GENETIC AND GENOMIC RESOURCES FOR GRAIN CEREALS IMPROVEMENT

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Finger and foxtail millets

7

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7.1 Introduction

Foxtail and finger millets are the second and third most important crops among millets after pearl millet. Foxtail millet is widely cultivated in Asia, Europe, North America, Australia, and North Africa for grains or forage, and an essential food for human consumption in China, India, Korea, and Japan (Austin, 2006). China ranks top in foxtail millet production with the annual cultivating area of about 2 million ha and an annual total grain production of about 6 Mt (Diao, 2011). Finger millet accounts for 12% of the global millets area and is grown in more than 25 countries in eastern and southern Africa, and across Asia from the Near East to the Far East. The major finger millet producing countries are Uganda, India, Nepal, and China (www.cgiar.org/our-research/crop-factsheets/millets/).

Foxtail and finger millets are good sources for micro and macronutrients with high nutraceutical and antioxidant properties. These crops are rich in protein, fat, crude fiber, iron, and other minerals and vitamins. Foxtail millet contains almost twice the amount of protein (11.2%) and fat (4%) as compared to rice, while finger millet contains over >10-fold higher calcium as compared to other cereals including rice and wheat (Saleh et al., 2013). Upadhyaya et al. (2011a) identified grain nutrients rich accessions in finger millet core collection (Upadhyaya et al., 2006a) having 37.66–65.23 mg/kg of Fe, 22.46–25.33 mg/kg of Zn, 3.86–4.89 g/kg of Ca, and 8.66–11.09% of protein. Similarly, Upadhyaya et al. (2011b) identified grain nutrients rich accessions in foxtail millet core collection (Upadhyaya et al., 2008) having 171.2–288.7 mg/kg of Ca, 58.2–68.0 mg/kg of Fe, 54.5–74.2 mg/kg of Zn, and 15.6–18.5% of protein. The husked grains of foxtail millet are used as food in Asia, southeastern Europe, and Africa. The flour is used for making cakes, porridges, and puddings. Foxtail millet is used in the preparation of beer and alcohol, especially in Russia and Myanmar, and for vinegar and wine in China, and primarily grown as bird feed, hay, and silage in Europe and the United States, while in China, the straw is an important fodder. Similarly, finger millet is used as food in Asia and Africa, and flour is used to prepare porridge and usually served with a side dish of vegetables, meat, or fish. In Africa, finger millet provides malt for making local beer and other alcoholic or nonalcoholic beverages. Finger millet straw is used as forage for cattle, sheep, and

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goats. In Uganda, the by-products of finger millet beer production are fed to chickens, pigs, and other animals (www.protabase.org).

Finger and foxtail millets are important ancient crops of dryland agriculture and the potential climate-resilient crops for food and nutritional security in the climate change scenario. However, mostly farmers cultivate unimproved varieties or traditional landraces that yields poorly. It is mainly because of unavailability of improved varieties, limited research efforts, and funding for these crops. Assessing genetic variability of germplasm collections, development, and use of genetic and genomic resources for breeding high-yielding cultivars, developing crop production and processing technologies, value addition for improving consumption, public private partnerships, and policy recommendations are needed to upscale these crops to make them more remunerative to farmers.

7.2 Origin, distribution, diversity, and taxonomy

7.2.1 Finger millet

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an allotetraploid evolved from its wild progenitor, *E. coracana* subsp. *africana*. The genus *Eleusine* contains about 10 species, both annuals and perennials, with three basic chromosome numbers 8, 9, and 10. Four are tetraploids, namely, *E. coracana* ($2n = 4x = 36$, AABB), *Eleusine africana* ($2n = 4x = 36$, AABB) and *Eleusine kigeziensis* ($2n = 4x = 36$, AADD), and *Eleusine reniformis* ($2n = 4x = 36$); Seven are diploids with a basic chromosome number of 8 in *Eleusine multiflora* ($2n = 2x = 16$, CC), 9 in *Eleusine indica* ($2n = 2x = 18$, AA), *Eleusine tristachya* ($2n = 18$, AA), *Eleusine floccifolia* ($2n = 18$, BB), *Eleusine intermedia* ($2n = 18$, AB), and *Eleusine verticillata* ($2n = 2x = 18$), and 10 in *Eleusine jaegeri* ($2n = 2x = 20$, DD) (Hiremath and Chennaveeraiah, 1982; Neves et al., 2005; Dwivedi et al., 2012). *E. coracana* subsp. *africana* is considered as a putative progenitor to cultivated finger millet, *E. coracana* subsp. *coracana*, and are completely cross-compatible and produce fertile hybrids (Mehra, 1962; Hiremath and Salimath, 1992).

Domestication of cultivated finger millet, *E. coracana* started around 5000 years ago in Western Uganda and the Ethiopian highlands and the crop extended to the Western Ghats of India around 3000 BC (Hilu et al., 1979; Hilu and de Wet, 1976). Cytologic analyses of hybrids, chloroplast DNA restriction analysis, and *in situ* hybridization of diploid and polyploidy species shows that *E. indica* is the "A" genome donor, while *E. floccifolia* is the "B" genome donor of cultivated *E. coracana* (Bisht and Mukai, 2001; Hiremath and Salimath, 1992; Hilu, 1988). Contrary to this, Liu et al. (2014) suggest *E. indica* as the primary A genome parent, while *E. tristachya* or its extinct sister or ancestor as the secondary A genome parent for derivation of *E. coracana*, while B genome donor is extinct. This is also supported by the close phylogenetic relationships of diploids, *E. indica* and *E. tristachya* with *E. africana*, *E. coracana*, and *E. kigeziensis* for cpDNA and nrDNA *Pepc4* (Neves et al., 2005; Liu et al., 2011b).

Isozyme and DNA marker analyses have revealed that cultivated finger millet has a narrow genetic base, but variation in the wild subspecies is considerably higher (Werth et al., 1994; Muza et al., 1995; Salimath et al., 1995a; Dagnachew et al., 2014). Considerable diversity is found in finger millet, wherein based on inflorescence morphology they can be grouped into races and subraces (Prasada Rao et al., 1993). The species *E. coracana* consists of two subspecies, *africana* (wild) and *coracana* (cultivated). The subsp. *africana* has two wild races, *africana* and *spontanea*, while subsp. *coracana* has four cultivated races; *elongata*, *plana*, *compacta*, and *vulgaris*. These cultivated races are further divided into subraces; *laxa*, *reclusa*, and *sparsa* in race *elongata*; *seriata*, *confundere*, and *grandigluma* in race *plana*; and *liliacea*, *stellata*, *incurvata*, and *digitata* in race *vulgaris*. The race *compacta* has no subraces (de Wet et al., 1984; Prasada Rao and de Wet, 1997).

7.2.2 Foxtail millet

Foxtail millet (*Setaria italica* (L.) P. Beauv.) is a member of the subfamily Panicoideae and the tribe Paniceae with chromosome number of $2n = 2x = 18$ (AA). It is an important ancient crop of dry land agriculture, grown since >10,500 years ago in China (Yang et al., 2012). The green foxtail, *Setaria viridis* ($2n = 2x = 18$, AA), is a wild ancestor of cultivated foxtail millet. The genus *Setaria* is organized into three gene pools based on observations drawn from interspecific hybridization and hybrid pollen fertility. The primary gene pool is composed of cultivated foxtail (*S. italica*) and its putative wild ancestor *S. viridis* (Harlan and de Wet, 1971). The secondary gene pool contains *Setaria adhaerans* ($2n = 2x = 18$) and two allotetraploids *Setaria verticillata* and *Setaria faberii* ($2n = 4x = 36$) (Li et al., 1942; Benabdelmouna et al., 2001). The tertiary gene pool contains *Setaria glauca* (or *Setaria pumila*, $4x$ to $8x$) in addition to many other wild species. Morphological and molecular studies on cultivated and green foxtail revealed large genetic diversity (Reddy et al., 2006; Upadhyaya et al., 2008; Vetriventhan et al., 2012; Wang et al., 2010a, 2012; Jia et al., 2013b).

