Compendium of Plant Genomes
Series Editor: Chittaranjan Kole

Rakesh K. Srivastava
C. Tara Satyavathi
Rajeev K. Varshney *Editors*

The Pearl Millet Genome

Springer

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Series Editor

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Whole-genome sequencing is at the cutting edge of life sciences in the new millennium. Since the first genome sequencing of the model plant *Arabidopsis thaliana* in 2000, whole genomes of about 100 plant species have been sequenced and genome sequences of several other plants are in the pipeline. Research publications on these genome initiatives are scattered on dedicated web sites and in journals with all too brief descriptions. The individual volumes elucidate the background history of the national and international genome initiatives; public and private partners involved; strategies and genomic resources and tools utilized; enumeration on the sequences and their assembly; repetitive sequences; gene annotation and genome duplication. In addition, synteny with other sequences, comparison of gene families and most importantly potential of the genome sequence information for gene pool characterization and genetic improvement of crop plants are described.

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This book series is dedicated to my wife Phullara and our children Sourav and Devleena

Chittaranjan Kole

Preface to the Series

Genome sequencing has emerged as the leading discipline in the plant sciences coinciding with the start of the new century. For much of the twentieth century, plant geneticists were only successful in delineating putative chromosomal location, function, and changes in genes indirectly through the use of a number of "markers" physically linked to them. These included visible or morphological, cytological, protein, and molecular or DNA markers. Among them, the first DNA marker, the RFLPs, introduced a revolutionary change in plant genetics and breeding in the mid-1980s, mainly because of their infinite number and thus potential to cover maximum chromosomal regions, phenotypic neutrality, absence of epistasis, and codominant nature. An array of other hybridization-based markers, PCR-based markers, and markers based on both facilitated construction of genetic linkage maps, mapping of genes controlling simply inherited traits, and even gene clusters (QTLs) controlling polygenic traits in a large number of model and crop plants. During this period, a number of new mapping populations beyond F_2 were utilized and a number of computer programs were developed for map construction, mapping of genes, and for mapping of polygenic clusters or QTLs. Molecular markers were also used in the studies of evolution and phylogenetic relationship, genetic diversity, DNA fingerprinting, and map-based cloning. Markers tightly linked to the genes were used in crop improvement employing the so-called marker-assisted selection. These strategies of molecular genetic mapping and molecular breeding made a spectacular impact during the last one and a half decades of the twentieth century. But still they remained "indirect" approaches for elucidation and utilization of plant genomes since much of the chromosomes remained unknown and the complete chemical depiction of them was yet to be unraveled.

Physical mapping of genomes was the obvious consequence that facilitated the development of the "genomic resources" including BAC and YAC libraries to develop physical maps in some plant genomes. Subsequently, integrated genetic–physical maps were also developed in many plants. This led to the concept of structural genomics. Later on, emphasis was laid on EST and transcriptome analysis to decipher the function of the active gene sequences leading to another concept defined as functional genomics. The advent of techniques of bacteriophage gene and DNA sequencing in the 1970s was extended to facilitate sequencing of these genomic resources in the last decade of the twentieth century.

As expected, sequencing of chromosomal regions would have led to too much data to store, characterize, and utilize with the-then available computer software could handle. But the development of information technology made the life of biologists easier by leading to a swift and sweet marriage of biology and informatics, and a new subject was born—bioinformatics.

Thus, the evolution of the concepts, strategies, and tools of sequencing and bioinformatics reinforced the subject of genomics—structural and functional. Today, genome sequencing has traveled much beyond biology and involves biophysics, biochemistry, and bioinformatics!

Thanks to the efforts of both public and private agencies, genome sequencing strategies are evolving very fast, leading to cheaper, quicker, and automated techniques right from clone-by-clone and whole-genome shotgun approaches to a succession of second-generation sequencing methods. The development of software of different generations facilitated this genome sequencing. At the same time, newer concepts and strategies were emerging to handle sequencing of the complex genomes, particularly the polyploids.

It became a reality to chemically—and so directly—define plant genomes, popularly called whole-genome sequencing or simply genome sequencing.

