

Compendium of Plant Genomes

Series Editor: Chittaranjan Kole

Anil Kumar · Salej Sood · B. Kalyana Babu ·
Sanjay Mohan Gupta · B. Dayakar Rao *Editors*

The Finger Millet Genome

Compendium of Plant Genomes

Series Editor

Chittaranjan Kole, President, International Climate Resilient Crop Genomics Consortium (ICRCGC), President, International Phytomedomics & Nutriomics Consortium (IPNC) and President, Genome India International (GII), Kolkata, India

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.

More information about this series at <https://link.springer.com/bookseries/11805>

Anil Kumar • Salej Sood •
B. Kalyana Babu • Sanjay Mohan Gupta •
B. Dayakar Rao
Editors

The Finger Millet Genome

Editors

Anil Kumar
Rani Lakshmi Bai Central
Agricultural University
Jhansi, India

Salej Sood
ICAR-Central Potato
Research Institute
Shimla, India

B. Kalyana Babu
ICAR-Indian Institute of Oil
Palm Research
Pedavegi, Andhra Pradesh, India

Sanjay Mohan Gupta
Defence Institute of Bio-Energy
Research (DIBER)
Haldwani, India

B. Dayakar Rao
ICAR-Indian Institute
of Millet Research
Hyderabad, India

ISSN 2199-4781

ISSN 2199-479X (electronic)

Compendium of Plant Genomes

ISBN 978-3-031-00867-2

ISBN 978-3-031-00868-9 (eBook)

<https://doi.org/10.1007/978-3-031-00868-9>

© The Editor(s) (if applicable) and The Author(s), under exclusive license to Springer
Nature Switzerland AG 2022

This work is subject to copyright. All rights are solely and exclusively licensed by the Publisher, whether the whole or part of the material is concerned, specifically the rights of translation, reprinting, reuse of illustrations, recitation, broadcasting, reproduction on microfilms or in any other physical way, and transmission or information storage and retrieval, electronic adaptation, computer software, or by similar or dissimilar methodology now known or hereafter developed. The use of general descriptive names, registered names, trademarks, service marks, etc. in this publication does not imply, even in the absence of a specific statement, that such names are exempt from the relevant protective laws and regulations and therefore free for general use.

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

This Springer imprint is published by the registered company Springer Nature Switzerland AG
The registered company address is: Gewerbestrasse 11, 6330 Cham, Switzerland

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 F₂ 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 the 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

1	History, Botanical and Taxonomic Description, Domestication, and Spread	1
	Salej Sood, B. Kalyana Babu, and Dinesh Joshi	
2	Economic, Nutritional, and Health Importance of Finger Millet	13
	Manoj Kumar Tripathi, Anil Kumar, Debabandhya Mohapatra, Rajpal S. Jadam, Shilpa S. Selvan, and C. Nickhil	
3	Genetic and Genomic Resources for Crop Improvement in Finger Millet	35
	P. Rajendrakumar and K. N. Ganapathy	
4	Paradigm Shift from Genetics to Genomics: Characterization of Diversity and Prospects of Molecular Markers	57
	Lalit Arya, Monika Singh, Amit Kumar Singh, and Manjusha Verma	
5	Molecular Mapping in Finger Millet	83
	K. V. Vijaya Kumar, Laavanya Rayaprolu, M. V. C. Gowda, Rajeev Gupta, and Santosh Deshpande	
6	The Complete Genome Sequence of Finger Millet	101
	H. B. Mahesh, K. G. Manasa, N. R. Raghavendra, Meghana Deepak Shirke, and Shailaja Hittalmani	
7	Comparative Genomics of Finger Millet	113
	B. Kalyana Babu, Salej Sood, Vikram Singh Gaur, and Anil Kumar	
8	Finger Millet Transcriptome Analysis Using High Throughput Sequencing Technologies	123
	Rajesh Kumar Pathak, Dev Bukhsh Singh, Dinesh Pandey, Vikram Singh Gaur, and Anil Kumar	
9	Seed Biology and Packaging of Finger Millet Using Omics Approaches for Nutritional Security	135
	Anil Kumar, Rajesh Kumar Pathak, Sanjay Mohan Gupta, and Salej Sood	

10	A Nutritional Crop Factory of Quality Seed Storage Proteins in Finger Millet for Combating Malnutrition	161
	Apoorv Tiwari, Supriya Gupta, Pramod W. Ramteke, and Anil Kumar	
11	Finger Millet Genome Analysis and Nutrient Transport	181
	T. Maharajan, T. P. Ajeesh Krishna, S. Ignacimuthu, and S. Antony Ceasar	
12	Finger Millet as Input Use Efficient and Organic by Default Crop	201
	Supriya Gupta, Sanjay Mohan Gupta, Kavita Gururani, Subodh Sinha, Rajeev Gupta, and Anil Kumar	
13	Molecular Basis of Biotic and Abiotic Stress Tolerance in Finger Millet	225
	Radha Shivhare, Anil Kumar, and Charu Lata	
14	Genetic Transformation for Crop Improvement and Biofortification	239
	Sanjay Mohan Gupta, Supriya Gupta, and Anil Kumar	
15	Novel Prospective on Suppression of Ageing by the Consumption of Finger Millet	261
	Anil Kumar, Madhu Rani, Rashmi Kumari, Pallavi Shah, Shalini Mani, and Salej Sood	
16	Holistic Value Chain Approach in Finger Millet	277
	B. Dayakar Rao, E. Kiranmai, D. Srenuja, and Vilas A Tonapi	



History, Botanical and Taxonomic Description, Domestication, and Spread

1

Salej Sood , B. Kalyana Babu,
and Dinesh Joshi

Abstract

Finger millet (*Eleusine coracana* L. Gaertn) is an annual small-seeded cereal mainly grown in Africa and Asia for both grain and forage. Once considered an orphan crop for subsistence agriculture, it is today's mainstream crop due to its exceptional adaptation qualities and nutritional importance. The name "finger millet" is derived from the shape of its panicles, where spikes look like fingers and thumb. The crop is a domesticated cereal of African origin that spread in pre-history to Asia and is associated with cultural history. Archeological findings suggest Ethiopian highlands as a primary center of origin of the crop, and its domestication happened in western Uganda to the area extending Ethiopian highlands. A long history of cultivation and large variability of finger millet landraces makes India the secondary center of diversity for the crop. The genus *Eleusine* has about

nine species which are found across African, Asian, and South American tropical and subtropical areas. Studies on different species of *Eleusine* suggest that the cultivated gene pool diversity in finger millet in Africa has originated from the weedy progenitor *E. africana*.

Finger millet is an annual, small grain self-pollinated allotetraploid ($2n = 4x = 36$) plant mainly grown in two major continents, Africa and Asia (Sood et al. 2017, 2019). It has wide adaptability and its cultivation extends from sea level to higher elevations in the Himalayas (Gupta et al. 2012). Finger millet has the ability to grow under harsh conditions in diverse environments and has great food value in terms of nutritional profile. It is grown in dry and semi-dry regions for both grains and forage. The crop has exceptional adaptation under low moisture conditions and provides assured harvest under dry spells in marginal areas, suitable for contingency crop planning (Sood et al. 2016). The grains can be stored for years and have many health-promoting benefits besides a very good nutritional profile. The finger millet forage is also highly palatable and nutritious. At the global level among millets, finger millet occupies the fourth place, after major coarse grains, i.e., sorghum, pearl millet, and a minor millet, foxtail millet (Gupta et al. 2012).

