



# Genomics-Assisted Crop Improvement

*Volume 1*

*Genomics Approaches and Platforms*

Rajeev K. Varshney  
Roberto Tuberosa  
*Editors*



Springer

# Genomics Assisted Crop Improvement Vol 1 Genomics Approaches And Platforms

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## **Genomics Assisted Crop Improvement Vol 1 Genomics Approaches And Platforms:**

*Genomics-Assisted Crop Improvement* R.K. Varshney, Roberto Tuberosa, 2007-12-12 Genomics research has great potential to revolutionize the discipline of plant breeding This two volume set provides a critical assessment of genomics tools and approaches for crop breeding Volume 1 entitled *Genomics Approaches and Platforms* illustrates state of the art genomics approaches and platforms presently available for crop improvement Volume 2 entitled *Genomics Applications in Crops* compiles crop specific studies that summarize both the achievements and limitations of genomics research for crop improvement We hope that these two volumes while providing new ideas and opportunities to those working in crop breeding will help graduate students and teachers to develop a better understanding of the applications of crop genomics to plant research and breeding *Genomics-Assisted Crop Improvement* Rajeev K. Varshney, Roberto Tuberosa, 2007-12-13 This superb volume provides a critical assessment of genomics tools and approaches for crop breeding Volume 1 presents the status and availability of genomic resources and platforms and also devises strategies and approaches for effectively exploiting genomics research Volume 2 goes into detail on a number of case studies of several important crop and plant species that summarize both the achievements and limitations of genomics research for crop improvement

*Genomics-Assisted Crop Improvement* Rajeev K. Varshney, Roberto Tuberosa, 2007-12-20 This superb volume provides a critical assessment of genomics tools and approaches for crop breeding Volume 1 presents the status and availability of genomic resources and platforms and also devises strategies and approaches for effectively exploiting genomics research Volume 2 goes into detail on a number of case studies of several important crop and plant species that summarize both the achievements and limitations of genomics research for crop improvement

**Proceedings of the 10th International Barley Genetics Symposium. Alexandria, Egypt 5-10 Apr 2008. ,** **Plant Breeding Reviews** Jules Janick, 2011-02-02 *Plant Breeding Reviews* presents state of the art reviews on plant breeding and genetics covering horticultural agronomic and forestry crops incorporating both traditional and molecular methods The contributions are authored by world authorities anonymously reviewed and edited by Professor Jules Janick of Purdue University USA The series is an indispensable resource for crop breeders plant scientists and teachers involved in crop improvement and genetic resources

**Bioinformatics for Plant Research and Crop Breeding** Jen-Tsung Chen, 2024-10-28 Explore and advance bioinformatics and systems biology tools for crop breeding programs in this practical resource for researchers Plant biology and crop breeding have produced an immense amount of data in recent years from genomics to interactome and beyond Bioinformatics tools which aim at analyzing the vast quantities of data produced by biological research and processes have developed at a rapid pace to meet the challenges of this vast data trove The resulting field of bioinformatics and systems biology is producing increasingly rich and transformative research Bioinformatics for Plant Research and Crop Breeding offers an overview of this field its recent advances and its wider applications Drawing on a range of analytical and data science tools its foundation on an in silico

platform acquired multi omics makes it indispensable for scientists and researchers alike. It promises to become ever more relevant as new techniques for generating and organizing data continue to transform the field. Bioinformatics for Plant Research and Crop Breeding readers will also find a focus on emerging trends in plant science, sustainable agriculture and global food security. Detailed discussion of topics including plant diversity, plant stresses, nanotechnology in agriculture and many others. Applications incorporating artificial intelligence, machine learning, deep learning and more. Bioinformatics for Plant Research and Crop Breeding is ideal for researchers and scientists interested in the potential of OMICs and bioinformatic tools to aid and develop crop improvement programs.

