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## Preface to the Series

Genome sequencing has emerged as the leading discipline in the plant sciences coinciding with the start of the new century. For much of the twentieth century, plant geneticists were only successful in delineating putative chromosomal location, function, and changes in genes indirectly through the use of a number of ‘markers’ physically linked to them. These included visible or morphological, cytological, protein, and molecular or DNA markers. Among them, the first DNA marker, the RFLPs, introduced a revolutionary change in plant genetics and breeding in the mid-1980s, mainly because of their infinite number and thus potential to cover maximum chromosomal regions, phenotypic neutrality, absence of epistasis, and codominant nature. An array of other hybridization-based markers PCR-based markers, and markers based on both facilitated construction of genetic linkage maps, mapping of genes controlling simply inherited traits and even gene clusters (QTLs) controlling polygenic traits in a large number of model and crop plants. During this period a number of new mapping populations beyond F<sub>2</sub> were utilized and a number of computer programs were developed for map construction, mapping of genes, and for mapping of polygenic clusters or QTLs. Molecular markers were also used in studies of evolution and phylogenetic relationship, genetic diversity, DNA-fingerprinting and map-based cloning. Markers tightly linked to the genes were used in crop improvement employing the so-called marker-assisted selection. These strategies of molecular genetic mapping and molecular breeding made a spectacular impact during the last one and a half decades of the twentieth century. But still they remained ‘indirect’ approaches for elucidation and utilization of plant genomes since much of the chromosomes remained unknown and the complete chemical depiction of them was yet to be unraveled.

Physical mapping of genomes was the obvious consequence that facilitated development of the ‘genomic resources’ including BAC and YAC libraries to develop physical maps in some plant genomes. Subsequently, integrated genetic-physical maps were also developed in many plants. This led to the concept of structural genomics. Later on, emphasis was laid on EST and transcriptome analysis to decipher the function of the active gene sequences leading to another concept defined as functional genomics. The advent of techniques of bacteriophage gene and DNA sequencing in the 1970s was extended to facilitate sequencing of these genomic resources in the last decade of the twentieth century.

As expected, sequencing of chromosomal regions would have led to too much data to store, characterize, and utilize with the-then available computer software could handle. But development of information technology made the life of biologists easier by leading to a swift and sweet marriage of biology and informatics and a new subject was born—bioinformatics.

Thus, evolution of the concepts, strategies and tools of sequencing and bioinformatics reinforced the subject of genomics—structural and functional. Today, genome sequencing has traveled much beyond biology and involves biophysics, biochemistry and bioinformatics!

Thanks to the efforts of both public and private agencies, genome sequencing strategies are evolving very fast, leading to cheaper, quicker and automated techniques right from clone-by-clone and whole-genome shotgun approaches to a succession of second generation sequencing methods. Development of software of different generations facilitated this genome sequencing. At the same time, newer concepts and strategies were emerging to handle sequencing of the complex genomes, particularly the polyploids.

It became a reality to chemically—and so directly—define plant genomes, popularly called whole-genome sequencing or simply genome sequencing.

The history of plant genome sequencing will always cite the sequencing of the genome of the model plant *Arabidopsis thaliana* in 2000 that was followed by sequencing the genome of the crop and model plant rice in 2002. Since then, the number of sequenced genomes of higher plants has been increasing exponentially, mainly due to the development of cheaper and quicker genomic techniques and, most importantly, development of collaborative platforms such as national and international consortia involving partners from public and/or private agencies.

As I write this preface for the first volume of the new series “Compendium of Plant Genomes”, a net search tells me that complete or nearly-complete whole-genome sequencing of 45 crop plants, eight crop and model plants, eight model plants, 15 crop progenitors and relatives, and three basal plants are accomplished, the majority of which are in the public domain. This means that we nowadays know many of our model and crop plants chemically, i.e., directly, and we may depict them and utilize them precisely better than ever. Genome sequencing has covered all groups of crop plants. Hence, information on the precise depiction of plant genomes and the scope of their utilization is growing rapidly every day. However, the information is scattered in research articles and review papers in journals and dedicated web pages of the consortia and databases. There is no compilation of plant genomes and the opportunity of using the information in sequence-assisted breeding or further genomic studies. This is the underlying rationale for starting this book series, with each volume dedicated to a particular plant.

Plant genome science has emerged as an important subject in academia, and the present compendium of plant genomes will be highly useful both to students and teaching faculties. Most importantly, research scientists involved in genomics research will have access to systematic deliberations on the plant genomes of their interest. Elucidation of plant genomes is not only of interest for the geneticists and breeders, but also for practitioners of an array of plant science disciplines, such as taxonomy, evolution, cytology,

physiology, pathology, entomology, nematology, crop production, bio-chemistry, and obviously bioinformatics. It must be mentioned that information regarding each plant genome is ever-growing. The contents of the volumes of this compendium are therefore focusing on the basic aspects of the genomes and their utility. They include information on the academic and/ or economic importance of the plants, description of their genomes from a molecular genetic and cytogenetic point of view, and the genomic resources developed. Detailed deliberations focus on the background history of the national and international genome initiatives, public and private partners involved, strategies and genomic resources and tools utilized, enumeration on the sequences and their assembly, repetitive sequences, gene annotation, and genome duplication. In addition, synteny with other sequences, comparison of gene families, and, most importantly, potential of the genome sequence information for gene pool characterization through genotyping by sequencing (GBS) and genetic improvement of crop plants have been described. As expected, there is a lot of variation of these topics in the volumes based on the information available on the crop, model, or reference plants.