Finger millet is a crop under the Poaceae family and Chloridoideae subfamily. It is the

S. Sood (✉)
ICAR-Central Potato Research Institute, Shimla
171001, HP, India
e-mail: salej.sood@icar.gov.in

B. K. Babu
ICAR-Indian Institute of Oil Palm Research,
Pedavegi, Andhra Pradesh, India

D. Joshi
ICAR-Vivekananda Institute of Hill Agriculture,
Almora, Uttarakhand, India

only millet that belongs to the tribe Chlorideae, whereas Piniceae is the tribe for all other millets. The finger millet panicles resemble the shape of the human thumb and fingers, therefore its English name has been given as “finger millet”.

Global estimates for precise area and production data on finger millet are not available. However, the literature estimates reveal that 5 million tons of finger millet grains were produced from 4 to 4.5 million ha area globally. The total production of finger millet in Africa was about 2 million tons, which was slightly lower than in India (2.2 million tons) (Sood et al. 2019). In Africa, finger millet is cultivated in eastern and southern African countries mainly Ethiopia, Kenya, Malawi, Tanzania, Uganda, Zaire, Zambia, and Zimbabwe. India and Nepal are the major finger millet producers in Asia, but the crop is also grown to some extent in China, Bhutan, Japan, and Sri Lanka. The latest estimates on area, production, and productivity of the crop in India are 67.2 thousand ha, 61.6 thousand tons, and 1332 kg/ha, respectively, which indicate a considerable decline in area, production, and productivity in comparison to previous years (Directorate of Economics & Statistics, Government of India, 2020, <https://eands.dacnet.nic.in/PDF/At%20a%20Glance%202019%20Eng.pdf>). Among various finger millet-producing states of India, Karnataka tops the list with >50% area, followed by Maharashtra and Uttarakhand (Chandra et al. 2020).

1.1 Origin and Phylogeny

Earlier botanists argued and suggested the origin of finger millet as India based on historical records and mention of finger millet by Sanskrit writers as ragi or rajika (De Candolle 1886; Dixit et al. 1987). Burkill (1935) proposed that *E. coracana* is the cultivated form ascended through selection in India from wild species *E. indica* (L) Gaertn. It was further stated that finger millet originated in India and Africa independently

(Vavilov 1951). More precise studies later explained that *E. coracana* is of African origin, domesticated in Western Uganda and Ethiopian highlands around 5000 years BC. The crop reached the Western Ghats in southern parts of India ~3000 BC (Hilu and De Wet 1976a; Hilu et al. 1979a, b; Fuller 2014).

The archaeological studies in Ethiopia dating back to the third millennium BC confirm the African origin of finger millet (Hilu et al. 1979a, b). Finger millet has two discrete races, African highland and Afro-asiatic lowland race. The former seems to be a derivative from *Eleusine africana*, which also resulted in the African lowland race. As per Hilu and De Wet (1976b), this African lowland race reached India as an Afro-Asiatic lowland race around 3000 BC. Wide phenotypic variability has been reported in African germplasm collections in comparison to Indian collections in many studies, strengthening the claim that Africa is the primary center of origin of finger millet. During its cultivation for years in the Indian subcontinent, the gene flow has resulted in great diversity in local and primitive crop cultivars, making India the secondary center of origin of the crop (Padulosi et al. 2009; Sood et al. 2016).

The cultivated finger millet species (*E. coracana*) is tetraploid with a basic chromosome number of 9 ($2n = 4x = 36$) (Sood et al. 2019). The species *E. africana* ($2n = 36$) exhibits great similarity with *E. coracana* in morphological features and gene flow occurs between them (Hilu and de Wet 1976b). First, the cytological studies showed that *E. indica* is one of the genome (AA) contributors to the cultivated species *E. coracana* and later chloroplast genome studies revealed *E. indica* to be the maternal genome donor of *E. africana*. The cytological studies also confirmed that *E. intermedia* and *E. tristachya* also belong to the genomic group “A” along with *E. indica* and these three species have a close genetic grouping (Mallikharjun et al., 2005). The results of genomic in situ hybridization and ribosomal DNA sites comparison on the

chromosomes of diploid and polyploid species inferred *E. indica* and *E. floccifolia* as two progenitors of *E. coracana* and *E. africana* (Bisht and Mukai 2000, 2001). Later, Neves et al. (2005) refuted *E. floccifolia* as a B genome donor based on genome analysis using nuclear internal transcribed spacers and plasmid trnT-trnF sequences. The results of molecular markers of *Pepc4* gene inferred that the species *E. coracana*, *E. africana* and *E. kigeziensis* are of allopolyploid origin (Liu et al. 2011), and strengthened the claim of two separate allopolyploidization origins for *E. africana*-*E. coracana* group and *E. kigeziensis*. However in both the cases, the diploid species group, *E. indica*-*E. tristachya* was recognized as the maternal parent (Liu et al. 2014), the paternal parents could not be traced for both the events as they might not exist now (Zhang et al. 2019). The placement of *Eleusine* in the subfamily Chloridoideae is undisputed.

1.2 Taxonomy and Classification

Eleusine is a small genus with 9–10 species distributed across continents mainly Africa, Asia, and South America in tropical and subtropical habitats (Hilu 1981; Phillips 1972). Out of the nine species, eight species, *E. coracana*, *E. africana*, *E. indica*, *E. kigeziensis*, *E. intermedia*, *E. multiflora*, *E. floccifolia*, and *E. jaegeri* (Phillips 1972) belong to East Africa, which is the center of diversity for the genus, *Eleusine*. The only species which has emerged outside Africa is *E. tristachya* (Neves 2011). This species is native to South America. The three species under the genus *Eleusine*, *E. coracana*, *E. tristachya*, and *E. indica* has wide adaptation ranging from sea level to high hills, while *E. jaegeri*, *E. floccifolia*, *E. kigeziensis*, *E. intermedia*, and *E. multiflora* are adapted to upland habitats and grow well in areas above 1,000 m amsl. Both diploid and polyploidy species are found in the genus *Eleusine* with three basic chromosome numbers ($x = 8, 9, 10$). The species has been classified into two separate groups, annual and perennial based on their growth habit.

The species under the genus *Eleusine* lack clear separation based on the taxonomic relationships, therefore, the gene pool does not have defined boundaries with respect to the primary, secondary, and tertiary gene pool species. However, phylogenetic studies in the *Eleusine* genus have categorized the species into three classes. Domesticated and wild forms of finger millet have been placed in the primary gene pool while diploid wild species progenitors constitute the secondary gene pool and all other species belong to the tertiary gene pool (Sood et al. 2019). The primary gene pool includes *E. coracana* subsp. *africana* and *Eleusine coracana* subsp. *coracana*, secondary gene pool comprises *E. indica*, *E. floccifolia*, and *E. tristachya* and the species *E. intermedia*, *E. jaegeri*, *E. kigeziensis*, *E. multiflora*, and *E. semisterlis* (syn. *E. compressa*) form the tertiary gene pool (Table 1.1).

The cultivated *Eleusine* form can be easily distinguished from wild forms based on its firm spikes and large and ball-shaped grains (Neves 2010). As discussed above, eight species of the *Eleusine* genus are native to Africa, which also includes the wild species *E. coracana* subspecies *africana* which has moved to America and Asia, particularly in warmer parts. Due to natural interbreeding between cultivated and wild finger millet species, many new hybrid combinations have appeared, most of which are lookalike companion weeds of the crop. This has been studied and demonstrated through scientific evidence using molecular markers that gene flow between subsp. *africana* and subsp. *coracana* has happened in nature (Dida et al. 2008).