**Genetics and Genomics of the Triticeae** Catherine Feuillet, Gary J. Muehlbauer, 2009-06-10. Sequencing of the model plant genomes such as those of *Arabidopsis thaliana* and rice has revolutionized our understanding of plant biology but it has yet to translate into the improvement of major crop species such as maize, wheat or barley. Moreover, the comparative genomic studies in cereals that have been performed in the past decade have revealed the limits of conservation between rice and the other cereal genomes. This has necessitated the development of genomic resources and programs for maize, sorghum, wheat and barley to serve as the foundation for future genome sequencing and the acceleration of genomic based improvement of these critically important crops. Cereals constitute over 50% of total crop production worldwide (<http://www.fao.org>) and cereal seeds are one of the most important renewable resources for food, feed and industrial raw materials. Crop species of the Triticeae tribe that comprise wheat, barley and rye are essential components of human and domestic animal nutrition. With 17% of all crop area, wheat is the staple food for 40% of the world's population while barley ranks fifth in the world production. Their domestication in the Fertile Crescent 10 000 years ago ushered in the beginning of agriculture and signified an important breakthrough in the advancement of civilization. Rye is second after wheat among grains most commonly used in the production of bread and is also very important for mixed animal feeds. It can be cultivated in poor soils and climates that are generally not suitable for other cereals. Extensive genetics and cytogenetics studies performed in the Triticeae species over the last 50 years have led to the characterization of their chromosomal composition and origins and have supported intensive work to create new genetic resources. Cytogenetic studies in wheat have allowed the identification and characterization of the different homoeologous genomes and have demonstrated the utility of studying wheat genome evolution as a model for the analysis of polyploidization, a major force in the evolution of the eukaryotic genomes. Barley with its diploid genome shows high collinearity with the other Triticeae genomes and therefore serves as a good template for supporting genomic analyses in the wheat and rye genomes. The knowledge gained from genetic studies in the Triticeae has also been used to produce Triticale, the first human made hybrid crop that results from a cross between wheat and rye and combines the nutrition quality and productivity of wheat with the ruggedness of rye. Despite the economic importance of the Triticeae species and the need for accelerated crop improvement based on genomics studies, the size 1.7 Gb for the bread wheat genome, i.e. 5x the human genome and 40 times the rice

genome high repeat content 80% and complexity polyploidy in wheat of their genomes often have been considered too challenging for efficient molecular analysis and genetic improvement in these species Consequently Triticeae genomics has lagged behind the genomic advances of other cereal crops for many years Recently however the situation has changed dramatically and robust genomic programs can be established in the Triticeae as a result of the convergence of several technology developments that have led to new more efficient scientific capabilities and resources such as whole genome and chromosome specific BAC libraries extensive EST collections transformation systems wild germplasm and mutant collections as well as DNA chips Currently the Triticeae genomics toolbox is comprised of 9 publicly available BAC libraries from diploid 5 tetraploid 1 and hexaploid 3 wheat 3 publicly available BAC libraries from barley and one BAC library from rye 3 wheat chromosome specific BAC libraries DNA chips including commercially available first generation chips from AFFYMETRIX containing 55 000 wheat and 22 000 barley genes A large number of wheat and barley genetic maps that are saturated by a significant number of markers The largest plant EST collection with 870 000 wheat ESTs 440 000 barley ESTs and about 10 000 rye ESTs Established protocols for stable transformation by biolistic and agrobacterium as well as a transient expression system using VIGS in wheat and barley and Large collections of well characterized cultivated and wild genetic resources International consortia such as the International Triticeae Mapping Initiative ITMI have advanced synergies in the Triticeae genetics community in the development of additional mapping populations and markers that have led to a dramatic improvement in the resolution of the genetic maps and the amount of molecular markers in the three species resulting in the accelerated utilization of molecular markers in selection programs Together with the development of the genomic resources the isolation of the first genes of agronomic interest by map based cloning has been enabled and has proven the feasibility of forging the link between genotype and phenotype in the Triticeae species Moreover the first analyses of BAC sequences from wheat and barley have allowed preliminary characterizations of their genome organization and composition as well as the first inter and intra specific comparative genomic studies These later have revealed important evolutionary mechanisms e g unequal crossing over illegitimate recombination that have shaped the wheat and barley genomes during their evolution These breakthroughs have demonstrated the feasibility of developing efficient genomic studies in the Triticeae and have led to the recent establishment of the International Wheat Genome Sequencing Consortium IWGSC <http://www.wheatgenome.org> and the International Barley Sequencing Consortium [www.isbc.org](http://www.isbc.org) that aim to sequence respectively the hexaploid wheat and barley genomes to accelerate gene discovery and crop improvement in the next decade Large projects aiming at the establishment of the physical maps as well as a better characterization of their composition and organization through large scale random sequencing projects have been initiated already Concurrently a number of projects have been launched to develop high throughput functional genomics in wheat and barley Transcriptomics proteomics and metabolomics analyses of traits of agronomic importance such as quality disease resistance drought and salt tolerance are underway in both species

