Chapter 14
Finger Millet (*Eleusine coracana* (L.) Gaertn.) Genetics and Breeding for Rapid Genetic Gains

S. Ramesh and T. V. Krishna

14.1 Introduction

Finger millet, commonly known as ragi/African millet, is one of the most ancient crops in the world. It belongs to family Poaceae. It is being cultivated in the arid and semi-arid tropics of Africa and Asia as a food and fodder crop. It is predominantly a rain-fed crop and sometimes it is cultivated under irrigation. It is a low water requirement crop and thus can grow well with a minimum rainfall between 300 and 400 mm. But it stands even up to 1500 mm. In India, it is generally cultivated as a rainy season crop. It is a tall growing herbaceous plant with a tough and robust root growth that enables it to endure and sustain extremely low levels of soil moisture. It supports millions of people living in relatively dry regions of Africa and Asia. Its stover makes an excellent fodder for livestock, especially for draught animals.

14.2 Nomenclature

Its nomenclature evokes much interest as it rings out religio-linguous overtones. Its generic name *Eleusine* is said to have been derived from Greek Goddess of cereals (Chalam and Venkateswarlu 1965). Burkil (1935) opined that it could have been named after Greek town *Eleusi-ne*. As for its specific name, it has been taken from its Ceylonese (Sri Lankan) name Kurukkan. The name finger millet could be obviously from the shape of its earhead, which resembles human palm and the fingers. The name African millet represents its African origin. But 'ragi' which is the common name of finger millet in southern parts of India is colloquial transformation of its Sanskrit name *Rajika*. Incidentally, Sanskrit was

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the widely prevailing lingua franca in ancient India during the period when ragi was acquiring agricultural significance in India.

14.3 Economic Importance

Grains are brick-red in color but some genotypes have white- to peach-colored grains. Grains are tasty, ground into powder (flour), and made into a number of products. Traditionally, foods like porridge (Uji), stiff porridge (Ugali), and local brew Busaa are made for general consumption in Africa. However, in India, the main dishes made are Mudde (dumplings), roti (leaven bread), and porridge (Vaidehi 1986). It is a high-quality energy food and its impact on human health is immense, particularly of working class. Ragi is regarded as a healthy food too. Most important and highly appreciated quality of ragi grain is its low glycemic index and absence of gluten in the grain that makes an ideal food for diabetic patients or those prone to diabetics, a deadly degenerative malady (Vaidehi 1986). Further, due to low protein efficiency ratio value, it is an antidote for obesity. The grain are rich in essential amino acids like methionine and lysine, which are difficult to find generally in grain-based foods (Devos 2005). These qualities might have triggered the awareness about the virtues of ragi and, accordingly, encouraged many countries to plan to include ragi in their diet and cropping systems in recent years. Further, Newman (2005) appreciated its great potential to become a specialty grain for food industry worldwide. Additionally, it is going to be a boon for the people living on subsistence economy in ecologically harsher and imbalanced dry farming zones.

14.4 Origin

Its nativity drew considerable attention and long and lengthy debates and now it is finally settled in favor of Ethiopian Highlands and from where it had moved further down to South Africa and then to India, around 3000–4000 BC (Hilu et al. 1979). But there were no empirical evidences as to when exactly it had entered India. However, Professor Sir J.B. Hutchinson in one of his books, *Essays on Crop Plant Evolution*, published in 1965, had mentioned that a few grains of finger millet along with one of its putative diploid progenitor, viz., *Eleusine indica*, were found in the charred debris in one of the Neolithic sites in Mysore district of Karnataka, India. The approximate age of these grains was reported to have been dated back to 1800 BC. Similar findings in Ethiopia were dated to third millennium BC (Hilu et al. 1979). This unequivocally established the fact that it is of African origin and from where it could have spread over to India later.

Further, for a number of years, it was considered that *Eleusine indica* was a putative parent of *Eleusine coracana*. The fact that *Eleusine indica* was discovered along with *Eleusine coracana* in the debris of excavation dating back to 1800 BC at

Neolithic sites in Mysore district of Karnataka, India, gave an impetus to the claim that it could have been native of India and *Eleusine indica* could have been a probable progenitor of *Eleusine coracana* (Hutchinson 1965). Subsequent cytological and morphological studies, however, elucidated that *Eleusine coracana* could have originated directly from *Eleusine africana* through selection and domestication of a large grain mutant (Hilu and de Wet 1976a, b). This strengthened the speculation and affirmed that it was a native of Africa. It was further confirmed from the findings of archaeological excavation in Ethiopia dating back to three millennium BC (Hilu et al. 1979). It is now an established fact that *Eleusine coracana* has an African origin. *Eleusine indica*, a diploid species with $2n = 18$ chromosomes, is one of the progenitors and the identity of the other donor of the tetraploid *Eleusine coracana* ($2n = 4x = 36$) is still in the realm of guessing.

Yet another evidence in favor of African origin had stemmed from the fact that *E. coracana*, a tetraploid with $2n = 36$ chromosomes, generally cultivated in India, had cytological and morphological features, which suggested that it was genetically conspecific to another tetraploid species *Eleusine africana* Kennedy O'Byrne with $2n = 36$ chromosomes, mostly found in Africa (Chennaveeriah and Hiremath 1974; Hilu and de Wet 1976a, b). Additionally, they observed that gene flow occurred freely between these two species. From this, they deduced that *Eleusine coracana* might have originated directly from *Eleusine africana*, possibly as a mutant, and subsequently selected for its larger grain size and then cultivated as finger millet, which are of two types: (1) African highland race, and (2) Afro-Asiatic lowland race. Hilu and de Wet (1976b) proposed that the African highland race was derived from *E. africana* and this then gave rise to African lowland race, which was then introduced to India. However, more authentic or clinching evidence that it was from East African origin came from the archaeological finding of finger millet in Ethiopia by Hilu et al. (1979), in which the finger millet-like grains were found in the debris, which were dated back to 3000 BC. Moreover, evidence for more ancient nature of *E. coracana* in India was derived from the archaeological finding of *Eleusine coracana* together with *Eleusine indica* near Halaguru, Mysore district of Karnataka, India, which were dated back to 1800 BC (Hutchinson 1965). Now both the races are designated as *Eleusine coracana*, subspecies *coracana*, and *Eleusine coracana*, subspecies *africana* (Acheampong et al. 1974–84).

14.5 Distribution

By virtue of its outstanding food and agricultural characteristics together with excellent nutraceutical properties, finger millet has spread to many countries in the world. Presently, it is found in almost all the eastern and southern African nations such as Kenya, Uganda, Zimbabwe, Tanzania, Rwanda, Zaire, and South Africa, besides Ethiopia. In Asia, India is the major ragi-growing country in the world. Besides, Nepal is slowly emerging as an important ragi-growing country. Malaysia, Indonesia, Japan, and China also figure in the ragi map of world. Recent reports

have alluded to the fact that it has made a beginning in the United States of America too. But presently, the grain is mostly used as bird feed. In India, its distribution is practically all over the country. Even in temperate Himalayas, it is being grown up to the elevation of 2300 m. But its concentration is in the states of Karnataka, Andhra Pradesh, Tamil Nadu, Maharashtra, Odisha, Jharkhand, and so on. Karnataka maintains the largest acreage and is a leading state in production.

