

Chittaranjan Kole *Editor*

Genomics and Breeding for Climate- Resilient Crops

Vol. 2 Target Traits



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*Dedicated to
Prof. Rajendra B. Lal
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Foreword by M. S. Swaminathan

I am very happy that Prof. Chittaranjan Kole and other eminent authors have prepared two books on Genomics and Breeding for Climate-Resilient Crops. These are timely publications since climate-smart agriculture is the need of the hour. Many of the crops formerly known as coarse cereals are both very nutrient rich and climate smart. It would therefore be more appropriate to refer to them as climate-smart nutricereals. In this connection I give below the views I expressed in an editorial which I wrote for *Science* under the title “Gene Banks for a Warming Planet” (Swaminathan 2009).

“At the International Congress of Genetics in New Delhi in 1983, I stressed the need for a conservation continuum, beginning with the revitalization of conservation of domesticated plants by farm families in all countries, and extending to the establishment of an international genetic resource repository maintained under permafrost conditions. Since then, thanks to the spread of participatory breeding and knowledge-management systems involving scientists and local communities, on-farm conservation and gene banks have become integral parts of national biodiversity conservation strategies. For example, there are now over 125,000 genetic strains of rice, of which over 100,000 are in a cryogenic gene bank maintained by the International Rice Research Institute (IRRI) in the Philippines. This gene pool is invaluable for adapting one of the world’s most important cereal grains to the consequences of global climate change.

We now largely depend on a few crops such as rice, wheat, corn, soybeans, and potatoes to sustain global food systems. However, their genetic homogeneity increases their vulnerability to abiotic and biotic stresses. If their production is affected by a natural calamity, their prices will increase and food-deficient countries are likely to face riots and worse. Important publications such as *Lost Crops of the Incas* and *Lost Crops of Africa* document the historic role of agrobiodiversity in ensuring food and health security. It has therefore become an urgent task to save vanishing ‘orphan crops.’ We also know that millets, tubers, and grain legumes are rich in micronutrients but require less irrigation than the major crops. These plants and others are also sources of genes that confer tolerance to drought, floods, and the increased salinity of soils.

Although plant conservation on farms and in the wild is the ideal approach to preserving genetic diversity in crop plants, these methods are constantly jeopardized by invasive species, human destruction of habitat, and market factors. Therefore, other preservation strategies become essential. There are many cryogenic gene banks around the world resembling that at IRRI, but each is very expensive to maintain. Now, thanks to an initiative of the Government of Norway and the Global Biodiversity Trust that began in 2007, the Svalbard Gene Vault located near the North Pole will conserve over four million accessions without the need for expensive cryogenics. The remote isolation and capacity of this facility should be sufficient to preserve a sample of the existing genetic variability of all economically important plants, a vast resource generated over the past 10,000 years of agricultural evolution.”

Mahatma Gandhi used to say that “nature provides for everybody’s need, but not for everyone’s greed.” Thus, we find in nature halophytes which are salinity tolerant, xerophytes, which are drought resistant, and many other crops adapted to different agroecological conditions. We should conserve this genetic wealth of inestimable value. We should also promote anticipatory research in order to learn how to scientifically checkmate the adverse impact of unfavorable weather. This book provides guidelines for such work.

I thank Prof. Chittaranjan Kole for this labor of love in the cause of sustainable food security. I also congratulate all his authors. I hope these books will help to make life better for people everywhere.

Prof. M. S. Swaminathan
Member of Parliament (Rajya Sabha),
India and Emeritus Chairman,
M S Swaminathan Research Foundation

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Foreword by Loren H. Rieseberg

In response to the remarkable rise of food prices in 2008, *The Economist* published an article titled, “Malthus, the false prophet: The pessimistic parson and early political economist remains as wrong as ever.” The authors argue that neo-Malthusian worries about our ability to feed 9.2 billion people in 2050 are mistaken, and that advances in agricultural productivity will be sufficient to feed the world.

I am less optimistic. Growth in crop yields has been decelerating for some time, a trend that is likely to be exacerbated by climate change and regional water scarcity. Nonetheless, the Food and Agriculture Organization of the United Nations contends that 90 % of the necessary increase in crop production globally must come from higher yields, since there is little opportunity for expanding the agricultural land base.

Should we be worried about this? I think so. While I may not make it to 2050, I have two small children who will (I hope). My wife tells me that we should not worry about things we cannot change. However, as genomicists, agronomists, and plant breeders, we have the knowledge and tools to develop more productive, sustainable, and resilient crops (and thus perversely prove *The Economist* to be correct in their dismissal of Malthus and predictions of a food crisis later this century).

The *Genomics and Breeding for Climate-Resilient Crops* provides a blueprint for meeting this most important challenge. The first volume discusses how new genomic tools and resources can be used to accelerate breeding, with the overall goal of maximizing crop productivity while minimizing resource use and environmental damage. An especially promising approach, in my view, is the use of genomic tools to identify and introduce valuable alleles from the wild relatives of crops into elite cultivars. It is this untapped variation in wild species—housed in seed banks around the world—that has the greatest chance of providing quantum jumps in yield.