Combined with the development of physical maps efficient gene isolation will be enabled and improved sequencing technologies and reduced sequencing costs will permit ultimately genome sequencing and access to the entire wheat and barley gene regulatory elements repertoire Because rye is closely related to wheat and barley in Triticeae evolution the latest developments in wheat and barley genomics will be of great use for developing rye genomics and for providing tools for rye improvement Finally a new model for temperate grasses has emerged in the past year with the development of the genetics and genomics including a 8x whole genome shotgun sequencing project of Brachypodium a member of the Poeae family that is more closely related to the Triticeae than rice and can provide valuable information for supporting Triticeae genomics in the near future These recent breakthroughs have yet to be reviewed in a single source of literature and current handbooks on wheat barley or rye are dedicated mainly to progress in genetics In Genetics and Genomics of the Triticeae we will aim to comprehensively review the recent progress in the development of structural and functional genomics tools in the Triticeae species and review the understanding of wheat barley and rye biology that has resulted from these new resources as well as to illuminate how this new found knowledge can be applied for the improvement of these essential species The book will be the seventh volume in the ambitious series of books Plant Genetics and Genomics Richard A Jorgensen series editor that will attempt to bring the field up to date on the genetics and genomics of important crop plants and genetic models It is our hope that the publication will be a useful and timely tool for researchers and students alike working with the Triticeae

**Advances in breeding techniques for cereal crops** Prof Frank Ordon, Prof. Wolfgang Friedt, 2019-06-28 Assesses performance of conventional techniques such as backcross and hybrid breeding in introducing new traits Maps current progress in methods to identify quantitative trait loci QTL linking phenotypic traits with genetic information for selection Shows comparative strengths and weaknesses of marker assisted selection MAS techniques such as genome wide association studies GWAS and nested association mapping NAM *Principles and Practices of Plant Genomics, Vol. 2* C Kole, Albert G. Abbott, 2008 The three volumes in this series containing 41 chapters contributed by over one hundred globally reputed scientists provide lucid deliberations on the concepts strategies tools methodologies and achievements of plant genomics presented in a typical class room approach Back cover **Crop Stress Management and Global Climate Change** José Luis Araus, Gustavo A. Slafer, 2011 Agriculture has shaped our planet into the world we know but its continued success is threatened by changing weather patterns Climate change is a diverse multifactorial phenomenon and the agronomic strategies we employ to combat its effects need to be case specific with significant regional differences With two major sections the first explaining the challenges posed by climate change and the second reviewing the current research avenues employed this book combines detailed discussion of physiological plant responses with practical experience on crop stress management and breeding Using a number of illustrative case studies it discusses how the stresses resulting from climate change could be overcome by assessing measuring and predicting environmental changes and stresses and identifying

opportunities for adapting to multifactorial change A global effort to combine climate change science with policy is desperately needed Climate change will continue to pose many challenges to agriculture in the future but by taking an integrative approach to predicting and adapting to change this book will inspire researchers to turn those challenges into opportunities

**Principles and Practices of Plant Genomics, Volume 3** Chittaranjan Kole,Albert G. Abbott,2008 The three volumes in this series containing 41 chapters contributed by over one hundred globally reputed scientists provide lucid deliberations on the concepts strategies tools methodologies and achievements of plant genomics presented in a typical class room approach Back cover

*Modern Variety Breeding for Present and Future Needs* Eucarpia. Congress,2008

Pre-breeding and Gene Discovery for Food and Renewable Energy Security Muhammad Sabran,2016 *Diversity of Plants* S. John Britto,2009 Inheritance of Resistance and Molecular Mapping of Soybean Aphid Resistance Genes in Soybean PI 567585A Menghan Liu,2010 *Genomics Assisted Breeding of Crops for Abiotic Stress Tolerance, Vol. II* Vijay Rani Rajpal,Deepmala Sehgal,Avinash Kumar,S.N. Raina,2019-07-01 The abiotic stresses like drought temperature cold salinity heavy metals etc affect a great deal on the yield performance of the agricultural crops To cope up with these challenges plant breeding programs world wide are focussing on the development of stress tolerant varieties in all crop species Significant genomic advances have been made for abiotic stress tolerance in various crop species in terms of availability of molecular markers QTL mapping genome wide association studies GWAS genomic selection GS strategies and transcriptome profiling The broad range of articles involving genomics and breeding approaches deepens our existing knowledge about complex traits The chapters are written by authorities in their respective fields This book provides comprehensive and consolidated account on the applications of the most recent findings and the progress made in genomics assisted breeding for tolerance to abiotic stresses in many important major crop species with a focus on applications of modern strategies for sustainable agriculture The book is especially intended for students molecular breeders and scientists working on the genomics assisted genetic improvement of crop species for abiotic stress tolerance