The history of plant genome sequencing will always cite the sequencing of the genome of the model plant Arabidopsis thaliana in 2000 that was followed by sequencing the genome of the crop and model plant rice in 2002. Since then, the number of sequenced genomes of higher plants has been increasing exponentially, mainly due to the development of cheaper and quicker genomic techniques and, most importantly, the development of collaborative platforms such as national and international consortia involving partners from public and/or private agencies.

As I write this preface for the first volume of the new series "Compendium of Plant Genomes," a net search tells me that complete or nearly complete whole-genome sequencing of 45 crop plants, eight crop and model plants, eight model plants, 15 crop progenitors and relatives, and three basal plants is accomplished, the majority of which are in the public domain. This means that we nowadays know many of our model and crop plants chemically, i.e., directly, and we may depict them and utilize them precisely better than ever. Genome sequencing has covered all groups of crop plants. Hence, information on the precise depiction of plant genomes and the scope of their utilization are growing rapidly every day. However, the information is scattered in research articles and review papers in journals and dedicated Web pages of the consortia and databases. There is no compilation of plant genomes and the opportunity of using the information in sequence-assisted breeding or further genomic studies. This is the underlying rationale for starting this book series, with each volume dedicated to a particular plant.

Plant genome science has emerged as an important subject in academia, and the present compendium of plant genomes will be highly useful to both students and teaching faculties. Most importantly, research scientists involved in genomics research will have access to systematic deliberations on the plant genomes of their interest. Elucidation of plant genomes is of interest not only for the geneticists and breeders, but also for practitioners of an array of plant science disciplines, such as taxonomy, evolution, cytology, physiology, pathology, entomology, nematology, crop production, biochemistry, and obviously bioinformatics. It must be mentioned that information regarding each plant genome is ever-growing. The contents of the volumes of this compendium are, therefore, focusing on the basic aspects of the genomes and their utility. They include information on the academic and/or economic importance of the plants, description of their genomes from a molecular genetic and cytogenetic point of view, and the genomic resources developed. Detailed deliberations focus on the background history of the national and international genome initiatives, public and private partners involved, strategies and genomic resources and tools utilized, enumeration on the sequences and their assembly, repetitive sequences, gene annotation, and genome duplication. In addition, synteny with other sequences, comparison of gene families, and, most importantly, the potential of the genome sequence information for gene pool characterization through genotyping by sequencing (GBS) and genetic improvement of crop plants have been described. As expected, there is a lot of variation of these topics in the volumes based on the information available on the crop, model, or reference plants.

I must confess that as the series editor, it has been a daunting task for me to work on such a huge and broad knowledge base that spans so many diverse plant species. However, pioneering scientists with lifetime experience and expertise on the particular crops did excellent jobs editing the respective volumes. I myself have been a small science worker on plant genomes since the mid-1980s and that provided me the opportunity to personally know several stalwarts of plant genomics from all over the globe. Most, if not all, of the volume editors are my longtime friends and colleagues. It has been highly comfortable and enriching for me to work with them on this book series. To be honest, while working on this series I have been and will remain a student first, a science worker second, and a series editor last. And, I must express my gratitude to the volume editors and the chapter authors for providing me the opportunity to work with them on this compendium.

I also wish to mention here my thanks and gratitude to Springer staff, particularly Dr. Christina Eckey and Dr. Jutta Lindenborn, for the earlier set of volumes and presently Ing. Zuzana Bernhart for all their timely help and support.

I always had to set aside additional hours to edit books beside my professional and personal commitments—hours I could and should have given to my wife, Phullara, and our kids, Sourav and Devleena. I must mention that they not only allowed me the freedom to take away those hours from them but also offered their support in the editing job itself. I am really not sure whether my dedication of this compendium to them will suffice to do justice to their sacrifices for the interest of science and the science community.

