimi overviewed theory on the molecular nature of postzygotic reproductive isolation in Chapter 4. A. Focà, M. C. Liberto and N. Marascio described next generation sequencing, microbiome evaluation, molecular microbiology and its impact on human health in Chapter 5. Proteomics and prostate cancer was demonstrated by Jae-Kyung Myung and Marianne D. Sadar in Chapter 6. Jayapal Manikandan and others have described RNA interference therapeutics in Chapter 7. Molecular mechanisms of hepatitis C virus entry were discussed by Mirjam B. Zeisel and Thomas F. Baumert in Chapter 8. Molecular phylogenetics for elucidation of evolutionary processes from biological data was discussed by Martina Talianova in Chapter 9. The

role of protein prenylation and processing in plant development, phytohormone signalling and secondary metabolism were discussed by Dring N. Crowell and Devarajan Thangadurai in Chapter 10. In Chapter 11, Ralf G. Dietzgen and his collaborators expound on the advantage of information systems like mangomics to support advanced mango breeding. In Chapter 12, Jeyabalan Sangeetha and her team overviewed the role of environmental genomics with special reference to understanding the impact of transgenic crops on soil quality, microbial diversity, and plant-associated communities. Mirza Hasanuzzaman and his colleagues have discussed biotechnological and genomic approaches for abiotic stress tolerance in crop plants in Chapter 13. Finally, molecular and genomic approaches of microbial remediation of petroleum contaminated soils have been discussed in Chapter 14.

The publication of this book was not solely the effort of only two of us. We owe a great debt of gratitude to all those who have so kindly contributed and deserves special credit for putting their valuable time and effort. In addition, we gratefully acknowledge Sandy Jones Sickels, Vice President, and Ashish Kumar, Publisher and President, at Apple Academic Press, Inc., for their keen interest and effort in bringing out this publication. Collectively, we hope the work will prove to be most useful in the understanding of past, present, and future scientific and technological innovations in these genomic and proteomic era.

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