14.6 Botany

Eleusine is a small genus comprising only 11 species. The chromosome numbers in the genus range from 18 to 45. Since there has been no reported species with less than 18 diploid chromosomes, it was proposed that its basic chromosome number could be $x = 9$. On this premise, 11 species in the genus are classified into diploids ($2n = 18$), tetraploids ($2n = 4x = 36$), and pentaploids ($2n = 5x = 45$). The diploids are *Eleusine obligostachya* Lam, *Eleusine coracana* (*Linn*), and *Eleusine verticillata* Roxb. The only pentaploid with 45 chromosomes is *Eleusine flagellifera.* It is apparent now that the species differentiation in the genus is based on the multiples of the basic chromosome number $x = 9$. Thus, there are altogether six diploids, four tetraploids, and one pentaploid.

Of all these species, *Eleusine coracana* is the only one that acquired agricultural significance both in Africa and India. It is a tall, annually growing herbaceous with a height of a meter or so, ending with an inflorescence called umbel or panicle, having finger-like spikes—and hence also called finger millet. Its growth habit is decumbent/erect/prostrate. Its stem is compressed with nodes, and thickness varies from 0.4 to 10.3 mm. It tillers profusely and they arise from the base of the plant (collar region). They vary from one to ten per plant, but not all of them are productive. Number of leaves varies according to height of the plant. They are long and linear with a prominent midrib, which tapers into an acuminate tip. They are generally glabrous and often found with ciliate margins. They are attached to the stem through a sheath, which firmly clasps the stem right from the internode. In addition to normal leaves, there is a flag leaf, arising from the lost internode, just below the thumb (odd) finger, which is situated a few millimeters or a centimeter down from the base of the panicle or earhead. The main stem and tillers end up in earhead, which consist of finger-like spikes. The earhead is borne on the peduncle whose length varies from 11.5 to 59.5 mm and width ranging from 11.9 to 15.56 mm. Number of fingers varies from four to five and sometimes even more. Little below the main fingers, generally, there is another finger, which is known as thumb finger. The shape and size of earhead vary. They are small, intermediate, and large. They are open or fist-like, the later due to incurved and compact fingers. Fingers consist of spikelets and are crowded into two overlapping rows on either side of the rachis. Each spikelet contains four to five flowers (florets). Flowers are bigger at the base than at the median line. There is a keel with short, stiff hairs. The florets are hermaphrodite, except the terminal florets. There

are three stamens with short anthers and long filaments; the lobes of anthers dehisce longitudinally; gynoecium is bicarpellary, unilocular, and with superior ovary. There are two broad and truncated lodicules that are present at the base of the ovary. The obovate ovary possesses a distinct style and plumose stigma. The florets open in basipetal successions in the spikelets (Umashankar and Setty 1977). Umashankar and Setty (1977) and Dodake and Dhonukshe (1998) observed that anthers dehisce around 3.00 am and pollination takes place immediately thereafter; though self-pollination is normally expected, some amount of outcrossing is also observed. However, the latter is genotype-specific (Fakrudin et al. 1998).

Seed is an achene. The seeds vary in color and shape. Seeds are covered by the glumes, but there are variations: exposed, partially covered, and completely covered. Partially covering categories are more frequent. There are differences in the grain color: white, light brown, copper brown, and purple brown. Copper brown types are more frequent (brick-red). Grains differ in shapes: round, reniform, and ovoid. Round-shaped grains are more frequent. Grain surface is either smooth or wrinkled; the former is more predominant.

14.7 Cytogenetics

*Eleusine coracana*hasattracted a great deal of attention, both in terms of origin and evolutionary points of view. There was a general perception that *Eleusine coracana* was a tetraploid form of diploid *Eleusine indica*, a grassy weed, ubiquitous in its distribution, endowed with diploid chromosome number of $2n = 18$ (Krishnaswamy 1951; Mehra 1963). Kempanna et al. (1976), however, carried out detailed karyomorphological studies of both the species, that is, *E. coracana* and *E. indica*, and compared them. The chromosomes of *E. coracana* (Table 14.1) were longer than those of *E. indica* (Table 14.2). Further, while *E. coracana* consisted of two satellite chromosomes (Fig. 14.1), *E. indica* consisted of only one satellite chromosome (Fig. 14.2). However, in both the species the satellite chromosomes were longer than those of others.

Further, Nayar et al. (1978) investigated karyotype of five diploid species (*Eleusine trystachya*; *Eleusine jaegeri*; *Eleusine floccifolia*; *Eleusine boronensis*; *E. indica*) and two tetraploid species (*E. africana*; *E. coracana*). While the three diploid species (*E. trystachya*; *E. jaegeri*; *E. floccifolia*) had two satellite pairs each, *E. boronensis* had two satellite pairs. Among tetraploids, *E. coracana* had two satellite pairs while *E. africana* had six satellite chromosomes. One of the satellite pair was longest in *E. coracana.* Further, karyotypes of four (*E. trystachya*; *E. jaegeri*; *E. floccifolia*; *E. indica*) out of five diploids were asymmetrical whereas those of *E. boronensis* were symmetrical. Among the five diploids, the total chromatin length was shortest in *E. indica*; it was longest in *E. trystachya*. Among the two tetraploids, the total chromatin length was shortest in *E. africana* (Table 14.3). All the diploids, except *E. indica*, were closely related to each other.

Table 14.1 Karyotype of *Eleusine coracana*

Chromosome number	Length (μm)	Arm ratio (μm)
1	3.090 ± 0.0203 satellite	1.1074 ± 0.0054
2	2.975 ± 0.0465 satellite	1.1071 ± 0.0063
3	2.890 ± 0.0663 special chromosome	1.1053 ± 0.0017
4	2.695 ± 0.0298	1.1026 ± 0.0017
5	2.630 ± 0.0289	1.1007 ± 0.0012
6	2.530 ± 0.0289	1.1083 ± 0.0014
7	2.489 ± 0.0416	1.1049 ± 0.0012
8	2.435 ± 0.0215	1.1029 ± 0.0010
9	2.390 ± 0.0340	1.1016 ± 0.0013
10	2.350 ± 0.0419	1.1061 ± 0.0013
11	2.290 ± 0.0419	1.1044 ± 0.0013
12	2.215 ± 0.0379	1.1036 ± 0.0014
13	2.200 ± 0.0368	1.1037 ± 0.0013
14	2.110 ± 0.0189	1.1089 ± 0.0009
15	2.050 ± 0.0275	1.1085 ± 0.0016
16	2.005 ± 0.0025	1.1005 ± 0.0005
17	2.000 ± 0.0000	1.000 ± 0.0000
18	1.900 ± 0.0000	1.111 ± 0.0000

