# Preface

Over the decades, in the fields of plant biology and crop breeding, a huge amount of sequencing data and omics-related information involving genomics, transcriptomics, proteomics, interactomics, and emerging integrative multiple omics, have been produced and inevitably continue to increase dramatically. In the meantime, bioinformatics tools have to be organized and upgraded fast to be capable of analyzing the resulting big raw data, which might reveal new aspects of biological mechanisms and networks as well as acquire the valuable genetic information of agronomic traits to aid in breeding programs of crops. Bioinformatics tools are powerful in solving biological problems by predicting novel functions of genes, protein-to-protein interactions, and biological networks. Nowadays, these tools are indispensable, and the knowledge of bioinformatics/computational biology/systems biology is increasingly prosperous; therefore, a timely summary of the emerging literature is necessary, which can provide a practical handbook for researchers and can also advance the future exploration of these tools and related research topics.

This book summarizes the current technical achievements in bioinformatics and presents their emerging applications in the research fields of plant science and agri-biotechnology for crop improvement. Also, it presents multiple omics-assisted molecular breeding which aim to the development of high-yield, high-quality, and stress-tolerant crops. In the topic of genetic mapping for interest genes, bioinformatics tools have been upgraded in a way to facilitate the identification of quantitative trait loci (QTLs), which might advance the efficiency of gene tagging, marker-assisted selection, and the understanding of genetics of complex traits and the identification of genetically related DNA markers. In the post-genomics and currently multiple omics era, a vast amount of genomic resources can be available in public databases. Meanwhile, machine learning algorithms came into being powerful enough to deal with a multilevel gene annotation process for predicting gene functions to fulfill crop improvement.

In modern times, the world has to face multiple crises that arise from changing climate and increasing human population and, consequently, serious environmental pollutants and food shortages. Therefore, agricultural biotechnology and molecular breeding are expected to solve the problems by mitigating the stress responses of crops and thereby supporting the global zero hunger of Sustainable Development Goals (SDGs) by the United Nations. For decades, plant scientists have started to develop climate-resilient agriculture by obtaining stress-tolerant crops using strategies to coordinate modern molecular tools; undoubtedly, bioinformatics has to be an essential component due to its multilevel

contributions to functional genomics-based crop improvement, particularly for designing future crops against changing climate. Each year, the global agricultural production suffers significant losses due to diseases caused by pests and pathogens, which leads a decrease in crop yield and quality. Unfortunately, under changing climate conditions, these damages may become more significant, meaning that a greater loss of food is foreseeable. Using bioinformatics tools together with multiple omics approaches, plant scientists are capable of deeply dissecting the interaction between plants and pests or pathogens, and the resulting knowledge might greatly benefit the development of crop protection.

In plant research, it is getting more and more critical to explore the knowledge of noncoding RNAs and one of the most powerful tools, bioinformatics, not only for genome-wide identification of interest RNAs and targets but also to be used for predicting their functions and interactions with players of cellular processes as well as the development of epigenomics. This book provides methods and applications of a critical type of emerging noncoding RNAs, namely microRNAs, with an emphasis on the molecular machinery for regulating plant growth and stress responses that can be unrevealing using bioinformatics tools.

Secondary metabolism research is thought to be critical for understanding plant stress responses and bioactivities of compounds derived from plants. The use of bioinformatics tools, such as molecular docking and computational simulation, can advance the prediction of molecular-level interactions concerning the system of ethnopharmacology and drug discovery. Also, this book presents how bioinformatics tools including machine learning and artificial intelligence can be applied to better understand the impact of secondary metabolites in plant defense systems, which can make considerable contributions to high-throughput metabolomics-related plant stress physiology and the development of stress-resilient agriculture.

This book presents recent advances and applications of bioinformatics/systems biology/multi-omics in plant biology and crop breeding based on an in silico platform acquired multi-omics big data, involving functional analysis, interaction network, regulatory mechanisms, and comparative analysis. The book would be an ideal reference for students, teachers, researchers, and experts in the field of plant science and crop breeding.

The editor is grateful for the instructions and help from the publisher. The editor is also extremely grateful for insightful and valuable chapters contributed by scientists and experts in the field.

*Jen-Tsung Chen*
*National University of Kaohsiung, Kaohsiung, Taiwan*