Several hypotheses regarding the origin and domestication have been proposed and a multiple domestication hypothesis has been widely accepted (de Wet et al., 1979; Li et al., 1995). Li et al. (1995) suggest a multiple domestication hypothesis with three centers, that is, China, Europe, and Afghanistan–Lebanon. A study by Hirano et al. (2011) on the geographical genetic structure of 425 landraces of foxtail millet and 12 accessions of green foxtail by transposon display (TD) as a genome-wide marker shows two clear genetic borders: (1) between accession from East Asia and those from other regions including Central, South, or Southeast Asia, and the Middle East, and (2) between West Europe and East Europe suggesting strong regional differentiations and a long history of the cultivation in each region, supporting multiple domestications events of foxtail millet.

Foxtail millet has abundant within-species diversity. Prasada Rao et al. (1987) suggested three races of foxtail millet based on the comparative morphology of the foxtail millet accessions: (1) race *moharia* is common in Europe, southeast Russia, Afghanistan, and Pakistan; (2) race *maxima* is common in eastern China, Georgia (Eurasia), Japan, Korea, Nepal, and northern India (it has also been introduced in

the United States); and (3) race *indica* is found in the remaining parts of India and Sri Lanka. These races can be further divided into 10 subraces (*aristata*, *fusiformis*, and *glabra* in *moharia*; *compacta*, *spongiosa*, and *assamense* in *maxima*; and *erecta*, *glabra*, *nana*, and *profusa* in *indica*). Later, Li et al. (1995) added the race *nana* along with *maxima*, *moharia*, and *indica* and described the plants that resemble the wild green millet, and are very short and slender, with many tillers, very short panicles with poor yield performance, and early maturity as a separate race *nana*.

7.3 Erosion of genetic diversity from the traditional areas

Loss of genetic diversity (genetic erosion), including the loss of individual genes or particular combinations of genes, and loss of varieties and crops occur rapidly in crops mainly because of replacement of traditional landraces by modern, high-yielding cultivars, natural catastrophes, and large-scale destruction and modification of natural habitats harboring wild species. Genetic erosion of foxtail and finger millets occurs mostly due to their neglect and often replacement with commercial or nonfood crops. Decline in finger millet cultivation in Socotra (an island in Yemen) and Kabale Highlands, Uganda has been reported (Bawazir and Bamousa, 2014; Mbabwine et al., 2005). Assessment of the status of plant genetic resources in Kabale Highlands, Uganda revealed that finger millet is one of the threatened crops where only few farmers cultivate finger millet and many have stopped its cultivation (Mbabwine et al., 2005). In India, the area under cultivation of foxtail and finger millets and other small millets declined mainly due to poor yield, unavailability of improved cultivars, and policy shift that focuses on rice and wheat.

7.4 Status of germplasm resource conservation

Large numbers of foxtail and finger millets germplasm accessions are available to the scientific community. Globally >46,000 foxtail millet and >37,000 finger millet germplasm accessions have been conserved *ex situ* in genebanks. The major collections of foxtail millet germplasm accessions are housed at China, India, France, and Japan, while India and African countries such as Kenya, Ethiopia, Uganda, and Zambia conserve major finger millet collections (Table 7.1).

7.5 Germplasm evaluation and maintenance

Foxtail and finger millets are highly self-pollinating crops, so there is no special regeneration and maintenance practice as in the case of cross-pollinated crops such as pearl millet. The field used for regeneration should not have grown the same crops in the previous year in order to avoid volunteer plants. Individual accessions can be planted in rows (4 m length) and harvested panicles by hand will be bulked to make up the accession. Considerable efforts have been made in foxtail and finger millets

Table 7.1 Major genebanks across the globe conserving foxtail and finger millet germplasm

Country	Institute	Germplasm accessions		
		Cultivated	Wild	Total
Finger millet				
India	National Bureau of Plant Genetic Resources (NBPGR)	9511	11	9522
	AICRP on Small Millets	6257	–	6257
	ICRISAT	5880	204	6084
	The Ramaiah Gene Bank, Tamil Nadu Agricultural University	2219	–	2219
	University of Agricultural Science, Banglore	1019	–	1019
Kenya	National Genebank of Kenya, Crop Plant Genetic Resources Centre, Muguga (KARI-NGBK)	2854	77	2931
Ethiopia	Ethiopian Institute of Biodiversity (EIB)	2173	–	2173
Uganda	Serere Agriculture and Animal Production Research Institute (SAARI)	1231	–	1231
Zambia	SADC Plant Genetic Resources Centre (SRGB)	1037	3	1040
Foxtail millet				
China	Institute of Crop Science, Chinese Academy of Agricultural Sciences (ICS-CAAS)	26233	–	26233
India	NBPGR	4384	8	4392
	AICRP on Small Millets	2512	–	2512
	ICRISAT	1488	54	1542
France	Laboratoire des Ressources Génétiques et Amélioration des Plantes Tropicales, (ORSTOM-MONTP)	3500	–	3500
Japan	Department of Genetic Resources I, National Institute of Agrobiological Sciences (NIAS)	2505	26	2531

Source: http://www.fao.org/wiews-archive/germplasm_query.htm; Institutes/genebanks with >1000 accessions considered for listing.

germplasm evaluation for various traits of economic interest, including biotic and abiotic stresses tolerance and grain nutritional content, and are discussed hereunder.

7.5.1 Agronomic traits

Large genetic variation for morphoagronomic traits has been found in foxtail (Li et al. 1995; Upadhyaya et al., 2008; Nirmalakumari and Vetriventhan, 2010) and finger millets (Upadhyaya et al., 2006a, 2007; Suryanarayana et al., 2014). For example, at the ICRISAT genebank, finger millet germplasm accessions conserved have large variation for days to flowering (50–120 days), plant height (30–240 cm), basal tillers (1–70),

Table 7.2 Diversity for agronomic traits in finger and foxtail millet active collection conserved at ICRISAT, Patancheru

Crop/trait	Mean	Range
Finger millet		
Days to flowering-rainy	80.4	50–120
Plant height (cm)-rainy	100.7	30–240
Basal tillers number	5.2	1–70
Flag leaf blade length (mm)	358.1	100–750
Flag leaf blade width (mm)	12.6	5–20
Flag leaf sheath length (mm)	102.5	8–280
Peduncle length (mm)	215.5	18–450
Panicle exsertion (mm)	113.5	0–360
Inflorescence length (mm)	93.1	10–320
Inflorescence width (mm)	78.4	7–460
Longest finger length (mm)	72.6	10–250
Longest finger width (mm)	11.6	2–50
Panicle branches number	7.7	2–27
Foxtail millet		
Days to flowering-rainy	53.5	32–135
Plant height (cm)-rainy	110.0	20–215
Basal tillers number	7.5	1–52
Flag leaf blade length (mm)	284.7	30–520
Flag leaf blade width (mm)	20.2	5–40
Flag leaf sheath length (mm)	138.5	50–260
Peduncle length (mm)	299.6	80–500
Panicle exsertion (mm)	162.5	10–360
Inflorescence length (mm)	163.1	10–390
Inflorescence width (mm	19.2	5–120
Weight of 5 panicles (g)	30.1	0.6–117

inflorescence length (10–320 mm), and so on; similarly in foxtail millet for days to flowering (32–135 days), plant height (20–215 cm), basal tillers number (1–52), inflorescence length (10–390 mm), and so on (Table 7.2). Upadhyaya et al. (2011b) identified 21 accessions of foxtail millet with higher grain yield compared to the best control cultivar. The ICRISAT global finger millet composite collection was evaluated for morphoagronomic traits and identified best-performing accessions for grain yield, early flowering, more number of fingers, high basal tiller number, and ear head length (Table 7.3).

