

Romesh Kumar Salgotra
Sajad Majeed Zargar *Editors*

Rediscovery of Genetic and Genomic Resources for Future Food Security

 Springer

Rediscovery of Genetic and Genomic Resources for Future Food Security

Romesh Kumar Salgotra
Sajad Majeed Zargar
Editors

Rediscovery of Genetic and Genomic Resources for Future Food Security

 Springer

Editors

Romesh Kumar Salgotra
School of Biotechnology
Sher-e-Kashmir University of Agricultural
Sciences & Technology of Jammu
Jammu, Jammu and Kashmir, India

Sajad Majeed Zargar
Division of Plant Biotechnology
Sher-e-Kashmir University of Agricultural
Sciences & Technology of Kashmir
Srinagar, Jammu and Kashmir, India

ISBN 978-981-15-0155-5

ISBN 978-981-15-0156-2 (eBook)

<https://doi.org/10.1007/978-981-15-0156-2>

© Springer Nature Singapore Pte Ltd. 2020

This work is subject to copyright. All rights are reserved by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed.

The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

The publisher, the authors, and the editors are safe to assume that the advice and information in this book are believed to be true and accurate at the date of publication. Neither the publisher nor the authors or the editors give a warranty, expressed or implied, with respect to the material contained herein or for any errors or omissions that may have been made. The publisher remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

This Springer imprint is published by the registered company Springer Nature Singapore Pte Ltd.

The registered company address is: 152 Beach Road, #21-01/04 Gateway East, Singapore 189721, Singapore

Preface

Plant genetic resources have supported humankind for several millennia. These resources are the basis for food security in addition to the sources of energy, animal feed, fibre and other ecosystem services. They are important in addressing the global challenges that are currently facing the human population, particularly the twin challenge of climate change and food scarcity. Owing to their great importance, effective conservation and sustainable utilization of these resources is critically important and has never been more urgent. Plant domestication is an evolutionary process in which humans have used wild species to develop new and altered forms of plants with morphological or physiological traits that meet human needs. Limited number of individuals of progenitor species were used by early farmers and the traits selected usually were related to overall yield, harvesting, and edibility. As a consequence, this strong selection process produced genetic bottlenecks of varying degrees that have resulted in a heterogeneous reduction in the level of genetic variation among annual herbaceous crops. The domestication process has resulted in reduced diversity at both the genome and morphological levels. The domestication has reduced or eliminated genetic diversity at certain loci in modern crops, thus limiting their potential for developing novel varieties with improved traits. Moreover, the selective approach during domestication had left behind various valuable alleles of biotic, abiotic stress resistance, yield and quality traits in the crop wild relative (CWR) species and landraces. There is urgent need to relook at and explore the available genetic resources for future food and nutritional security.

Crop evolution under domestication has led to increased productivity of crop species, but at the same time has narrowed their genetic basis. The potential of the genetic diversity stored in CWRs and landraces for use in crop improvement appears to be much greater than we previously imagined. Recent increases in the use of wild resources have occurred because of the recognition of the usefulness of CWRs along with the availability of various genomic resources. With the advent of modern technologies, such as next-generation sequencing (NGS) and other omics-based high throughput techniques, various genomic resources have promised to revolutionize genetics, plant breeding and biotechnology through molecular characterization, transcript profiling and cloning of whole genomes to understand the structure, function and evolution of genes. A combination of Genome-Wide Association Studies (GWASs) and next-generation-mapping populations have improved our ability to connect phenotypes and genotypes and explore the genetic diversity of

wild relatives for crop improvement. The combination of these approaches with the promise of improved genomic technologies provides an opportunity for comparative genomics to apply our understanding of the past to the future for crop improvement. These genomic resources can be deployed to rediscover and explore the new genes/alleles and traits from CWRs for developing novel crop varieties resistance to various biotic and abiotic stresses, and other quality traits.

Genomic approaches have been widely used to identify genes or genomic regions controlling complex traits. High-throughput next-generation sequencing technologies offer opportunities to efficiently discover SNPs associated with important traits in landraces and crop wild relatives of both diploid and polyploid plant species. With recent significant cost reductions, scientists are now able to genotype thousands of individuals by genotyping-by-sequencing (GBS) or resequencing. With the availability of increasing numbers of SNPs and phenotypic data, researchers have been able to validate and fine-map previously identified genes and to discover novel genomic regions underlying valuable agronomic traits in crop wild species by association mapping. The availability of genome-wide data and efficient phenotyping approaches will continue to accelerate the discovery of genes controlling superior traits in CWRs. Other functional omics approaches, including transcriptomics, proteomics and metabolomics, have provided alternative opportunities for global analysis of regulatory genes, expressed proteins or metabolite candidates underlying important traits in CWRs. These omics approaches are also particularly suitable for dissection of the variation in CWRs for further utilization in crop improvement. However, the development of a high-throughput phenotyping pipeline remains challenging, especially in the field conditions. Some of the genomic regions associated with domestication traits have enhanced our understanding of their genetic basis, and will encourage further investigation to see whether allelic variation in those regions in wild relatives can additionally benefit crop improvement.

Rapid progress in advanced biotechnologies that can bridge genotype-phenotype gaps will facilitate the use of CWRs for crop improvement. Thus a number of QTL and SNPs associated with agronomically and ecologically important traits have been identified in wild species by linkage analyses, GWAS and/or combined “omics” approaches. The rapid improvement of biotechnological tools, such as diverse omics approaches, has resulted in promising advances, and no doubt will become routine in plant breeding programmes. Advanced biotechnologies are continuously being developed and will accelerate the conservation and use of genetic diversity retained in CWRs, resulting in agriculture sustainability. Utility of these resources is important in increasing the resilience and productivity of agricultural production systems. However, despite their importance, utility of these resources is poor. This book reviews the real and potential application of the current advances in genomics-based technologies in exploring and utilization of these resources for crop improvement. This book also describes in detail about exploring the untapped genes and traits for crop improvement from wild species which had been ignored during the domestication process. This will also give insight about how to utilize untapped and unexplored genetic diversity of wild species, wild relatives and landraces for crop improvement.

Rediscovery of Genetic and Genomic Resources for Future Food Security is designed to focus on the importance of plant genetic resources in achieving food security in the near future. It describes how the recent genomic resources techniques can be efficiently used in plant breeding programmes to achieve food security in the future. This book describes in detail about exploring the new genes and traits for crop improvement from wild species at the shortest possible time. The book also gives insight about how to utilize untapped and unexplored genetic diversity of wild species, wild relatives and landraces for crop improvement. It breaks the mould, offering an impressive array of balanced analyses, fresh ideas and perspectives, and thoughtful and realistic prescriptions which could help in the sustainable utilization of plant genetic resources with modern biotechnological techniques. The presentation style of the book is easy to follow and comprehend. Professionals, researchers and students are constantly reminded of previous topics of relevance to current topics being discussed. This book is not only an excellent teaching tool, but it is also a suitable reference source for professionals.