The second volume is a natural extension of the first, focusing on the key traits (drought tolerance, heat tolerance, water use efficiency, disease resistance, nitrogen use efficiency, nitrogen fixation, and carbon sequestration) necessary for climate-resilient agriculture. Any hope we have of ameliorating the impact of climate change on crop productivity rests on our ability to manipulate these traits.

This twin book project is timely, as the world is slowly waking up to the fact that a global food crisis of enormous proportions is brewing (indeed, I suspect that it will arrive long before 2050). As a consequence, these volumes are likely to form the basis of new courses on climate change and agriculture at academic institutions, to influence policy-makers worldwide, and to provide motivation and guidance to funding agencies. With sufficient investment in agricultural research and public breeding programs, I hope that my worries about filling 9.2 billion bellies are unfounded and that human ingenuity will once again trump Malthusian pessimism.

Loren H. Rieseberg
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Foreword by Calvin O. Qualset

We are in the midst of a new era in crop improvement by genetic means with unprecedented ability to manipulate genes beyond Harlan's genepool compatibility circles. Still, wide hybridizations are difficult to produce, but the ability to introduce genes by parasexual means widens the genepool to include "any gene from any species" in the breeders' repertoire. Genomics provides the bases for such events. On the other side of the technological advances is the realization that our globe is under change due to anthropological causes, and perhaps by other forces. Climate change is a reality, but also is the reality that climate change is not predictable on a day-to-day or even annual basis. Agriculturalists will tell you that climate change occurs every year—sometimes for a succession of years. Our natural resources include atmospheric properties that effect climate change and our other natural resources—soil, biological, and water—are subjected to perturbations that can be detrimental and ultimately affect the sustainability of humankind.

It is a pleasure to see this comprehensive two-volume treatment dedicated to the subject of modifying the resiliency of crops to mitigate the impacts of long-term climate changes. But how about short-term climatic effects? These are the reality in agriculture, and we cannot say that crop breeders have been unaware of the short-term effects. Research programs over many decades have been dedicated to fitting crops to their environments, much as natural selection has adapted organisms to their environments. For example, latitudinal adaptation of crops or forest trees is genetically determined. The genetic bases are generally understood and those genetic effects may be exploited to produce climate-resilient crops. As early as 1921 Mooers' classic paper "Agronomic Placement of Varieties" (Mooers 1921) showed how crop management decisions could stabilize and maximize the performance of crop varieties that differed in their genetic potentials, such as maize. He pioneered what is now known as the regression approach to visualizing genotype \times environment interaction that has become a mainstay for characterizing genotype performance in variable environments. He was able to show that certain varieties had greater resilience than others and that "placement" of varieties should match their potential and the environmental potential that he called soil quality.

Coping with the vagaries of environment has long been an issue in food, feed, and fiber production and these two volumes are relevant to the current concerns about climate change and to the stabilization of sustainable yields. Now, more than ever, integration of scientific approaches is necessary to mitigate the impacts of climate on crop production, including soil science, pest control, water management, human nutrition requirements, recognition of climatic variances, and, yes, socio-economic factors. Most of these topics are found in these two remarkable volumes, written by global experts.

I encourage the reading of the chapters on history, principles, and methods in Volume 1, as well as the innovative chapters on critical crop traits for resilience in Volume 2.

Calvin O. Qualset
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Foreword by Ronald L. Phillips

As crop scientists, we are inherently charged with preserving, protecting, and defending the world's food supply, much like the oath that a US President may take when assuming office. Our profession takes seriously the need to *preserve* the germplasm that exists around the world—evidenced by the major seed banks for a large variety of crops. We also do our best to *protect* the food supply by responding to various biotic and abiotic stresses via conventional breeding and genetic engineering approaches. *Defending* the world's food supply takes various forms such as policies that provide open access to valuable materials or via intellectual property rights that encourage the development of new types of products, including those for feed, fiber, biofuels, nutritionally improved types, and even medical applications.

The environment causes many difficult situations—and always has—such as the dust bowl in the US during the 1930s. Drought still plagues many areas of the globe and is one of the myriad of conditions that cannot be well-predicted in advance. Then we have the complication that the genotype being grown interacts with the environment in a very complex fashion making difficult the development of improved types.

Genomic approaches add to our understanding of many of the environmental issues. Data from genomic sequencing now provide the basic framework on which to gain information for enhancing the understanding of such phenomena as genotype \times environment interactions, gene expression related to environmental stresses, and provide clues as to how to apply the information for the betterment of agriculture. Marker-assisted selection is being employed in most modern plant-breeding programs with considerable success. For example, the *Sub1a* gene that provides impressive flooding tolerance in rice can be transferred from one variety to another by marker-assisted conventional breeding in 2.5 years or less.

In addition to various challenges traditionally faced by crop scientists, we now have the specter of even more extreme and variable conditions under which crops are grown. Climate change is a reality; however one of the debatable questions deals with whether it is man-made. Do you believe it or not? My question is “Does it matter?” Underpinning any belief about climate change is the fact that climate determines the very future of the world's food supply. Research must be focused on mitigating the often devastating effects of climate, which appear to be increasingly serious.

