

Preface

Rice (*Oryza sativa*) is one of the most important staple food crops in the world. Breeding efforts to improve the agronomical quality of rice have been conducted, and studies on rice from the viewpoint of basic biological interest have also been carried out. In 1991, a book entitled *Rice* (edited by Dr. Bajaj) was published as the 14th volume in the series *Biotechnology in Agriculture and Forestry* (BAF), detailing rice research activities at that time, and focusing mainly on cell and tissue culture and genetic variability. Studies on rice have fundamentally advanced since then, whose outcomes are mentioned below. This is a good reason to compile a new volume on rice.

The situation regarding rice research has markedly changed in the last 16 years. First, the genomic sequences of rice were completely determined by the International Rice Genome Sequencing Project in 2004. Since the genome sequence of *Arabidopsis thaliana* had been determined in 2000, rice became the second species in the seed plants to have its genome well understood. Second, the technology to transform rice by the *Agrobacterium*-mediated method was developed and is now established. In classical phytopathology, Poaceae (including rice) has not been considered as a host for *Agrobacterium*. This transformation method is relatively easy and reproducible as compared to conventional transformation methods using protoplasts, and is now widely used in rice research. As a result, the *Agrobacterium*-mediated transformation method allows rice researchers to analyze the functions of the gene of interest by producing transgenic rice. Third, molecular techniques and tools to isolate genes and to analyze their functions have become available. Many important genes have been isolated by map-based cloning methods as well as tagging methods using endogenous transposons and exogenous elements. In addition, reverse genetic studies have become possible by screening of knockout lines, by making knockdown lines and by using the TILLING (targeting induced local lesions in genomes) method. Genome-wide expression analyses such as microarray and MPSS (massively parallel signature sequencing) for rice research have also developed and will provide a wealth of information in rice in the form of functional genomic studies, as in other model organisms.

Such technical advances promote rice from a local experimental material to a model organism not only for applied research to improve crops, but also for basic research to understand molecular and cellular activities in monocots. As a result, many excellent studies that uncover critical biological function have been published

recently and some of them have had a huge impact on plant sciences. For example, the receptor for gibberellin (GA), a key phytohormone, was discovered in rice research, and studies on GA signaling in rice have advanced much more than in *Arabidopsis*. A large number of other basic studies to reveal gene function and evolution of rice and applied studies to improve the yield and quality of rice are now being developed.

Considering these situations, we have compiled a volume on the recent advances in rice research, many of which have been greatly facilitated by the information derived from the complete sequence of the rice genome. Therefore, this book is a completely new edition on rice in the genomics era. It is comprised of four sections and 26 chapters. Each chapter is written by expert scientists in their respective fields of rice research.

The grass family includes many important crops other than rice, such as wheat, maize and barley, providing most of the staple food for human-beings in the world. The alignment of the cereal genome showed extensive conservation of gene order or synteny among grasses. This syntenic relationship has already been exploited in map-based cloning of agronomic genes using homologues in rice. Therefore, results from rice research will have a great impact on other cereal crops as well. According to information from the series editors of BAF, a new volume on maize is being prepared, which would complement the contents of this volume. We hope that this book will become an valuable resource for fundamental and applied research in rice as well as a reference for broad-spectrum research in other plants.

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