Source: Kempanna et al. (1976)

Table 14.2 Karyotype of *Eleusine indica*

Chromosome number	Length (μm)	Arm ratio (μm)
1	2.85 ± 0.0055 satellite	1.1025 ± 0.0008
2	2.189 ± 0.006 special chromosome	1.3222 ± 0.0072
3	2.19 ± 0.0068 special chromosome	1.1046 ± 0.001
4	2.13 ± 0.0067	1.1057 ± 0.0013
5	2.07 ± 0.0057	1.1047 ± 0.0014
6	2.03 ± 0.0055	1.1061 ± 0.0081
7	1.96 ± 0.0065	1.1057 ± 0.0014
8	1.885 ± 0.0055	1.1060 ± 0.0015
9	1.73 ± 1.1059	1.1059 ± 0.0015

14.8 Genetic Resources

Genetic resources are the wealth/treasure for continuous genetic improvement of economically important crops to cater to the needs of present and future generations. Considering the importance of finger millet for food security, especially in production systems with frequent drought spells, concerted efforts have led to collection and conservation of a large number of germplasm accessions at different institutes/universities (Table 14.4).

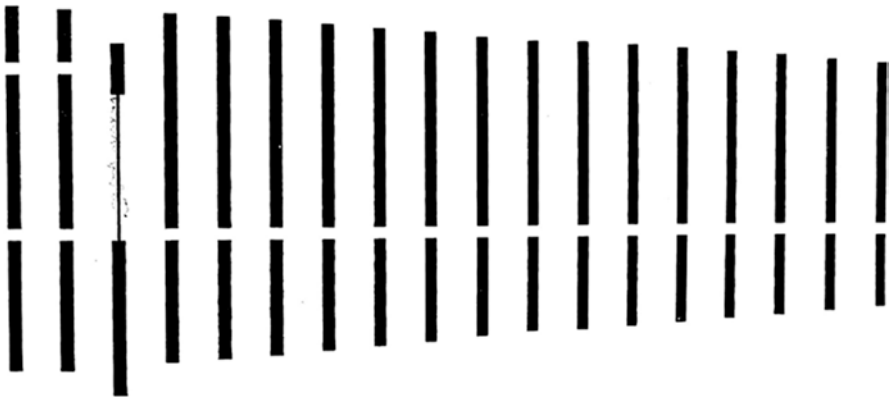

Fig. 14.1 Ideogram showing the average length and arm ratio of the 18 pairs of chromosomes in *Eleusine indica*

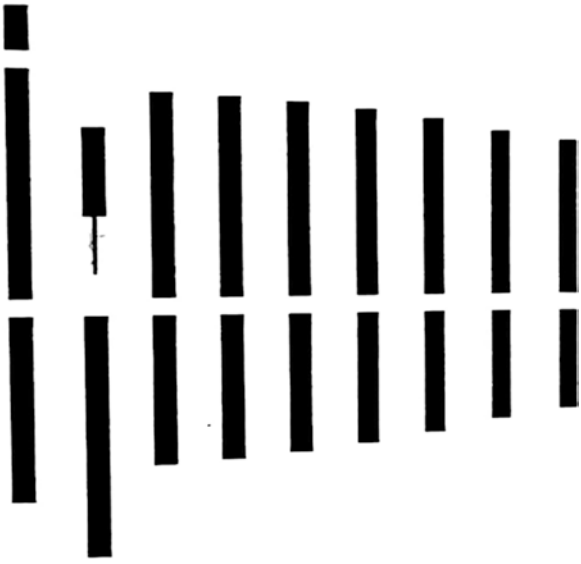

Fig. 14.2 Ideogram showing the length and arm ratio of nine pairs of *Eleusine indica*

The largest collection of finger millet genetic resources is held in institutes located in India, for example, National Bureau of Plant Genetic Resources (NBPGR), New Delhi, International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Patancheru, and University of Agricultural Sciences (UAS), Bengaluru. Several researchers have attempted to evaluate and characterize fairly large numbers of germplasm accessions. For example, Kempanna and Tirumalachar (1968), Mallanna et al. (1978), and Bhaskariah and Mallanna (1997) evaluated 619, 925, and 1064 *E. coracana* accessions, respectively, in various years. They reported considerable

Table 14.3 Comparison of karyotypes of five diploids and two tetraploid species of *Eleusine*

Sl. no.	Name of the species	Ploidy level	Type of karyotype	Length of chromosomal range (μm)	Total chromatin length (μm)
1	*Eleusine trystachya*	Diploid	5 M + 4 SM	2.40–3.40	51.12
2	*Eleusine jaegeri*		4 M + 5 SM	1.92–3.30	46.74
3	*Eleusine floccifolia*		4 M + 5 SM	2.25–2.76	44.88
4	*Eleusine boronensis*		3 M + 6 SM	2.32–3.60	48.24
5	*Eleusine indica*		2 M + 7 SM	1.40–2.36	29.12
6	*Eleusine coracana*	Tetraploid	12 M + 6 SM	1.80–3.48	81.00
7	*Eleusine africana*		8 M + 10 SM	0.88–2.84	68.00

Source: Nayar et al. (1978)
M median centric, *SM* sub-median centric

Table 14.4 Significant germplasm collections of finger millet

Sl. no.	Institution	Headquarters	Number of accessions
1	National Bureau of Plant Genetic Resources (NBPGR)	New Delhi, India	9522
2	International Crops Research Institute for Semi-Arid Tropics (ICRISAT)	Patancheru, India	6804
3	All India Coordinated Minor Millet Project (AICMMP)	University of Agricultural Sciences (UAS) Bengaluru, India	6257
4	Kenya Agricultural Research Institute (KARI)	Muguga, Kenya	2875
5	Institute of Biodiversity Conservation (IBC)	Addis Ababa, Ethiopia	2156
6	USDA Agricultural Research Service (USDA-ARS)	Griffin, USA	1452
7	Serere Agricultural and Animal Production Research Institute (SAARI)	Soroti, Uganda	1231
8	SADC Plant Genetic Resource Centre	Lusaka, Zambia	1037
9	Central Plant Breeding and Biotechnology Division, Nepal Agricultural Research Council (CPBBD)	Kathmandu, Nepal	869
10	National Center for Genetic Resources Preservation	Fort Collins, USA	702
11	National Institute of Agrobiological Sciences (NIAS)	Kannondai, Japan	565
12	Mt. Makulu Central Research Station	Chilanga, Zambia	390
13	Institute of Crop Germplasm Resources, Chinese Academy of Agricultural Sciences (ICGR-CAAS)	Beijing, China	300

Source: Goron and Raizada (2015); Dwivedi et al. (2012)

variability in both qualitative and quantitative traits. There have been several other numerous efforts to evaluate the germplasm accessions, but with limited numbers. In an effort to broaden the genetic base of finger millet cultivars, Gowda and Sheriff (1986) generated variability from inter-species (*E. coracana* × *E. africana*) crosses and reported significant variability in most of the economically important traits. The natural variability that existed among the accessions has been exploited to identify high-yielding cultivars as a short-term strategy to cater to immediate needs of the farmers.