In this unique book project, the need is emphasized for meaningful and efficient phenotyping, including innovative techniques, as well as the use of model organisms such as *Arabidopsis*, *Medicago truncatula*, and *Lotus japonicas*. The effectiveness of plant breeding is well established; improved methods of phenotyping and testing for various traits will only enhance the contributions of plant breeding. Attention to the thousands of accessions of various crops in germ-plasm banks in terms of phenotyping would speed the movement of such materials into prebreeding programs. As with the search for durable disease resistance, breeding for “durable” resilience to important climate traits will require detailed understanding of the underlying genetics reviewed in these volumes. The shift of flowering time is a trait of interest with considerable underlying genetic information. Selection for flowering in the cooler part of the day, for example, may avoid some of the dramatic effects of high temperature on grain production.

These volumes on Genomics and Breeding for Climate-Resilient Crops are carefully designed to provide up-to-date insights on research accomplished as well as what is needed to preserve, protect, and defend our food supply. There is a logical and systematic progression of thought throughout the two volumes and numerous ideas are presented on climate change topics. As the Earth’s temperature is rising, huge ice caps are melting, highs and lows of rainfall are hitting extremes, and carbon dioxide is changing the pH of oceans, we must take action on developing a comprehensive program to reduce the effects of climate threats on our food supply. International cooperation is needed, and these volumes reflect the international interest in the goal of developing climate-resilient crops. The environmental events that bring dramatic headlines in news programs and magazines demand that crop scientists employ the most effective technologies to circumvent the reduction in food supply due to climate. This is especially important given that another billion people exist on this planet every 14 years, and they must have an adequate food supply. This two-book project is a welcome contribution to the future of genomics and breeding for climate-resilient crops.

Ronald L. Phillips
Regents Professor Emeritus
University of Minnesota, USA

Foreword by J. Perry Gustafson

The UN projects that by 2050 World food production will need to increase by a minimum of 70 % to feed a projected World population of more than nine billion. This 70 % increase will not be enough to improve the diets of the one billion hungry people in the world; it will only be enough to keep the same diet the world has today. It is clear that extraordinary improvements in agricultural productivity will be necessary. World food production has been steadily increasing from approx. 2.94 billion metric tons (BT) in 1961 to approx. 8.27 BT in 2007. Most importantly, this dramatic increase in food production was produced on approximately the same amount of land currently under production as was under production in 1950. Thus, the increase in production was the result of improved crop cultivars, crop technology advances, and better management practices. Projections indicate that world food production between now and 2050 can be increased to meet population demands for improved dietary standards provided that existing and newly developed technology is utilized to genetically improve cultivars, and that the world works very hard to improve crop management. This all needs to be accomplished without causing any additional adverse effects on the environment, and while clearly avoiding the cultivation of new land. Plant breeders will have to pay close attention to the effects of global warming on food production. However, the chapters in this book clearly show that current advances in technology are capable of doing so and of dramatically decreasing the time to deliver genetic improvements into the field. These include techniques, which bypass some traditional approaches to seed production. Introducing gene complexes by genetic manipulation from related species has a long and successful history and with the addition of new genetic engineering techniques will continue into the future. Arguably, the carefully coordinated application of all existing and new technologies discussed in the two volumes will be critically important to feed an ever-increasing population, sustaining the productivity of arable lands, and maintaining our fragile environment.

J. Perry Gustafson
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Preface

Climate change is expected to enormously affect life on the Earth. It will cause drastic changes in the environment and ecology and thus will severely impact agriculture. Therefore, it poses a serious challenge for global food security. It is expected to cause drastic changes in agroclimatic conditions including temperature, rainfall, soil nutrients and health, and incidence of pathogens and pests leading to striking reduction in crop yields due to global warming, water scarcity, changes of rainfall patterns resulting in increasingly frequent drought and flood, and other extreme weather events. Plant pathogens and pests may also evolve quickly with more virulent pathotypes and biotypes and so may extend their geographical spread leading to epidemics and severity due to climate change. Furthermore, elevated CO₂ levels will also reduce the nutritional quality of most crops and some crops may even become more toxic due to changes in the chemical composition of their tissues. Climate change will also cause elevation of greenhouse gas emission. The most grave and still unknown concern, however, involves the critical effects that interactions among various biotic and abiotic excesses or paucities will have on crops and cropping systems making the task of feeding a world population of nine billion by 2050 extremely challenging.

Several eminent scientists from different parts of the world are planning to put significant effort into combating or mitigating the threat to food security due to climate change. We organized an international workshop on Climate Change during the 20th International Conference on the Status of Plant and Animal Genome Research (PAG conference) held during January 2012 in San Diego, California and established the International Climate Resilient Crop Genomics Consortium (ICRCGC) with a membership of over 30 active scientists from over ten countries (<http://www.climatechange-genomics.org>). Recently, many more scientists have become interested in this critical topic and we organized a special international workshop on Genomics and Breeding of Climate-Resilient Crops for Future Food Security during the 6th International Crop Science Congress held during August 6–10, 2012 in Bento Goncalves, Brazil followed by a brain-storming discussion to formulate the future strategies and work plans for combating climate change. We recently organized another two workshops on this subject in January 2013 in

San Diego, California during the 21st PAG conference. ICRCGC is now preparing a white paper for more serious and broad dialogs to initiate international and multi-disciplinary efforts to combat climate change using genetic resources and advanced genomics and breeding tools.