7.5.2 Grain nutrients

At ICRISAT, finger millet core collection accessions assessed for genetic variability for grain nutrient contents and identified 15 promising accessions each for grain Fe (37.66–65.23 mg/kg), Zn (22.46–25.33 mg/kg), Ca (3.86–4.89 g/kg), and protein (8.66–11.09%) contents, and 24 accessions were selected based on their superiority over

Table 7.3 Germplasm/cultivars reported as sources for agronomic and nutritional traits and resistant/tolerant to biotic and abiotic stresses in finger millet and foxtail millet

Trait	Germplasm/cultivar sources	References
Finger millet		
Early flowering	IE# 49, 120, 189, 196, 234, 501, 509, 581, 588, 600, 641, 694, 847, 2030, 2093, 2158, 2275, 2293, 2322, 2323, 2957, 3104, 3537, 3543, 4425, 4431, 4432, 4442, 4711, 4734, 4755, 4759, 6013, 6550	Bharathi (2011)
Basal tillers	IE# 2296, 2034, 4711, 2293, 2299, 2608, 2619, 5145, 6553, 847, 2408, 2534, 3987, 1013, 120, 2042, 2091, 2106, 2139, 2146, 2233, 2288, 2367, 2410, 2504, 2645, 2657, 2674	Bharathi (2011)
Finger number	IE# 6033, 3790, 4586, 6059, 3111, 4476, 3106, 2914, 4677, 5733, 5875, 5877, 4257, 5105, 5563, 6510, 4297, 2957, 5689, 5956, 4563, 3120, 2816, 6013, 2303, 2591, 6252, 6241, 4866	Bharathi (2011)
Head length	IE# 2223, 2621, 2789, 6553, 3581, 3431, 3722, 6512, 2108, 2781, 3046, 2486, 5321, 3704, 798, 3489, 5022, 2591, 2608, 4476, 2611, 3531, 2336, 4125, 4658, 6546	Bharathi (2011)
Forage yield	IE# 2117, 24, 2568, 2651, 2753, 2796, 2811, 2880, 2942, 2979, 3789, 50, 672, 715, 860, 908, 916, 96, 99	Bharathi (2011)
Grain yield	IEs 94, 2340, 2498, 2578, 2587, 2683, 2773, 2903, 2983, 2992, 3194, 3790, 3802, 4600, 4974, 5198, 5472, 3663, 3693, 3744, 4121, 4310, 4679, 5862, 6142, 6236, 667, 1010, 2299, 2590, 2678, 2684, 2698, 2712, 2756, 2827, 2872, 3135, 3136, 3270	Bharathi (2011)
Iron	IE# 4708, 2921, 4709, 588, 5736, 4476, 942, 4734, 5794, 4107, 7338, 2093, 5870, 4443, 817	Upadhyaya et al. (2011a)
Zinc	IE #3120, 7508, 6546, 3025, 7386, 7407, 615, 712, 5788, 633, 2008, 1023, 886, 4817, 510	Upadhyaya et al. (2011a)
Calcium	IE# 4476, 2030, 6546, 4708, 2568, 2957, 6537, 2608, 2572, 2921, 4443, 2780, 4866, 7386, 4709, CO# 9, 11, GE 2491, Malawi # 1305, 1314, 1861, 1866, 1895, 1907, 1915, 1940, 1952, IE# 3156, 3184, 3799, 3802	Upadhyaya et al. (2011a); Vadivoo et al. (1998)
Protein	IE #6537, 9, 4709, 4708, 6541, 2921, 6546, 4476, 4443, 588, 6013, 2093, 4817, 3120, 3101, Malawi# 1305, 1314, 1861, 1907, 1958, 2049, MS# 174, 887, 1168, 2777, 2784, 2869, GE# 37, 60, 1106, 2491, 2500, CO# 7, 9, IE# 3156, 3184	Upadhyaya et al. (2011a); Vadivoo et al. (1998)

(Continued)

Table 7.3 Germplasm/cultivars reported as sources for agronomic and nutritional traits and resistant/tolerant to biotic and abiotic stresses in finger millet and foxtail millet *(cont.)*

Trait	Germplasm/cultivar sources	References
Blast	ED 201-5A, ICM 401, PRM 9802, SANJI 1, TNAU 1009, VL# 234, 324, 328, 330, 332, 333, Genotype no. 2400, 4313, 4914, 4915, 4929, 4966, 5102, 5126, 5148, IE #1055, 2821, 2872, 4121, 4491, 4570, 5066, 5091, 5537	Kumar and Kumar (2009); Mantur et al. (2001); Babu et al. (2013b);
Drought	PR202, VL315, PES 400, PRM# 8107, 8112, VL 315	Bhatt et al. (2011); Gupta et al. (2014a)
Heat stress	GP # 3, 111, 153	Babu et al. (2013a)
Salinity	GPU 48, Indaf 5, Co 12, Trichy 1, IE #518, 2034, 2217, 2790, 2872, 3045, 3077, 3391, 3470, 3973, 4073, 4329, 4671, 4673, 4757, 4789, 4795, 4797, 5066, 6154, 6165, 6326	Shailaja and Thirumeni (2007); Vijayalakshmi et al. (2014); Krishnamurthy et al. (2014b)
Foxtail millet		
Grain yield	ISe# 710, 969, 1820, 388, 842, 49, 1888, 90, 364, 1767, 362, 1808, 846, 869, 1511, 909, 1846, 1610, 795, 1458, 1704	Upadhyaya et al. (2011b)
Early flowering	ISe# 1312, 1151, 1227, 1201, 1234, 1335, 1286, 1161, 1320, 1647, 1638, 1037, 1181, 1563, 1254, 1204, 1547, 1187, 403, 1118, 1163	Upadhyaya et al. (2011b)
Calcium	ISe# 1227, 1181, 1059, 1419, 827, 751, 1474, 1685, 900, 840, 1629, 1851, 769, 1581, 1286, 1136, 1161, 1773, 931, 869, 663	Upadhyaya et al. (2011b)
Iron	ISe# 1151, 1286, 1400, 1305, 1332, 1059, 1581, 1320, 1312, 144, 1163, 1460, 160, 1037, 1597, 1009, 1161, 1704, 1187, 1745, 838, GPUS# 14, 18, S 130, SiA# 2619, 326, 2599, ATPS 83, ISC 247, TNAU 43	Upadhyaya et al. (2011b); Philip and Maloo (1996)
Zinc	ISe# 1286, 748, 1387, 195, 1134, 1408, 1419, 1161, 900, 1820, 1320, 1654, 1704, 1605, 403, 1808, 751, 1674, 144, 1234, 985	Upadhyaya et al. (2011b)
Protein	ISe# 1312, 1227, 1789, 1254, 1541, 827, 748, 1305, 1647, 1335, 751, 1118, 1134, 1151, 195, 1234, 1067, 1419, 144, 735, 1161	Upadhyaya et al. (2011b)
Blast	GPUS-6, AZJ-11, SIA-2592, SIA-2593, SIA-2596, SIA-2606, SiA-2608, RSE-62, Niangu 1, Jinan 8337, ISe #375, 376, 748, 751, 769, 771, 785, 846, 1059, 1067, 1137, 1181, 1187, 1201, 1204, 1258, 1286, 1320, 1335, 1387, 1419, 1541, 1547, 1563, 1575, 1593, 1685, 1704	Jain et al. (1991); Tian and Quan (1995); Zhang and Guan (1995); Sharma et al. (2014)

Table 7.3 Germplasm/cultivars reported as sources for agronomic and nutritional traits and resistant/tolerant to biotic and abiotic stresses in finger millet and foxtail millet *(cont.)*

Trait	Germplasm/cultivar sources	References
Brown spot	GPUS# 26, 27, SiA #3039, 3059, 3064, 3066, 3088, TNAU #213, 235, 225, DHGR# 2061, 2062	Kumar and Kumar (2009)
Banded leaf and sheath blight	RFM# 82, 83, 84, 85, 87, 88, 90, 93, 94, 95, 96, 97	Jain et al. (2014)
Downy mildew	Luyu 2, Luyu 6, Wanchi 1, Yugengze and Baisu from Japan, Pingrangsu, Qiushusu and Duolangsu, ISe# 25, 30-1, 172, 274, 465, Meera (SR 16), Tie Gu 7, Longgu 28, Jingu 16, Jingu 11, Lugu No 7, Yugo No 3, Lujin 3, Beihuang, Zhenggu 2	Wang et al. (1997); Maloo et al. (2001); Wang et al. (1998a); Jiyaju (1989); Jiyaju and Yuzhi (1993); Dwivedi et al. (2012)
Smut	Jingu 16, Lugu No 7, K8763, Sarativskoye 2, Sarativskoye 3, Sarativskoye 6, Veselepodolyanskoye 632, Barnaulskoye 80, Gorilinka, Tie Gu 7	Jiyaju (1989); Jiyaju and Yuzhi (1993); Wang et al. (1998a)
Rust	Lugu No 7, Yugu No 2, Yugu No 3, Niangu 1	Jiyaju and Yuzhi (1993); Tian and Quan (1995)
Drought	BSi-1, EM 15/BSi 467, EM 8/BSi 467, Tie Gu 7, Jinan 8337	Begum et al. (2013); Wang et al. (1998a); Zhang and Guan (1995)
Lodging	Tie Gu 7, Longgu 28, Nenxian 13, Jingu 11, Yugu No. 1, Yugu No. 2, Yegu 5, Yanggu, Liuyuexian 2, Cang 155, Gufeng 1, An 4844, Heng 8735, Ji 9409, Pin 324, Zheng 9188, Pin 540, Cang 409, An 7169, An 9217, Bao 182	Wang et al. (1998a); Jiyaju (1989); Chen and Qi (1993); Tian et al. (2010); Dwivedi et al. (2012)
Salinity	ISe #254, 869, 1851, 96, 388, 480, 995, 1629, 969, 1888, Honggu, Xiaohuanggu, and Sanbianchou, ICERI 5, ICERI 6	Ardie et al. (2015); Krishnamurthy et al. (2014a); Tian et al. (2008)