1.3 *Eleusine* Germplasm Collections

India holds the largest germplasm collections of 10,507 accessions in the National Bureau of Plant Genetic Resources, New Delhi, under long-term conservation. Although most of these accessions belong to cultivated species and are indigenous, the collection also contains 6 wild species. ICRISAT in India holds about 5,957

Table 1.1 *Eleusine* species, habitat, and salient features

Species	Vernacular name	2n chromosome numbers & genome formula	Gene pool	Geographical distribution	Growth habit and important features
<i>Eleusine coracana</i> subsp. <i>coracana</i> (L.) Gaertn	Ragi, <i>Koracan</i> , <i>Coracan</i> , Kodra, Kodo, Mandal, Nachni, <i>Wimbi</i> , <i>Hawere</i> , <i>Khawke</i> , <i>Mulirubi</i> , <i>Mugumbi</i> , <i>Limbi</i> , <i>Lupodo</i> , <i>Malesi</i> , <i>Lipoke</i> , <i>Usanje</i> , <i>Mawe</i> , <i>Koddo</i> , <i>Bulo</i> , <i>Bule</i> , etc	36 (x = 9), AABB	Primary	Indian subcontinent (India, Nepal), East Africa (Uganda, Kenya, Ethiopia)	Growth habit—Annual; robust culm; digitate or subdigitate panicle/ inflorescence with 3–10 fingers, thick and firm, fingers straight or incurved and 4–14 cm long, width 9–15 mm Black, brown to reddish, and white globular grains used for food and fermented alcoholic drinks and therapeutic usages, straw is used as fodder
<i>E. coracana</i> subsp. <i>africana</i> Kennedy-O'Byrne	-	36 (x = 9), AABB	Primary	Africa, mainly in eastern and southern uplands (Malawi, Kenya, Rhodesia, Tanzania), and Arabia	Growth habit—Annual; moderately robust culm, up to 100 cm length; Glabrous soft leaves digitate or subdigitate panicle with 3–17 fingers, which are 3.5–15.5 cm long and 4–7 mm wide Black to brown ovate-oblong grains, which are about 1.2–1.6 mm long, It is a weed but used as a forage grass
<i>E. indica</i> (L.) Gaertn	Goosegrass, crows foot grass, wiregrass	18 (x = 9), AA	Secondary	Cosmopolitan weed of African origin; mostly tropics and subtropics	Growth habit—Annual; Slender culms; soft, glabrous leaves; digitate or subdigitate panicle with 3–8 narrow fingers, which are mostly straight and around 5–10 cm long, 3–6 mm wide; Elliptic black grains with conspicuous ridges on the surface It is a weed but used as a forage grass and has medicinal value
<i>E. floccifolia</i> (Forssk.) Spreng	<i>Akirma</i> , <i>akrma</i> , <i>dagoo</i> , <i>garrgorr</i>	18 (x = 9), BB	Secondary	Ethiopia, Somalia, Kenya, Yemen, Eritrea	Growth habit—Perennial; moderately robust tough culms with an approximate height of 20–70 cm; 8–55 cm long folded leaf blades; subdigitate

(continued)

Table 1.1 (continued)

Species	Vernacular name	2n chromosome numbers & genome formula	Gene pool	Geographical distribution	Growth habit and important features
					panicle with 2–10 fingers, which are mostly straight, 2.5–12 cm long, and 3.5–6 mm wide; Blackish elliptic to oblong grains, 0.9–1.4 mm long
<i>E. tristachya</i> (Lam.) Lam	–	18 (x = 9), AA	Secondary	South America, Brazil	Growth habit—short-lived Annual/Perennial; decumbent 10–45 cm long culms, internodes elliptical in section; 6–25 cm long and 1–4 mm wide leaf blades; digitate panicle with 2–3 straight fingers, fingers 1–4 cm long and 5–16 mm wide; dark brown to blackish oblong to trigonous grains with punctiform hilum; It is a weed but has potential as a fodder crop
<i>E. intermedia</i> (Chiov.) S. M. Phillips	–	18 (x = 9), AB	Tertiary	Kenya, Ethiopia	Growth habit—Perennial; moderately vigorous culms; herbaceous glabrous leaves; sub-digitate to a racemose panicle with 4–15 straight fingers, which are 5–12 cm long and 4–8 mm wide; black elliptic to trigonous grains
<i>E. jaegeri</i> Pilger	Manyata grass, <i>mafutiana</i> , <i>akirma</i> , <i>dagoo</i> , <i>titima</i>	20 (x = 10), DD	Tertiary	Tanzania, Uganda	Growth habit—Perennial; Vigorous culms; Leather-type leaves with rough margins; subdigitate or racemose panicle with 2–10 straight fingers, which are about 4–17 cm long and 3–7 mm wide; Black elliptic/ oblong to trigonous grains

(continued)

Table 1.1 (continued)

Species	Vernacular name	2n chromosome numbers & genome formula	Gene pool	Geographical distribution	Growth habit and important features
<i>E. kigeziensis</i> S. M. Phillips	–	36 (x = 9), AADD	Tertiary	Uganda, Congo, Burundi, Rwanda, Ethiopia	Growth habit—Perennial; Robust culms; Soft and Glabrous leaves; digitate panicle with 2–7 straight fingers, 7.5–14 cm long and 4.5–5.5 mm wide; Black elliptic to trigonous grains
<i>E. multiflora</i> Hochst. ex A. Rich	–	16 (x = 8), CC	Tertiary	Eritrea, Kenya, Ethiopia, Tanzania	Growth habit—Annual; Slender around 45 cm long culms; Soft, wide, and flat leaves; racemose panicle with 3–8 short wide curved fingers, 1–4 cm long and 8–16 mm wide; black oblong-compressed grains with a ridged surface; It is a weedy species but has potential as a valuable forage grass
<i>E. semisterilis</i> S. M. Phillips	–	Cytologically unknown	–	Kenya (Maybe extinct now)	Growth habit—Perennial; slender, erect, 145 cm high culms; leaf blades linear and loosely folded; subdigitate panicle with around 9 fingers which could be 5–15 cm long, laxly arranged spikelets in the fingers; black obovate grains

Source Phillips 1972; Liu et al. 2011; Sood et al. 2019; <http://www.theplantlist.org/browse/A/Poaceae/Eleusine/>

global accessions, of which 105 are of wild species. The major collection of wild species of finger millet is conserved and maintained at Agricultural Research Station, Griffin, Georgia, USDA, which has 17 wild species (*E. floccifolia*, *E. indica*, *E. jaegeri*, *E. multiflora*, and *E. tristachya*) out of the total collection of 766 accessions. Eastern Africa, which is the primary center of origin of the crop, Kenya, Zimbabwe, Uganda, and Zambia hold about 1902, 1158, 1155, and 497 accessions. Besides, many other South Asian

and African countries hold small germplasm collections (Sood et al. 2019). The global finger millet collection at ICRISAT has been characterized and core, as well as the mini-core set, have been developed for use in breeding and genomics studies (Upadhyaya et al. 2006). Although global diversity of finger millet has been conserved and important accessions have been identified, the wild species particularly, *E. coracana* subsp. *africana* and progenitors also need due attention (Neves 2010).

Based on compactness and shape of inflorescence, finger millet germplasm has been classified into races and subraces. The salient characters of races and subraces under each species are given in Table 1.2 (Prasada Rao et al. 1993; Bharathi 2011).

1.4 Crop Adaptation and Floral Biology

Finger millet has wide adaptation and can be grown in a wide habitat because of its hardy nature and short growing season. Being a C4 crop, it is highly efficient in adapting to environmental fluctuations and climate change. It can be grown from coastal plains to high hills, between 500 and 2,400 m above sea level (Fig. 1a). The genotype response although varies with agro-ecologies. Short-duration varieties are generally adapted to highlands and medium to long-duration cultivars do well in plains and tropical areas. The crop completes its life cycle in 75–160 days. It is generally grown in drylands as a rainfed crop but irrigated crop does well in terms of grain yield and the potential yield under irrigated conditions is around 5–6 t/ha. The crop can tolerate some waterlogging, but water stagnation severely affects crop productivity. Finger millet volunteers, shattering types are common in crop fields and difficult to identify early in the season. They look like normal plants but their seed starts shattering even in the immature stage itself.