New Delhi, India Chittaranjan Kole

Contents

Global Millet Trends, Outlook, Challenges, and Opportunities

Kumara Charyulu Deevi, Nedumaran Swamikannu and Jyosthnaa Padmanabhan

1 Introduction

Millets are a group of small-seeded coarse cereals grown mainly in Asia and Africa. They are grown on soils which typically are too poor to support any other crop. They are significant contributors to the food security of the people living in Africa and Asia. They are grown mostly in developing countries (McDonough et al. 2000) located in Africa (Niger, Nigeria, Sudan, Mali, Burkina Faso) and Asia (India, China, Pakistan, Myanmar, Nepal) for food, feed, and fodder. Millets account for <1% of global cereal production and 3% of coarse cereal production. They are thinly traded with <2% of total millet production being exported. The most important millets by area cultivated and production quantities are pearl millet, finger millet, proso millet, and foxtail millet. The area covered by these millets, excluding sorghum, is 76% for pearl millet, 19% for finger millet, 9% for tef, and 4% for fonio (Obilana 2003). Sorghum and pearl millet are the two most important global members in the millets group, and these two have the largest area among the millets and occupy the fifth and sixth positions in total global crops, respectively, after rice, wheat, maize, and barley. With this background, the present chapter starts by highlighting the importance of millets, especially pearl millet in Asia and Africa. It also describes the major producing regions and trends in area, production and productivity across major growing countries in the world. Pattern of millets utilization among different regions is also furnished. The economic impacts of pearl millet research across different ecologies are reviewed and tabulated. The region-wise projected millet demand and supply between 2030 and 2050 are summarized and the widening gap among them identified. Major challenges in millets cultivation across ecologies are summarized and the potential opportunities among those are discussed at the end.

1.1 Importance of Pearl Millet

Pearl millet (*Pennisetum glaucum* R. Br.) is an important crop in the semiarid and arid ecologies of South Asia (SA) and sub-Saharan Africa (SSA) that are characteristically challenged by low and erratic rainfall and high mean temperature and simultaneously have soils with low organic carbon and poor water-holding capacity (Serba et al. 2020). Pearl millet is valued for its nutrient-rich grain for human consumption (Parthasarathy Rao et al. 2006) and its green fodder and dry stover for livestock (Andrews and Kumar 1992; Parthasarathy Rao and Hall 2003) and forms the basis of livelihood and nutritional security for >90 million people in

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SSA and SA (Serba et al. 2020). Pearl millet demand is anticipated to increase in the future because of increasing human and livestock populations in SSA and SA and as a healthy food and other industrial uses (Rai et al. 2008). Its cultivation may further extend in the areas where maize and sorghum are cultivated because of depleting water resources. Pearl millet production is likely to become more challenging because of predicted intense drought stress, rise in temperature, and greater disease incidences in SSA (Sultan et al. 2013) and SA (Rama Rao et al. 2019). Therefore, its production must be increased at a much faster rate and more so in challenging agro-ecologies.

Presently, millets are cultivated mostly in Africa (~ 20 million ha) and Asia (~ 11 million ha). In Asia, India has the largest area (~ 10 million ha) under this crop. Global area, production, and productivity data for millets are not available separately for all kinds of millets in FAOSTAT. Hence, the present study used millets data which include pearl millet and other small millets. Approximately, pearl millet represents about 3/4th of global millet area in the world. Africa accounts for about 64% of global millet area while Asia represents nearly 34%. Rest of the world only occupies 2% of global millet area. In most parts of the world, pearl millet is grown as a subsistence crop for local consumption. Commercial millet production is risky, especially in Africa, because the absence of large market outlets means that fluctuations in output cause significant price fluctuations, particularly in areas where millet is the main food crop. Apart from grain production, millet is also cultivated for grazing, green fodder, or silage. Livestock are an important component of most millet production systems, and millet crop residues contribute significantly to fodder supplies (Parthasarathy Rao and Hall 2003).

2 Global Millet Production and Utilization

African countries account for 63% of the global area under millets and 48% of global production (Table 1). Much of the crop is grown on marginal lands with low inputs and consequently yields in this region are relatively low. Asian countries are the second most important block of millet producers, accounting for 34% of the global area and 49% of the global production. Yields are close to double here compared to Africa, as improved/hybrid seeds are widely used (Kumara Charyulu et al. 2014), though the total area in these countries has been falling as farmers shift to other, more remunerative crops.

