

Mohar Singh · Sandeep Kumar *Editors*

Broadening the Genetic Base of Grain Cereals

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Mohar Singh
ICAR-National Bureau of Plant
Genetic Resources Regional Station
Shimla, HP, India

Sandeep Kumar
ICAR-National Bureau of Plant
Genetic Resources
New Delhi, India

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Preface

Worldwide, majority of grain cereals have intrinsically a narrow genetic base which has been exploited to the maximum levels of productivity. Further breakthroughs in enhancing yield and improving stability in future crop cultivars require the identification of useful materials with desirable traits of interest and their incorporation into the elite genetic background. Knowledge, access, and use of genetic diversity available in cultivated and wild relatives are essential for broadening the genetic base of cultivated species. In view of this context, an effort has been made to bring together the rather scattered research work done in this useful area in the form of an edited collection, a compilation that should be of great value to the researchers across the world. The book comprises a total of ten chapters on different cereals and millets, contributed by eminent researchers from various reputed institutions of the world. The introductory chapter describes some key issues linked to bottlenecks and wild species utilization on current trends of interspecific hybridization. The subsequent chapters deal with different aspects related to widening the genetic base of cultivated gene pool. Each chapter provides detailed information on crop genepool, evolutionary relationships and systematic assessment of gene flow, gene flow constraints, level of diversity in crop germplasm, production related problems, traits of importance for widening the genetic base, wide hybridization, barriers to wide hybridization, methods of wide hybridization, and genome mapping and genomics status of each candidate crop. The editors are extremely thankful to all authors for their significant contributions to this book. The entire process of preparing the manuscript was marked by cordial collegiality. Thanks are also due to Ms. Megha Bakshi working as Project Assistant with editors for her assistance during the preparation of this multi-authored edited book in terms of compilation, edited chapter processing, and typographical scientific work. We are also indebted to Springer India for their excellent professional support in the completion of this project. Despite several rounds of proofreading and our best efforts, the book may still have some scientific, technical, and printing errors. We will appreciate if these omissions are brought to our notice, so that they may be rectified in future editions. Finally, we hope this book will be very useful to researchers and other readers across the world.

Shimla, India
New Delhi, India

Mohar Singh
Sandeep Kumar

Contents

1	Introduction	1
	Mohar Singh and Sandeep Kumar	
2	Wheat	9
	W. Tadesse, S. Rajaram, F.C. Ogbonnaya, M. Sanchez-Garcia, Q. Sohail, and M. Baum	
3	Rice	27
	Kuldeep Singh, Kumari Neelam, Amanpreet Kaur, and Karminderbir Kaur	
4	Maize	67
	Firoz Hossain, Vignesh Muthusamy, Jayant S. Bhat, Shailendra K. Jha, Rajkumar Zunjare, Abhijit Das, Konsam Sarika, and Rajesh Kumar	
5	Barley	89
	Naval Kishore, Vishnu Kumar, and R.P.S. Verma	
6	Oats	127
	Rahul Kapoor and Chinka Batra	
7	Sorghum	163
	Pummy Kumari, S.K. Pahuja, Satyawana Arya, and J.V. Patil	
8	Pearl Millet	205
	H.P. Yadav, S.K. Gupta, B.S. Rajpurohit, and Nisha Pareek	
9	Finger Millet	225
	Salej Sood and B. Kalyana Babu	
10	Foxtail and Barnyard Millets	257
	Sandeep Kumar, N. Dikshit, Mohar Singh, and J.C. Rana	

About the Editors

Mohar Singh is currently working as Senior Scientist (Plant Breeding) at the National Bureau of Plant Genetic Resources Regional Station in Shimla, India. Dr. Singh received his doctoral degree in Plant Breeding from the Himachal Pradesh Agricultural University in Palampur, India. He has been working on the genetic and genomic resources of pulses, cereals, and potential crops for the last several years. He has identified several useful gene sources for various traits of interest in wild *Cicer* and *Lens* species, some of which have since been introgressed into the cultivated background for diversification of the cultivated gene pool. Dr. Singh has published more than 50 research papers in journals of national and international repute. He also holds two textbooks and three edited books to his credit.

Sandeep Kumar is presently working as Senior Scientist (Biochemistry) at the Germplasm Evaluation Division, National Bureau of Plant Genetic Resources (NBPGR), an institute of the Indian Council of Agricultural Research (ICAR), New Delhi, since December 22, 2010. Earlier, he worked as a Scientist (Biochemistry) at the Directorate of Rapeseed-Mustard Research, Sewar, Bharatpur, which is also an institute of the ICAR. He received his master's and doctoral degrees in Biochemistry from Chaudhary Charan Singh Haryana Agricultural University, Hisar, Haryana. He has substantial experience in teaching various graduate and postgraduate courses at SBS PGI, Balawala, Dehradun, and graduate courses at D.N. College, Hisar. He has also researched biochemical aspects in various groups of crops including cereals, oilseeds, and forages. Presently, his research focuses on the nutritional and other biochemical aspects of cereals and oilseeds. He has to his credit one book as co-editor and more than 45 scientific publications published in journals of national and international repute.