Jammu, Jammu and Kashmir, India
Srinagar, Jammu and Kashmir, India

Romesh Kumar Salgotra
Sajad Majeed Zargar

Contents

1	Potential of Genetic and Genomic Resources for Genetic Improvement of Food Crops	1
	Romesh Kumar Salgotra and Sajad Majeed Zargar	
2	Untapped Genetic Diversity of Wild Relatives for Crop Improvement	25
	Zoran Jovovic, Violeta Andjelkovic, Novo Przulj, and Dragan Mandic	
3	Molecular Approaches for Harvesting Natural Diversity for Crop Improvement	67
	Pawan Saini, Pooja Saini, Jashan Jot Kaur, Rose Mary Francies, Mudasir Gani, Ambavane Ajinkya Rajendra, Narender Negi, Ashok Jagtap, Amar Kadam, Charan Singh, and Shailendra Singh Chauhan	
4	Omics and Plant Genetic Resources: Towards Mining Potential Genes	171
	Nagesha N and Praveen L. Bennur	
5	Genetic and Genomic Resources and Their Exploitation for Unlocking Genetic Potential from the Wild Relatives	193
	Mehfuz Hasan, Abu Sayeed Md. Hasibuzzaman, Hasan Muhammad Abdullah, and Md. Mehboob Hasan Kallol	
6	Role of Gene Banks in Maintaining Crop Genetic Resources	211
	Parvaze A. Sofi, Sajad M. Zargar, Rakeeb A. Mir, and Romesh Kumar Salgotra	
7	Exploring Genetic Resources for Identification of Potential Novel Genes for Crop Improvement	225
	Pankaj Pandotra, Parshant Bakshi, Anil Kumar Singh, and Suphla Gupta	

8	Next-Generation Sequencing Technologies and Their Implications for Efficient Utilization of Genetic Resources	239
	Mehak Gupta, Romesh Kumar Salgotra, and Bhagirath Singh Chauhan	
9	Comparative Genomics for Exploring New Genes and Traits for Crop Improvement	251
	Gayatri Jamwal and Inderpal Singh Bijral	
10	Potential of Wild Species in the Scenario of Climate Change.	263
	Suzana Jordanovska, Zoran Jovovic, and Violeta Andjelkovic	
11	Role of Wild Relatives for Development of Climate-Resilient Varieties.	303
	Manmohan Sharma, Punya, and Bharat Bhushan Gupta	
12	Strategies for Conservation of Genetic Resources	315
	Jahangir Ahmad Dar, Masrat Kareem, Sajad Majeed Zargar, Aijaz A. Wani, Sheezan Rasool, and Kaisar A. Bhat	
13	Crop Landraces: Present Threats and Opportunities for Conservation	335
	Rakeeb Ahmad Mir, Arjun Sharma, and Reetika Mahajan	
14	Future Threats and Opportunities Facing Crop Wild Relatives and Landrace Diversity.	351
	Chainika Gupta, Romesh Kumar Salgotra, and Gulshan Mahajan	

Contributors

Hasan Muhammad Abdullah GIS and Remote Sensing Lab, Department of Agroforestry and Environment, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh

Violeta Andjelkovic Maize Research Institute ‘Zemun Polje’, Belgrade, Serbia

Parshant Bakshi Division of Fruit Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, Jammu, Jammu and Kashmir, India

Praveen L. Bennur Department of Plant Bioechnology, College of Agriculture, UAS, GKVK, Bangalore, Karnataka, India

Kaisar A. Bhat Proteomics Laboratory, Division of Plant Biotechnology, SKUAST-K, Srinagar, Jammu and Kashmir, India

Inderpal Singh Bijral Sher-E-Kashmir University of Agricultural Sciences and Technology, Jammu, Jammu and Kashmir, India

Bhagirath Singh Chauhan Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Gatton, QLD, Australia

Shailendra Singh Chauhan CSB–Central Sericultural Research & Training Institute (CSR&TI), Pampore, Jammu and Kashmir, India

Jahangir Ahmad Dar Proteomics Laboratory, Division of Plant Biotechnology, SKUAST-K, Srinagar, Jammu and Kashmir, India

Rose Mary Francies Department of Seed Science and Technology, Kerala Agricultural University (KAU), Thrissur, Kerala, India

Mudasir Gani CSB–Central Sericultural Research & Training Institute (CSR&TI), Pampore, Jammu and Kashmir, India

Bharat Bhushan Gupta Division of Plant Breeding and Genetics, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu, Jammu and Kashmir, India

Chainika Gupta School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu, Jammu and Kashmir, India

Mehak Gupta School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu, Jammu and Kashmir, India

Suphla Gupta Plant Biotechnology Division, Council for Scientific and Industrial Research (CSIR), Indian Institute of Integrated Medicine (IIIM), Jammu, India

Mehfuz Hasan Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh

Abu Sayeed Md. Hasibuzzaman Department of Genetics and Plant Breeding, Bangabandhu Sheikh Mujibur Rahman Agricultural University, Gazipur, Bangladesh

Ashok Jagtap School of Agricultural Biotechnology, Punjab Agricultural University (PAU), Ludhiana, Punjab, India

Gayatri Jamwal Sher-E-Kashmir University of Agricultural Sciences and Technology, Jammu, Jammu and Kashmir, India

Suzana Jordanovska Institute of Agriculture Skopje, University “Ss Cyrilus and Methodius” in Skopje, Skopje, Republic of Macedonia

Zoran Jovic Biotechnical Faculty Podgorica, University of Montenegro, Podgorica, Montenegro

Amar Kadam Department of Biotechnology, Lokmangal College of Agricultural Biotechnology, Mahatma Phule Krishi Vidyapeeth (MPKV), Solapur, Maharashtra, India

Md. Mehboob Hasan Kallol Senior Management Counsellor and Head, Computer Services Division, Bangladesh Institute of Management (BIM), Dhaka, Bangladesh

Masrat Kareem Department of Botany, University of Kashmir, Srinagar, Jammu and Kashmir, India

Jashan Jot Kaur Department of Plant Breeding and Genetics, Punjab Agricultural University (PAU), Ludhiana, Punjab, India