control cultivars for two or more grain nutrients (Upadhyaya et al., 2011a) (Table 7.3). Vadivoo et al. (1998) reported a wide range of variation for protein (6.7–12.3%) and calcium (162–487 mg/100 g of grain) in finger millet and identified 20 and 16 genotypes with significantly higher protein and calcium content, respectively (Table 7.3).

Similarly in foxtail millet, Upadhyaya et al. (2011b) identified 21 diverse accessions with agronomically (earliness and high grain yield) and nutritionally (high seed protein, 15.6–18.5%; Ca, 171.2–288.7 mg/kg; Fe, 58.2–68.0 mg/kg; and Zn, 54.5–74.2 mg/kg) superior traits (Table 7.3). Seed protein, fat, starch, and amino acids content in 259 foxtail millet cultivars from six provinces in China showed a wide range

of variation (g/100 g) for protein (11.85–20.58), fat (2.82–4.47), starch (65.59–74.12), and amino acids (Yang et al., 2013). Philip and Maloo (1996) evaluated 40 genotypes of foxtail millet varieties for their Fe content and grouped the varieties with high Fe content. Li et al. (2009) evaluated vitamin E contents of 400 foxtail millet accessions, and identified accessions with high vitamin E content. Shao et al. (2014) evaluated folic acid (vitamin B9) content in 245 foxtail millet traditional varieties originating from different regions in Shanxi, China showing wide genetic variations (0.37–2.37 μg/g) and a total of 24 varieties with higher folic acid content were identified, among them, Jingu 21, a major leading cultivar, recorded folic acid content of 2 μg/g.

7.5.3 Biotic stress

Blast caused by *Pyricularia grisea* is a very prominent disease in finger millet, which affects the productivity, utilization, and trade in Eastern and Southern Africa and South Asia. The average loss due to blast has been reported to be around 28–36% (Nagaraja et al., 2007), and in certain areas yield losses could be as high as 80–90% (Vishwanath et al., 1986; Rao, 1990). At ICRISAT, a comprehensive disease severity assessment (rating) scale has been developed for leaf, neck, and finger blast based on the qualitative and quantitative differences of lesions observed on plants infected with blast pathogen (Babu et al., 2013b). In mini core collection, 66 accessions with combined resistance to leaf, neck, and finger blast have been identified, of which nine genotypes also have desirable agronomic traits such as early flowering, medium plant height, and semicompact to compact inflorescence (Babu et al., 2013b). In addition, many researchers have also evaluated finger millet genotypes and reported sources of resistance to blast disease (Table 7.3).

The most serious diseases of foxtail millet are blast (*Pyricularia setariae)*, downy mildew (*Sclerospora graminicola*), rust (*Uromyces setariae-italiae*), and smut (*Ustilago crameri*) (Dwivedi et al., 2012; http://database.prota.org/PROTAhtml/Setaria%20italica_En.htm). At ICRISAT, foxtail millet core collection accessions were evaluated for blast resistance in field and greenhouse under artificial inoculation conditions and identified 21 accessions resistant to neck and head blast under field evaluation and 11 accessions had seedling leaf blast resistance in the greenhouse. Further evaluation against four isolates of blast pathogen led to the identification of 16 accessions with resistance to leaf, sheath, neck, and head blast to at least one isolate, and two accessions (ISe 1181 and ISe 1547) showed free from head blast infection and are resistant to leaf, neck, and sheath blast against four isolates (Sharma et al., 2014). Many studies on screening foxtail millet germplasm accessions or cultivars against blast, brown spot, banded leaf, and sheath blight diseases have been carried out and sources for resistance have been reported (Table 7.3).

7.5.4 Abiotic stress

7.5.4.1 Drought

Foxtail millet is a relatively drought-tolerant crop compared to other cereals. Significant correlations between agronomic traits like panicle weight, grain weight per

panicle, plant height, length of rachis, and 1000-grain-weight, and physiologic parameters like relative chlorophyll, soluble protein, malondialdehyde (MDA), and superoxide dismutase (SOD) with drought-resistant index (DRI) under drought condition were reported (Zhang et al., 2012b). Various drought screening studies employing different methods had enabled identification of drought-tolerant genotypes in foxtail millet (Table 7.3). Screening of 17,313 accessions of foxtail millet genotypes from China for drought tolerance using seedling survival under repeated drought stress led to grouping of accessions into five grades with grade 1 being the most drought tolerant, which included the cultivar, Yugu1 (Li, 1997). A quick and simple screening technique for screening foxtail millet drought tolerance using mannitol or polyethylene glycol (PEG-6000) tests has been used and suggested relative water content and germination rate under osmotic stress as indicators of drought tolerance at the seedling stage (Zhang et al., 2005; Zhu et al., 2008). Lata et al. (2011) used lipid peroxidation measure to assess membrane integrity under stress as biochemical marker to screen 107 cultivars and classified the genotypes as highly tolerant, tolerant, sensitive, and highly sensitive.

In finger millet, drought reduced leaf area, dry matter accumulation, seed weight, radiation use efficiency, biomass, and yield (Maqsood and Ali, 2007). Drought stress induced increase in the activity of superoxide dismutase, ascorbate peroxidase, and glutathione reductase in tolerant varieties (PR 202 and VL 315), while lower in susceptible varieties (PES 400 and VR 708) (Bhatt et al., 2011). Ascorbate peroxidase:superoxide dismutase ratio, which is a crucial factor in alleviating drought stress, was higher in drought-tolerant varieties compared to susceptible varieties under stress. The susceptible varieties recorded maximum stress-induced damage, wherein higher accumulation of MDA and hydrogen peroxide was found (Bhatt et al. 2011). Neshamba (2010) studied the variability of drought tolerance in finger millet and identified 16 drought-tolerant accessions than the best check.

7.5.4.2 Heat stress

In finger millet, high-temperature stress caused significant influence on growth, development, and yield. Traits that influence yield, such as panicle number, finger number, finger length, seed number, and seed weight, were significantly reduced by high-temperature stress (Opole et al., 2010; Babu et al., 2013a). Babu et al. (2013a) established a temperature induction response (TIR) technique for screening high-temperature tolerance at seedling stage in finger millet, wherein they standardized the sublethal, that is, challenging temperatures 38–54°C (for 5 h) and lethal temperatures as 57°C (for 2 h) and found some thermotolerant genotypes (Table 7.3).

7.5.4.3 Salinity

Foxtail and finger millets are the potential crops for salt-affected soils (Krishnamurthy et al., 2014a, 2014b). Most recently at ICRISAT, Krishnamurthy et al. (2014b) studied the finger millet crop response to salinity in terms of total shoot or grain biomass at maturity using mini core collection and grouped the accessions into tolerant (22), moderately tolerant (20), sensitive (21), and the sensitive and late ones (5) based on yield

under saline condition (Table 7.3). Similarly, Krishnamurthy et al. (2014a) screened the foxtail millet core collection under saline condition in pot culture, which revealed a large variation for salinity tolerance and identified salinity-tolerant accessions (Table 7.3).

7.5.4.4 Lodging

Lodging is a constraint in many crops, including finger and foxtail millets mainly due to soft stalk that are prone to lodging and crop management and environmental factors. In foxtail millet, Tian et al. (2010) suggested lodging coefficient as a suitable indicator for field selection for lodging resistance. Foxtail millet landraces and improved varieties that resist lodging have been reported from China (Table 7.3). Reddy et al. (2009) reported that 25.29% of the finger millet germplasm from East African countries assembled at ICRISAT were of nonlodging types, mostly from Uganda and Kenya, which could be used as sources to transfer the trait into new breeding lines after multienvironment evaluation.