The height of finger millet plants varies from 30 to 150 cm and mostly medium height cultivars are grown in India (100–130 cm). Finger millet inflorescence is in the whorl of 2–11 digitate, straight or slightly curved spikes (Fig. 1b and c). The spike is 8–15 cm long and 1.3 cm broad. In each spike, about 50–70 spikelets are arranged alternatively on one side of the rachis (Gupta et al. 2012). Each spikelet contains 3–13 florets. The florets have three stamens and the gynoecium is bi-carpellary, uni-locular with a superior ovary having two styles with feathery branched stigma (Seetharam et al. 2003). The anthers surround the stigma, which ensures self-

pollination. Finger millet grains vary in shape from round-oblong/oval, and white -reddish-brown in grain color (Fig. 1.2). The surface of finger millet grains is finely grooved and its pericarp is fused to the surface of the grain. Finger millet wild relatives have seed shattering trait, and at maturity seeds disperse naturally from the panicle, the cultivated species lost the seed shattering trait during domestication but it varies from cultivar to cultivar (de wet et al. 1984). Some cultivars are hard threshers while others still disperse some seed naturally at maturity.

The pollination system studies in finger millet revealed that pollen dust covers the stigma before it comes out of the lemma, leaving no or little chance for cross-pollination (Gupta et al. 2012). The spikelets opening follows the top to the bottom pattern in each spike, and florets in the spikelets open from bottom to top. The studies suggest that one floret in the spikelet opens per day. The flowering completes in around 5–7 days. Anthesis happens early morning between 1.00 and 5.00 a.m., when anthers dehisce to pollinate their stigmas (Gowda 1997). Dodake and Dhonukshe (1998) reported that pollen grains remain viable in finger millet for about 20 min, while stigma receptivity stays for up to 5 h. The estimation of natural crossing does not exceed 1% in finger millet (Seetharam 1998). Inter-varietal hybridization using the contact method (Ayyangar 1934) is the simplest and easiest way for recombination breeding. For successful hybridization, genotypes having dominant character such as pigmentation on nodes are used as the male parent. This helps in the identification of true hybrids in the F₁ generation. However, inducing male sterility through hot water treatment for 5 min at a temperature of 48–52 °C of immature inflorescence on the 3rd to 4th day of emergence was effective in getting few true hybrid seeds (Sood et al. 2019). Genetic male sterility (GMS) and partial GMS source have been identified in the crop but are of little use due to maintenance problem and varying level of sterility/fertility in different locations (Gupta et al. 1997; Gowda et al. 2014; Sood et al. 2019).

Table 1.2 Races and subraces in finger millet germplasm and their features

Species	Subspecies	Race	Subrace(s)	Salient features
<i>E. Coracana</i>	<i>Coracana</i>	<i>Elongata</i>	<i>liliaceae, stellata, incurvata, and digitata</i>	This race is commonly found in Africa and Asia. It has long slender 10–24 cm long panicles with digitately arranged spreading fingers, which curve outward on maturity. In the subrace <i>liliaceae</i> , the fingers in the panicle are reflexed, while subrace <i>stellata</i> contains twisted fingers. As the name suggests, subrace <i>incurvata</i> have incurved fingers that give a fist-like appearance, and subrace <i>digitata</i> has top curved fingers
		<i>Plana</i>	<i>seriata, confundere, and grandigluma</i>	This race <i>plana</i> has large 8–15 mm long spikelets, which are arranged on the rachis as even rows of two and look like a flat ribbon. The subrace <i>seriata</i> has serially arranged spikelets on the rachis, which gives ribbon-like appearance, the subrace <i>confundere</i> contains numerous fertile florets which upon grain filling at maturity give a compact look to the panicle, the <i>grandigluma</i> subrace is characterized by very large pointed glumes, which are longer than spikelets
		<i>Compacta</i>		The race <i>compacta</i> members are commonly stated as cockscomb finger millets. The spikelets have 9 or more florets. Fingers incurve at the tip to form a fist-like panicle
		<i>Vulgaris</i>	<i>laxa, reclusa, and sparsa</i>	The race <i>vulgaris</i> is the most distinct among all the four races of finger millet based on phenotype. It has long slender panicle branches, which are arranged digitately, and spikelets have 4–8 florets. The moderate number of florets in the spikelets give a semi-compact appearance and fingers incurve at maturity. As the name suggests, <i>laxa</i> subrace has long open fingers and spikelets arranged in thin rows on the rachis of the panicle fingers. This subrace resembles the wild <i>Africana</i> race. The subrace <i>reclusa</i> is characterized by short open fingers, which do not curve. The <i>sparsa</i> subrace is also characterized by open fingers, however, the spikelets arrangement on the panicle has naked space in between the clusters of spikelets
<i>E. africana</i>	<i>africana</i>	<i>africana</i>	–	The panicles in the race <i>africana</i> are long and thin, i.e., around 8–17 cm long and about 5 mm wide. The spikelets on the rachis are arranged in two rows on one side with 4–9 flowers. The glumes are short <5 mm, smaller than the spikelet
		<i>spontanea</i>	–	The features of race <i>spontanea</i> match with race <i>africana</i> . The race <i>spontanea</i> contains derivatives of hybridization between <i>E. coracana</i> and <i>E. africana</i>

Source Bharathi (2011)



Fig. 1.1 Finger millet crop in Uttarakhand hills, India. **a** Crop stand of improved variety VL 376. **b** Immature panicles of finger millet variety VL 376. **c** Mature panicles of finger millet variety VL 376

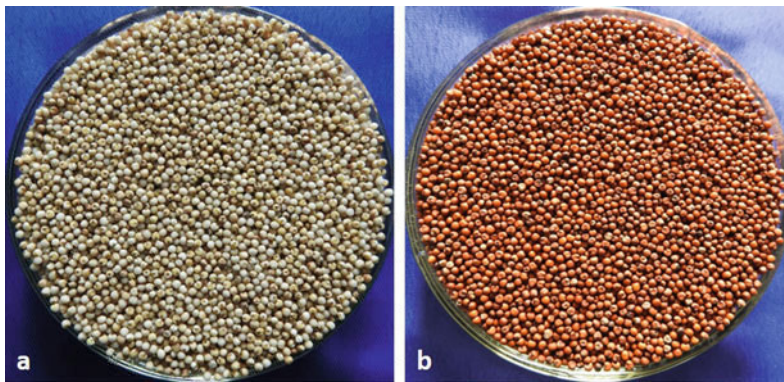


Fig. 1.2 Cleaned finger millet grains after threshing. **a** White grains of finger millet variety VL 382. **b** Reddish-brown grains of finger millet variety VL 376

1.5 Genome Size

Using Feulgen microspectrophotometry, nuclear DNA content of *Eleusine* spp. was first reported by Hiremath and Salimath (1991), which was later substantiated by Mysore and Baird (1997) with more accurate analysis using laser flow cytometry. The 2C DNA content of different *Eleusine* species varied from 1.51 to 3.87 pg. The cultivated species, *E. coracana* was found to have 3.36–3.87 pg 2C DNA followed by *E. coracana* subsp. *africana* (3.34 pg), *E. indica* (1.61–1.76 pg), *E. tristachya* (1.51 pg), *E. floccifolia* (2.0 pg), *E. multiflora* (2.65 pg), and *E. jaegeri* (1.90 pg). A recent study reported 1.20, 1.84, 1.14, 1.21, 2.52 pg 2C DNA content in *E.*

jaegeri, *E. multiflora*, *E. tristachya*, *E. indica*, and *E. coracana* subsp. *africana*, respectively (Hittalmani et al. 2017). In their study, the cultivated species *E. coracana* was found to have 3.01 pg 2C DNA content and 1453 Mb genome size. The analysis of genome size of wild species showed a range of 580 Mb in *E. jaegeri* to 1217 Mb in *E. coracana* subsp. *africana*. *E. coracana* subsp. *Coracana*, and *E. coracana* subsp. *africana* were found to have almost similar genome size which was attributed to the domestication of *E. coracana* subsp. *coracana* from *E. coracana* subsp. *africana* (Hittalmani et al. 2017). Although in comparison to many types of grass and other plants, the genome size of the *Eleusine* species is small, still it is too large for genomics studies (Neves 2010).