Gulshan Mahajan Queensland Alliance for Agriculture and Food Innovation (QAAFI), The University of Queensland, Gatton, QLD, Australia

Reetika Mahajan Division of Plant Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar, Jammu and Kashmir, India

Dragan Mandic Agricultural Institute of Republic of Srpska, Banja Luka, Republic of Srpska, Bosnia and Herzegovina

Rakeeb Ahmad Mir Department of Biotechnology, School of Biosciences and Biotechnology, BGSB University, Rajouri, Jammu and Kashmir, India

Nagesha N Department of Plant Bioechnology, College of Agriculture, UAS, GKVK, Bangalore, Karnataka, India

Narender Negi ICAR–National Bureau of Plant Genetic Resources (NBPGR), Shimla, Himachal Pradesh, India

Pankaj Pandotra Division of Fruit Science, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, Jammu, Jammu and Kashmir, India

Novo Przulj Faculty of Agriculture, University of Banja Luka, Banja Luka, Republic of Srpska, Bosnia and Herzegovina

Punya School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu, Jammu and Kashmir, India

Ambavane Ajinkya Rajendra Department of Seed Science and Technology, Kerala Agricultural University (KAU), Thrissur, Kerala, India

Sheezan Rasool Proteomics Laboratory, Division of Plant Biotechnology, SKUAST-K, Srinagar, Jammu and Kashmir, India

Pawan Saini CSB–Central Sericultural Research & Training Institute (CSR&TI), Pampore, Jammu and Kashmir, India

Pooja Saini Department of Biotechnology, Eternal University, Baru Sahib, Himachal Pradesh, India

Romesh Kumar Salgotra School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu, Jammu, Jammu and Kashmir, India

Arjun Sharma Department of Biotechnology, School of Biosciences and Biotechnology, BGSB University, Rajouri, Jammu and Kashmir, India

Manmohan Sharma School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Jammu, Jammu and Kashmir, India

Anil Kumar Singh School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, (SKUAST-J), Chatha, Jammu, Jammu and Kashmir, India

Charan Singh ICAR–Indian Institute of Wheat and Barley Research (IIWBR), Karnal, Haryana, India

Parvaze A. Sofi Dry Land Agricultural Research Station, SKUAST, Kashmir, Jammu and Kashmir, India

Aijaz A. Wani Department of Botany, University of Kashmir, Srinagar, Jammu and Kashmir, India

Sajad Majeed Zargar Division of Plant Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar, Jammu and Kashmir, India

About the Editor and Co-editor



Romesh Kumar Salgotra, PhD, is currently a Professor and Coordinator, School of Biotechnology at Sher-e-Kashmir University of Agricultural Sciences & Technology of Jammu (SKUAST-Jammu) in India. Dr. Salgotra received his PhD in Plant Breeding and Genetics in 1999 from CSK Himachal Pradesh Krishi Vishwavidyalaya, Palampur, India. He was previously an Endeavour Executive Fellow of Queensland Alliance for Agriculture and Food Innovation (QAAFI) at the University of Queensland, Australia. He has worked in different capacities as Junior Scientist and Senior Scientist at SKUAST-Jammu under All India Co-ordinated Rice Improvement Project, National Rice Research Institute (NRRI), Hyderabad, and *Central Research Institute for Dryland Agriculture (CRIDA)*, Hyderabad, India. He has also worked as Agriculture Extension Officer in Govt. of Jammu and Kashmir, India. Dr. Salgotra is a recipient of BOYSCAST Fellowship, Tennessee University, USA. He was awarded the prestigious Norman E. Borlaug Fellowship by United States Agriculture Development (USDA) during 2015. He has participated in Genetic Resources and Intellectual Property Rights Programme (GRIP) under Swedish International Development Agency (SIDA), Sweden, and follow-up programme at Pretoria, South Africa. He has received several awards for his work and research. He was the member and representative of Global Forum for Innovative Agriculture (GFIA), Abu Dhabi, UAE. Dr. Salgotra was also one of the members of delegation in the Joint Committee on Science and Technology, Govt. of India, held at Belgrade, Serbia, in 2017. He has chaired a session in International Association of Science & Technology

Development for Computational Bioscience held at Cambridge, Massachusetts, USA. He has more than 50 peer-reviewed publications and has delivered numerous oral and poster presentations in national and international meetings/conferences. He has been affiliated with several internationally reputed journals and is also reviewer of reputed journals *Scientific Reports*, *PLOS One*, *Plant Cell Reports*, *BMC Genetics*, *Rice Science*, *Journal of Integrative Agriculture*, *Australian Journal of Crop Science*, *SABRAO* and many others. He has guided MSc and PhD students under his supervision. Dr. Salgotra has received several grants for research projects from national and international funding agencies.



Sajad Majeed Zargar, PhD is currently an Assistant Professor at Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir (SKUAST Kashmir), India. He was previously a visiting professor at the Nara Institute of Science and Technology, Japan. He has worked as an Assistant Professor at SKUAST Jammu, Baba Ghulam Shah Badshah University, Rajouri (BGSB), India. He has also worked as a scientist at Advanta India Limited, Hyderabad, India, and TERI (The Energy and Resources Institute), New Delhi, India. Dr. Zargar is a recipient of the CREST overseas fellowship from DBT, India, and is also recipient of the Goho grant from the Govt. of Japan. He has received several awards for his work and research. He is also a member and representative of INPPO (International Plant Proteomics Organization). His editorial activities and scientific memberships include publishing research and review articles in international journals and as a reviewer. He has been affiliated with several internationally reputed journals and is also reviewer of reputed journals, *Frontiers in Plant Science*, *3 Biotech*, *Scientia Horticulturae*, *Methods in Ecology and Evolution*, *Australian Journal of Crop Science* and many others. Dr. Zargar has been invited to give many lectures at professional meetings and workshops and has received grants for research projects under his supervision.

