Preface

Publishing a scientific research monograph not only requires extraordinary accumulation of data derived from technical endeavors that often spans a decade, but also requires the authors to invest many months or even years of writing. Writing and publishing a book offers the authors neither benefit nor satisfaction when taking into consideration the myriad of factors such as contemporary fast-paced research rhythm combined with professional title and salary promotions, research grant proposals and project evaluations, the high cost of book publications, limited number of readers, and the relatively small market. Nevertheless, there are multitudes of factors that motivated us in striving to compose and publish this book. First and foremost, there is a need for achieving breakthrough research in order to develop competitive wheat varieties. According to Li and Wan (2012), the demand for wheat production in China is projected to increase by at least 28 % by 2020. With the continuous depletion of arable land in China, the only way to meet this demand is to develop innovative varieties with high yield. It is true that the conventional breeding has made great contributions to the increased wheat production in China since 1949, and the techniques for field selections are still irreplaceable at present. However, this traditional breeding method has a number of disadvantages including selections being based only on phenotype, which inherently results in low efficiency and less superior varieties. For example, several major commercial varieties in China, such as Jimai 22, Aikang 58, Zhoumai 18, and Shanon 20, perform well within the boundaries of their plant habits and stress tolerances, but to reach another breakthrough presents entirely new sets of significant challenges. The development of super varieties with multiple beneficial traits controlled by collective elite alleles requires molecular markers to identify, track, and accumulate these superb genes, which needs the multidisciplinary knowledge (Peleman and Vander Vort 2003). Secondly, there is a need for combining molecular breeding and conventional breeding. Since the advent of modern molecular biology techniques represented by PCR, rapid developments in plant genetic diversity analysis and identification and cloning of elite genes have been made over the last three decades. The wealth of data in regard to genomics, proteomics, metabolomics, and

phenotypes and numerous patents are too many to mention. It is my belief that "molecular breeding" and "molecular design breeding" are still at the stages of concept development and project applications. This is largely due to the poor combination of molecular breeding with traditional breeding. The current scientific research system is the cause of the "mismatch"—researchers on molecular breeding are mainly scattered in the confines of academic institutions and/or universities within which they do not fully understand or consider the needs of conventional breeding, while the conventional breeders who often work at local breeding stations and agricultural corporations have less interest in the "molecular design breeding" (it is "computer breeding" according to them). Furthermore, because wheat genome is characterized by its immense size and enormous complexity of QTLs, trait selections based on only one or a few molecular markers from populations with diverse backgrounds and environments are often not ideal. For example, genes with large grain gene/QTL and grain weight may not be necessarily high. Similarly, lines with disease resistant gene/QTL may be susceptible to diseases in the field. Having worked at Shandong Agricultural University for several decades, the author takes advantage of the unique situations experienced in both traditional breeding and molecular breeding and implemented the synthesis of the two breeding approaches with good results. This book publishes the summaries of my team research results and my past 16 years' research experience. Thirdly, we wish to express our gratitude for the monumental support from the national science and technology policy for many of our wheat breeding projects. Over the last decade, we have received research funds for a number of national research projects, including the State "973" program (No. 2009CB118301) for molecular improvement of high-yield wheat and development of molecular breeding elements aiming for creating super wheat high yield (supported by the Ministry of National Science and Technology); four projects (No. 30471082, 30671270, 30971764, and 31171554) supported by the Natural Science Foundation of China; two projects on wheat transformation supported by the National Development and Reform Commission; and the Mega Project on "Development and commercialization of super wheat varieties in Shandong Province." The success of these milestone projects and the wealth of research data presented in this volume are the results of the continuous support we received over the past ten years from the state and province, which allowed me and all of my team members (including all the graduated students) to focus and conduct these studies. By publishing this book, it is my intention to express my sincere thanks to the state and provincial leadership as well as all of the counterparts in China for their support and inspiration during this painstaking period of research.

