

Preface

My continuous association with rice research dates back to 1990, when I started as a postdoctoral research fellow at CSIRO Plant Industry thanks to the generous support of the Rockefeller Foundation under its International Rice Biotechnology Program. By that time, rice had already been recognized as a model species for cereal biotechnology, not only because of its status as a staple food for resource-poor Asia with half the world's population and the urgent need to increase the rice production to meet the growing demand, but also because of well understood rice genetics and the availability of a large number of molecular markers. Progress with transgene delivery and expression has been more rapid with rice than with any other cereal because of the efficient rice tissue culture and transformation systems developed over the years.

In the mid-1990s, rice was further established as a model species for cereal genome research, because of its small genome size, ease with which it could be transformed, and its gene order and gene sequence similarities with other cereals. A consortium of publicly funded laboratories formed The International Rice Genome Sequencing Project (IRGSP) in 1997 to produce a high-quality, map-based sequence of the rice genome using the cultivar Nipponbare of *Oryza sativa* ssp. *japonica*.

I was fortunate enough to continue to work on rice even after the conclusion of our Rockefeller-funded project in 1997, thanks to the support and encouragement of CSIRO Plant Industry's then Chief Dr. Jim Peacock and Genomics Program leader Dr. Liz Dennis. We knew that with the imminent availability of the complete rice genome sequence, the challenge to the scientific community would be in identifying functions for each of the expected 25,000 to 50,000 plant genes. Along with a few other groups worldwide, we embarked on developing functional genomics tools and resources in the form of transposon insertional mutants and mutagens. Genome-wide research tools, resources, and approaches such as data mining for structural similarities, gene expression profiling at the RNA level with expressed sequence tags (ESTs), microarray and DNA chip-based analyses, gene expression profiling at the protein level (proteomics), gene knockouts or loss of function studies with naturally occurring alleles, induced deletion mutants and insertional mutants, and gene expression

knock-down (gene silencing) studies with RNAi have all become integral parts of plant functional genomics including that of rice.

I have been in touch with these facets of Rice Functional Genomics through my involvement as a member of the International Rice Functional Genomics Consortium, a voluntary organization with a mandate to coordinate research in the post-sequencing functional genomics era by exploring ways to consolidate international rice functional genomics resources and to build common strategies to achieve our common goals. We, as a scientific community, still have a long way to go in fully understanding the key genes controlling important agronomic characters before they can be exploited by classical or transformation breeding for crop improvement.

The chapters in this book focus on most of the aforementioned aspects of rice functional genomics and are authored by leading researchers in their respective fields. I am indebted to chapter coordinators, coauthors, and reviewers for their extremely valuable contributions. Sincere thanks to my colleagues at CSIRO Plant Industry—Drs. Qian-Hao Zhu, John Watson, and Andrew Eamens, for assisting me with technical editing of various chapters. My thanks to Drs. Danny Llewellyn, Peter Waterhouse, Ming-Bo Wang, Alan Richardson, Chris Helliwell, Xue-Rong Zhou, Mr Neil Smith, Miss Kerrie Ramm, and others for proofreading the chapters. I thank Springer for inviting me to edit this book, which has been a challenging and rewarding experience for me.

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