Abbreviations

ABA	Abscisic acid
AB-QTL	Advanced back crossed QTL
AFLPs	Amplified fragment length polymorphisms
AM	Association mapping
AMPRIL	Arabidopsis multiparent RIL
ATI	Accelerated Trait Introgression
BACs	Bacterial artificial chromosomes
BCP	Biofortification Challenge Program
BILs	Backcross inbred lines
BNF	Biological nitrogen fixation
BGCI	Botanic Gardens Conservation International
BLAST	Basic Local Alignment Search Tool
<i>Bt</i>	<i>Bacillus thuringiensis</i>
CAPS	Cleaved amplified polymorphic sequence
CBD	Convention on Biological Diversity
CC	Core collection
cDNA	Complementary deoxy ribose nucleic acid
CGA	Candidate gene approach
CGD	Crop genetic diversity
CGRs	Crop genetic resources
CGIAR	Consultative Group for International Agricultural Research
CIAT	International Center for Tropical Agriculture
CIFOR	Center for International Forestry Research
CIMMYT	International Maize and Wheat Improvement Center
CIP	International Potato Centre
CMS	Cytoplasmic genic male sterility
CRISPR-cas9	Clustered regularly interspaced short palindromic repeats-associated protein 9
CRS	Core reference set
CSSLs	Chromosome segment substitution lines
CMT3	Chromomethylase 3
CWR	Crop wild relatives
CO ₂	Carbon dioxide
DArT	Diversity array technology

DH	Doubled haploid
DHPLC	Denaturing high-performance liquid chromatography
DCL	DICER like enzymes
DNA	Deoxy-ribose nucleic acid
DREB	Dehydration responsive element binding
DS	Domestication syndrome
DT	Drought tolerance
EcoTILLING	Eco Type TILLING
EST	Expressed sequence tag
FACE	Free-air carbon dioxide enrichment
FAO	Food and Agriculture Organization
FAnGR	Farm Animal Genetic Resources
GDP	Gross domestic product
GIS	Geographic information system
GAB	Genomic-assisted breeding
GBS	Genotyping-by-sequencing
GC	Gateway cloning
GolS	Galactinol synthase
GenoSIS	Genome Spatial Information System
GEBV	Genomic estimated breeding value
GM	Genetic modification
GMOs	Genetically modified organisms
GPS	Global positioning system
GR	Green revolution
GS	Genome selection
GWAS	Genome-wide association studies
GWE	Genome-wide editing
GWP	Genome-wide prediction
HDB	Homology-directed recombination
HNVs	High natural values
HSPs	Heat shock proteins
HTPs	High-throughput phenotyping
HTPPs	High-throughput phenotyping platforms
HYVs	High yielding varieties
IAEA	International Atomic Energy Agency
IARI	Indian Agricultural Research Institute
IBP	International Biological Program
ICARDA	International Center for Agricultural Research in the Dry Areas
ICRAF	International Council for Research in Agroforestry
ICRISAT	International Crops Research Institute for the Semi-Arid Tropics
IFPRI	International Food Policy Research Institute
IHF	Integration Host Factor
IITA	International Institute of Tropical Agriculture
ILRI	International Livestock Research Institute
IPCC	Intergovernmental Panel on Climate Change

IBPGR	International Board for Plant Genetic Resources
ICC	International Co-ordinating Council
ICN	International Conference on Nutrition
InDels	Insertions or deletions
IFAD	International Fund for Agricultural Development
ILO	International Labour Organisation
IME	Institution of Mechanical Engineers
INIBAP	International Network for the Improvement of Banana and Plantain
IRRI	International Rice Research Institute
ITPGRFA	International Undertaking on Plant Genetic Resources for Food and Agriculture
IUCN	International Union for Conservation of Nature
IWMI	International Water Management Institute
KASP	Kompetitive allele specific PCR
LEA	Late embryogenesis abundant proteins
LPS	Low-pressure storage
LOS	Low-oxygen storage
LN	Liquid nitrogen
LD	Linkage disequilibrium
LR	Landraces
MAB	Marker-assisted breeding
MABC	Marker-assisted backcrossing
MAGIC	Multi-parent advanced generation intercross
MAGP	Marker-assisted gene pyramiding
MARS	Marker-assisted recurrent selection
MAS	Marker-assisted selection
MBC	Map-based cloning
MS	Mass spectrometry
MSBP	Millennium Seed Bank Project
MoEFCC	Ministry of Environment, Forest and Climate Change
MPCA	Medicinal Plant Protection Area
NAM	Nested association mapping
NAFIS	National Bank for Agriculture and Rural Development, All India Rural Financial Inclusion Survey
NAGS	National Active Germplasm Sites
NBPGR	National Bureau of Plant Genetic Resources
NERICA	New Rice for Africa
NGOs	Non-governmental organizations
NHEJ	Non-homologous end joining
NIDM	National Institute of Disaster Management
NILs	Near isogenic lines
NGS	Next-generation sequencing
PAMP	Pathogen-associated molecular pattern
PCR	Polymerase chain reaction
PGR	Plant genetic resources

PGRFA	Plant Genetic Resource for Food and Agriculture
PoU	Prevalence of undernourishment
PROSEA	Plant Resources of Southeast Asia
PPP	Plant protection products
PTM	Post-translational modifications
QTL	Quantitative trait loci
RILs	Recombinant inbred lines
RAD-seq	Restriction-site-associated DNA sequencing
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
RGA	Rapid Generation Advancement
RGPs	Restoration of gene pools
RNA	Ribose nucleic acid
RNAi	RNA interference
RISC	RNA-induced silencing complex
ROS	Reactive oxygen species
SADC	Southern African Development Community
SARP	Sequence-related amplified polymorphism
SCAR	Sequence-characterized amplified region
SDGs	Sustainable development goals
SGS	Second-generation sequencing
siRNA	Small interfering RNA
SNPs	Single nucleotide polymorphism
SMRT	Single-Molecule Real-Time Sequencer
SNVs	Single nucleotide variations
SSD	Single-seed descent
SSLPs	Simple sequence length polymorphisms
SSR	Simple sequence repeats
STRs	Short tandem repeats
STS	Sequence tagged site
TAC	Technical Advisory Committee
TALENs	Transcription activator-like effector nucleases
TCA	Tricarboxylic acid cycle
TFs	Transcription factors
TGS	Third-generation sequencing technologies
TILLING	Targeting-induced local lesions in genomes
UCDP	Uppsala Conflict Data Program
UNCED	United Nations Conference on Environment and Development
UNFAO	United Nations Food and Agriculture Organization
UNEP	United Nations Environment Programme
UNESCO	United Nations Education, Scientific and Cultural Organization
UNHCR	United Nation Higher Commission for Refugees
UNICEF	United Nations International Children's Emergency Fund
UNIX	Uniplexed Information and Computing System
USEPA	United States Environmental Protection Agency

VIR	N. I. Vavilov All-Union Scientific Research Institute of Plant Industry
WGP	Whole genome prediction
WGS	Whole-genome shotgun sequence
WEF	World Economic Forum
WEPs	Wild edible plants
WHO	World Health Organization
ZNFs	Zinc finger nucleases