7.5.4.5 Waterlogging

Finger millet is relatively tolerant to waterlogging as well as drought, while foxtail millet is susceptible to waterlogging but tolerant to drought (Kono et al., 1987). Prolonged waterlogging decreased total root number in finger millet, but increased in foxtail millet (Kono et al., 1988). Zegada-Lizarazu and Iijima (2005) reported significant reduction of water use efficiency (WUE) in these crops under waterlogging, while under drought condition significant reduction was for shoot dry weight and leaf area. Few varieties were reported as tolerant to waterlogging in foxtail millet like Jinan 8337 (Zhang and Guan, 1995) and Lugu 7 (Chen and Qi, 1993); however, extensive screening has not been reported in both crops.

7.6 Use of germplasm in crop improvement

Germplasm resources provide a pool of genes for breeding high-yielding, biotic- and abiotic-resistant cultivars. Systematic breeding efforts and utilization of genetic resources are limited in finger and foxtail millets. Use of germplasm accessions can be enhanced if small subsets of a few hundred germplasm accessions, which represent the entire diversity present in the crop species, are available. At ICRISAT, Upadhyaya et al. (2006a, 2008) formed core collections in finger and foxtail millets (Table 7.4). For establishing core collection in foxtail millet, entire germplasm accessions were stratified into three taxonomic races (*indica*, *maxima*, and *moharia*). Principal coordinate analysis was performed on 12 qualitative traits for each of the biological races separately that resulted in the formation of 29 clusters. From each cluster, 10% of the accessions were selected to constitute a core collection of 155 accessions (Upadhyaya et al., 2008). Similarly, the entire germplasm collection of finger millet was stratified into four regions: Africa, Asia, America, and Europe. The information on country of origin was not available for 181 accessions, which were grouped into “unknown”

Table 7.4 Representative germplasm subsets of foxtail and finger millets germplasm collection

Crop	Germplasm subsets	No. of accessions used	No. of traits/SSRs involved	No. of accessions in subset	References
Finger millet	Core	5940	14	622	Upadhyaya et al. (2006a)
	Core	4511		551	Gowda et al. (2007b)
	Core	1000	23	77	Haradari et al. (2012)
	Mini core	622	20	80	Upadhyaya et al. (2010)
	Composite collection	–	–	1000	Upadhyaya et al. (2005)
	Reference set	1000	19	300	Upadhyaya (2008a)
Foxtail millet	Core	1474	23	155	Upadhyaya et al. (2008)
	Core	1478	23	156 and 78	Gowda et al. (2007a)
	Mini core	155	21	35	Upadhyaya et al. (2011b)
	Composite collection	–	–	500	Upadhyaya et al. (2006b)
	Reference set	500	20 SSRs	200	Upadhyaya (2008b)

region. A principal component analysis (PCA) was performed on the accessions from each region. A hierarchical cluster analysis was conducted on the first five PCA scores in each region separately. From each cluster, about 10% accessions were randomly selected to form the core collection (Upadhyaya et al. 2006a). Core collections of finger and foxtail millets developed at ICRISAT were further evaluated under multiple environments for morphoagronomic traits and formed core of core called mini core collections (Upadhyaya et al., 2010, 2011b, Table 7.4). Gowda et al. (2007a, 2007b) developed core collections in foxtail and finger millets. The core and mini core collection approaches provide an effective mechanism for proper exploitation of germplasm resources for trait identification and allele mining.

ICRISAT currently conserves 6,804 accessions (including 204 wild accessions) of finger millet and 1,542 accessions (including 54 wild accessions) of foxtail millet, and a total of 41,956 and 16,435 seed samples of finger and foxtail millets, respectively, were supplied to 50 and 53 countries, respectively. It includes a total of 35 sets of finger millet, and 24 sets of foxtail millet core/mini core collection/reference set. Among the germplasm accessions supplied, five accessions of finger millet were released

directly as varieties in Zambia (IE 2929, IE 2947), Uganda (IE 2440, IE 4625), and Kenya (IE 4115).

Wild foxtail genotypes that are highly exposed to herbicides evolved to be resistant to some herbicides were utilized to transfer the herbicide resistance into cultivated foxtail millet, which enables the use of herbicides in foxtail millet cultivation. For example, the herbicide sethoxydim-resistant green foxtail millet collected in a cultivated field in Manitoba, Canada (population UM131) was found to be 3000 times more resistant to sethoxydim than the wild type (Wang and Darmency, 1997) and 54, 29, 11 times more resistant to tralkoxydim, diclofop-methyl, and fenoxaprop-*p*-ethyl than the wild type, respectively (Heap and Morrison, 1996). Wang and Darmency (1997) transferred sethoxydim resistance from green foxtail to breed foxtail millet with improved herbicide resistance.

Various male-sterile lines of foxtail millet have been identified having dominant, recessive genes and photo/thermosensitive nuclear system (Cui et al., 1979; Wang et al., 1993, 2002, 2010b; Zhao et al., 1996; Hao et al., 2009), gene interaction male-sterile lines (Hu et al., 1986), cytoplasmic male sterility (Zhu et al., 1991), and cytoplasmic-nuclear male-sterile type (Zhi et al., 2007). These lines are potential sources for heterosis breeding in foxtail millet and have been used in developing hybrid cultivars in China. For example, Zhangzagu 5, a high yielding hybrid cultivar, was released from Zhangjiakou Academy of Agricultural Sciences, Hebei Province (Liu et al. 2014). Most of the currently released Chinese spring foxtail millet male-sterile lines were derived from Chang10A, whose cytoplasm was contributed by Qinyuanmujizui (Liu et al., 2011a; Wang et al., 1998b), while most summer foxtail millet male-sterile lines were derived from Huangmi1A with the cytoplasm from Dahuanggu (Liu et al., 1996, 2006). In the case of finger millet, Gupta et al. (1997) reported a genetic male-sterile line, INFM 95001, identified through treating the finger millet germplasm accession IE 3318 (=SDFM 63 from Zimbabwe) with ethyl methane sulfonate (EMS), would facilitate crossing for the production of finger millet hybrid progenies to generate new segregants to enhance genetic recombination in recurrent selection programs for finger millet improvement.

7.7 Limitations in germplasm use

Though considerable numbers of germplasm accessions are available nationally and internationally in foxtail and finger millets (Table 7.1), breeders continue to use only a limited number of accessions. Therefore, a large number of valuable accessions remain unexplored mainly due to nonavailability of precise data on traits of economic interest, limited research efforts, and funding. Forming representative core and mini core collections from the entire collection can enhance the use of germplasm in breeding programs because of the reduced size of collections that capture the diversity of entire collections of the particular species. Interestingly, representative germplasm subsets like core, mini core, and composite collections, and genotyping-based reference sets are available in both crops (Table 7.4) that can serve as potential resources for crop improvement and for genomic studies.