Considering that the genetic resources held at NBPGR, New Delhi, ICRISAT, Patancheru, and UAS, Bengaluru, are unwieldy for precise characterization and evaluation and that there is possibility of occurrence of duplicates due to repeated sampling of same accession and/or assigning different names/identity to the same accession, core sets consisting of varying numbers of accessions have been developed. A team of scientists under the leadership of Dr. A. Seetharam, Former Project Coordinator of All India Coordinated Small Millets Improvement Project (AICSMIP), University of Agricultural Sciences (UAS), Bengaluru, India, developed a core set of 551 accessions based on phenotypic evaluation of global collection of 5669 accessions during 1996–2005 in India at four locations, namely Almora (in the Himalayas), Ranchi (North India), and Vizianagaram and Bengaluru (in the Deccan plateau region). This core set comprised the accessions originating from ten countries representing Africa (primary center of diversity), the Indian subcontinent (secondary center of diversity), and others (Table 14.5; Seetharam et al. 2005).

The core set of accessions have been deposited at the National Active Germplasm Site, AICSMIP, Bengaluru, India. Subsequently, Upadhyaya et al. (2006) also developed a core set of 622 accessions from a total of 5940 accessions held at International Crops Research Institute for Semi-Arid Tropics (ICRISAT), Hyderabad, India, based on 14 quantitative traits. Newman (2005) of Plant Genetic

Table 14.5 Country representation of core set of finger millet germplasm accessions

Country	No. of accessions
India	379
Malawi	55
Kenya	48
Uganda	24
Zambia	12
Zimbabwe	07
Tanzania	04
Sri Lanka	03
Japan	03
Others	14

Resource Conservation Unit at Griffin, USA, developed yet another core set of 80 accessions, representing over 90% variability in the base collection of 700 accessions. The core set is suggested for evaluation across target production environments and years to identify widely/specifically adapted and stable accessions to foster enhanced access and use of finger millet germplasm in cultivar development. The core sets are considered as first-look sources of genetic resources for use in crop improvement programs. The availability of core sets is expected to result in enhanced utilization of genetic resources in crop breeding programs, which is the key to develop cultivars with broad genetic base, which contribute to sustainable production of finger millet.

14.9 Genetics

14.9.1 Qualitative Traits

Several researchers have reported the number and mode of action of genes controlling easily observable/assayable and highly heritable traits such as stem, earhead, and grain color. These traits are controlled by one to three genes (Table 14.6).

These traits could be used as diagnostic markers of germplasm accessions for maintaining their identity and purity. They help minimize duplication and avoid mistakes in labeling the germplasm accessions and thereby enable their easy retrieval from the collection. They can also be used in detecting true hybrids considering that developing hybrids in finger millet is tedious owing to tiny florets. They

Table 14.6 Genetics of qualitative traits in finger millet

Trait	Number of genes	Mode of action	Reference
Plant pigmentation: purple/green	One	Purple is dominant over green	Ravikumar and Seetharam (1990)
Length of rachis	Two dominant genes: E_1 and E_2	Complementary epistasis	Vijayaraghavan and Warier (1949)
Earhead color (purple vs. green)	One with two alleles P and p	Purple dominant over green; P > p	Ayyangar and Warier (1933)
Glume cover: complete/partial	Three genes	Complementary epistasis	Ayyangar and Warier (1931)
Grain color: purple/green; brown/green	Two genes	Purple and brown colors are dominant over green; duplicate dominant	Shanthakumar and Gowda (1998)
Genetic male sterility (GMS)	One	Fertility is dominant over sterility	Gupta et al. (1997)

are found useful in conducting Distinctness (D), Uniformity (U), and Stability (S) test, a mandatory requirement for protecting varieties under Protection of Plant Varieties and Farmers' Rights (PPV&FR) Act of India and such other similar Acts that are in vogue in other countries.

14.9.2 Quantitative Traits

Owing to the difficulty in effecting crosses, attempts to investigate genetics of quantitative traits are limited. Review of a few such studies (Sumathi et al. 2005; Gurunathan et al. 2006; Gupta and Kumar 2009; Shailaja et al. 2009) has indicated that most of the economically important traits such as grain yield and its components are controlled by genes with predominantly dominant mode of action.

14.10 Breeding

Major efforts to breed finger millet were concentrated in India. Breeding finger millet in Africa is rather limited. Breeding is predominantly focused on improving grain yield and its components and resistance to blast disease.

14.10.1 Breeding for Productivity Per Se Traits in India

Tyagi and Rawat (1989) bred two varieties, Pant Mandu 3 and PES 110, in Uttarkhand state of India in the Himalayas. Both were tolerant to leaf, finger, and neck blasts. The former matured in 95 days. It was 80–85 cm tall with compact and curved spikes and the seed was light brown in color. The variety PES 110 matured in 115–120 days, and had medium-sized top. First-ever attempt on breeding finger millet was initiated by Dr. Leslie C. Coleman in the then Mysore state (now Karnataka) in India by about 1900 AD. He made several collections of finger millet accessions from Mysore and Madras province (now Tamil Nadu) in South India and quantified variability in farmer-preferred traits at Hebbal, Bengaluru, India. From this initial attempt, he identified seven different types based on earhead shape and color. A few of them produced long and open earheads with green color, while others produced small, closed, compact purple-pigmented earheads. This study led him to isolate a high-yielding genotype from locally cultivated, nondescript variety "Madayyanagiri." It was a tall, purple-pigmented variety having a better yield structure than its parental stock and was found suitable for dryland cultivation. It was released in the state of Mysore in 1922 (Coleman 1922). It had remained as a variety

for a pretty long time. At the same time, Tamil Nadu developed and released two varieties CO 1 and CO 10, which combined good yields with better protein content.