Potential of Genetic and Genomic Resources for Genetic Improvement of Food Crops

1

Romesh Kumar Salgotra and Sajad Majeed Zargar

Contents

1.1	Introduction.....	3
1.2	Importance of Genetic and Genomic Resources.....	4
1.3	Genetic and Genomic Resources for Crop Improvement.....	8
1.4	Important PGR in Crop Improvement.....	14
1.5	Role of PGR and Genomic Resources in Industries.....	15
1.6	Implication of Genomic Resources for PGR Conservation.....	16
1.7	Impediments to the Use of PGR in Crop Improvement.....	17
1.8	Challenges.....	18
1.9	Conclusion.....	18
	References.....	19

Abstract

Plant genetic resources (PGR) are the major natural resources on which human being has relied on for their livelihood, and their demand will increase in the future due to the continuing growth of population. Scientifically use of PGR is important in increasing the resilience and productivity of agricultural production systems for future food security. However, despite their importance in crop improvement, utility of these resources has been poor. With the advent of new high-throughput technologies like next-generation sequencing (NGS), new genomic resources have been generated. The advancement in genomic tools and

R. K. Salgotra (✉)

School of Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Jammu, Chatha, Jammu, Jammu and Kashmir, India

S. M. Zargar

Division of Plant Biotechnology, Sher-e-Kashmir University of Agricultural Sciences and Technology of Kashmir, Srinagar, Jammu and Kashmir, India

© Springer Nature Singapore Pte Ltd. 2020

R. K. Salgotra, S. M. Zargar (eds.), *Rediscovery of Genetic and Genomic Resources for Future Food Security*, https://doi.org/10.1007/978-981-15-0156-2_1

1

reduction in their costs are bringing many more plants within the range of genome- and transcriptome-level analysis. The genomic resources thus generated will be useful for genetic improvement of crops through applications of resources such as marker-assisted breeding (MAB) for gene introgression, mapping quantitative trait loci (QTLs) or identifying new or rare alleles associated with a particular trait. The effective and complementary use of all of genomic resources and available PGR will be required for meeting the challenge posed by the world's expanding demand for food. This chapter focuses on how genomic resources can be used in PGR for crop improvement particularly for major food crops. The real and potential application of the current advances in genomic technologies can be used for efficient utilization of PGR for crop improvement to secure food security.

Acronyms

AB-QTL	Advanced backcrossed QTL
AM	Association mapping
CGA	Candidate gene approach
CGIAR	Consultative Group for International Agricultural Research
CMS	Cytoplasmic genic male sterility
CRS	Core reference set
CWR	Crop wild relatives
DH	Doubled haploid
EcoTILLING	Ecotype TILLING
EST	Expressed sequence tag
GAB	Genomic-assisted breeding
LD	Linkage disequilibrium
MAB	Marker-assisted breeding
MAS	Marker-assisted selection
NGS	Next-generation sequencing
PCR	Polymerase chain reaction
PGRs	Plant genetic resources
QTLs	Quantitative trait loci
RAD-seq	Restriction-site-associated DNA sequencing
RAPD	Random amplified polymorphic DNA
RFLP	Restriction fragment length polymorphism
SCAR	Sequence characterized amplified region
SNPs	Single nucleotide polymorphism
SSR	Simple sequence repeats
STS	Sequence tagged site
TILLING	Targeting induced local lesions in genomes

1.1 Introduction

Genetic resources are sometimes called the “first resource” of the natural resources which can be used for crop improvement. At one level, plant genetic resources (PGRs) include all the individuals of a species, particularly if it is threatened with extinction. PGRs also include populations, gene pools or races of a species which possess important attributes not found uniformly throughout the species. PGR can also be defined as all materials such as wild species, wild relatives, landraces, etc. that are available for improvement of a cultivated plant species. Breeding lines and research materials, such as mutant, genetic or chromosomal stocks, are also genetic resources and are important in animal and plant breeding and in all phases of biological research. Finally, genetic resources can refer to genes themselves, maintained in selected individuals or cloned and maintained in plasmids. The effort required to utilize these resources in crop improvement is enormous but well justified as the genetic diversity present in these represents a critical component in the world’s fight against hunger. These resources are the basis for food security which can be efficiently utilized for crop improvement through various biotechnological interventions.

To feed the ever-increasing population in the scenario of climate change, the demand for the development resilient crop cultivars is imperative. Development of such cultivars through conventional plant breeding methods depends on the availability of natural genetic variations in PGR of a given crop species. Moreover, genetic variability that exists is very low and needs to be widened for further improving the productivity of the crop. Further, there is a need to protect the loss of genetic diversity in several plant species. Efforts have been made since long to collect, conserve and evaluate PGRs, to support the plant breeders with diverse genetic materials, to widen the genetic base and to create new varieties to enhance the crop productivity. Out of 240,000 plant species, only 25–30 are used for human consumption, and of these, rice, wheat and maize together constitute about 75% of global grain production (Cordain 1999). Therefore, conservation, multiplication and sustainable utilization of the existing PGRs, which comprise cultivars, landraces and wild relatives, are essential to combat the food security.

In classical plant breeding, PGR may also include those genetic materials that do not have any immediate use for the plant breeders (Hallauer and Miranda 1981). To satisfy the ever-increasing demands of a growing human population for more food, plant breeders require access to new genetic diversity in plant species (Brozynska et al. 2016). According to the extended gene pool concept, PGR may be divided into primary gene pool, secondary gene pool, tertiary gene pool and isolated genes (Harlan and de Wet 1971). The primary gene pool comprises of the crop species itself and other species that can be easily crossable. The secondary gene pool consists of related species that are more difficult to cross with the target crop. In this case crossing is less successful, and if crossing is there, the progenies are partially sterile. The tertiary gene pool is composed of species which can only be crossed by employing techniques like embryo rescue or protoplast fusion. In fourth class PGR, the isolated genes, may derive from related or unrelated plant species, from animals

or microorganisms. The importance of the different classes of PGR for crop improvement depends on the target crop species. The utility of PGR is important in increasing the productivity and production of food crops. However, despite their importance, utility of genetic resources has been poor. The array of PGR together with new genomic resources and other technological tools provides us with a healthy solution to meet the world's future food demands. PGRs or genomic resources alone will not serve the purpose; rather, the complementary utilization of these resources will be required for crop improvement to meet the food requirements.