7.8 Germplasm enhancement through wide crosses

Foxtail and finger millets are self-fertilizing crops with some amount of cross-pollination occurring in foxtail millet (4%) (Li et al., 1935) and finger millet (1%) mediated by wind (Jansen and Ong, 1996; Purseglove, 1972). Floral morphology and anthesis behavior make them the most difficult species for hybridization; however, emasculation and crossing techniques have been reported (Li et al., 1935; Richardson, 1958; Siles et al., 2001). The interspecific hybridization studies in finger millet were mostly with the view to determine genome relationship; however, these studies provide basic information on crossability and barriers, genome relationship, and so on. Interspecific F_1 hybrids, *E. indica* × *E. floccifolia* and *E. tristachya* × *E. indica* were made to investigate species genome affinity and crossing barriers, suggesting that genomes of *E. floccifolia* and *E. tristachya* are homologous to *E. indica* (Salimath et al., 1995b). Later, Mallikharjun et al. (2005) made an interspecific hybridization involving two tetraploid species (*E. coracana* and *E. africana*) and four diploid species, namely, *E. intermedia*, *E. indica*, *E. floccifolia*, and *E. tristachya* ($2n = 2x = 18$), and suggested *E. indica* with AA genome as the pivotal donor species in the evolution of *E. africana* and *E. coracana*. The crosses *E. intermedia* × *E. coracana*, *E. tristachya* × *E. coracana*, *E. africana* × *E. indica*, *E. africana* × *E. floccifolia* and *E. intermedia* × *E. africana* showed crossability of 3.2–8.3%, and the resultant triploid hybrids showed normal growth and substantial flowering, but the anthers were mostly shriveled with little content in them resulting in drastic reduction of pollen stainability (2–8%) in F_1 hybrids and all these plants were completely sterile (Mallikharjun et al., 2005). The hybrid between *E. coracana* × *E. africana* was found to be intermediate between parents for most of the traits such as productive tillers, finger length, finger number and days to 50% flowering, and exhibits reduced pollen fertility compared to their parents (Shet et al., 2010b). Interspecific hybrids were successfully produced, when *E. intermedia* was used as a female parent in two crosses involving *E. indica* and *E. floccifolia* and as male parent with *E. tristachya*; however, all F_1's were completely sterile and reciprocal crosses in all the three combinations (*E. intermedia* × *E. indica*, *E. intermedia* × *E. floccifolia* and *E. tristachya* × *E. intermedia*) did not yield F_1 hybrids. The F_1 hybrids showed characteristics that were intermediate in nature or similar to one of the parents (Devarumath et al., 2005). Evaluation and utilization of wild gene pool for crop improvement has received limited research attention. *E. africana* is a close relative of the cultivated species of *E. coracana*. Earlier reports indicate that gene transfer from *E. africana* to *E. coracana* is feasible and useful in breeding. *E. africana* has more tillering ability (15–20), high drought tolerance capacity, matures early (95–100 days), and has more fingers per ear and long finger length (Shet et al., 2010b). Interspecific hybridization between *E. africana* and cultivated finger millet varieties (HR 911, PR 201, Indaf 8, HR911, and PR 202) were attempted in order to transfer some of the desirable characters from wild species to the popular cultivars. The hybrids were intermediate for productive tillers, finger length, finger number, and days to 50% flowering and exhibited reduced pollen fertility (Shet et al., 2009, 2010a).

The green millet (*S. viridis*) could be an interesting source for improvement of foxtail millet without a complex and time-consuming breeding strategy as only two backcross generations associated with selection are enough to eliminate weedy characters and to return to the cultivated type (Naciri et al., 1992). Zangre and Darmency (1993) reported that it could be possible to recover the cultivated type using a simple selection procedure in F_2 and F_3. Darmency et al. (1987) demonstrated the potential of interspecific hybridization between cultivated foxtail millet and its wild progenitor green foxtail, and polyploidization to improve the traits of foxtail millet. The tetraploidization resulted in a shift in characteristics toward the crop species; especially, a twofold increase in seed weight was noticed. Nonadditive effects were found for most characters, except for the seed shedding, which was found to be encoded by at least four loci. Cultivated type plants were easily recovered in the diploid and the tetraploid F_2 (Darmency et al., 1987). Interspecific hybridizations between foxtail millet cultivars and a green foxtail resistant to the herbicides have also been made to transfer herbicide resistance into cultivated foxtail millet and obtained resistant genotypes (Darmency and Pernès, 1985; Wang and Darmency, 1997; Darmency et al., 1987). Recently, Qie et al. (2014) made an interspecific hybridization between *S. italica* × *S. viridis* and identified QTLs that contribute to germination and early seedling drought tolerance. They found that both *S. viridis* and *S. italica* contributed favorable alleles for drought tolerance indicating that wild *S. viridis* populations may serve as a reservoir for novel stress tolerance alleles, which could be employed in foxtail millet breeding.

7.9 Integration of genomic and genetic resources in crop improvement

7.9.1 Molecular markers and genome sequence

Genomic resources, like availability of molecular markers, linkage maps, and genome sequence, are essential for gene tagging, quantitative trait loci (QTL) mapping, and marker-assistant selection for rapid crop improvement. However, these genomic resources are limited in finger millet. As a result, limited numbers of markers have been developed (Table 7.5). The Bio-Innovate Program has initiated a finger millet genome-sequencing project by partnering with the African Orphan Crop Consortium. This initiative is being coordinated by ICRISAT, Nairobi in partnership with Biosciences eastern and central Africa (BecA) Hub, University of California, University of Georgia (UGA), and the Swedish University of Agricultural Sciences (SLU).

In foxtail millet, large numbers of molecular markers have been developed like SSR (simple sequence repeat), expressed sequence tag–simple sequence repeat (EST–SSR), intron length polymorphic (ILP), transposable element (TE), and microRNA (miRNA)-based markers during pregenome sequence era. The major breakthrough in the area of *Setaria* genomics is the release of two reference genome sequences (Bennetzen et al., 2012; Zhang et al., 2012a). Zhang et al. (2012a) sequenced the

Table 7.5 Genomic resources of finger and foxtail millets

DNA markers	No. of markers	References
Finger millet		
Nucleotide binding site (NBS); leucine-rich repeat (LRR)	9	Panwar et al. (2011)
EST–SSR	17	Arya et al. (2009)
	11	Panwar et al. (2011)
	30	Naga et al. (2012)
	545	Babu et al. (2014d)
	58	Babu et al. (2014c)
	74	Babu et al. (2014b)
	56	Nirgude et al. (2014)
SSR	82	Dida et al. (2007)
	27	Reddy et al. (2011)
	49	Musia (2013)
Foxtail millet		
EST–SSRs	26	Jia et al. (2007)
	12	Obidiegwu et al. (2013)
	447	Kumari et al. (2013)
SSR	269	Jia et al. (2009)
	143	Zhao et al. (2012)
	172	Gupta et al. (2012)
	64	Gupta et al. (2013)
	45	Lin et al. 2011
	35	Sato et al. (2013)
	21,294	Pandey et al. (2013)
	788	Zhang et al. (2014)
Intron length polymorphism (ILP) markers	98	Gupta et al. (2011)
	5,123	Muthamilarasan et al. (2014)
Transposable elements (TE) based markers	20,278	Yadav et al. (2014a)
SV (Structural variants)	152	Bai et al. (2013)
microRNA-based genetic markers	176	Yadav et al. (2014b)

foxtail cv. "Zhang gu" and a predicted genome size of ~485 Mb. Zhang et al. (2012a) also sequenced another genotype of foxtail millet named "A2," a photothermosensitive male-sterile line and identified 542,322 single nucleotide polymorphisms (SNPs), 33,587 small insertion and deletions (indels), and 10,839 structural variants (SV) between A2 and Zhang gu. The sequence analysis showed the presence of 38,801 genes, out of which ~82% were expressed. Bennetzen et al. (2012) sequenced foxtail millet accession "Yugu1" and green foxtail accession "A10." The final genomic sequence assembly contains ~400 Mb of assembly covering ~80% of the genome, showing the presence of 24,000–29,000 expressed genes. The availability of foxtail millet genome sequence in the public domain has enabled large-scale development of genomic

resources through sequence scanning for microsatellite repeat-motifs and physical mapping of markers on chromosomes (Pandey et al., 2013; Zhang et al., 2014; Xu et al., 2013). Next-generation sequencing technologies enable large-scale genotyping and sequencing of germplasm accessions, which enables genome-wide variation analysis and scanning sequence variations like SNP, indels polymorphisms, and SV (Bai et al., 2013; Jia et al., 2013a) (Table 7.5). Foxtail millet core and finger millet mini core collections of ICRISAT germplasm accessions were genotyped for rapid SNP characterization through genotyping-by-sequencing (GBS) approach – a new low-cost, high-throughput sequencing technology. It will enable the study of the population genetics and structure for effective use of these materials for genetic and genomic research (H.D. Upadhyaya, personal communication).

