

Preface

The past decade has seen a tremendous shift toward using next-generation sequencing (NGS) technologies for development of powerful tools to identify underlying genes for both simple and complex traits. The advent of NGS and high-throughput genotyping technologies have reduced the genotyping cost significantly and made it possible to use genome-wide marker data for prediction of phenotype to help reduce the cost of phenotyping. Integration of genomics tools with conventional breeding can forge new directions to meet environmental challenges efficiently in less time and more accurately. First-generation molecular breeding approaches (marker-assisted backcrossing (MABC) and marker-assisted recurrent selection (MARS)) require a lengthy process for developing genetic populations for identification of linked markers for a few simply inherited traits but failed to improve complex traits such as yield and drought tolerance due to their technical and genetic limitations. In the case of complex traits which are generally controlled by large number of genes/quantitative trait loci (QTLs) with small effect, “genomic selection (GS)” has gained momentum in plant breeding due to the decline in the genotyping cost. One of the strengths of GS lies in the ability to select an individual without phenotypic data (predicting the individual’s breeding value) based on a prediction model trained with phenotypes and genotypes. However, practicing GS is not as simple as MABC and MARS and requires an understanding of complex statistical models. GS has been widely used in cattle breeding and more recently has gained popularity among plant breeders. This book is a timely effort to compile details about GS for users providing basic as well as advanced understanding. The content of this book will serve as a useful reference for users, covering the germplasm to be used, phenotyping evaluation, marker genotyping methods, and statistical models involved in genomic selection.

A total of 21 authors (Contributors) have contributed to the nine chapters of the book. The editors of this volume are grateful to all the authors for their contributions and for their commendable effort in summarizing the published/unpublished research work in a comprehensive, up-to-date manner. In addition, the cooperation they have extended in terms of timely completion and revision of chapters from

time to time is well appreciated. While editing this book, the strong support received from many other colleagues (Drs. Aaron Lorenz, Isabel Vales, John M. Hickey, and José Crossa) to review the chapters is greatly appreciated. Their constructive comments and suggestions have been instrumental to further improve the chapters.

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We hope that this book will be helpful and useful to students, young researchers, and crop specialists.

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