In plant genome about 50–60,000 genetic loci are present, and in crop improvement, the correct combination of specific alleles is required. The knowledge of where these alleles are best found and how these can be combined in a single species is important for crop improvement. With the emergence of NGS techniques with reduced cost, various genomic resources such as genome sequences, functional genomic resources including microarrays and RNA-seq, sufficient numbers of molecular markers, expressed sequence tags (ESTs) and high-density genetic maps are causing a rapid acceleration of genetics and genomic research of crops. The completion of reference genome sequences of important crops and the ability to perform high-throughput resequencing are providing opportunities for improving our understanding of the PGR for utilization in crop improvement. This is leading to an increase in our knowledge of the genes that are linked to many agronomical and quality traits. These genomic resources have the potential to accelerate gene discovery which are being introgressed/pyramided in crops to enhance crop productivity to ensure food security. This chapter focuses on the potential use of PGR and genomic resources to meet the continually expanding demand for major food crops. This reviews the real and potential application of the current advances in genomic technologies in improving the utilization of these resources. This will also indicate how potentially these resources and technological tools can be used for crop improvement to meet food security in the future.

1.2 Importance of Genetic and Genomic Resources

Genetic and genomic resources play a significant role in crop improvement particularly in the development of crop varieties with desirable characters. To meet the challenge posed by demand for food, the complementary utilization of genetic resources with available genomic will be required. Genetic resources can efficiently be used in crop improvement with the help of the current advances in genomic technologies.

1.2.1 Genetic Resources

Genetic resources play a significant role in agriculture, particularly in crop variety development and improvement programmes. PGR diversity provides the major sources of important genes for diseases and insect pest resistance and yield and quality improvement. Genetic resources form the natural variations that have been

utilized to support human kind for several millennia. They include primitive forms of cultivated crop species and landraces, modern cultivars, obsolete cultivars, breeding lines and genetic stocks and related wild species. These resources are the basis for food security in addition to being sources of energy, animal feed, fibre as well as other ecosystem services. They are important in addressing the global challenges such as climate change, global population growth and food scarcity. PGRs are fundamental to our efforts to improve agricultural productivity. These resources, fortunately stored in gene banks around the world and owing to their great importance, effective conservation and sustainable utilization of PGR, are critically important to food security, as evidenced by the huge number of accessions that are conserved in gene banks for various species. It is clear that enormous progress has been made in conserving important germplasm in gene banks, but these genetic resources remain unexploited because of a variety of factors. Genetic approaches have a long history of use in conservation, but the transition to genomic technologies is only just beginning. Earlier very limited biotechnological interventions and genomic resources were available and are the main limitations for exploitation of genetic resources (Supple and Shapiro 2018). With the development of various genomic techniques, the genetic resources can be used efficiently for crop improvement.

PGRs are the most important components of agrobiodiversity. The introgression of genes in wheat crop which provided the foundation for the “Green Revolution” demonstrated the tremendous impact of genetic resources on crop production (Hoisington et al. 1999). Food security mainly depends on the wise use and conservation of agricultural biodiversity and genetic resources (Esquinas-Alcazar 2005). Since importance have been given to relatively small number of crop species for global food security, it is particularly important that their genetic diversity is conserved effectively and managed wisely. So far, only a small part of the total genetic variability has been characterized and used for crop improvement. Owing to their great importance, effective conservation and sustainable utilization of PGR are imperative for food security.

1. *Wild relatives*: The major portion in PGR in plant species is contributed by wild relatives. Wild species possess numerous desirable characters such as genes for biotic and abiotic resistance and nutritional value enhancement for crop improvement. Due to some crossability barriers, wild species are difficult to cross with cultivated genotypes. However, crossability between cultivated varieties and wild species can be overcome using embryo rescue, genetic engineering and protoplast fusion techniques for transferring some useful traits from wild relatives to cultivated genotypes. The wild relatives possess desirable nutritional traits such as protein content in wheat, calcium content and provitamin A in potatoes and tomatoes, respectively.
2. *Landraces*: The indigenous varieties selected by the local people from the traditionally grown germplasm are termed as landraces. And development of varieties from these selected germplasm is called as landrace varieties. These varieties also possess numerous genes for biotic and abiotic resistance. These landraces are grown under species environmental conditions and areas but possess a

number of important traits to be used in crop improvement. Although landrace varieties are low yielding, these are tolerant to major stress factors such as water regime, drought, frost, soil salinity and heat.

1.2.2 Genomic Resources

With the advancement in high-throughput techniques and cost reduction of next-generation sequencing (NGS), many genomic resources such as genome sequences, high-throughput analysis of gene expression, numbers of molecular markers, ESTs and high-density genetic maps have paved the way to the genetic engineering and molecular breeding of plants for crop improvement. The application of these genomic resources to crop species can contribute efficiently to solve the problems of nutritional deficiency and biotic and abiotic stresses. In the last decade, the emphasis on crop improvement using novel genomic tools has shifted toward the identification and functional analysis of miRNAs, one of the hottest research fields in plant sciences (Sun 2012). For the last three decades, globally different genomic resources are being effectively used for identifying the important genes and alleles from the genetic resources to be used in breeding programmes (Fig. 1.1). The following are the various genomic resources which are being used for crop improvement:

1. *Quantitative trait loci*: A number of agronomic traits are controlled by many genes, and these traits are called as quantitative or complex traits. A quantitative trait locus (QTL) represents a region of a genome that contains genes associated with a particular quantitative trait such as yield, grain weight, protein content,

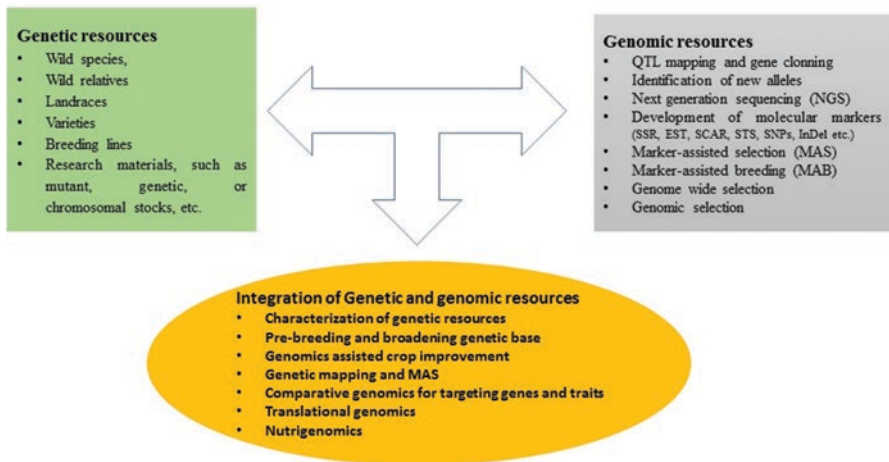


Fig. 1.1 A schematic illustration of the integration of genetic and genomic resources for crop improvement

etc. (Collard et al. 2005). Such regions are associated with the agronomic/phenotypic traits of the plant species. However, their identification in the genome is very difficult because of the interactions between QTL, absolute number of QTL, epistasis and other sources of variation (Doerge 2002). These genes/QTLs are identified and tagged by using molecular markers (Mohan et al. 1997). A tight association between the gene of interest and molecular markers led to marker-assisted breeding (MAB) programme in crop improvement. This will also help in the construction of genetic map based on molecular markers (Francia et al. 2005).