Globally, the area under millets has come down from 35 to 32 million ha during the last decade (2011–2020) period. The millet cropped area is much stable in Africa region while it has declined significantly in case of Asia region. Except in case of Europe, millet cropped area under Americas and Oceania regions exhibited stability during study period. The global millet production has declined marginally due to reduction in area. Africa region (specifically West Central Africa) indicated remarkable

Table 1 Area planted to millets by region, 2018–20

Region	Area (‘000 ha)	Production (‘000 tons)	Productivity (kg/ha)
Global	31,862 (100)	30,142 (100)	945
Africa	20,128 (63.2)	14,488 (48.0)	718
Eastern Africa	1331 (4.2)	1954 (6.5)	1468
Western Africa	13,813 (43.3)	10,082 (33.4)	729
Americas	183 (0.5)	287 (0.9)	1580
Asia	11,100 (34.8)	14,791 (49.1)	1331
Europe	413 (1.3)	539 (1.8)	1297
Oceania	35 (0.1)	36 (0.1)	1018

Note Figures in the parenthesis indicates % to column total decline in crop production during the last decade. The reasons might be significant millet area reduction in Nigeria coupled with decline in mean productivity levels in the region. Contrary to area trend in Asia, the millet production has increased marginally due to enhancement in productivity over last one decade (Kumara Charyulu et al. 2017). The production has significantly gone down in Europe when compared with Americas and Oceania regions. Overall, millets area and production have come down globally and across major regions during the last decade period.

2.1 Region-Wise Production and Productivity Trends

Region-wise long-term trends of millets production and productivity levels across major regions are summarized in Figs. 1 and 2 respectively. The global millet production is almost stable (hovering around 28 m tons) during the last twenty years period. The production in case of Africa has gone up and reached to a peak during 2008 (19 m tons) and afterwards it has come down to 13 m tons. The production in Asia region has not changed much

