

# Genomic Selection for Crop Improvement

Rajeev K. Varshney • Manish Roorkiwal  
Mark E. Sorrells  
Editors

# Genomic Selection for Crop Improvement

New Molecular Breeding Strategies  
for Crop Improvement

 Springer

*Editors*

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# Foreword

Today the world is facing an unprecedented challenge: how to feed a growing population predicted to reach over 9.1 billion people by 2050 on a resource base threatened by climate change and with limited options for bringing new arable land under cultivation. Associated challenges of high levels of women and child malnutrition in Asia and sub-Saharan Africa and environmental degradation add to the complexity threatening our future.

To meet these challenges, farmers need improved varieties of crops which give higher productivity and economic returns while withstanding risks induced by climate change such as high temperatures, changing spatial and temporal rainfall distribution, and emerging pests and diseases. These new varieties must also provide consumers, both rural and urban, with access to food that is highly nutritious and safe.

A key task before the agricultural research community is to integrate genomics into modern crop improvement to unlock the genetic diversity of food crops in ways that maximize the availability of improved varieties with the range of production and resilience traits (drought, heat, disease, and pest tolerance) alongside improved nutritional value. Modern genomics provides new tools for increasing both the yield and quality of crop products. Next-generation breeding will need to draw on genomics as the “best bet” for sustainably eradicating hunger, malnutrition, and poverty. Genomics coupled with advanced analytics and precision phenotyping can dramatically increase our capacity to utilize genetic diversity and develop highly nutritious, stress-tolerant crop varieties faster and cheaper than ever before and so respond with urgency to the realization of the Sustainable Development Goals by 2030.

Despite rates of genetic gain leveling off in many cropping systems, significant efforts in genetic improvement have helped increase productivity and develop climate-resilient varieties. Next-generation sequencing technologies are reducing drastically the cost of genotyping and enabling genome-wide marker data to support the design, development, and delivery of robust and nutritious crop varieties.

*Genomic Selection for Crop Improvement* is a timely resource to fill the gap between genome science and crop breeding. In capturing the insights of global leaders on genomics and crop improvement, I am confident that this resource will advance our collective understanding and application of modern tools to unlock our wealth of crop genetic diversity to deliver resilience and profitably for farmers and nutritional value to consumers.

ICRISAT  
Patancheru, Telangana, India  
October 17, 2017

Dr. David Bergvinson

# 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.

The editors also would like to thank their respective families for their cooperation and moral support as the editorial work for this book took away precious moments that they should have spent together with their families. RKV is thankful to Monika, his wife, for her constant encouragement and support and Prakhar (son) and Preksha (daughter) for their love and cooperation. Similarly, MR is grateful to his wife (Shweta) for her support and encouragement in doing editorial responsibilities in addition to research duties at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), with special thanks to Divit (son) for his fondness. RKV and MR would also like to extend their sincerest thanks to Dr. David J. Bergvinson, Director General, ICRISAT, and Dr. Peter S. Carberry, Deputy Director General-Research, ICRISAT, for their help and support.

RKV and MR are also grateful to their colleagues from Center of Excellence in Genomics (CEG), Research Program - Genetic Gains, ICRISAT, and the collaborators for their direct/indirect suggestions during planning of the book. The cooperation and help received from Eric Stannard, Eric Hardy, and Rekha Udaiyar of Springer during various stages of the development and completion of this book project is gratefully acknowledged.

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

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