2. *Molecular markers*: With the advances in NGS and molecular marker technology, a number molecular markers such as restriction fragment length polymorphism (RFLP), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), simple sequence repeats (SSR), sequence tagged site (STS), expressed sequence tag (EST), sequence characterized amplified region (SCAR), single nucleotide polymorphism (SNPs), insertion-deletion (InDel), etc. were developed. These molecular markers have been successfully used in the construction of genetic maps, indirect selection of desired traits in segregating and advanced breeding materials. Today molecular markers become the choice of markers for genetic diversity studies of crop plants. Molecular markers could be used in various crops such as wheat, apple, pear, plum, etc. for identification of desired traits. These markers successfully help in the development of biotic and abiotic stress-resistant varieties (Salgotra et al. 2015).
3. *Marker-assisted selection*: There has been considerable progress during the last two and half decades in mapping and tagging many agronomical desirable traits with molecular markers, which form the basis for marker-assisted selection (MAS). In MAS, molecular markers are used to assist in the selection of target traits of interest such as resistance genes for diseases and insect pests and selection of quality traits of fruit trees (Dirlewanger et al. 2004). MAS has been successfully used in introgression of a number of genes in rice crop varieties which are susceptible to lodging, diseases and insect pests.
4. *Genome-wide association studies (GWAS)*: Association mapping (AM) is an alternative to classical linkage mapping to explicate the genetic basis of complex traits particularly for abiotic stresses (Abdurakhmonov and Abdurakimov 2008; Zhao et al. 2011). Linkage mapping based on biparental progeny has been useful for identification of major genes and QTL mapping (Komatsuda et al. 2007). But linkage mapping based on biparental progeny suffers from several drawbacks (Cosart et al. 2011). The shortcomings of the biparental-based linkage mapping are well addressed in association genetics in several crops (Gupta et al. 2005; Hall et al. 2010; Maccaferri et al. 2011). Further advantages of biparental linkage analysis, along with association mapping in nested association mapping in single unified mapping population, are used for the genome-wide dissection of complex traits (Yu et al. 2008).
5. *Whole-genome de novo sequencing*: In several decades “Sanger sequencing” remained predominant for decoding the genomes. The whole-genome sequenc-

ing in less time and low cost is the major landmark discovery in omics. Earlier a small-genome sequencing requires huge funds in multi-institutional efforts. With the advancement of NGS technologies, genome sequencing has become much faster, low cost and efficient by several folds. After the introduction of the first 454 NGS platform, several platforms were introduced such as Illumina, ABI SOLiD, Helicos, PacBio, Ion Torrent and Oxford Nanopore. The whole-genome sequencing of plants has generated huge genomic resources such as development of molecular markers, comparative genomics, gene expression through transcriptome, etc.

6. *Genome resequencing for the discovery of genome-wide variation*: A reference genome is generated once the genome of a plant is sequenced. The reference genome is for studying genetic resources of the same species or related species to detect genetic variations. Thus, whole-genome resequencing of several accessions/genotypes enables to generate useful genomic resources and information. This has also removed bottlenecks of ascertainment bias (i.e. the presence of rare alleles) obtained through biparental mapping population in the estimation of linkage disequilibrium (LD) and genetic relationships between genotypes (Cosart et al. 2011). Genome Project 1001 is one of the largest projects started in 2008 for resequencing of 1001 *Arabidopsis thaliana* to know/discover genome-wide sequence variations. In China genome sequencing project of 3000 rice accessions is ongoing to discover genome-wide sequence variations among the genotypes.

1.3 Genetic and Genomic Resources for Crop Improvement

Conventional research inputs have contributed in solving some of the constraints limiting crop productivity. However, limitations, such as complex genome, narrow genetic base, poor fertility in distant crosses, transferring important genes from wild relatives, susceptibility to biotic and abiotic stresses and long duration to breed elite cultivars, hinder crop improvement programmes (Salgotra et al. 2015). However, the modern biotechnological techniques and genomic resources can overcome the problem of identification of important genes and alleles in the wild and unrelated species. The identified important genes and alleles can be easily transferred in cultivated species embryo rescue techniques, and linkage drag can be minimized with the use of genomic resources such as MAS, MAB, QTL mapping, etc. There are various biotechnological strategies to solve the problems faced by the breeders which can be adopted for PGR to enhance the crop productivity on sustainable basis.

Genetic resources are the basic material for selection and improvement of crop species through breeding to ensure food security for the rapidly increasing population. Different aspects related to PGR such as collection, conservation, evaluation, management and utilization are, however, needed to be done eminently. Biotechnological tools have proved useful in a number of ways to improve the conservation and management of PGR (Hodgkin et al. 2001). Molecular markers help

in DNA profiling, identification and verification of accession identity and genetic contamination (Collard et al. 2005; Spooner et al. 2005; Weising et al. 2005) and also have been used to identify eco-geographic races within the domesticated or wild gene pools of crop species (Yu et al. 2003). Different genomic resources have emerged with the availability of high-throughput techniques and sequence of various crop species genomes through NGS techniques. Presently, existing biotechnological approaches also overcome challenges of embryo rescue and somatic hybridization for effective utilization and enhancement of PGR in crop improvement (Rao et al. 2003; Zimnoch-Guzowska et al. 2003). Bringing together plant breeders and biotechnologists is an eminent need for effective utilization of genomic resources techniques in plant breeding programmes. The following are recent genomic resources techniques which can be efficiently used in plant breeding programmes to achieve food security in the future.