These were all pure-line selections from the landraces. Hybridization was difficult with the crop as the florets in the spikes were small and embedded in the densely crowded spikelets. To overcome this difficulty, Ramaswamy et al. (1994) suggested "contact method of hybridization." In this method, earheads of the two selected varieties are tied together and covered with grease-proof paper bags. Subsequently, seeds are collected from the earheads after they mature, seedlings from such seeds are raised, and plants harboring traits from both the parents are selected as true hybrids. A few popular varieties like Purna, Annapurna, and Cauvery were identified through pedigree selection from segregating populations derived from crosses developed using contact method of hybridization at Mandya Centre in India. While the variety "Cauvery" was suitable for dryland ecosystem, "Purna" and "Annapurna" were suitable for both dry and irrigated ecosystems. Following the "contact method of hybridization," the first-ever Indo-African variety HR 374 was developed, which was a cross between EC 4840 and HES 927 (now IE 927). This was a very high yielder. It was released for cultivation in Karnataka in 1997. Another variety, HR 911, a cross between UAS 1 and IE 927, was adaptable to both rainy (June–October/November) and summer (February–May) seasons and was released for cultivation during 1985 (Gowda and Sheriff 1986). These "Indaf" series varieties had a very high yield potential and replaced almost all the earlier released varieties. These varieties brought a paradigm shift in ragi production scenario in India.

At Mandya Centre, a regional research station of UAS, Bengaluru, Lakshmanaiah in 1970s and 1980s extensively used exotic accessions, IE 927, IE 929, and IE 980 R, and developed a series of Indaf (Indian × African accessions) varieties (Indaf 1–9) with high-yielding ability (Fig. 14.3). Indaf 1 was more suitable for kharif season and Indaf 5 for summer season, and Indaf 9 was good for late rainy season. Subsequently, Indaf 1 and Indaf 5 were replaced by a better variety Indaf 8. Indaf 7 was released for postrainy season. Gowda and Sheriff (1986) developed another variety from a cross between PR 209 and IE 927, which had high yield potential in respect of both grain and stover, besides tolerance to drought and lodging. It was released for transitional zone in southern Karnataka. To improve grain quality with high protein, a variety "Hamsa" was crossed with brown-seeded variety IE 927 and developed Indaf 11 with better protein quality. In extensive field trials for 3 years during 1981 through 1984, three new varieties, HR 911, Indaf 8, and Indaf 5, were developed. Gowda et al. (1999) developed a variety HR 391, which was suitable for rain-fed cultivation in dry belt of southern Karnataka. It matured in 118–120 days. Gowda et al. (1999) developed a dual-purpose variety MR 2 for Southern Transition belt of Karnataka. It was a hybrid derivative of PR 202 × IE 927, developed at Mandya Centre. It had superior grain yield together with tolerance to drought and lodging. Of late, germplasm unit (GPU)series of varieties (Fig. 14.4) such as GPU 28, GPU 45, GPU 48, GPU 66, and GPU 67 has been developed and released for commercial production. Sundareshan and Prasad (1983) reported a variety CO 12, which was a selection

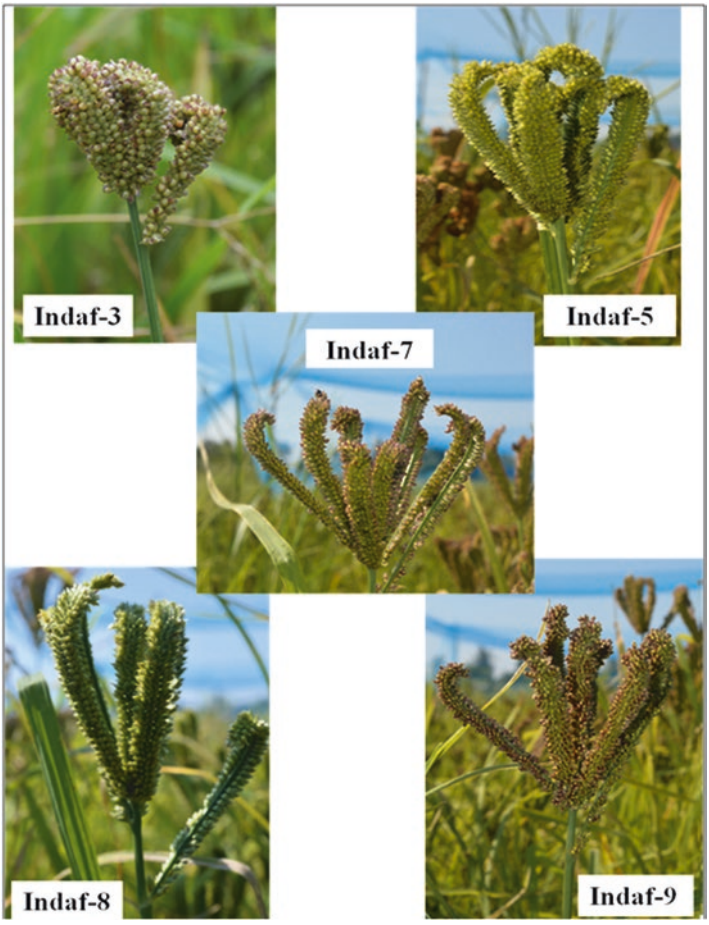

Fig. 14.3 Photographs of panicles of Indaf series finger millet varieties derived from Indian × African germplasm crosses

having medium duration and matured in 85–100 days. It was suitable for Tamil Nadu in India. It was developed at Directorate of Wheat Research at Karnal in Haryana in North-West India. A comprehensive list of varieties released for commercial production in India is presented in Table 14.7.

14.10.2 Breeding Finger Millet in Africa

Gupta et al. (1989–90) identified a high-yielding genotype from a germplasm accession P 1462703 and registered in Zimbabwe in 1986. It matured in 87 days and had a medium grain size with good malting ability. Subsequently, Mnyenyembe (1990)

Fig. 14.4 Photographs of germplasm unit (GPU) series of finger millet varieties

identified an early maturing variety "FMVI" from a landrace with good brewing ability in Zimbabwe. It matured in 90–115 days and was blast and drought resistant. Mnyenyembe (1990) tested 25 selections at seven locations in Malawi during 1974–1975 and identified a high-yielding selection. Subsequently, he identified two more high-yielding selections. Based on advanced early maturing varietal trials involving 25 selections at four locations in Zambia, Gupta et al. (1989–90) identified a highest-yielding variety "SDRM 3" that accounted for an increase of 42% over the check variety.