The central strategy of combating climate change will obviously involve the development of climate-resilient crop cultivars with broader genome plasticity allowing wider adaptability, broader genome elasticity with potential for high response to phenotypic, chemotypic, and molecular selection and above all durable and robust resistance to biotic and abiotic stresses. However, genomics and breeding for climate-resilient crops are relatively new fields of study and research and given the seriousness of the threats of climate change will obviously be included in course curricula in academic institutes and in frontier programs of agricultural research organizations at national and international levels. This topic is expected to be of increasing interest to policy-makers, social activists, and both public and private sector agencies supporting agricultural research. There are a few critical and comprehensive reviews on this subject and a number of publications are also available on the assessment of the impact of climate change on agriculture and suggested strategies to circumvent the severe effects to ensure food security. These deliberations are, however, scattered over the pages of newspapers, newsletters, journals, and web sites. Hence, a compilation of narratives on the concepts, strategies, tools, and related issues was felt to be lacking and this was the guiding force behind the inception of this two-volume work on Genomics and Breeding for Climate-Resilient Crops.

Volume 1 “Genomics and Breeding for Climate-Resilient Crops: Concepts and Strategies”

Volume 1 of this book deliberates on the basic concepts and strategies of genomics and breeding for developing climate-resilient crop varieties. In recent years considerable gains have been made in our understanding of plant genome organization and gene expression. In large part this has been achieved through the study of “model species,” i.e., species in which genetics and genomics are more tractable than in many crop plants. The best known and most developed of these models is *Arabidopsis thaliana*, the DNA sequence of which was published in 2000. Subsequently, a number of different model species have been developed and the number of crop species that feed the world with sequenced genomes has also increased.

Progress in developing the resources, tools, and approaches to allow more rapid development of improved crops has been significant in the last decade. These include genomics, transcriptomics and metabolomics as well as nondestructive, dynamic high-throughput phenotyping (phenomics), and novel approaches to germ-plasm characterization and population improvement. It is timely therefore to

provide a detailed analysis of where we are now and what progress can be expected in the near future. This description of the “state of the art” is presented in Volume 1.

The first chapter of Volume 1 by Abberton provides an introduction to the potential damaging effects of climate change on agriculture leading to future food insecurity and narrates the required integrated approaches to address this serious threat. It elucidates on the role of plant improvement and the requirement of judicious deployment of genomic tools for utilization of genetic diversity and precision high-throughput phenotyping as supplementary strategies for developing climate-resilient crop varieties.

At the heart of crop improvement are genetic resources, their collection, characterization, and utilization. The contribution of Pignone and Hammer (Chap. 2) shows ways in which the use of genetic resources can be targeted at the challenges of a changing climate. Genetic resources offer a vast reservoir of important novel traits and allelic variation for traits. Increasingly, genomics tools are being brought to bear on the variation collected in genebanks.

De Pace and coauthors in Chap. 3 detail modern methods of identifying traits for incorporation into selection criteria for new cultivars and to uncover the underlying genetic control of variation in these traits. They present reasons as to why paleoclimate and vegetation-type reconstruction from fossil records and species vicariance help in understanding the long-term dynamics of plant features and trait evolution associated with dispersal and climate changes. Comparative genomics demonstrated as alleles for those plant features (i.e., plant morphology and phenophase alteration), and for biotic (response to bacterial and fungal pathogens) and abiotic (i.e., drought, flooding) stress resistance are still part of the standing genetic endowment of the living gene pools of the crop and forest plant species and allied wild relatives. Therefore, recapitulation of evolutionary and domestication processes using various genomic tools will provide innovative molecular breeding methods to explore and select the genetic variants needed for forest and crop adaptation to climate change pressures.

Subsequent chapters deal more explicitly with how modern genetics and genomics can be used within crop improvement programs. Dwiyanti and Yamada (Chap. 4) describe genetic mapping and identification of quantitative trait loci (QTL) for traits involved in responses to changing climate. Generally, QTLs related to climate change response are complex and largely affected by environmental conditions. Nevertheless, researchers have succeeded in identifying several major QTLs and applying the knowledge in crop breeding. Various genomics tools are now available in crop species that have been the subject of most research, particularly maize but now increasingly rice and other cereals. Progress in wheat has been slow due to the limited extent of genetic variation in the crop and its hexaploid nature, but next-generation sequencing (NGS) approaches are changing this rapidly. Genome sequencing with ever-increasing speed and reducing costs brings with it the potential for “genotyping by sequencing,” which when allied with sophisticated statistical approaches is likely to allow the potential of genome-wide or genomic selection (GWS) to be realized more effectively. Knowledge of QTLs in model species and advances in genomic tools can be applied to crop plants with limited genomic information.

Adaptation to climate change would require convergence of appropriate technologies, policies, and institutional innovations and Chap. 5 by Prasanna and coauthors focuses on some of the promising genomic tools and strategies that can enhance time- and cost-effectiveness of breeding for climate-resilient major cereal crops, particularly maize. They deliberate on employment of modern breeding strategies such as high-density genotyping, whole-genome re-sequencing, high-throughput and precise phenotyping, and genomics-assisted breeding including genome-wide association studies, breeder-ready marker development, rapid-cycle genomic selection, marker-assisted recurrent selection, and crop modeling.