1.6 Genetic Improvement

This spatial isolation of the crop in India and Africa has led to the appearance of two genetically and morphologically diverse gene pools. However, studies conducted on genetic diversity in African and Indian collections presented much larger variation for inflorescence color in African accessions in comparison to Indian collections. Many studies conducted on the phenotypic evaluation of Indian and African germplasm showed wide variation for inflorescence types in both gene pools. The studies reported that most Indian accessions inflorescence belong to race *vulgaris*, i.e., they have semi-compact to compact ears while varied ear types extending from open to fist-shaped, mostly belonging to two major races *plana* and *compacta* were found in African accessions. Accessions in both the gene pools also vary for many quantitative traits (Naik et al. 1993). More diversity in the African gene pool has been attributed to gene flow from wild species *E. africana* into cultivated finger millet.

Various DNA-based molecular markers have been used to study the genetic diversity of the finger millet gene pool. Both genomic and genic simple sequence repeat (SSR) markers have been used markers for profiling finger millet accessions to study the genetic diversity. Due to the nonavailability of SSRs earlier studies used random amplified polymorphic DNA (RAPD) markers. Most of these studies clustered the finger millet accessions into two major groups, belonging to two distinct gene pools, i.e., African and Indian gene pools. In a study of Indian accessions, DNA markers could clearly classify accessions of North India and southern India. The South Indian accessions were found to be genetically close to African accessions. The results of genetic diversity studies substantiate that accessions of southern India are closer to African genotypes due to their origin from wild species *E. africana*, however, the north and northeast accessions are different and the uniqueness of such gene pool needs to be explored (Panwar et al. 2010a, b).

The introduction and use of African germplasm in India resulted in a higher genetic gain in finger millet breeding. Indo-African crosses in finger millet generated more variability and diverse parents resulted in higher productivity of finger millet, which increased >50% in Karnataka State and around 60 percent in Tamil Nadu State in India (Seetharam 1982; Nagarajan and Raveendran 1983). Blast is the major biotic stress affecting finger millet productivity and the identification of stable sources of resistance is the key to developing resistant genotypes. Screening of diverse germplasm particularly African germplasm has resulted in the identification of stable sources of resistance for the blast in finger millet, which has been used to develop resistant varieties through recombination breeding (Seetharam 1998). To date, more than 30 finger millet varieties have been released in India, where the major breeding objectives were maturity duration, grain yield, fodder yield, and disease resistance. The least emphasis was laid on nutritional quality traits earlier but now the nutritional quality is the integral component of finger millet breeding programs in India and Africa.

References

- Ayyangar GNR (1934) Recent work in the genetics of millets in India. *Madras Agric J* 22:16–26
- Bharathi A (2011) Phenotypic and genotypic diversity of global finger millet (*Eleusine coracana* (L.) Gaertn.) composite collection. PhD thesis, Tamil Nadu Agricultural University, Coimbatore, India
- Bisht MS, Mukai Y (2000) Mapping of rDNA on the chromosomes of *Eleusine* species by fluorescence in situ hybridization. *Genes Genet Syst* 75:343–348
- Bisht MS, Mukai Y (2001) Genomic in situ hybridization identifies genome donor of finger millet (*Eleusine coracana*). *Theor Appl Genet* 102:825–832
- Burkill IH (1935) A dictionary of economic products of Malaya peninsula. Crown Agents of the Colonies, London
- Chandra AK, Chandora R, Sood S, Malhotra N (2020) Global production, demand and supply. In: Singh M, Sood S (eds) Millets and pseudo-cereals-genetic resources and breeding advancements. Woodhead Publishing, Elsevier, pp 7–18