Table 14.7 Finger millet varieties released in India

Sl. no.	Name of variety	Year of release	Pedigree	Institution developed
1	Chhattisgarh Ragi-2 (BR-36)	2018	PR-202 × GE-669	Indira Gandhi Krishi Vishwavidyalaya (IGKVV), Jagdalpur
2	DHFM-78-3	2018	GE 1219 × Indaf 8	University of Agricultural Sciences (UAS), Dharwad
3	Dapoli-2 (SCN-6)	2017	Soma-clone of Dapoli-1	Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth (BSKKV), Dapoli
4	CO 15	2017	CO 11 × PR 202	Tamil Nadu Agricultural University (TNAU), Coimbatore, Tamil Nadu
5	GNN-7	2017	Pure-line selection	Navsari Agricultural University (NAU), Gujarat
6	VL-379	2017	GE-440 × VL-149	Indian Council of Agricultural Research - Vivekananda Parvatiya Krishi Anusandhan Sansthan (ICAR-VPKAS), Almora
7	KMR 340	2016	OUAT-2 × WRT-4	UAS, Bengaluru
8	VL 376	2016	GE 4172 × VL Ragi 149	ICAR-VPKAS, Almora
9	GNN-6	2016	Selection from local germplasm WN-259	NAU, Waghai
10	GN-5	2016	Selection from local germplasm WWN-20	NAU, Waghai
11	VL Mandua-348	2016	VL Ragi 146 × VL Ragi 149	ICAR-VPKAS, Almora
12	VL 352	2012	VR 708 × VL 149	VPKAS, Almora, Uttarakhand
13	Indira Ragi-1	2012	HR 911 × GE 669	Agricultural Research Station (ARS), Jagdalpur, Chhattisgarh
14	PPR 2700 (Vakula)	2012	KM 55 × U 22/B	ARS, Perumallapalli, AP
15	VR 396 (Hima)	2012	IE 2695 × PR 202	ARS, Vizianagaram, AP
16	KMR 204	2012	GPU 26 × GE 1409	Vishweshwaraiah Canal (VC) Farm, Mandya, Karnataka
17	OEB 532	2012	GPU 26 × L5	Orissa University of Agriculture and Technology (OUAT), Berhampur, Odisha
18	OEB 526	2012	SDFM 30 × PE244	OUAT, Odisha
19	KOPN 235 (Phule Nachni)	2011	Pure-line selection	Mahatma Phule Krishi Vidyapeeth (MPKV), Rahuri
20	VL 347	2010	VR 708 × VL 149	VPKAS, Almora, Uttarakhand
21	PRM 2	2010	Pure-line selection	GB Pant University of Agriculture and Technology (GBPUAT), Uttarakhand
22	GPU 67	2009	Selection from GE 5331	UAS, Bengaluru

(continued)

Table 14.7 (continued)

Sl. no.	Name of variety	Year of release	Pedigree	Institution developed
23	KMR 301 (Gowri)	2009	MR 1 × GE 1409	UAS, Bengaluru
24	GPU 66	2009	PR 202 × GPU 28	UAS, Bengaluru
25	VR 847 (Srichaitanya)	2009	GPU 26 × L5	ARS, Vizianagaram, Andhra Pradesh
26	GN 5	2009	Pure-line selection	NAU, Waghai, Gujarat
27	ML 365	2008	IE 1012 × Indaf 5	UAS, Bengaluru
28	Paiyur 2	2008	VL 145 × Selection 10	TNAU, Coimbatore
29	VR 762 (Bharathi)	2006	Pure-line selection from VMEC 134	ARS, Vizianagaram, AP
30	VL 324	2006	VL 162 × IE 3808	VPKAS, Almora, Uttarakhand
31	PRM 1	2006	Pure-line selection Ekeshwar local	GBPAUT, Ranichauri, Uttarakhand
32	VL 332	2006	VL 127 × IE 1213824	VPKAS, Almora, Uttarakhand
33	GN 4	2006	Selection from WN228	NAU, Waghai, Gujarat
34	GPU 48 (Ratna)	2005	GPU 26 × L 5	PC Unit, UAS, GKVK, Bengaluru
35	DHRS 1	2005	Pure-line selection	ARS, Hanumanamatti, Karnataka
36	VL 315	2004	SDFM 69 × VL 231	VPKAS, Almora, Uttarakhand
37	Co 14 (TNAU 946)	2004	Malawi 1305 × Co 13	TNAU, Coimbatore
38	MR 6 (Divya)	2004	African white × ROH2	UAS, Bengaluru
39	GPU 45	2001	GPU 26 × L5	UAS, Bengaluru
40	OEB 10 (Chilika)	2001	GE 68 × GE 156	OUAT, Berhampur, Odisha
41	L 5	1999	Malawi × Indaf 9	ARS, Nagenahalli, Karnataka
42	OUAT 2 (Surya)	1999	Mutant of C09	OUAT, Berhampur
43	BM 9–1 (Bhairabi)	1999	Mutant of Budha Mandia	OUAT, Berhampur
44	PR 230 (Maruthi)	1998	Pure-line selection	Regional Agricultural Research Station (RARS), Andhra Pradesh
45	VR 708	1998	Pure-line selection-VNEC36	ARS, Vizianagaram, Andhra Pradesh
46	GPU 28	1998	Indaf 5 × (Indaf 9 × IE1012)	UAS, Bengaluru
47	GPU 26	1997	Indaf 5 × Advanced line derived from Indaf 9 × IE1012	UAS, Bengaluru
48	BM 11–1 (Rushikulya)	1996	Mutant of Buddha Mandia	OUAT, Berhampur
49	PR 2614 (Saptagiri)	1995	MR 1 × Kalyani	ARS, Perumallapalli
50	BM 2 (Birsa Marua)	1995	Pure-line selection	Birsa Agricultural University (BAU), Ranchi, Jharkhand

(continued)

Table 14.7 (continued)

Sl. no.	Name of variety	Year of release	Pedigree	Institution developed
51	VL 146	1995	VL 201 × IE 882	VPKAS, Almora, Uttarakhand
52	MR 2 (Akshaya)	1994	Indaf 5 × PR 202	UAS, Bengaluru
53	KM 65	1994	Pure-line selection	Chandra Shekhar Azad University of Agriculture & Technology (CSAUA&T), Kanpur
54	DAPOLI 1	1994	Selection from Mutant no. 50/1	BSKKV, Dapoli, Maharashtra
55	PPR 2350 (Padmavathi)	1993	Pure-line selection	ARS, Perumallapalli
56	GN 3	1993	KM13 × GN 2	Gujarat Agricultural University (GAU), Gujarat
57	A 404	1993	Introduction from AP	Birsa Agricultural University (BAU), Ranchi
58	PR 1158–9 Goutami)	1992	Godavari × U22	ARS, Vizianagaram
59	VR 520 (Suraj)	1992	Pure-line selection from VN2507/19	ARS, Vizianagaram
60	INDAF 15	1991	IE 67 × IE 927	UAS, Bengaluru
61	VL 149	1991	VL 204 × IE 882	VPKAS, Almora, Uttarakhand
62	MR 1	1990	Hamsa × IE 927	UAS, Bengaluru
63	VL 124	1989	Pure-line selection	VPKAS, Almora, Uttarakhand
64	TRY 1 (SSRC 247)	1989	Pure-line selection HR374	TNAU, Coimbatore
65	RAU 8	1989	BR 407 × Ranchi local	Dr. Rajendra Prasad Central Agriculture University, formerly Rajendra Agricultural University (RAU), Dholi, Bihar
66	KM 13	1989	Pure-line selection	CSAUA&T, Kanpur
67	PES 400 (Pant Mandua 3)	1989	Pure-line selection	GBPUAT, Pantnagar
68	Co 13 (TNAU 294)	1989	Co7 × TAH 107	TNAU, Coimbatore,
69	HR 911 (KBR 1)	1985	UAS 1 × IE 927	UAS, Bengaluru
70	INDAF 9 (Chitta)	1985	K1 × IE 980R	UAS, Bengaluru
71	VL 204	1985	Pure-line selection	VPKAS Almora, Uttarakhand
72	Simhadri	1985	Pure-line selection from VN311	ARS, Vizianagaram
73	PR 1044 (Ratnagiri)	1985	Pure-line selection local Mettachody variety/PM 629	ARS, Peddapuram
74	PES 110	1985	Pure-line selection	GBPUAT, Pantnagar

