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Rice is one of the most important crops with enormous socio-economic importance. It is the staple food for nearly half of the world's population with more than 90 % of the crop grown in developing countries. In order to feed the growing population, rice production must increase steadily over the next decades. However, arable land is becoming more and more scarce and hence new cultivars that combine higher yield with superior grain quality are needed. It is becoming obvious that this can be achieved only by using new tools of molecular biology and genomics. However, the interest in rice genetics is not stimulated only by rice improvement programmes. Last decade witnessed a surprising change of rice from a crop with a poor genetics to a model of plant genetic research. Rice is the second species whose genome has been almost completely sequenced and became a model for genomics of cereals.

The proceedings of the Fourth International Symposium, which was hosted by The International Rice Research Institute, have been published as a paperback. The book consists of an introductory part, four parts with the plenary lectures, and three workshop reports. In addition to the Foreword by R.P. Cantrell and the Opening Address by G.W. Padolina, the introductory part contains two papers that present overviews on the development of rice genetics and genomics and the application of Mendelian genetics in rice breeding. The third paper is a report from the Rockefeller Foundation who has been supporting the International Programme on Rice Biotechnology.

Proceedings of plenary lectures constitute the core of the book. The section on molecular markers genetic diversity and evolution presents seven papers that focus on the evolution and domestication of rice, its genome structure, molecular markers, genetic mapping and marker-assisted selection. This part of the book also contains a paper on genetic and molecular basis of heterosis and a paper presenting rice as a central genome for the genetics of all cereals.

The largest section of the proceedings focuses on structural and functional genomics. The first of the nine papers of this section is an update on the Rice Genome Sequencing Project. The next two papers discuss the strategies for finishing genomic sequence and development of physical maps of rice. Five articles deal with the functional genomics, namely the use of natural occurring allelic variation, deletion mutants, transposon gene tagging and insertional mutagenesis. The last paper in this section is on rice bioinformatics.

The third section of the symposium proceedings focuses on gene isolation and function. Six papers deal with a range of targets, ranging from cloning genes for blast resistance, the analysis of molecular signalling in disease resistance, evolution of disease resistance genes, to isolation of candidate genes for tolerance of abiotic stress. The last two papers of this section deal with the molecular dissection of cell death and tools for achieving synthetic apomixis. Five papers have been included in the fourth section on genetic transformation. The topics include engineering for virus resistance, transgenic approaches for generating rice tolerant of dehydration stress, high-level expression of C4 photosynthetic genes in transgenic rice, and finally transgene integration, organization and expression. The final part of the book are reports on three symposium workshops: Rice molecular breeding workshop, Functional Genomics Workshop, and Bioinformatics workshop.

As it happens, it takes some time before a symposium proceedings are published, making some of the information outdated. This is especially true for rice genome sequencing. Despite this, the book is a valuable source of information for rice geneticists and biotechnologists. All papers have been written by leading scientists, they are well arranged and include numerous graphs and schemes and some colour figures. As rice has become an important model for plant genetics and genomics, the book is of general interest to researchers and students working in these areas.

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