Genomics-assisted Crop Improvement Rajeev K. Varshney,Roberto Tuberosa,2007 **Genetic Engineering News** ,2003 **Translational Genomics for Crop Breeding, 2 Volume Set** Rajeev Varshney,Roberto Tuberosa,2013-12-04 The Genomics Applications in Crop Improvement two volume set brings together a diverse field of international experts in plant breeding genomics to share their experiences in the field from success stories to lessons learnt In recent years advances in genetics and genomics have greatly enhanced our understanding of the structural and functional aspects of plant genomes Several novel genetic and genomics approaches such as association genetics advanced back cross QTL analysis allele mining comparative and functional genomics transcriptomics proteomics etc offer unprecedented opportunities to examine crop genetic variation and utilize this variability for breeding purposes Enhancing the prediction of the phenotype from a genotype using genomics tools is referred to as genomics assisted breeding To date genomics assisted breeding has shown its potential for crop

improvement in several crops however these successes have been largely restricted to temperate cereal and legume crops and others such as Eucalyptus sugarcane tomato and other vegetables crops Moreover while success stories are available for improving resistance to biotic stresses only a few examples are available on development of superior lines for abiotic stresses These volumes will allow researchers the tools to begin to apply these technologies more broadly and will hopefully lead to lasting improvements in a wide variety of economically important crops Volume One Biotic Stress focuses on genomic assisted advances for improving economically important crops against biotic stressors such as viruses fungi nematodes and bacteria Looking at key advances in crops such as rice barley wheat and potato amongst others Volume Two Abiotic Stress Quality and Yield Improvement focuses on advances improving crop resistance to abiotic stresses such as extreme heat drought flooding as well as advances made in quality and yield improvement Chapters examine advances in such key crops as rice maize and sugarcane among others Two volumes covering important topics in crop genomics and applying that information to breeding improved varieties of economically important crops Volumes cover improving resistance to abiotic and biotic stressors as well as breeding efforts to improve yield and quality Includes chapters on current challenges for plant breeders such as fusarium disease in wheat and cyst nematodes in soybean crops Organized by crop with chapters covering a variety of topics for each including disease resistance drought tolerance salinity tolerance and overall improvement of yield Written by an international team of experts This book is intended for crop science researchers plant biologists geneticists physiologists cellular and molecular biologists and advanced students in related fields will also find this set useful Smart Breeding Kailash Chandra,Subhash Chand,Ravi Prakash Saini,Rohit Sharma,2024-02-13 This new volume focuses on novel breeding and biotechnological approaches for crop improvement covering recent advances in molecular breeding and plant breeding such as pre breeding reverse breeding allele mining next generation sequencing etc The authors consider the important necessity and development of climate resilient crops that can withstand hostility or adversities of climate without substantially compromising yield and discuss ways to mitigate plant stress The recent developments in breeding and biotechnological approaches concerning crop improvement that are discussed in the book include molecular markers their genesis and their significant applications for crop improvement QTL mapping a modern breeding approach for mapping quantitative traits pulse molecular breeding and genomics and approaches for precise gene alterations in the genome of organisms by using genome editing Other techniques include reverse breeding a technique that allows breeders to develop parental lines directly from the heterozygous plant within a shorter time frame pre breeding approaches for biotic and abiotic stress management in crop plants allele mining as a way to find existing variations in an organism s gene pool by scanning the entire gene marker assisted selection where molecular markers have played a significant role in accelerating breeding programs and next generation sequencing NGS platforms in crop improvement where the authors summarize the technical know how of each sequencing platform and its merits and demerits The book introduces the design and importance of



Mutmap and its variant in modern breeding a novel gene mapping approaches that allows rapid identification of causal nucleotide changes of mutants by whole genome resequencing Examples and case studies of the various approaches are included as well with several examples of marker assisted selection of rice and maize crop and other agriculturally important crops This informative volume will enhance readers knowledge about the recent developments in breeding and biotechnological approaches concerning crop improvement

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