I must confess that as the series editor it has been a daunting task for me to work on such a huge and broad knowledge base that spans so many diverse plant species. However, pioneering scientists with life-time experience and expertise on the particular crops did excellent jobs editing the respective volumes. I myself have been a small science worker on plant genomes since the mid-1980s and that provided me the opportunity to personally know several stalwarts of plant genomics from all over the globe. Most, if not all, of the volume editors are my longtime friends and colleagues. It has been highly comfortable and enriching for me to work with them on this book series. To be honest, while working on this series I have been and will remain a student first, a science worker second, and a series editor last. And I must express my gratitude to the volume editors and the chapter authors for providing me the opportunity to work with them on this compendium.

I also wish to mention here my thanks and gratitude to the Springer staff, Dr. Christina Eckey and Dr. Jutta Lindenborn in particular, for all their constant and cordial support right from the inception of the idea.

I always had to set aside additional hours to edit books besides my professional and personal commitments—hours I could and should have given to my wife, Phullara, and our kids, Sourav, and Devleena. I must mention that they not only allowed me the freedom to take away those hours from them but also offered their support in the editing job itself. I am really not sure whether my dedication of this compendium to them will suffice to do justice to their sacrifices for the interest of science and the science community.

Kalyani, India

Chittaranjan Kole

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## Preface

The chickpea, (also known as Bengal gram *Cicer arietinum* L.) is an important legume crop cultivated in >55 countries across the globe. Its wider adaptation to tropical, subtropical, and temperate regions climates makes it as the second most important widely cultivated cool season legume. Chickpeas are widely cultivated for seed as seeds are rich in protein, fiber, and essential amino acids hence very important in vegetarian diets in Indian subcontinent. Besides improving human health it also contributes to soil fertility through biological nitrogen fixation. Cultivated chickpea has originated in southeast Turkey, and *Cicer reticulatum* is considered as its progenitor. Desi (small seeded) and kabuli (large seeded) are two types of chickpea which occupy 85 and 15% of total cultivated area. Climate changes have been posing challenges continuously by reducing chickpea yields through abiotic and biotic stresses. Although about 350 chickpea varieties have been released using conventional breeding approaches, selection for yield *per se* has not been much rewarding in past until the use of modern breeding approaches.

During the last two decades, several crop genomes have been sequenced, which empowered scientists with new tools for developing climate smart crops. Genome sequence information also further increased our understanding of physiological responses, phenotypes and transformed genetics research and crop breeding. The year 2013 is considered as very important year for chickpea research community, as both desi and kabuli genomes have been decoded and several thousand of genetic markers, millions of genome variations that can be used for chickpea improvement have been reported. Besides, several hundreds of germplasm lines as well as release varieties of chickpea were re-sequenced to understand the genome dynamics, evolutionary history, and diversity that can be harnessed for chickpea improvement.

In view of above, this book in the genome compendium series has been planned to provide comprehensive information related to chickpea genome. The book comprises of 12 chapters that provide a detailed overview of economic importance of chickpea, botany, cytogenetics, genetics, genomics tools available and efforts toward breeding climate resilient chickpeas. In addition, the book also provides deeper insights and future perspective of using the chickpea genome information for chickpea improvement. A total of 20 authors, representing six countries from four continents have contributed eleven chapters for this volume. The editors of this volume are grateful to all

the authors for their contribution in writing chapters of high quality. We are also thankful to the reviewers for their constructive suggestions and corrections helping us in improving the quality of the chapters. The editors are also thankful to Dr. David Bergvinson, Director General, ICRISAT and Dr. Peter Carberry, Deputy Director General—Research, ICRISAT for their support. We would like to thank Prof. Chittaranajan Kole, Editor-in-Chief, Genome Compendium Series for asking us to contribute on this important subject as well as to Springer in general and Abirami Purushothaman, Shahid Mohammad, Naresh Kumar Mani, Christina Eckey, Jutta Lindenborn in particular for their help and support.

We also appreciate and recognize cooperation and moral support from our family members for sparing us precious time for editorial work that we should have spent with our respective families. RKV acknowledges the help and support of his wife (Monika), son (Prakhar), and daughter (Preksha) who allowed their time to be taken away to fulfill RKV's editorial responsibilities in addition to research and other administrative duties at ICRISAT. Similarly, MT is grateful to his wife (Jaya), daughter (Sirivarshini), and son (Vishwanath) for their support in doing editorial responsibilities in addition to research activities at ICRISAT. FM acknowledges the support and patience of his wife Linda during the writing and editing of contributions to this volume. Editors would also like to thank their friends and collaborators from chickpea research community especially Liu Xin, Xun Xu (BGI, Shenzhen, China), and NP Singh (ICAR-Indian Institute of Pulses Research, Kanpur, India) for their encouragement and support in various ways.

We hope that our efforts in compiling the information on different aspects of chickpea will help the chickpea research community in enhancing better understanding about the chickpea biology and developing research strategies for chickpea improvement. This book will also benefit students, academicians, and policy makers in updating their knowledge on recent advances in chickpea research.

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