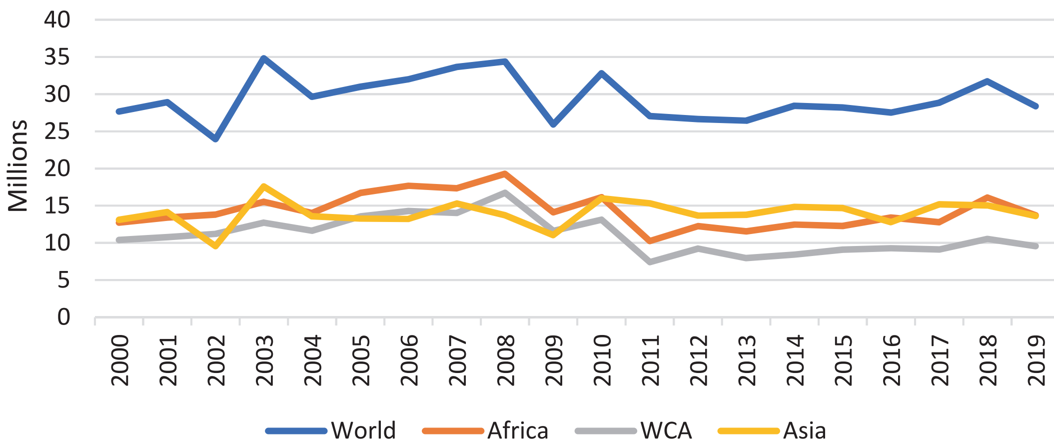

Fig. 1 Region-wise production trends, 2000–2019

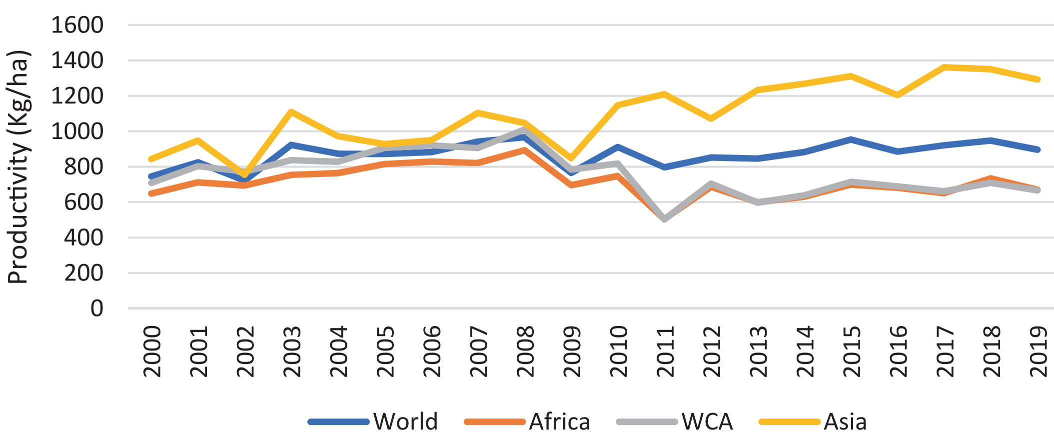

Fig. 2 Region-wise productivity trends, 2000–2019

(13 m tons) over study period (2000–2019). In case of Western Central Africa (WCA) region, there is significant decline in millet production (10.4–9.5 m tons) during two decades period (Fig. 1).

Historical region-wise productivity trends during 2000–2019 across major millet growing regions are furnished in Fig. 2. Among all, Asia region exhibited consistent productivity growth and has increased from 800 to nearly 1400 kg per ha. This may be due to access and adoption of improved cultivars combined with improved management practices in Asia (Yadav et al. 2021; Venkata Rao et al. 2018). Millet productivity level in case of world is stable and hovering between 800 and 900 kg per ha. The mean productivity scenario in case of Africa and WCA has consistently been declined over time (from 800 to 600 kg per ha). Decline in cropped area during study period coupled with decrease in productivity levels in Africa led to significant decline in crop production in the region (Jukanti et al. 2016; Pucher 2018).

2.2 Major Millet Producing Countries

The performance of millet over last one decade across major producing countries in the world is furnished in Table 2. With respect to acreage, the top 10 countries include seven in Africa (Niger, Nigeria, Sudan, Mali, Burkina Faso, Chad, and Senegal) and three in Asia (India, China, and Pakistan). Among all major countries, India stood on the top in terms of cropped area followed by Niger and Nigeria. There is significant decline (about 25%) in millet cropped area in India during the study period. The production has marginally reduced due to enhancement in productivity by 20%. The millet cropped area is stable in case of Niger (7 m ha) with marginal improvement in productivity. Nigeria has lost almost 50% of the cropped area and production due to decline in productivity (– 20%) during the study period. Millet cropped area under Mali, Sudan, Angola, Burkina Faso, Chad, China, and Ethiopia have expanded

Table 2 Millet performance across major countries, 2009–2019

Country	2009–11			2017–19			% change		
	Area	Production	Yield	Area	Production	Yield	Area	Production	Yield
India	11,158	11,576	1037	8921	11,142	1248	– 25.1	– 3.8	20.3
Mali	1660	1428	913	2101	1737	830	21.0	21.6	– 9.1
Niger	6939	3092	444	6954	3639	523	0.2	17.7	17.8
Nigeria	3659	3790	979	2421	1873	781	– 51.1	– 50.6	– 20.2
Sudan	NA	NA	NA	3093	1553	477	NA	NA	NA
Angola	197	43	217	274	63	232	39.1	46.5	6.9
Burkina Faso	1253	982	780	1264	995	785	0.9	1.3	0.6
Chad	1067	469	421	1189	711	598	11.4	51.6	42.0
China	780	1455	1867	846	2396	2841	8.5	64.7	52.2
Ethiopia	403	603	1494	452	1064	2349	12.2	76.5	57.2
Nepal	268	298	1112	263	311	1183	– 1.9	4.4	6.4
Pakistan	494	314	636	488	357	733	– 1.2	13.7	15.3
Russian Fed	355	425	1058	258	324	1247	– 27.3	– 23.8	17.9
Senegal	954	701	724	917	860	937	– 3.9	22.7	29.4
Tanzania	365	353	975	282	337	1206	– 22.7	– 4.5	23.7

Note Area in '000 ha; production in '000 tons and yield in kg/ha