The strategy for climate-resilient agriculture should be to maximize crop production with minimal or no damage to the environment. This would demand changes in the approaches to crop improvement, and in the deployment of recent techniques involving genomics in crop research. Designer crops have to be developed with enhanced efficiency in the use of radiation energy, nutrients, and water; they also have to fit the system of conservation agriculture including zero tillage. Talukdar and Talukdar (Chap. 6) describe recent changes in strategies and approaches to crop breeding highlighting the progress of genomic tools in meeting the challenges of climate change in agriculture.

Of course a major modern tool for the improvement of specific traits is genetic engineering. To date, this technology has been widely employed but only for a few traits in a small number of crops. Developments in genetic engineering have been instrumental for commercial application in the production of transgenic plants for biotic and abiotic stresses. It has tremendous potential in agriculture and especially for important traits related to climate change. Yadav and coauthors (Chap. 7) address the challenge of deploying this technique for important complex traits that are central to climate adaptation.

New approaches to selection are required to take full advantage of the pace at which new genomic knowledge is being acquired. Ceccarelli and coauthors (Chap. 8) and Murphy and coauthors (Chap. 9) explain how participatory breeding, where farmers are involved in the selection process, can be focused on adaptation.

In Chap. 8, Ceccarelli and coauthors show how climate changes have affected humanity for a long time, and how crops and people have reacted and adjusted to changes. As biodiversity has sometimes been negatively affected by modern crop production, they discuss how participatory plant breeding, by exploiting specific adaptation and farmers' knowledge, can positively contribute not only to crops' adaptation to climate changes but to increase biodiversity and to increase production directly in the hands of the farmers, thus also improving the accessibility and availability of food.

Murphy and coauthors (Chap. 9) explain how participatory breeding can be focused on adaptation. Evolutionary breeding has been shown to efficiently increase fitness, disease resistance, and related yield components in self-pollinating cereals while maintaining a broad-based genetic diversity in the field. Through buffering of biotic and abiotic stresses, increased on-farm genetic diversity can be important to maintaining yield stability across time and space. Inclusion of on-farm selection of diverse evolutionary breeding populations within and across fluctuating

environments has the potential to greatly increase the scope of genotypically plastic cultivars capable of adaptation to unpredictable climate-induced environmental change.

Modern crop improvement in both its genomics and phenomics components is increasingly data rich. Edwards (Chap. 10) summarizes the role and importance of bioinformatics in integrating these data and converting them to usable knowledge has been emphasized greatly over the past two decades and is now being increasingly reflected in the public sector and commercial programs throughout the world.

Chapter 11 by Lybbert and coauthors deals with the critical issue of international collaboration and the importance of international funding to facilitate the exchange of knowledge and germplasm required to achieve success in global crop development. The benefits of climate-resilient crops are often complex and the adoption of these crops will require international collaboration and coordination of public and private sectors. Support for networking and funding of collaborative research and extension activities will determine global success in the development of climate-resilient crops and their impact on food security.

However, the importance of regulation and intellectual property is pervasive in the area of modern crop improvement and not restricted to genetic engineering. These issues are considered by Blakeney (Chap. 12). Similarly, sociopolitical consideration extends across the whole of the application of genomics, its translation into the development of cultivars and farmers' access to them and the ability to incorporate them into their operations as enumerated by Hughes and coauthors in Chap. 13.

Volume 2 “Genomics and Breeding for Climate-Resilient Crops: Target Traits”

In many cases breeders seek improvements in yield and yield per unit of input, however, factors limiting yield are many and various and often these factors must be addressed directly in targeted approaches. Volume 2 elucidates the genomic and breeding approaches for genetic improvement in the major target traits covered in its 13 chapters.

In the majority of crop species, the timing of flowering represents a key adaptive trait, with a major impact on yield. In Chap. 1, Bentley and coauthors review the genetic determinants and environmental cues that influence flowering time in a range of crop species. They deliberate on the consequences of climate change on crop adaptation mediated by flowering and discuss the breeding targets and methodologies to mitigate detrimental yield.

Plant growth and development are largely dependent on the root system due to its crucial role in water and mineral uptake affecting overall plant growth and architecture. Most agricultural crops have a remarkable level of genetic variation in root morphology that can be harnessed for improving crop adaptation to several

abiotic stresses. The importance of roots and roots traits (size, architecture, interactions with soil, exudation, etc.) has long been recognized, but progress has been slow due to difficulty in phenotyping and screening techniques. However, genomics approaches allied to the development of noninvasive dynamic imaging techniques capable of phenotyping root traits and largely effecting QTL identification to facilitate marker-assisted selection will bring significant new opportunities for crop improvement as enunciated in Chap. 2 by Silvas and coauthors.

Two of the major abiotic stresses involve responses to low or high temperatures. Because of the need to feed an ever-increasing global population, attempts at agricultural production are being extended into marginal locations, including those at higher altitudes where growth conditions are suboptimal due to the cold stresses commonly encountered. Amongst the traits associated with survival under such conditions, the acquisition of genes for freezing tolerance is considered of primary importance with gene improvement targeted specifically at the timeliness of engagement, the maintenance, and the subsequent release of cold acclimation mechanisms necessary to ensure a winter survival appropriate to the region of crop growth, followed by rapid recovery to ensure good crop yields once the threats of encountering further freezing temperatures are diminished. Humphreys and Gasior (Chap. 3) deliberate the detailed effects of cold on crop growth and development and ultimately on crop yield, and the strategies and tools for developing crop varieties with improved tolerance to winter and freezing.