(continued)

Table 14.7 (continued)

Sl. no.	Name of variety	Year of release	Pedigree	Institution developed
75	Co 12	1985	Pure-line selection from PR722	TNAU, Coimbatore
76	NILCHAL (B-4-10-56)	1985	Mutant of IE 642	OUAT, Bhubaneswar
77	PAIYUR 1	1985	Pure-line selection from PR 722	TNAU, Coimbatore
78	BM 1 (IE 723)	1985	Pure-line selection	BAU, Ranchi
79	K 7	1982	GO 8 × K2	TNAU, Coimbatore
80	GN 2	1982	Pure-line selection from Gujarat local	GAU, Gujarat
81	INDAF 8	1982	Ullubele × IE 929	UAS, Bengaluru
82	K 6	1982	Natural Mutant from local	TNAU, Coimbatore
83	K5	1982	Sarada × EC 158	TNAU, Coimbatore
84	Co 11 (EC 4849)	1982	Pure-line selection from MS2584	TNAU, Coimbatore
85	INDAF 7 (Hasta)	1981	Annapurna × IE 927	UAS, Bengaluru
86	NIRMAL	1980	Pure-line selection from genetic collection from Nepal	CSAUA&T, Kanpur
87	VL 101	1978	Pure-line selection from IE 524	VPKAS, Almora, Uttarakhand
88	INDAF 5	1977	Kaveri × IE 929	UAS, Bengaluru
89	INDAF 3	1976	Kaveri × IE 927	UAS, Bengaluru
90	PR 202 (Godavari)	1976	Pure-line selection from Mettachudyragi of Araku variety	ARS, Peddapuram, Andhra Pradesh
91	INDAF 1	1976	Ullubele × IE 929	UAS, Bengaluru
92	Co 10	1976	Pure-line selection Maruaragi	TNAU, Coimbatore
93	HPB 7–6	1976	Hamsa × Poorna	UAS, Bengaluru
94	GN 1 (Gujarat Nagli 1)	1976	Pure-line selection from local selection of Dangs	GAU, Gujarat
95	HR 374	1975	EC 4840 × IE 927	UAS, Bengaluru
96	Kalyani	1972	Pure-line selection from CR 652	ARS, Perumallapalli
97	Shakti	1972	R0013 × H 22	UAS, Bengaluru
98	Dibya Sinha	1971	Mutant of AKP 7	Centre for Pulses Research (CPR), Berhampur
99	AKP 7 (Sarada)	1971	Pure-line selection	RARS, Anakapalli, AP
100	CO 9	1970	EC 4336 × PLR 1	TNAU, Coimbatore
101	Hamsa	1967	Pure-line selection	UAS, Bengaluru

(continued)

Table 14.7 (continued)

Sl. no.	Name of variety	Year of release	Pedigree	Institution developed
102	CO 8	1963	Pure-line selection from natural cross of MS6502	TNAU, Coimbatore
103	Cauvery	1962	Ullubele × H 22	UAS, Bengaluru
104	Annapurna	1962	K 1 × Aruna	UAS, Bengaluru
105	AKP 2	1962	Pure-line selection from Anakapalli local	RARS, Anakapalli
106	Udaya	1959	K 1 × Aruna	UAS, Bengaluru
107	Poorna	1959	Co 1 × Aruna	UAS, Bengaluru
108	VZM 1	1958	Pure-line selection	ARS, Vizianagaram, AP
109	VZM 2	1958	Pure-line selection	ARS, Vizianagaram, AP
110	Aruna	1956	Pure-line selection from local Giddaragi	UAS, Bengaluru
111	Co 5	1953	Pure-line selection	TNAU, Coimbatore
112	Co 7	1953	Pure-line selection from Cuddapah rajanpet ragi	TNAU, Coimbatore
113	Co 1	1942	Selection from Gidda Aryam (EC 593)	TNAU, Coimbatore
114	Co 2	1942	Pure-line selection from Udumalpet ragi (EC 3517)	TNAU, Coimbatore
115	Co 3	1942	Mutant of Co 1	TNAU, Coimbatore
116	Co 4	1942	Pure-line selection from Palladam ragi	TNAU, Coimbatore
117	Hagari 1 (Farm Ragi)	1941	Mutant from Gidda Aryam	Karnataka State Department of Agriculture (KSDA), Karnataka
118	ES 11 (Gidda Ragi)	1939	Selection from Giddaragi	KSDA, Karnataka
119	ES 13	1939	Selection from Kari giddaragi	KSDA, Karnataka
120	K1 (Kolar Gidda Ragi)	1939	Selection from Kolargiddaragi	KSDA, Karnataka
121	R 0870	1939	Pure-line selection from EC 47 of Coimbatore	KSDA, Karnataka
122	CO 6	1935	EC 1540 × EC 2945	TNAU, Coimbatore
123	H 22	1918	Pure-line selection from local ragi	KSDA, Karnataka

Source: Compendium of varieties in small millets, 2014. Compiled by MVC Gowda, YA Nanja Reddy, N Pushpalatha, M Deepika, CK Pramila, and Sachin S Jadhav, Project Coordinating Unit, All India Coordinated Small Millets Improvement Project, GKVK, Bangalore

14.10.3 Breeding for Resistance to Blast Disease

Finger millet production is constrained by: several fungal diseases such as blast (*Magnaporthe grisea*), seedling and leaf blight (*Helminthosporium nodulosum*), Cercospora leaf spot (*Cercospora eleusinis*), foot rot (*Sclerotium rolfsii*), smut (*Melanopsichium eleusis*), downy mildew (*Sclerospora macrospora*), dmaping off (*Pythium aphanidermatum*), banded blight (*Rhizoctonia solani*), sheath blight (*Marasmius candidus*), leaf spot (*Curvularia lunata*), Ozonium wilt (*Ozonium taxanum*), and rust (*Uromyces eragrostidis*); bacterial diseases such as bacterial blight (*Xanthomonas coracanae*), bacterial leaf spot (*Xanthomonas eleusinae*), and bacterial leaf stripe (*Pseudomonas eleusinae*); and viral diseases such as ragi mottle streak, ragi severe mosaic, and ragi streak. However, both in India and Africa, blast disease is the most devastating biotic production constraint in finger millet. Hence, most breeding programs aim at enhancing levels of resistance to blast disease along with grain yield potential.