- De Candolle A (1886) Origin of cultivated plants. Hafner Publishing Co., New York
- deWet JMJ, Prasada Rao KE, Brink DG, Mengesha MH (1984) Systematic evolution of *Eleusinecoracana* (Gramineae). *Amer J Bot* 7:550–557
- Dida MM, Wanyera N, Dunn MLH, Bennetzen JL, Devos KM (2008) Population structure and diversity in finger millet (*Eleusine coracana*) germplasm. *Trop Plant Biol* 1:131–141
- Dixit A, Dixit SS, VishnuMittre (1987) The occurrence of *Eleusine africana* Kennedy-O' Byrne in India and its significance in the origin of *Eleusine coracana*. *Proc Indian Acad Sci (plant Science)* 85:1–10
- Dodake SS, Dhonukshe BL (1998) Variability in floral structure and floral biology of finger millet (*Eleusine coracana* (L.) Gaertn.). *Indian J Genet* 58:107–112
- Fuller DQ (2014) Finger millet: origins and development. In: Smith C (ed) *Encyclopedia of global archaeology*. Springer, pp 2783–2785. <https://doi.org/10.1007/978-1-4419-0465-2>
- Gowda BTS (1997) Genetic enhancement and breeding strategies in finger millet (*Eleusine coracana* Gaertn.). In: National seminar on small millets, 23-24 April 1997, Coimbatore, India, pp 16–18 (Extended summaries)
- Gowda MVC, Pushpalatha N, Jhadav SS, Satish RG, Boronayaka MB, Sujay V, Pramila CK, Manasa KG, Gowda J, Ravishankar P, Krishnappa M, Narasimhamurthy DN (2014) PS-1 (IC0598201; INGR14015), a finger millet (*Eleusine coracana*) germplasm with partial sterility, useful in hybridization and easy maintenance. *Indian J Plant Genet Resour* 27(2):192
- Gupta SC, Muza FR, Andrews DJ (1997) Registration of INFM 95001 finger millet genetic male sterile line. *Crop Sci* 37:1409
- Gupta A, Sood S, Agrawal PK, Bhatt JC (2012). Floral biology and pollination system in small millets. *Eur J Plant Sci Biotechnol* 6(2):80–86
- Hilu KW (1981) Taxonomic status of the disputable *Eleusine compressa* (Gramineae). *Kew Bull* 36:559–562
- Hilu KW, De Wet JMJ (1976a) Domestication of *Eleusinecoracana*. *Econ Bot* 30:199–208
- Hilu KW, DeWet JMJ (1976b) Racial evolution of finger millet, *Eleusine coracana*. *Amer J Bot* 63:1311–1318
- Hilu KW, De Wet JMJ, Harlan JR (1979a) Archaeobotanical studies of *Eleusine coracana* ssp. *coracana* (finger millet). *Amer J Bot* 63:330–333
- Hilu KW, deWet JMJ, Harlan JR (1979b) Archaeobotany and the origin of finger millet. *Amer J Bot* 66:330–333
- Hittalmani S, Mahesh, HB, Deepak Shirke M, Biradar H, Uday G, Aruna YR, Lohithaswa HC, Mohanrao A (2017) Genome and Transcriptome sequence of Finger millet (*Eleusine coracana* (L.) Gaertn.) provides insights into drought tolerance and nutraceutical properties. *BMC Genomics* 18:465. <https://doi.org/10.1186/s12864-017-3850-z>
- Hiremath SC, Salimath SS (1991) Quantitative nuclear DNA changes in Eleusine (Gramineae). *Pl Syst Evol* 178:225–233
- Liu Q, Jiang B, Wen J, Peterson PM (2014) Low-copy nuclear gene and McGISH resolves polyploid history of *Eleusine coracana* and morphological character evolution in Eleusine. *Turkish J Bot* 38:1–12
- Liu Q, Triplett JK, Wen J, Peterson PM (2011). Allotetraploid origin and divergence in Eleusine (Chloridoideae, Poaceae): evidence from low-copy nuclear gene phylogenies and a plastid gene chronogram. *Ann Bot-London* 108:1287–1298
- Mysore KS and Baird V (1997) Nuclear DNA content in species of Eleusine (Gramineae): a critical re-evaluation using laser flow cytometry. *Plant Syst Evol* 207:1–11
- Nagarajan C, Raveendran TS (1983) Germplasm mobilization and utilization in finger millet in Tamil Nadu. National Seminar on Finger Millet-Genetics and Breeding, UAS, Bangalore, India
- Naik BJ, Shankare Gowda BT, Seetharam A (1993) Pattern of variability in relation to domestication of finger millet in Africa and India. In: Riley KW, Gupta SC, Seetharam A, Mushonga JN (ed) *Advances in small millets*, Oxford and IBH Publishing Co. Pvt. Ltd. New Delhi, pp 347–364
- Neves SS (2011) Eleusine. C. Kole (ed.), *Wild Crop Relatives: Genomic and Breeding Resources, Millets and Grasses*, Springer-Verlag Berlin Heidelberg, pp 113–133
- Padulosi S, Bhag Mal, BalaRavi S, Gowda J, Gowda KTK, Shanthakumar G, Yenagi N and Dutta M (2009) Food Security and Climate Change: Role of Plant Genetic Resources of Minor Millets. *Indian J Plant Genet Res* 22(1):1–16
- Phillips SM (1972) A survey of the Eleusine Gaertn. (Gramineae) in Africa. *Kew Bull* 27:251–270
- Panwar P, Saini RK, Sharma N, Yadav D, Kumar A (2010a) Efficiency of RAPD, SSR and cytochrome P450 gene based markers in accessing genetic variability amongst finger millet (*Eleusine coracana*) accessions. *Mol Biol Rep.* 37(8):4075–4082. <https://doi.org/10.1007/s11033-010-0067-5>
- Panwar P, Nath M, Yadav VK and Kumar A (2010b) Comparative evaluation of genetic diversity using RAPD, SSR and cytochrome P450 gene based markers with respect to calcium content in finger millet (*Eleusine coracana* L. Gaertn.). *J Genet* 89:121–133. <https://doi.org/10.1007/s12041-010-0052-8>
- Prasada Rao KE, De Wet JMJ, Gopal Reddy V, Mengesha MH (1993) Diversity in the small millets collection at ICRISAT. In: Riley KW, Gupta SC, Seetharam A Mushonga JN (ed) *Advances in Small Millets*, Oxford & IBH Publishing Co, New Delhi, India pp 331–346
- Seetharam A (1982) Finger millet improvement. *Indian Farming* 32(3):3–6
- Seetharam A (1998) Small millets research: achievements during 1947-97. *Indian J Agricul Sci* 68 (8):431–438

- Sood S, Joshi DC, Chandra A, Kumar A (2019) Phenomics and genomics of finger millet: current status and future prospects. *Planta*. <https://doi.org/10.1007/s00425-019-03159-6>
- Sood S, Kant L, Pattanayak A (2017) Finger millet (*Eleusine coracana* (L.) Gaertn.)-A minor crop for sustainable food and nutritional security. *Asian J Chem* 29(4):707–710
- Sood S, Kumar A, Babu BK, Gaur VS, Pandey D, Kant L, Pattanayak A (2016) Gene discovery and advances in finger millet [*Eleusine coracana* (L.) Gaertn.] genomics-an important nutri-cereal of future. *Front Plant Sci* 7:1634. <https://doi.org/10.3389/fpls.2016.01634>.
- Upadhyaya HD, Gowda CLL, Pundir RPS, Reddy VG, Singh S (2006) Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. *Genet Resour Crop Evol* 53:679–685
- Vavilov NI (1951) The origin, variation, immunity and breeding of cultivated plants. The Roland Press Co., New York
- Zhang H, Hall N, Goertzen LR, Chen CY, Peatman E, Patel J and McElroy JS (2019) Transcriptome analysis reveals unique relationships among *Eleusine* species and heritage of *Eleusine coracana*. *G3: Genes Genomes Genetics* 9:2029–2036. <https://doi.org/10.1534/g3.119.400214>



Economic, Nutritional, and Health Importance of Finger Millet

2

Manoj Kumar Tripathi, Anil Kumar,
Debabandhya Mohapatra,
Rajpal S. Jadam, Shilpa S. Selvan,
and C. Nickhil

Abstract

Finger millet (*Eleusine coracana*) is a principal cereal crop in many regions, where low-income people are more. Finger millet grains have predominant differences in color as white, brown, and light brown varieties, great value nutritional compounds, high quantity of phytochemicals molecules, enriched with several amino acids (essential), availability of several crucial minerals compounds, and also gluten-free status. Although the grain is rich in several bioactive and nutritionally valuable compounds, finger millet is enormously ignored and remains extensively underutilized. The biochemical composition of finger millet grains has significant contribution in reducing several human health risks such as metabolic diabetic conditions, high blood pressure, and digestive tract illness. Several traditional processing methods are now available and important for proper uti-

lization of grains, for example, malting, soaking, cooking, fermentation, and popping. The available processing methods play a crucial role in improving the nutritive and organoleptic properties and are also very effective in the reduction of anti-nutritional compounds such as phenols, phytic acids, and tannins in finger millet. Very few studies are available for finger millet utilization and there is an urgent need for further studies on bioactive compounds, improved processing means, nutraceuticals, and product formulations.

2.1 Introduction

Millets are grown as major and significant crops in several regions of the world. Millet crops are recognized as very healthy grain that can be grown on minimal lands with lower water levels. Short growing season under dry- and high-temperature conditions is favorable for their higher productivity. Majority of millet grows and ripens within 70–90 days of the growing period. Millet crops mainly comprise finger millet *Eleusine coracana* (L.), sorghum (*Sorghum bicolor* (L.), kodo millet (*Paspalum scrobiculatum* L.), little millet (*Panicum sumatrense*), foxtail millet (*Setaria italica* (L.), pearl millet *Pennisetum glaucum* (L.), proso millet (*Panicum miliaceum* L.), barnyard millet *Echinochloa colona* (L.) and *Echinochloa crusgalli* (L.). In

M. K. Tripathi (✉) · D. Mohapatra · R. S. Jadam ·
S. S. Selvan · C. Nickhil
ICAR-Central Institute of Agricultural Engineering,
Bhopal MP-462038, India
e-mail: manoj.tripathi1@icar.gov.in

A. Kumar
Rani Lakshmi Bai Central Agricultural University,
Uttar Pradesh, Jhansi, India

the developed world, the importance of millets is not very high. At the present condition, the traditional foods are mainly in use for food purposes and major technologies for the purpose of the development of ready-to-cook foods are inadequate. It is found that millet crops have nutritive and health potential comparable to major cereals and many technologies for processing for food development are also available but the use of millet for food is quite limited to major populations in the world and rural populations at the domestic level. The reasons for this are the lack of some more innovative processing technologies, easy to handle, ready to cook, ready to eat, and safety aspects at commercial levels for populations of urban people. In the current scenario, the novel healthy foods products are recognized if their nutritional status is proper and that will also help in convincing the consumer. Major urban consumers prefer breakfast cereals, pasta, noodles, and baked products like bread and biscuits in food.