Porch and Hall (Chap. 4) describe crop improvement with respect to heat tolerance. Many current environments experience high temperatures that reduce crop yield, and projected increases in temperature could reduce grain or fruit yield by about 10 % per °C increase in temperature. Yet, relatively little effort has been devoted to breeding for heat tolerance. However, for a few crop species, heat-resistant cultivars have been bred by conventional hybridization and selection for heat tolerance during reproductive development. The successes that have been achieved are described and provide blueprints, whereby heat-resistant cultivars could be bred for many annual crop species. Molecular approaches to enhance breeding for heat tolerance are also discussed.

A major focus of this volume is on water: drought stress and water use efficiency important for interactions with soil including effects on flooding propensity. Crop improvement has had limited success in developing new cultivars with enhanced adaptation to drought-prone environments, although it has been pursued for various decades. Research on the mechanisms underlying the efficient use of water by crops and water productivity remains essential for succeeding in this endeavor. They may be improved through genetic enhancement. Advances in genetics, “omics,” precise phenotyping and physiology coupled with new developments in bioinformatics and phenomics can provide new insights into traits that enhance adaptation to water scarcity. Chapter 5 by Ortiz provides an update on research advances and breeding main grain crops for drought-prone environments.

For several decades now, plant breeders have been selecting for high water use efficiency as a way to increase agricultural productivity in water-limited environments. Water use efficiency is the ratio between carbon gain

(photosynthesis) and water loss (transpiration), which inherently occurs during stomatal opening. High water use efficiency is generally associated with greater drought tolerance, but this does not always equate to greater productivity. There are few studies that have demonstrated improvements in water use efficiency that lead to improved yields. Chapter 6 by Bramley and coauthors describe the multifarious hydraulic and biochemical processes controlling plant water loss and photosynthesis. They show that water use efficiency is predominantly driven by plant hydraulic properties, and genes that are mostly involved in gas exchange. Genetic variation for these properties exists in agricultural crops, but research needs to be directed towards examining the influence of high water use efficiency on yield production in targeted environments.

The enormous diversity in rice and its adaptation to contrasting hydrological and edaphic conditions made it one of the crops most acquiescent to genetic manipulation to keep up with the increasing adversities of climate change, including the increasing flood incidences predicted by several climate models. A classical example is presented in Chap. 7 by Ismail, summarizing the progress in breeding for flood tolerance in rice and prospects for future improvements to cope with further deteriorations projected in rainfed lowlands of the tropics. A case was presented where deployment of the *SUBIA* gene that confers tolerance to submergence during the vegetative stage resulted in considerable impacts in farmers' fields in flood-prone areas, with yield advantages of 1 to over 3 t ha⁻¹ following 4–18 days of complete submergence. This is a classic example of the use of genomic tools to resolve current issues and cope with further adversities of climate change, while keeping up with the rising demands for more food.

Clearly responses to biotic stresses, and postharvest losses, are crucial aspects in maintaining yield in many environments and often diseases and insects are a major cause of biomass loss.

Chapter 8 by Bariana and coauthors summarizes the role of genomics in the breeding of disease-resistant crop cultivars. Various selection technologies used in cereal and pulse improvement programs are discussed. Current information on disease response linked markers is reviewed in light of their implementation. The potential use of whole genome molecular scanning in breeding disease-resistant crops is also explored. The role of information management in programs aimed at the application of genomics to crop improvement is emphasized.

Agricultural research has for decades focused on gathering crucial information on the biochemical, genetic, and molecular realms that deal with plant–insect interactions in changing ecosystems. Environmental conditions, which include the overall conditions of climate change, are a reality that needs to be considered as one of the crucial phenomena of changing ecosystems when planning future crop improvement, security, and/or pest management strategies. In the context of climate change in Chap. 9 Emani and Hunter attempt to integrate past and present research in classical and molecular breeding, transgenic technology, and pest management. The integrated approach will direct present research efforts that aim at creating plant–insect pest interaction climate change models that reliably advise future strategies to develop improved insect-resistant, climate-resilient plant varieties.

One of the foundations of the increases in crop productivity in the past has been improved nutrient availability, especially nitrogen and phosphorus. The increases in crop production that are needed to meet the demands of a growing world population will require greater supply and uptake of essential nutrients by plants. Even in the absence of climate change, there is a need to improve the nutrient use efficiency of our present cropping systems to make better use of nonrenewable resources and to minimize the adverse environmental effects of the over-use of fertilizers. Moreover, in many parts of the world, the nutrient concentration of staple food crops is low, and significant gains in the health of communities can be achieved by biofortification of grain. Breeding crop varieties that are better able to use poorly available sources of nutrients in the soil or which can respond better to inputs of nutrients is an important aspect of increasing nutrient use efficiency. The uptake and use of nitrogen and phosphorus by crop plants are complex processes and to date, there has been limited success in improving nutrient use efficiency using conventional approaches. Advanced genetic techniques allied to traditional plant breeding may play an important role in improving nutrient use efficiency. McDonald and coauthors present a review on the importance of improving nitrogen use efficiency and on research accomplished so far for that purpose in Chap. 10.