Dependable knowledge on physical, biochemical, and genetic basis and availability of sources of resistance to blast help enhance the effectiveness of breeding finger millet for blast disease resistance. Several researchers have unraveled mechanism of resistance to blast disease in finger millet. Thicker leaf epidermis-cum-cuticle, higher stomatal frequency and size (Sanath Kumar et al. 2002), higher peroxidase activity, higher polyphenol oxidase, phenyl alanine ammoniase, and total phenol contents (Somappa 1999), and cytoplasm granulation (Madhukeshwara 1990) were found associated with resistance to blast disease in finger millet. Both additive and nonadditive gene effects played significant role in the expression of resistance to blast disease (Seetharam and Ravikumar 1993; Ravikumar and Seetharam 1994; Byregowda et al. 1997, 1999).

14.10.3.1 Sources of Resistance to Blast Disease

Thomas (1941) was the pioneer to report the existence of variation in responses to blast disease in finger millet. Subsequently, several researchers have attempted screening finger millet germplasm accessions/landraces/varieties/advanced breeding lines and identified numerous sources of resistance to blast disease (Table 14.8).

14.10.3.2 Breeding for Resistance to Blast Disease

African genotypes such as IE 927, IE 929, IE 922, and IE 978 had high productivity potential besides resistance to blast disease. Further, Mallanna et al. (1978) found that PR 202 and IE 927 had combined resistance to both blast and sclerotium wilt diseases. Concerted efforts led to the development and release of high yielding and blast disease resistant varieties such as GPU 28 at UAS, Bengaluru, India. It is highly popular and the ruling variety in southern parts of Karnataka state. Latha

Table 14.8 Source of resistance to blast disease in finger millet

Sl. no.	Germplasm accessions/varieties	Reference
1	TAH-91-1, TAH-8	Pall (1992)
2	APV-27	Rath and Mishra (1975)
3	TE-882, IE 1941, U.47, U-10, U.45, GE.304, GE.713	Seetharam and Viswanath (1983)
4	IE.1012, HPB 96–11, MR.1, MR2, MR3	Viswanath and Lucy Chennamma (1987)
5	GE Nos. 75, 669, 866, 1309, 1407, 1409	Ravikumar and Seetharam (1990)
6	TNAU 551	Ramaswamy (1995)
7	GE.2400, 4913, 4914, 4915	Mantur et al. (2002)
8	GE. Nos. 250, 261, 263, 320, 338, 344, 352, 416, 357, 371, 383, 396, 398, 400, 406, 409	Sanath Kumar et al. (2002)
9	MR.1, GPU-56, GPU.58, VL.321	Ramappa et al. (2002a, b, c)

et al. (2005) have established reproducible protocols for in-vitro plant regeneration and genetic transformation for development of leaf blast disease resistant finger millet using particle-in low gene-mediated method.

14.11 Genomics-Assisted Breeding

Conventional phenotype-based breeding of finger millet has been effective in developing farmer-preferred traits. However, further genetic improvement to cater to the ever-changing needs of the farmers, consumers, and processing industries and to address the challenges posed by climate change requires the use of genomic tools. The genomic tools such as markers, genetic engineering, and genome editing have proved effective to enhance genetic gains per breeding cycle and unit time. Use of DNA markers in finger millet breeding research is still in infancy as they are being developed only recently. Nevertheless, sequence independent marker systems such as random amplification of polymorphic DNA (RAPD; Fakrudin et al. 2004; Das et al. 2009; Das and Misra 2010) and amplified fragment length polymorphism (AFLP; Dida et al. 2007) have been used to detect and characterize genetic variation among germplasm accessions and breeding lines. However, the information obtained from these markers is not reliable due to their poor reproducibility. Hence, sequence-dependent simple sequence repeat (SSR) and single nucleotide polymorphism (SNP) are highly preferred by researchers owing to their simple codominant inheritance and amenability for automation and high reproducibility. Using 1740 expressed sequence tags (EST), Arya et al. (2009) developed EST-SSR markers. Recently, Hittalmani et al. (2017) based on draft whole-genome sequence have developed a large number of genomic and EST-SSR-based markers. SSR markers being easily assayable even on simple agarose system are markers of choice by the

breeders. These markers could be used in various applications in finger millet genetics and breeding research, such as in: (1) developing fingerprint to identify duplicate germplasm accessions, (2) characterizing and assessing genetic variability in working germplasm and/or breeding lines, (3) selecting genetically diverse genotype for effecting crosses to generate variability to identify genotypes with best combination of traits, (4) identifying genomic regions/quantitative traits loci (QTL) controlling economically important traits, and (5) developing fingerprint varieties for protecting intellectual property rights associated with cultivars. Identification and validation of QTL paves way for implementation of marker-assisted selection (MAS). The use of MAS is yet to be initiated in finger millet. As a prelude to implement MAS, Dida et al. (2007) generated first-ever genetic map of the tetraploid finger millet in inter-subspecies population derived from a cross between *E. coracana* spp. *coracana* cv. Okhole-1 and its wild progenitor *E. coracana* ssp. *africana* accession MD 20 using restriction fragment length polymorphism and AFLP, EST-SSR, and genomic SSR-based markers. Assignment of linkage groups to A and B genomes was performed by comparing the hybridization pattern of probes in Okhole-1, MD 20, and *Eleusine indica* acc. MD 36. The map spanned 721 cM on the A genome and 787 cM on the B genome. Such studies need to be carried out to identify and validate QTL controlling economically important traits for implementation of MAS in finger millet.

Finger millet has ten-fold higher calcium in grains compared to other cereals and relatively high levels of drought tolerance. Identification of functional validation of candidate genes/regulatory genes controlling economically important traits such as moisture stress tolerance (Parvathi et al. 2013; Parvathi and Nataraja 2017; Ramegowda et al. 2017), salinity tolerance (Ramegowda et al. 2012), calcium transport capacity (Kanwal et al. 2014), and phosphate transport capacity (Pudake et al. 2017), coupled with efficient protocol for genetic transformation (Latha et al. 2005), is expected enhance the use of precision breeding tools such as genome editing in finger millet for rapid genetic gains per selection cycle and per unit time.

14.12 Future Prospects

The expected increased incidence of existing, and emergence of new, biotic and abiotic stresses driven by imminent climate change (IPCC 2007) warrants accelerated breeding for these production constraints. There is a need for deployment of genomic tools such as DNA markers, especially SSR and SNP markers, to enhance the pace and precision of breeding finger millet. The SSR and SNP markers should be routinely used for discovery of QTL controlling economically important traits followed by genomic selection to complement phenotype-based selection to accelerate genetic gains per breeding cycle and unit time. Genome editing tools are expected to enhance genetic gains for traits controlled by functionally well-characterized genes. While we do not claim an exhaustive review, we hope that this chapter would benefit all those who are interested in finger millet breeding.

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