7.9.2 Genetic maps

The first genetic map of foxtail millet genome was reported by Wang et al. (1998c) using RFLP markers. They constructed intra- and inter-specific maps. The intraspecific map was based on the cross, Longgu 25 × Pagoda flower green comprised of nine linkage groups aligned with nine foxtail millet chromosomes using trisomic lines, and it spanned 964 cM. Furthermore, the intraspecific map was compared to an interspecific map developed based on *S. italica* (cv.B100) × *S. viridis* (acc.A10), which showed that the order of the markers and the genetic distances between the loci are highly conserved. Later these intra- and interspecific genetic maps were enriched with additional markers (Devos et al., 1998; Jia et al., 2009; Mauro-Herrera et al., 2013). In addition, many other groups also developed linkage maps, for example, Zhang et al. (2012a) constructed a genetic map from a cross between Zhang gu and A2, and mapped 751 markers including 118 SNPs and 641 SVs; Qie et al. (2014) constructed a genetic map based on an interspecific cross between *S. italica* cv. Yugu 1 and *S. viridis* acc. W53; and Sato et al. (2013) developed genetic map using two F_2 populations (JP. No. 73913 × JP No. 222613 and JP. No. 73913 × JP No. 71640).

In finger millet, Dida et al. (2007) generated the first genetic map based on interspecific F_2 population of the cross between *E. coracana* subsp. *coracana* cv. Okhale-1 and its wild progenitor *E. coracana* subsp. *africana* acc. MD20 using RFLP, AFLP, EST, and SSR markers. Assignment of linkage groups to the A and B genome was done by comparing the hybridization patterns of probes in Okhale-1, MD 20, and *E. indica* (A genome donor to *E. coracana*) acc. MD-36. The maps span 721 and 787 cM for the A and B genome, respectively, covering all 18 finger millet chromosomes at least partially.

A number of studies on comparative genomics involving foxtail millet and finger millet with other members of the grass family have been previously reported (Devos et al., 1998, 2000; Doust et al., 2004; Srinivasachary et al., 2007; Kumari et al., 2013; Muthamilarasan et al., 2014; Pandey et al., 2013). These studies revealed close relationships of the *gramineous* crops indicating syntenic relationship among the chromosomes of foxtail millet with other *gramineous* crops like sorghum, maize, rice, and so on.

7.10 Utilization of genetic and genomic resources

In finger and foxtail millet, core and mini core collections have been developed at ICRISAT (Upadhyaya et al., 2006a, 2008, 2010, 2011b). In addition, with the support from the Generation Challenge Programme, ICRISAT scientists have developed composite collections of finger millet consisting of 1000 accessions (Upadhyaya et al., 2005), and foxtail millet consisting of 500 accessions (Upadhyaya et al., 2006b). Composite collections have been genotyped with SSR markers and genotype-based reference sets have been established in these crops (Upadhyaya, 2008a, 2008b) (Table 7.4). These germplasm subsets represent diversity of the entire collections of the particular species, and are ideal genetic resources for genomic studies and are being used.

Molecular markers have been utilized successfully for phylogeny, genetic structure and diversity, and QTL identification in foxtail millet. Genetic loci responsible for tiller number, axillary branch number, *spikelet-tipped bristles*, *Waxy* gene, and male sterility in foxtail millet have been reported (Wang et al., 1998c, 2013; Devos et al., 1998; Doust et al., 2004, 2005; Doust and Kellogg, 2006; Sato et al. 2013). Qie et al. (2014) reported the genomic regions controlling germination and early seedling drought tolerance in foxtail millet, where the wild green foxtail genotype and the foxtail millet cultivar contributed favorable alleles for the traits, indicating that wild *S. viridis* populations may serve as a reservoir of novel alleles for stress tolerance, which could be employed in foxtail millet breeding. Association of an SNP in a novel DREB2-like gene SiDREB2 with stress tolerance was reported in foxtail millet, and an allele-specific marker for dehydration tolerance has been developed (Lata et al., 2011). Through association mapping approach, genomic regions linked with agronomic traits have been reported in foxtail millet using SSR markers (Vetriventhan, 2011; Gupta et al., 2014b). The advent of next-generation sequencing technologies has enabled large-scale genotyping and resequencing of germplasm accessions. Most recently, Jia et al. (2013a) identified 512 loci associated with 47 agronomic traits through genome-wide association mapping by sequencing 916 diverse foxtail millet varieties (Jia et al., 2013a).

Considerable efforts have also been made in the case of finger millet on utilization of markers and QTL identification. Panwar et al. (2011) designed functional markers based on the nucleotide sequences of different NBS-LRR domain containing blast-resistant genes of cereals. Several primers gave unique bands linked with disease resistance exhibiting clear polymorphism between blast resistant and susceptible genotypes of finger millet. Nirgude et al. (2014) developed EST–SSRs utilizing nucleotide sequences of different candidate genes like *opaque2 modifiers* and calmodulin (CALcium-MODULated proteIN) cereals. The *opaque2 modifier* specific EST–SSRs could differentiate the finger millet genotypes into high, medium, and low protein containing genotypes, while calcium-dependent candidate gene based EST–SSRs could differentiate the genotypes based on the calcium content with few exceptions. These results indicate the possible role of genic-SSRs in governing trait variations and could be utilized in germplasm characterization for particular traits like disease resistance and calcium content. Using association-mapping approach, QTLs for agronomic traits, blast disease, and tryptophan and protein content have been identified in finger millet (Babu et al., 2014c, 2014a, 2014b).

7.11 Conclusions

Finger and foxtail millets are the most important crops mostly grown under marginal areas with limited resources. Foxtail millet is a major crop in India, China, and Japan, while finger millet is an important crop in India and African countries. Foxtail and finger millet germplasm accessions conserved globally, reported to have large genetic variation at both phenotypic and molecular level, enable mining of alleles for important traits for yield improvement. Germplasm sets, such as core, mini core, composite, and reference sets, established in these crops have huge applicability in genetic and genomic research, and crop improvement. These crops along with other small millets are considered as "nutri-cereals" owing to their rich nutritional and health benefits; however, few attempts have been made to understand the genetics and genomics of the nutritional trait. Foxtail millet has received more research attention and is considered as a model species to explore plant architectural traits, evolutionary genomics, and physiologic attributes of the C_4 Panicoid crops. In the case of finger millet, genome sequencing has been initiated, and will be available to researchers. Increased use of genetic and genomic resources will guide breeders in developing climate-resilient cultivars in these "nutri-cereals" to enhance food and nutritional security.

References

Ardie, S.W., Khumaida, N., Nur, A., Fauziah, N., 2015. Early identification of salt tolerant foxtail millet (*Setaria italica* L. Beauv.). Proc. Food Sci. 3, 303–312.

Arya, L., Verma, M., Gupta, V.K., Karihaloo, J.L., 2009. Development of EST–SSRs in finger millet (*Eleusine coracana* ssp. *coracana*) and their transferability to pearl millet (*Pennisetum glaucum*). J. Plant Biochem. Biotechnol. 18 (1), 97–100.

Austin, D.F., 2006. Fox-tail millets (*Setaria*: Poaceae) – abandoned food in two hemispheres. Econ. Bot. 60 (2), 143–158.

Babu, D.V., Sudhakar, P., Reddy, Y.S.K., 2013a. Screening of thermotolerant ragi genotypes at seedling stage using TIR technique. Bioscan 8 (4), 1493–1495.

Babu, T.K., Thakur, R.P., Upadhyaya, H.D., Reddy, P.N., Sharma, R., Girish, A.G., et al., 2013b. Resistance to blast (*Magnaporthe grisea*) in a mini-core collection of finger millet germplasm. Eur. J. Plant Pathol. 135, 299–311.

Babu, B.K., Agrawal, P.K., Pandey, D., Jaiswal, J.P., Kumar, A., 2014a. Association mapping of agro-morphological characters among the global collection of finger millet genotypes using genomic SSR markers. Mol. Biol. Rep. 41 (8), 5287–5297.

Babu, B.K., Agrawal, P.K., Pandey, D., Kumar, A., 2014b. Comparative genomics and association mapping approaches for opaque2 modifier genes in finger millet accessions using genic, genomic and candidate gene-based simple sequence repeat markers. Mol. Breed. 34 (3), 1261–1279.

Babu, B.K., Dinesh, P., Agrawal, P.K., Sood, S., Chandrashekara, C., Bhatt, J.C., et al., 2014c. Comparative genomics and association mapping approaches for blast resistant genes in finger millet using SSRs. PloS ONE 9 (6), e99182.

Babu, B.K., Pandey, D., Agrawal, P.K., Sood, S., Kumar, A., 2014d. *In-silico* mining, type and frequency analysis of genic microsatellites of finger millet (*Eleusine coracana* (L.)

Gaertn.): a comparative genomic analysis of NBS-LRR regions of finger millet with rice. Mol. Biol. Rep. 41 (5), 3081–3090.