Increasing demands for healthy foods populations are concentrated on agriculture practices and the production of such types of crops. Consumption of millet grain will increase if process technologies for processing are accessible commercially in millet-consuming countries. Divergence use of food production may play a major role in encouraging production and consumption. The use of whole multigrain food and multigrain substitute are good options for healthy food and healing dietary alteration. Encouraging consumption of millet grain foods is now in practice to decrease the frequency of several diseases in the urban population.

The use of millet grains for food purposes is important in human history, predominantly in Asia and Africa, and has also been cultivated in East Asia for the past 10,000 years. Millet crops are very reliable crops for drought and infertile soils in comparison to other grain crops. The yield of millet on a per hectare basis can improve greatly by suitable irrigation and justifiable soil supplements. The use of advanced breeds of millet can meaningfully increase farm yield production.

2.2 Economic and Nutritional Importance

Keeping up with ideal worldwide public well-being needs promotion of food involved in health and elongation of aging instead of only prevention of chronic illnesses. Presently, there is a greater advancement in medical and health science but we are also facing problems of negative impacts of medicines and their economic burden. In ancient times, it was a well-known dogma that food is the medicine and medicine is the food which specifies that nutrition and its components play a significant role in grand health welfare (Dev et al. 2011). Therefore, the emergent call for healthy food foodstuffs is encouraging revolution and advance in the global scenario. This direction of research and development is mainly concerned with nutrition and health components are designated as nutraceuticals (Chauhan et al. 2013; Keservani et al. 2010; Dev et al. 2011). Several health information advocate the health benefits of nutraceuticals as avoidance and defence against numerous chronic disorders. Therefore, any important change of nutrients due to inopportune nutritive issues affects the health outcome. Presence of health values, whole-grain cereals can be admired as key nutraceutical applicants for human intake and a better lifestyle. This chapter presents a view of finger millet (*Eleusine coracana*), which have several nutritional and nutraceutical qualities to encounter worldwide nutritional disability.

Finger millet comes from the Poaceae family and is usually famous as ragi or madua in India, dagusa in Ethiopia, and rapoko in South Africa (Ignacimuthu and Ceasar 2012). Worldwide, 12–13% of the total millet-producing area is used in finger millet cultivation in more than 25 countries of Africa and Asia and practiced as a major staple food for individuals living with very restricted economic capital. Finger millet can be cultivated on marginal lands, and high altitudes with drought and saline conditions. It needs slight irrigation with little agricultural support but maintains ideal yields.

Finger millet has been reported as the greatest nutritive among all main cereals (National Research Council 1996) and is also thought of as a potential super cereal by the United States National Academies (National Research Council 1996). In view of nutrition, it is extensively rich in minerals which are greater than some key cereal as wheat and rice (Vadivoo et al. 1998; Antony and Chandra 1998). It is reported to be a great source of calcium in comparison to other cereals such as rice, wheat or maize, and milk. Higher contents of iron and fiber, favor this crop as more nutritive. Finger millet has major important amino acids (essential) such as lysine (McDonough et al. 2000) and methionine. Finger millet is also a rich source of some important polyunsaturated fatty acids, for example, linoleic acid and α -linolenic acid (Fernandez et al. 2003), helpful in the brain and nervous system development (Birch et al. 2007; Jacobson et al. 2008). Finger millet is also a good source of vitamins such as thiamine, riboflavin, niacin, and tocopherols (Obilana et al. 2002).

Cultivation and utilization of finger millet are mainly restricted in developing countries with minor farmers having inadequate agricultural resources and referred to as grain of poor people (National Research Council 1996). Even with established health benefits, only a restricted advancement has been made in use as a functional food. Although it has immense potential as nutritional and therapeutic food, it remained underutilized by the common people due to either unfamiliarity or hesitation.

Presently, the commercialization and marketing strategies of finger millet grain increase its opportunities for yield and formulation of several value-added products. Hence, there is an urgent necessity to advance processing technologies such as steaming, soaking, malting, and fermentation for improving the value of the final products. Divergence of value-added foodstuffs would also improve finger millet commercialization aspects. Its exceptional malting value makes it appropriate as a raw substrate for the brewing industry (Taylor et al. 2006). Truly, promoting and demonstrating finger millet and other millets as a healthy food product with

greater nutrient excellence shall rise its use in populations who are really aware of their health (Shobana et al. 2013). Numerous reports have emphasized the impact of underutilized grain such as finger millet on revenue generation in both national as well as global markets (Chadha and Oluoch 2007). In case of a developing country like India, by value addition to millet assumed nearly increased two- to threefold farmer incomes and created new employment openings, mainly for females (Vijayalakshmi et al. 2010). This is a great opening to grow markets for non-staple crops which may be a source of income in poor populations (Kahane et al. 2013).

2.3 Finger Millet Grains

Grains of finger millet have low glycemic index and gluten-free crops. (Muthamilarasan et al. 2016; Manjula and Visvanathan 2014). Due to low glycemic index properties, finger millet is found to be a good option for populations with conditions of gluten ingestion and diabetic conditions. Finger millets with the presence of low glycemic index grain may be useful in controlling blood glucose levels (Jideani and Jideani 2011). Finger millet grains are rich in dietary fiber, calcium, and iron minerals in comparison to other cereal grains (Sood et al. 2016). The presence of these minerals is found to be useful in the decline of several diseases such as coronary, cardiovascular, obesity, and diabetic conditions (Kaur et al. 2014; Ramashia et al. 2018). In some reports, it was found that grains of finger millet are very rich in polyphenols and phytates compounds which are familiar to affect the accessibility of some important minerals.

2.4 Morphology of Finger Millet

The grains of the major cultivar of finger millet are brown while a very few with white and red color (Ramashia 2018). Finger millet grains differ from approximately 1.0 to 1.5 mm in diameter (Gull et al. 2014; Siwela 2009). The main

structural portions of the finger millet grains are pericarp, germ, and endosperm. The pericarp is an outer layer and contains three layers as epicarp, mesocarp, and endocarp (Ramashia 2018). The pericarp layer is removed during processing as a nonedible part. (Patel and Verma 2015). The endosperm portion is near the seed coat which is utilized in flour making (Palanisamy et al. 2012).

Finger millet is presently used as a significant primary food in various areas of Asia (Gari 2001) as a major functional food. This grain has tremendous potential for boosting food security and rural development and enhances nutritional value (Oduori 2005). Finger millet may play an important role in improving the nutritive and therapeutic features of formulated foods. Millet grain seed is an edible part and a good source of several biochemical components such as phytochemicals, food fibers, polyphenols, and minerals. The presence of essential amino acid, methionine, and several other micro and macronutrients which are not present in poor people's diets make this grain more valuable (Schaafsma 2000).

2.5 Specialty of Finger Millet

Finger millet is presently used as significant primary food in various areas of Asia (Gari 2001) as a major functional food. This grain has tremendous potential for boosting food security, rural development and enhances nutritional value (Oduori 2005). Finger millet may play important role in improving the nutritive and therapeutic features of formulated foods. Millet grain seed is an edible part and a good source of several biochemical components such as phytochemicals, food fibers, polyphenols, and minerals. The presence of essential amino acid, methionine, and several other micro and macronutrients which are not present in poor people's diets make this grain more valuable (Schaafsma 2000).

The soluble dietary fiber present in enough amounts in grains may support in proper regulation of blood glucose and serum cholesterol level (Anderson 1980). It is particularly suggested as healthy food for diabetic persons.