1.3.1 Pre-breeding and Broadening Genetic Base

A significant proportion of gene bank collections comprises wild species, which represent the primary, secondary and tertiary gene pool (Harlan and de Wet 1971). These genetic resources have immense value in terms of the useful genes and alleles to improve the gene pool of crop species. Earlier breeders are reluctant to use these valuable resources in their breeding programmes because of linkage drag. For example, breeders in Japan have faced challenges in developing elite varieties with resistance against blast and also possessing good quality traits because of the co-introduction of desirable alleles for blast resistance and the undesirable ones controlling poor grain quality (Fukuoka et al. 2009). While such associations could be because of pleiotropy, they have in most cases been found to be because of tightly linked genes (Fukuoka et al. 2009). Breaking this linkage is usually costly and time-consuming. Most breeders therefore prefer to reuse their usually limited working collections, thereby leading to release of varieties with narrow genetic diversity. This narrow genetic base negatively affects the resilience, productivity and sustainability of agricultural production systems. Pre-breeding is therefore an important activity that helps to improve the genetic value, attractiveness as well as suitability of gene bank materials to breeders. Presently, certain predictive models have been developed which have the capacity to predict those SNP variations that are most likely to lead to deleterious phenotypic effects (Xu 2010). The biotechnological tools can identify the materials with such SNP alleles which can be eliminated from breeding programmes at an early stage. Plant breeders are also reluctant to use wild species due to linkage drag and their unwillingness to disrupt the favourable linkage blocks in their breeding materials.

With the use of high-throughput sequencing and genotyping approaches, it is now possible to obtain cross-specific sequence markers such as SNPs that can be used to saturate the genetic background of both parents (Henry et al. 2010). Using SNP markers, it is possible to monitor the degree of introgression of specific alleles or genomic regions in the offspring (Sharma et al. 2013; McNally et al. 2009).

This monitoring ensures that the genome of the recurrent parent can be efficiently regained, and the tracking of both desired and undesired alien alleles ensures that only narrow segments of the wild species, preferably having only the desired allele, are introgressed (Henry et al. 2010). To minimize linkage drag, it is recommended that the markers to monitor the introgression should be as close as possible to the desired genomic region (Hospital 2001). The use of genic or functional markers linked to the gene of interest is preferable. Deep sequencing of the genomic region controlling a particular trait can help identify the loci/alleles responsible for the undesirable trait and thus select recombinants lacking this undesirable allele (Fukuoka et al. 2009; Varshney et al. 2014). Genomics therefore plays an important role in the identification of both beneficial and deleterious alleles as well as facilitating the transfer of the beneficial ones during crop improvement. This minimizes the challenges associated with wild and unadapted materials, thereby enhancing their utility in crop improvement.

1.3.2 Genomic-Assisted Crop Improvement

Genomic technology has been applied in gene identification laying good foundation for functional genomics research, and to aid us in understanding the gene expression and biological activity, genomics initiatives are focused on fundamental elements of plant biology with regard to growth, development, reproduction, photosynthesis and responses to environmental conditions and pathogens. Cereal genomics carries the strength to shape the future of agriculture and its sustainability (Tuberosa et al. 2002). The better prediction of the phenotype that a particular genotype will produce is a primary goal of genomics-based breeding. Analysis of the crop genome architecture and their expressed components is now possible with the development in crop genomics and subsequently leads to an increase in our knowledge of the genes that are linked to key agronomically important complex traits particularly in major crop species. DNA-based molecular markers including SNPs have played a pivotal role in detecting the genetic variation available in germplasm collections and breeding lines. These DNA markers can be generated in large numbers and can prove to be very useful for a variety of purposes relevant to crop improvement. Their association with genes/QTLs controlling the traits of economic importance has also been utilized in some cases for indirect MAS. Other uses of molecular markers include gene introgression through backcrossing, germplasm characterization, genetic diagnostics, characterization of transformants, study of genome organization and phylogenetic analysis.

Various sets of diverse molecular markers have been developed for many major crop species and are being used extensively for the development of saturated molecular, genetic and physical maps and for the identification of genes or QTL controlling traits of economic importance through MAS (Varshney et al. 2005; Varshney et al. 2006). With the use of genomic resources, various traits of crops have been improved (Table 1.1). Together with MAS other approaches like association

Table 1.1 Potential use of genetic and genomic resources for crop improvement

Crop	Breeding strategies	Objective	References
Maize	AB-QTL	Improved hybrid performance for yield, grain moisture and plant height	Ho et al. (2002)
	MAS	Conversion of normal maize lines into quality protein maize (QPM)	Babu et al. (2004)
	MAS	Improvement of drought adaptation	Ribaut and Ragot (2006)
Barley	Introgression, MAS	Enhancement of tolerance to boron toxicity in two-rowed barley	Emebiri et al. (2009)
	Introgression, MAS	Resistance to barley yellow mosaic virus I–III from donor line “Y4”	Okada et al. (2003)
Rice	Introgression, AB-QTL	Identification of yield-improving QTLs from <i>O. rufipogon</i>	Xiao et al. (1998)
	Pyramiding	Bacterial blight (BB) resistance (<i>X. oryzae</i> pv. <i>oryzae</i>) into elite rice variety PR 106	Singh et al. (2001)
	Pyramiding	Bacterial blight (BB) resistance (<i>X. oryzae</i> pv. <i>oryzae</i>) into elite rice variety Samba Mahsuri	Sundaram et al. (2010)
	MAS	Introgression of locus conferring submergence tolerance from cultivar “FR13A” into “Swarna”	Xu et al. (2006)
Wheat	Introgression	Stacking of QTL for <i>Fusarium</i> head blight (FHB) resistance from non-adapted sources in an elite spring wheat background	Miedaner et al. (2006)
	MAS	Leaf rust resistance (<i>Puccinia triticina</i>), stripe rust resistance (<i>P. striiformis</i>), leaf, stripe and stem rust resistance gene complex	Chicaiza et al. (2006)
	MAS	Introduction of six <i>Fusarium</i> head blight QTLs, orange blossom wheat midge resistance (<i>Sm1</i>) and leaf rust resistance (<i>Lr21</i>)	Somers et al. (2005)
	MAS	Introduction of three <i>Fusarium</i> head blight QTLs into an elite winter wheat breeding population	Wilde et al. (2008)
	Introgression	Leaf rust resistance gene <i>Lr58</i> from <i>A. triuncialis</i>	Kuraparthi et al. (2011)

Source: *Journal of Plant Science & Research*

mapping (Ersoz 2007), functional genomics (Schna 1998), genetical genomics (Jansen and Nap 2001), allele mining (Varshney et al. 2005), targeting induced local lesions in genomes (TILLING) and ecotype TILLING (EcoTILLING) (Till 2007) have been available from the past decade.

Development in cereal genomics play a key role in crop improvement for better understanding of the biological mechanisms which can improve the decision-making process for more efficient breeding strategies for screening and selecting superior genotypes (Varshney et al. 2005). These advances and development will provide opportunity for efficient transfer of information systems from model species and major crops to orphan crops (Naylor et al. 2004).