Mohar Singh and Sandeep Kumar

Abstract

The human population growth has passed seven billion figures and is assumed to reach nine billion by 2050 (UN 2013). With such a higher population increasing rate, the amount of food we produce today will not be sufficient in the coming years to keep all alive, healthy and wealthy, which develops substantial pressure on the agricultural production system. Agricultural production demands are expected to increase in the twenty-first century with demands for cereals in particular expected to rise by 70 % from 2007 to 2050 (FAO 2012). Besides, the need of biomass for bioenergy and biorefineries is also expected to increase considerably. There are, however, fewer possibilities to increase the area under agriculture substantially for enhancing production systems in the world. Global climate change is also going to affect the production potential more adversely mainly due to increase in temperatures which in terms reduce the photosynthetic capacity of important agricultural crop plants. Further, water is expected to become a limiting factor in most of areas, and the pressure from devastating pathogens and pests is also assumed to increase, substantially. However, challenges of meeting future cereal production demands as mentioned above will be entirely dependent on the development of potential cultivars well adapted to the altered growing conditions. The tailoring of genetically potential crop varieties with high and stable yield, adequate quality attributes and low environment impact will in turn be dependent on the available invaluable wild/weedy genetic resources and their subsequent selection and utilization for diversification of culti-

M. Singh (✉)
ICAR-National Bureau of Plant Genetic Resources
Regional Station, Shimla, HP 171 004, India
e-mail: singhmohar_2003@yahoo.com

S. Kumar
ICAR-National Bureau of Plant Genetic Resources,
Pusa Campus, New Delhi 110 012, India
e-mail: kumarsandeep_biochem@rediffmail.com

vated gene pool. Gene banks across the globe are primarily focusing on plant genetic resources management activities of elite germplasm. But there is an urgent need for active involvement with all stakeholders to enhance the utilization of crop wild relatives. There is considerable germplasm availability of cereals including collections of adapted varieties and genetic stocks carrying useful traits of interest through to landraces and crop wild relatives. However, this richness of plant genetic diversity is greatly underutilized, with important traits not being exploited into the cultivated genetic background. The conservation of genetic resources must be linked to their enhanced and sustainable use if they carry potential traits to play a pivotal role under adverse situations. Pre-breeding approach provides us a useful tool that can be used for the introgression of demanding traits of interest into suitable, agronomically adapted genetic backgrounds.

Keywords

Base broadening • Yield enhancement • Wild species • Grain cereals

The human population growth has passed seven billion figures and is assumed to reach nine billion by 2050 (UN 2013). With such a higher population increasing rate, the amount of food we produce today will not be sufficient in the coming years to keep all alive, healthy and wealthy, which develops substantial pressure on the agricultural production system. Agricultural production demands are expected to increase in the twenty-first century with demands for cereals in particular expected to rise by 70 % from 2007 to 2050 (FAO 2012). Besides, the need of biomass for bioenergy and biorefineries is also expected to increase considerably. There are, however, fewer possibilities to increase the area under agriculture substantially for enhancing production systems in the world. Global climate change is also going to affect the production potential more adversely mainly due to increase in temperatures which in terms reduce the photosynthetic capacity of important agricultural crop plants. Further, water is expected to become a limiting factor in most of areas, and the pressure from devastating pathogens and pests is also assumed to increase, substantially. However, challenges of meeting future cereal production demands as mentioned above will be entirely dependent on the development of potential culti-

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1.1 Traits of Importance for Base Broadening

1.1.1 Abiotic Stresses

Tolerance to prevailing abiotic stresses such as drought, cold, salinity, heat, water logging, nutrient use efficiency and mineral toxicity has traditionally enabled cereal crops to cope with the major stresses with a balance of useful characters. In view of climate changing scenario, shifts in the prevalence of some abiotic stresses with drought being increasingly important, given the effect of climate change on the amount of precipitation and its distribution over the growing seasons in most parts of the world. Therefore, it is expected that the agricultural areas will experience enhanced or novel abiotic stresses making it increasingly urgent to develop cereals that can withstand such environmental changes, in order to increase or even just to maintain current yield levels.