Properly processed and regular use in diets of finger millet is well-known to decrease the threat of diabetic conditions (Gopalan 1981) and gastrointestinal tract illnesses (Tovey 1994). Many health-promoting roles was reported in finger millet which evidences its use as nutraceutical food, nutritive, feed, cultural, and medicinal in industrial and economic prospective. It is also reported as a wonder grain because it has a wide variety of range, abiotic stress tolerant, higher storage, and very rich in nutraceutical compounds.

2.6 Nutritive Value

Finger millet grains contain major nutrients which are essential for human use. Grains are extensively rich in protein, dietary fiber, minerals, and some anti-nutritional compounds such as phytates and phenolic compounds. Several studies suggest that finger millet has a decent quantity of beneficial compounds as dietary fibers which is healthy for digestion. Finger millet grains have a very low amount of fat that is appropriate for dietary sources. Finger millet is the best source of some important minerals like calcium, phosphorus, potassium, sodium, etc., and vitamin B complex. Millets also have significant amounts of essential amino acids specifically rich in sulfur. Finger millet grain is also known for amino acids arginine, histidine, lysine, tryptophan, phenylalanine, tyrosine and methionine.

Finger millet grains are also utilized as a whole which is simply consumable with good flavor (Thapliyal and Singh 2015). Finger millet can be served as good source of vitamins and fatty acids (Rurinda et al. 2014). Important health aid of the grains is low discharge of glucose molecules during digestion into the bloodstream (Chappalwar et al. 2013; Mamatha and Begum 2013), which reduces the demand for glucose frequently and reduces constipation (Vanithasri et al. 2012). Millet grains are also linked with lowering the threat of diabetes, effective in blood pressure, cholesterol control, cancer, and cardiovascular diseases (Pradeep and Sreerama 2015; Subastri et al. 2015) (Table 2.1) (Asharani et al. 2010).

Table 2.1 Some important compounds of finger millet grains associated with health (Chandra et al. 2018; Sarita and Singh 2016; Thilagavathi et al. 2015)

Compounds	Biological functions
Phytic acid	Lowering body cholesterol
Phenolic and Tannin compounds	Role in healing and metabolic aging conditions Useful in several cancer and cardiovascular conditions Effective in blood pressure and diabetes
Ferulic acid	In tissue repair Encourage wound curing
Dietary fiber	Help in hypoglycemic and hypolipidemic conditions Effective in serum cholesterol control Effective in atherosclerosis Anti-cancerous properties
Magnesium	As cofactor for enzyme systems Blood glucose control, Blood pressure regulation
Phosphorus	Formation of bones and teeth Body growth and maintenance Repair of cells and tissues

2.6.1 Mineral, Vitamin, and Fatty Acid Content

Finger millet grains are rich in essential minerals, for example, calcium (Ca) and phosphorus (P) and play significant roles in children's development and pregnancy condition (Jideani 2012; Chappalwar et al. 2013). Their role is also very important in obesity, diabetes, and malnutrition (Jayasinghe et al. 2013; Manjula et al. 2015). Regular consumption of finger millet can be very effective for calcium deficiency (Towo et al. 2006). Phosphorus, whose concentration varies from 130.0 to 283.0 mg/g, is also one of the important minerals found in finger millet grains which contribute to the energy metabolic

pathway and tissue repairing in the human body (Vanithasri et al. 2012; Ramashia et al. 2018). Some other important minerals present in finger millet grains are iron (3–20%) (Shukla and Srivastava 2014; Rajiv et al. 2011) and magnesium. Both the minerals play a role in the control of blood pressure, asthma, and heart attack (Saleh et al. 2013; Verma and Patel 2013; Prashantha and Muralikrishna 2014). Several reports indicate that finger millet grains have more nutritive value than other millets (Devi et al. 2014; Dlamini and Siwela 2015) (Table 2.2).

Vitamins are also one of the important micronutrient components essential for proper growth and maintenance of the human body and deficiency of vitamins may cause several

Table 2.2 Nutritional composition (proximate and minerals) of finger millet (Dlamini and Siwela 2015; Devi et al. 2014)

Finger millet	Proximate composition (%)					
	Moisture	Carbohydrates	Dietary fiber	Fat	Protein	Minerals
	7.15–13.1	75.0–83.3	15–22.0	1.8	7.7	2.7
	Common minerals composition (mg/100 g)					
	Phosphorus	Potassium	Magnesium	Calcium	Sodium	Iron
	130–250.0	430–490	78–201	398.0	49.0	3.3–14.89

Table 2.3 Major vitamin content and fatty acids of finger millet (Ramashia 2018; Saleh et al. 2013; Ramashia 2018; Serna-Saldivar 2010)

Finger millet	Vitamins composition (mg/100 g)				
	Vit A (Retinol)	Vit B ₁ (Thiamine)	Vit B ₂ (Riboflavin)	Niacin	Vit C (Ascorbic acid)
	–	0.2–0.48	0.12	1.0–1.30	0.0–1.0
	Fatty acid compositions (g/100 g of total fats)				
	Palmitic acid	Linoleic acid	Oleic acid	Linolenic acid	
	21.1–24.7	24.2	49.8	1.3–4.40	

deficiencies diseases. Finger millet grains contain a good amount of water-soluble vitamins and fat specifically vitamins A and B complex (Table 2.3) (Devi et al. 2014; Chappalwar et al. 2013).

Grains of finger millet also comprise several major essential fatty acids such as linolenic and palmitic acids, which are critical in the improvement of the brain and nerves (Kunyanga et al. 2013; Muthamilarasan et al. 2016). There are very low contents of fatty acids, which have a better shelf life and are helpful in body weight management (Gunashree et al. 2014; Singh et al. 2012; Verma and Patel 2013). Low content of fat and dietary fiber with higher amounts of carbohydrates in finger millet are important for nutritive and physiological aids (Vanithasri et al. 2012; Banusha and Vasantharuba 2013).

2.6.2 Amino Acids Content

Finger millet is very rich in some important essential amino acids. A good amount of approximately 44% of essential amino acids are found in finger millet grains, which mainly include methionine, cysteine and tryptophan, lysine, isoleucine, leucine and phenylalanine, and threonine (Singh and Raghuvanshi 2012; Ramashia et al. 2018; Sood et al. 2017). These components also work in nutrition as well as health aspects (Thapliyal and Singh 2015). The amount of amino acid methionine was reported to be higher than any millet source (Prashantha and Muralikrishna 2014; Singh et al. 2012).

2.6.3 Anti-nutritional Composition of Finger Millet

Some important anti-nutritional compounds reported in Finger millets are phytate, tannins, trypsin inhibitors, and flavonoids. These anti-nutritional compounds are reported to reduce the nutritional properties of finger millet grains (Palanisamy et al. 2012). The major polyphenolic compounds of finger millet are phenolic acids and tannins and the quantity of flavonoids is reported as minor components. The presence of polyphenolic compounds is responsible to keep a good body's immune system against pathogens and clinical conditions (Udeh et al. 2017; Siwela et al. 2007; Devi et al. 2014). Tannins present in the outer layer of finger millet grains function as a physical barrier against fungal pathogens attack (Devi et al. 2014) and are also reported as an important role in several biological functions. A negative impact was reported in case of some anti-nutritional compounds, which are concentrated in finger millet and this compound reduces the digestibility of some nutrient compounds and the absorption of some important minerals.

Tannin compounds are also reported to affect growth due to their adverse impact on the function of some important body organs such as the pancreas, thyroid gland, and liver. These tannin compounds also influence the color, flavor, and nutritional quality of food products developed from finger millet grains. Tannin compounds were also reported for antioxidant activity and help in aging and the avoidance of some important metabolic diseases (Shibairo et al.