Nitrogen assimilation and fixation underlie the advances of the green revolution and limit the impact of both agriculture and environmental plant productivity on carbon sequestration. For a number of years the potential importance of legumes in crop rotations across many agroecosystems has been recognized. However, the limited extent to which this potential has been realized has been disappointing. Legumes do not just contribute in terms of food, feed, and fertility but are also important as fuel wood and could help more with respect to carbon sequestration. However, their key attribute and a major reason why they are so important for the future of world agriculture is the nitrogen-fixing symbioses they form with nodulating bacteria. Genetic and genomic tools have been applied powerfully in recent years to understand the control of the legume–rhizobia interaction utilizing model legumes, particularly *Medicago truncatula* and *Lotus japonicus* and the great challenge is to deploy this information in the improvement of the major grain and forage legumes (Lightfoot, Chap. 11). However, the world’s major nitrogen sink crops are the grasses and cereals. Equally, the world’s major carbon sink crops are trees and wetland plants. These crops and plants could be made more efficient in their use of nitrogen and consequently, water. Scientists have tried many transgenes in many crops to achieve these improvements with good rates of success. Stacks of genes, and new sets of transgenes hold promise to deliver significant improvements across the world’s major crops. On the basis of these discoveries efforts to develop genetically, or even transgenically altered environmental plants might also help to slow global warming.

Carbon sequestration in plants has been proposed as a possible moderator or solution to the rising levels of atmospheric carbon dioxide (CO₂) threatening to alter global temperature and climate. Chapter 12 by Cseke and coauthors

examines the different mechanisms of carbon sequestration within the Earth's natural carbon cycle with a special focus on events associated with plant development. This chapter outlines the specific chemical and biological processes that allow plants to capture, allocate, and provide for long-term storage of CO₂ in the form of both above-ground and below-ground biomass. They specifically examine the contribution of mycorrhizal and other soil community-level interactions as an important reminder that healthy soils are required for the uptake of nutrients needed for efficient carbon sequestration. This chapter provides a perspective on molecular approaches to enhancing carbon sequestration in biological systems.

Gases that trap heat in the atmosphere are referred to as greenhouse gases. Four major greenhouse gases that are abundant in the atmosphere today are carbon dioxide, methane, nitrous oxide, and fluorocarbons. These are naturally occurring [greenhouse gases](#) because they are potentially essential to keeping the Earth's temperature warm. However, man-made activities have increased the number of these gases, resulting in more heat getting trapped in the atmosphere. Among these gases, [carbon dioxide](#) has the highest concentration in the atmosphere. Chapter 13 by Abberton deliberates on greenhouse gas emission and carbon sequestration.

The chapters of Volume I "Genomics and Breeding for Climate-Resilient Crops: Concepts and Strategies" were contributed by 38 scientists from 14 countries including Australia, China, France, Germany, India, Italy, Japan, Kenya, Nigeria, Netherlands, Philippines, UK, USA, and Zimbabwe. The chapters of Volume 2 "Genomics and Breeding for Climate-Resilient Crops: Target Traits" were contributed by 48 scientists from nine countries including Australia, Brazil, Germany, India, Japan, Philippines, Sweden, USA, and UK. Altogether 84 scientists from 16 countries authored the 26 chapters of the two volumes. I wish to extend my thanks and gratitude to all these eminent scientists for their excellent contributions and constant cooperation.

I have been working with Springer since 2006 and edited several book series, and I have developed a cordial relationship with all the staff involved. I wish to thank Dr. Christina Eckey and Dr. Jutta Lindenborn for their constant guidance and cooperation right from the planning up to the completion of this book project. It was highly enriching and comfortable to work with them all along.

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required to attain sustainable food security in the future. I express my deep regards and gratitude to them for sharing their wisdom and philosophy and also for all the generosity, affection, encouragement, and inspiration they showered upon me!

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Abbreviations

AAT	Alanine aminotransferase
ABA	Abscisic acid
ABP9	ABA-responsive cis-elements binding protein 9
ABRE	ABA-responsive elements
ADH	Alcohol dehydrogenase
ADP	Adenosine diphosphate
AFP	Antifreeze protein
AG	<i>AGAMOUS</i> gene
AGI	Arabidopsis Genome Initiative
<i>AGL24</i>	<i>AGAMOUS-LIKE 24</i> gene
AHB1	<i>Arabidopsis</i> hemoglobin
ALAT	Alanine aminotransferase
AM	Arbuscular mycorrhizae
AM	Association mapping
ANN	Artificial neural network
ANOVA	Analysis of variance
AOC	Allene oxide cyclase
AON	Autoregulation of nodulation
AOS	Allene oxide synthase
<i>AP1</i>	<i>APETALA1</i> gene
<i>AP2</i>	<i>APETALA2</i> gene
<i>AP3</i>	<i>APETALA3</i> gene
APase	Acid phosphatase
APX	Ascorbate peroxidase
AQP	Aquaporin
ARF	Auxin-responsive factor
ASE	Allele-specific expression
ASI	Anthesis-silking interval
ATP	Adenosine triphosphate
<i>AtSAP5</i>	<i>Arabidopsis thaliana</i> stress-associated protein 5
AVRDC	Asian Vegetable Research and Development Center