1.1.2 Biotic Stresses

Plant pathogens cause considerable yield losses in cereal production, reducing crop quality and threatening food safety. Disease prevention and control are thus a prerequisite for competitive cereal production with the breeding of genetically disease-resistant crops being one of the most environmentally and economically desirable ways to manage plant diseases. The prevalence of different plant diseases is changing due to changing environmental conditions, including global climate change, but also changes in agricultural production with trends towards larger areas planted to fewer and/or genetically more uniform varieties, reduced crop rotation and soil tillage, loss of biodiversity, changing use of pesticides, and global trade. In such a changing environmental and economical context, plant diseases will inevitably appear and compromise crop production in regions where they did not represent a problem before, as is already being seen with the emergence of a new strain of heat-tolerant wheat yellow rust and increasing problems with

Fusarium head blight and *Ramularia* leaf spot. Understanding the host-pathogen biology is the first step towards minimizing the risks represented by plant diseases. Durable, both race non-specific and race-specific, resistance incorporated into high-yielding genotypes is the main method to manage diseases of cereals.

1.1.3 Quality Parameters

Cereal grains provide carbohydrates, protein, minerals, dietary fibre, vitamins and various functional molecules with medicinal properties. Increasing the future production potential of cereals and increasing/maintaining the nutritional traits make the task more challenging for the breeders. Wild species in general had higher content of micronutrients and vitamins which can be used for biofortification of the cultivated species. Further, high fibre content and functional biomolecules or nutraceuticals are other biochemical components where wild species can play a major role in development of materials containing higher concentration of these components.

New durable and efficient sources of resistance/nutritional traits will have to be sought, in the case of cereals, from landraces and from wild relatives of the crops. This appears to be an insignificant part of cereal germplasm accessions that are conserved in various gene banks across the world. Knowledge, access, and use of diversity available in the cultivated and wild relatives are essential for broadening the genetic base of cultivars to sustain crop improvement. An overview of the existing level of diversity and the genetic base of major grain cereals is presented in this chapter based on the contributions made by respective crop experts collated in this book.

1.2 Wheat

Wheat is one of the most important staple food crops for 35% of the world's population and is becoming important in the developing countries (CIMMYT 2011). To meet the demand for tailoring high-yielding and stress-resistant crop

varieties, it is a prerequisite to widen the genetic base of cultivated gene pool (Khalighi et al. 2008). The narrow genetic base of cultivated genotypes has limited the plant breeders' progress towards further improvement (Rejesus et al. 1996). Therefore, there is an urgent need to exploit new sources of variation, and incorporating them into cultivated backgrounds is one of the basic and fundamental ways of most of the wheat breeding programmes (Baghizadeh and Khosravi 2011). However, landraces and their wild relatives are base genetic materials for diversity maintenance and improvement (Baghizadeh and Khosravi 2011). The wild relatives of cultivated wheat are considered as potential sources of useful alleles for genetic base widening (Khalighi et al. 2008), because of high polymorphism found in wild gene resources, and that can be useful for wheat crop improvement (Cenkci et al. 2008). Introduction of useful genes from *Aegilops* can contribute to traits like major yield contributing component characters, quality and resistance to various biotic and abiotic stresses (Schneider et al. 2008). Likewise, *Aegilops* species are also reservoirs of invaluable genes for resistance against heat and drought (Zaharieva et al. 2001a; Molnár et al. 2004), salinity (Colmer et al. 2006) and cold (Monneveux et al. 2000) stresses. Many of these wild species contain valuable genes for resistance to various pathogens (Aghaee-Sarbarzeh et al. 2001; Schneider et al. 2008). Besides, *Aegilops* can also contribute to yield through modification of physiology of cultivated gene pool by increasing the size of flag leaf and thus biomass production (Monneveux et al. 2000); *Ae. kotschy* and *Ae. tauschii* also possess high iron and zinc content (Chhuneja et al. 2006).

1.3 Rice

The worldwide demand for rice is estimated to increase from 676 million tons in 2010 to 852 million tons in 2035 with an overall increase of 26% in the next 25 years (Khush 2013). To achieve this target, new rice varieties with higher yield potential and greater yield stability are vital

to relieve the growing pressure of greater rice production. Rice is bestowed with tremendous genetic diversity of which only a small fraction has been used for its improvement. Today, yield stagnation in rice is a proven fact rather than mere perception, and further yield jump does not seem to be forthcoming with present set of genetic material being used in most of the cross-breeding programmes. In order to achieve high yield potential and breaking yield plateau, utilization of wild gene pool can widen the genetic base of cultivated varieties. The genus *Oryza* of the Gramineae family consisted of 24 species. Among these, two species *O. sativa* and *O. glaberrima* are cultivated and the remaining 22 are wild species. The wild species have either $2n=24$ or $2n=48$ chromosomes representing AA, BB, CC, BBCC, CCDD, EE, FF, GG and HHJJ genomes. The genes from the cultivated rice (*O. sativa*) and its closely related wild species, having AA genome (*O. nivara*, *O. rufipogon*, *O. glumaepatula*, *O. longistaminata* and *O. meridionalis*), can be easily transferred to cultivated species by conventional hybridization and backcrossing procedures (Brar and Khush 1997).