Based on the foundation of the molecular biology and bioinformatics, Belgian scientist Peleman et al. (2003) recently proposed a novel breeding concept known as "breeding by design." This idea consists of three core concepts: mapping QTL-associated agronomic traits; evaluating the allelic variations at these loci; and implementing molecular design breeding. The premise of the research conducted by my laboratory over the past ten years was based on the concepts of molecular breeding and molecular design breeding. Constructive data (e.g., creations of molecular elements and molecular markers) derived from the research have been

successfully applied to traditional breeding programs, enabling us to make the right cross combinations followed by good pedigree selections. This book compiles wheat molecular genetics map construction and genetic diagnosis of major wheat traits (QTL analysis). The book is divided into seven chapters. Chapters 1 and 2 mainly introduce "research progress of crop quantitative traits" and "the core concept and research methods of quantitative traits," which establish the necessary backgrounds for the contents of the subsequent chapters. Chapter 3 presents "six wheat genetic molecular maps" established by us with the details of map characteristics and their merits of applications. Chapters 4–7 discuss the following subjects: genetic analyses of QTLs associated primarily with wheat yield, quality, physiology, and stress resistance, respectively, have obtained more than 120 major QTLs of dozens of major traits and their molecular markers as well. In order to give readers a comprehensive understanding of the latest research progress, the volume presents not only the results of QTL mapping and efficacy analysis of each major QTL primarily based on our own research projects, but also, in addition, the summaries of similar projects at both home and abroad.

Introduction of the concepts and methods consists of only about 10 % of this volume, and the bulk of the content—more than 90 %—contains the summary of our research data, thereby indicating that this is not a biotechnological book with emphasis on the foundations of methodology and techniques. Rather, this book begins with establishment of molecular genetic maps, QTL analyses, followed by molecular marker-assisted breeding, thereby resulting in a science monograph with a comprehensive and in-depth research system. Ultimately, this publication is not only the collection of the findings of the emerging and ever-evolving wheat molecular marker breeding, but also the prerequisite for the implementations of the newly proposed "molecular design breeding."

The contents of this book are contributed by the members of my Wheat Quality Breeding Team stationed at the State Key Laboratory of Crop Biology, Shandong Agricultural University. Data presented in this volume are the results of several generations of wheat breeding efforts evidenced by development of a novel wheat variety (PH82-2-2) with high protein content and other superior qualities in the 1980s (awarded a 2nd Prize by the National Technology Invention); creations of seven new wheat varieties with high yield and superior quality over the past ten years, including Shannong Youmain #2 (evaluated at the provincial level in 2001 and at the state level in 2009), #3, Shannong #11 and #12 (evaluated at the provincial level in 2003, 2004, and 2005, respectively), #19 and #20 (evaluated at the state level in 2010 and 2011, respectively), and #26 (evaluated at the state level in 2014); and the comprehensive understanding of advantages and disadvantages of the conventional wheat breeding programs. The author has 36 years of career endeavors divided equally between teaching and research, with primary focus on plant physiology and biochemistry in addition to plant genetics and breeding. The fundamental knowledge of these two disciplines enabled me to successfully combine the traditional breeding with the modern molecular biology. For instance, the establishment of various genetic populations (RIL, DH, CIL, ad NL) began as early as 1998, which laid the foundation for the subsequent QTL mapping and molecular

marker-assisted breeding. The rate of selected variety combinations versus cross combinations has increased from 1/1000 by traditional breeding to 1/500 by this strategy, whereas the selected lines for potential varieties from traditional breeding are only 1/1,000,000 compared to 1/10,000 using our selection system. Furthermore, land requirement for breeding studies is about 50 % less than that of a decade ago, and the cost of breeding has decreased significantly, while breeding efficiency has experienced remarkable improvement.

During my nearly 40 years of breeding experience, I have presided over a number of programs on molecular breeding and molecular design breeding at the state level. Participating in writing this book includes young faculty members, graduate students who have left the author's laboratory and are currently working across the country, and those who are currently still in their graduate programs at both Ph.D. and master levels, as well as the field technicians. Each of them provided his/her utmost effort to contribute to this publication. However, due to the rapid development of molecular biology and marker-assisted breeding technology, over time it is inevitable to identify insufficient information in this book. We hope that this volume would provide service and impart knowledge to the readers, but at the same time, we also welcome the readers to submit comments, feedbacks, or concerns.

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