BAC	Bacterial artificial chromosome
BC	Backcross
BCA	Belowground carbon allocation
BGMV	Bean golden mosaic virus
<i>bHLH</i>	Basic helix-loop-helix
BIL	Backcross inbred line
BLB	Bacterial leaf blight
BNI	Biological nitrification inhibition
BR	Brassinosteroid
<i>Bt</i>	<i>Bacillus thuringiensis</i>
<i>BTC1</i>	<i>BOLTING TIME CONTROL 1</i> gene
BVOC	Biogenic volatile compounds
bZIP	Basic leucine zipper protein
CA	Cold acclimation
<i>CAB2</i>	<i>CHLOROPHYLL A/B BINDING PROTEIN 2</i> gene
<i>CAL</i>	<i>CAULIFLOWER</i> gene
CAM	Carboxylic acid metabolism
CAM	Crassulacean acid metabolism
CaMV	Cauliflower mosaic virus
CAT	Catalase
CAX1	Calcium exchanger 1
CBF	C-repeat binding factor
<i>CCA1</i>	<i>CIRCADIAN CLOCK-ASSOCIATED 1</i> gene
<i>CCR2</i>	<i>COLD AND CIRCADIAN-REGULATED 2</i> gene
CDF	Cation diffusion facilitator
<i>CDF1</i>	<i>CYCLING DOF FACTOR 1</i> gene
cDNA	Complementary DNA
CDPK	Calcium-dependent protein kinase
CE	Cation efflux
<i>CEN</i>	<i>CENTRORADIALIS</i> gene
CGIAR	Consultative Group on International Agricultural Research
CID	Carbon isotope discrimination
CIMMYT	International Maize and Wheat Improvement Center
CIPK	CBL-interacting protein kinase
CIRAD	Centre International de Reseaux Agriculture and Development
CLE	Clavata3/ESR-related peptide
CLV3	Clavata3
<i>CO</i>	<i>CONSTANS</i> gene
Col	Columbia
COR	Cold-regulated
CP	Crude protein
CRT	C-repeat
<i>CRY1</i>	<i>CRYPTOCHROME 1</i> gene
<i>CRY2</i>	<i>CRYPTOCHROME 2</i> gene
CSP	Cold-shock protein

CSSLs	Chromosome segment substitution lines
CT	Condensed tannins
CTD	Canopy temperature depression
CV	Coefficient of variation
DAM	Dormancy-associated MADS-box
<i>DAM</i>	Dormancy-associated MADS-box genes
DArT	Diversity array technology
DEG	Differentially expressed gene
<i>DF1</i>	<i>DELAYED FLOWERING 1</i> gene
DH	Doubled haploid
DHL	Doubled haploid line
DIMBOA	2,4-Dihydroxy-7-methoxy-2H-1,4-benzoxazin-3-one
DREB	Dehydration-responsive element-binding protein
DREB1	Dehydration-responsive element-binding protein 1
ds-cDNA	Double-stranded cDNA
<i>DTH8</i>	<i>DAYS TO HEADING 8</i> gene
<i>EBS</i>	<i>EARLY BOLTING IN SHORT DAYS</i> gene
ECM	Ectomycorrhizae
<i>Ef7</i>	<i>Early flowering 7</i> gene
<i>Ehd1</i>	<i>Early heading date 1</i> gene
<i>Ehd2</i>	<i>Early heading date 2</i> gene
<i>Ehd3</i>	<i>Early heading date 3</i> gene
EIN	Expression interaction network
<i>ELF3</i>	<i>EARLY FLOWERING 3</i> gene
EPA	Environmental Protection Agency
ERF	Ethylene-responsive factor
ESK1	<i>ESKIMO1</i> mutation
EST	Expressed sequence tag
ET	Evapotranspiration
EU	European Union
FACE	Free-air carbon dioxide enrichment
FAO	Food and Agricultural Organization
<i>FAR1</i>	<i>FAR-RED IMPAIRED RESPONSE 1</i> gene
FGAS	Functional genomics of abiotic stress
<i>FHY3</i>	<i>FAR-RED ELONGATED HYPOCOTYL 3</i> gene
<i>FKF1</i>	<i>FLAVIN-BINDING, KELCH REPEAT, F-BOX 1</i> gene
<i>FLC</i>	<i>FLOWERING LOCUS C</i> gene
<i>FpCBF</i>	<i>Festuca pratensis CBF</i> gene
<i>FPF1</i>	<i>FLOWERING PROMOTING FACTOR 1</i>
<i>Fr-A1</i>	Frost resistance QTL (on chromosome 5A in <i>Triticum</i> spp.)
<i>Fr-A2</i>	Frost resistance QTL (on chromosome 5A in <i>Triticum</i> spp.)
<i>Fr-Am2</i>	Frost resistance QTL (on chromosome 5A in <i>Triticum monococcum</i>)
<i>Fr-H2</i>	Frost resistance QTL (on chromosome 5A in <i>Barley</i>)
<i>FRI</i>	<i>FRIGIDA</i> gene