1.4 Maize

Maize originated in Mexico and Central America and belongs to the tribe Maydae of family Poaceae. Genetic resources especially crop wild relatives and landraces harbour novel alleles/genes for imparting resistance/tolerance to various agro-morphological traits and biotic and abiotic stresses including nutritional quality traits. Among wild relatives, teosintes and *Tripsacum* are native to Mexico and Central America, while *Coix*, *Chionachne*, *Trilobachne* and *Polytoxa* originated in Southeast Asia. Likewise, interspecific compatibility between maize and teosinte develops hybrids. While generation of crosses between maize and *Tripsacum* species is difficult, Asiatic genera possess high degree of cross-incompatibility with maize. However, landrace accessions possessing unexplored alleles/genes serve as valuable donors for important traits of interest. These invaluable germplasm resources

can be systematically and effectively utilized in genetic enhancement and to widen the genetic base of cultivated varieties to develop high-yielding and nutritious germplasm resilience to desirable traits.

1.5 Barley

Barley being the earliest domesticated cereal is one of today's major crops. Wide adaptation of barley to ecogeographic conditions and higher response to low input and stressful environments make it cultivable globally. It is self-pollinating and a true diploid ($2n=2x=14$) and therefore is considered as an ideal genetic material for basic research purposes. Besides other sources of genetic variation, barley landraces continue to be an important tool of genetic diversity conserved *ex situ* in gene banks. Gene flow involving wild progenitors and domesticated cultivars has attracted breeders' interest in order to broaden the genetic base of barley. Biotic and abiotic factors affecting barley yield have to be determined specifically. There is little or no opportunity for interspecific gene transfer in nature between the other species of genus *Hordeum* as there is no chromosome pairing at meiosis with few exceptions. Wheat-barley hybridization has the potential to incorporate favourable characteristics of stem strength and winter hardiness of wheat into barley. Use of DNA markers and high-throughput techniques in barley has enhanced the precision for introgressing specific traits of importance for diversification of cultivated gene pool. Consensus maps have allowed comparative mapping to explore information available in other crop species. Recent approaches like advanced backcross QTL (AB-QTL) analysis and association mapping (AM) studies have aided in understanding of the complex agronomic traits in barley. Further, interspecific and intergeneric hybridization in barley can be beneficial for introgression of useful traits in the barley genetic background. Owing to health benefits of barley, industrial interest for introduction of different barley products in human diets has increased considerably. Further, efforts are in progress to sequence the barley

genome by the International Barley Genome Sequencing Consortium. The future barley breeding programme should combine the application of new tools and techniques with traditional and efficient plant breeding methods to achieve desired goals rapidly.

1.6 Oats

Oats rank sixth in world cereal production and are being grown as multipurpose crop for grain, pasture and forage or as a rotation crop in several segments of the world. The collection of germplasm and the conservation of gene pools of cultivated and related wild/weedy species are essential for crop improvement. The main focus is to summarize recent knowledge and significant achievements on genetic resources activities including plant taxonomy, diversity, collection, conservation, characterization, evaluation, and utilization in breeding of oats for diversification of cultivated varieties. Wild species of *Avena* are grouped into three gene pools depending on their interfertility with cultivated hexaploid oat. As far as wide hybridization is concerned, resistance to powdery mildew was introduced to breeding materials with the use of germplasm from *A. sterilis* (Hayes and Jones 1966), *A. barbata* (Aung et al. 1977; Thomas et al. 1980) and diploids *A. pilosa* (Hoppe and Kummer 1991; Sebesta et al. 1986), *A. hirtula* (Thomas 1968), *A. ventricosa* (Thomas 1970) and *A. prostrata* (Griffiths 1984; Morikawa 1995). In more recent findings of Herrmann (Yu and Herrmann 2006), the resistance was transferred from the tetraploid perennial oat *A. macrostachya*.

1.7 Sorghum

Sorghum [*Sorghum bicolor* (L.) Moench] is the world's fifth most important multipurpose cereal crop, valued for its grain, stalks and leaves. It is considered as drought, heat and insect resistant. Its small diploid genome ($2n=20$) and phenotypic diversity make it an ideal C_4 grass model (Mace et al. 2013). The *Sorghum* genus consists