Bai, H., Cao, Y., Quan, J., Dong, L., Li, Z., Zhu, Y., et al., 2013. Identifying the genome-wide sequence variations and developing new molecular markers for genetics research by re-sequencing a landrace cultivar of foxtail millet. PLoS ONE 8, e73514.

Bawazir, A.A., Bamousa, A.S., 2014. Biodiversity and conservation of plant genetic resources on Socotra. Discourse J. Agric. Food Sci. 2 (7), 217–224.

Begum, F., Sultana, R., Nessa, A., 2013. Screening of drought tolerant foxtail millet (*Setaria italica* Beauv.) germplasm. Bangladesh J. Sci. Ind. Res. 48 (4), 265–270.

Benabdelmouna, A., Abirached-Darmency, M., Darmency, H., 2001. Phylogenetic and genomic relationships in *Setaria italica* and its close relatives based on the molecular diversity and chromosomal organization of 5S and 18S-5.8S-25S rDNA genes. Theor. Appl. Genet. 103, 668–677.

Bennetzen, J.L., Schmutz, J., Wang, H., Percifield, R., Hawkins, J., Pontaroli, A.C., et al., 2012. Reference genome sequence of the model plant *Setaria*. Nat. Biotechnol. 30, 555–561.

Bharathi, A., 2011. Phenotypic and genotypic diversity of global finger millet (*Eleusine coracana* (L.) gaertn.) composite collection. PhD Thesis. Tamil Nadu Agricultural University, Coimbatore, Tamil Nadu.

Bhatt, D., Negi, M., Sharma, P., Saxena, S.C., Dobriyal, A.K., Arora, S., 2011. Responses to drought induced oxidative stress in five finger millet varieties differing in their geographical distribution. Physiol. Mol. Biol. Plants 17 (4), 347–353.

Bisht, M.S., Mukai, Y., 2001. Genomic *in situ* hybridization identifies genome donor of finger millet (*Eleusine coracana*). Theor. Appl. Genet. 102, 825–832.

Chen, J., Qi, Y., 1993. Recent developments in foxtail millet cultivation and research in China. In: Riley, K.W., Gupta, S.C., Seetharam, A., Mushonga, J.N. (Eds.), Advances in Small Millets. Oxford and IBH Publishing Co, New Delhi, pp. 101–107.

Cui, W.S., Du, G., Zhao, Z.H., 1979. The selection and utilization of male sterile line/Shanxi 280 of foxtail millet. Sci. Agric. Sin. 12, 43–46, (in Chinese).

Dagnachew, L., De Villiers, S., Sewalem, T., Dida, M., Masresha, F., Kimani, W., et al., 2014. Genetic diversity and eco-geographical distribution of *Eleusine* species collected from Ethiopia. Afr. Crop Sci. J. 22 (1), 45–58.

Darmency, H., Pernès, J., 1985. Use of wild *Setaria viridis* (L.) Beauv. to improve triazine resistance in cultivated *S. italica* (L.) by hybridization. Weed Res. 25, 175–179.

Darmency, H., Ouin, C., Pernès, J., 1987. Breeding foxtail millet (*Setaria italica*) for quantitative traits after interspecific hybridization and polyploidization. Genome 29, 453–456.

de Wet, J.M.J., Oestry-Stidd, L.L., Cubero, J.L., 1979. Origins and evolution of foxtail millet. J. d'agriculture traditionnelle et de botanique appliquée 26, 53–63.

de Wet, J.M.J., Prasada Rao, K.E., Brink, D.E., Mengesha, M.H., 1984. Systematic and evolution of *Eleusine coracana* (Gramineae). Am. J. Bot. 71, 550–557.

Devarumath, R.M., Hiremath, S.C., Rao, S.R., Kumar, A., Bewal, S., 2005. Genome analysis of finger millet *E. coracana* by interspecific hybridization among diploid wild species of *Eleusine* (Poaceae). Cytologia 70 (4), 427–434.

Devos, K.M., Wang, Z.M., Beales, C.J., Sasaki, T., Gale, M.D., 1998. Comparative genetic maps of foxtail millet (*Setaria italica*) and rice (*Oryza sativa*). Theor. Appl. Genet. 96, 63–68.

Devos, K.M., Pittaway, T.S., Reynolds, A., Gale, M.D., 2000. Comparative mapping reveals a complex relationship between the pearl millet genome and those of foxtail millet and rice. Theor. Appl. Genet. 100, 190–198.

Diao, X.M., 2011. Current status of foxtail millet production in China and future development directions. The Industrial Production and Development System of Foxtail Millet in China. Chinese Agricultural Science and Technology Press, Beijing, pp. 20–30.

Dida, M.M., Srinivasachary, Ramakrishnan, S., Bennetzen, J.L., Gale, M.D., Devos, K.M., 2007. The genetic map of finger millet, *Eleusine coracana*. Theor. Appl. Genet. 114, 321–332.

Doust, A.N., Kellogg, E.A., 2006. Effect of genotype and environment on branching in weedy green millet (*Setaria viridis*) and domesticated foxtail millet (*Setaria italica*) (Poaceae). Mol. Ecol. 15, 1335–1349.

Doust, A.N., Devos, K.M., Gadberry, M.D., Gale, M.D., Kellogg, E.A., 2004. Genetic control of branching in foxtail millet. Proc. Natl. Acad. Sci. USA 101 (24), 9045–9050.

Doust, A.N., Devos, K.M., Gadberry, M.D., Gale, M.D., Kellogg, E.A., 2005. The genetic basis for inflorescence variation between foxtail and green millet (Poaceae). Genetics 169 (3), 1659–1672.

Dwivedi, S., Upadhyaya, H.D., Senthilvel, S., Hash, C.T., Fukunaga, K., Diao, X., et al., 2012. Millets: genetic and genomic resources. Plant Breed. Rev. 35, 247–375.

Gowda, J., Rekha, D., Krishnappa, M., 2007a. Methods of constructing core set using agro-morphological traits in foxtail millet [*Setaria italica* (L.) Beauv.]. J. Plant Genet. Res. 20 (3), 193–198.

Gowda, J., Somu, G., Mathur, P.N., 2007b. Formation of core set in finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm using geographical origin and morpho-agronomic characters. Indian J. Plant Genet. Res. 20, 38–42.

Gupta, S.C., Muza, F.R., Andrews, D.J., 1997. Registration of INFM 95001 finger millet genetic male sterile line. Crop Sci. 37, 1409.

Gupta, S., Kumari, K., Das, J., Lata, C., Puranik, S., Prasad, M., 2011. Development and utilization of novel intron length polymorphic markers in foxtail millet (*Setaria italica* (L.) P. Beauv.). Genome 54, 586–602.

Gupta, S., Kumari, K., Sahu, P.P., Vidapu, S., Prasad, M., 2012. Sequence-based novel genomic microsatellite markers for robust genotyping purposes in foxtail millet [*Setaria italica* (L.) P. Beauv.]. Plant Cell Rep. 31, 323–337.

Gupta, S., Kumari, K., Muthamilarasan, M., Subramanian, A., Prasad, M., 2013. Development and utilization of novel SSRs in foxtail millet [*Setaria italica* (L.) P. Beauv.]. Plant Breed. 132 (4), 367–374.

Gupta, S., Garg, R., Kumar, S., Sengar, R.S., 2014a. Assessment of finger millet (*Eleusine coracana* L.) genotypes for drought tolerance at early seedling growth stages. Vegetos 27 (3), 227–230.

Gupta, S., Kumari, K., Muthamilarasan, M., Parida, S.K., Prasad, M., 2014b. Population structure and association mapping of yield contributing agronomic traits in foxtail millet. Plant Cell Rep. 33, 881–893.

Hao, X.F., Wang, J.Z., Wang, G.Q., Wang, L.Y., Wang, X.Y., 2009. AFLP analysis of photo sensitive male sterile gene in millet. J. Shanxi Agric. Sci. 37, 10, (in Chinese).

Haradari, C., Gowda, J., Ugalat, J., 2012. Formation of core set in Indian and African finger millet [*Eleusine coracana* (L.) Gaertn.] germplasm accessions. Indian J. Genet. 72 (3), 358–363.

Harlan, J.R., de Wet, J.M.J., 1971. Towards a rational taxonomy of cultivated plants. Taxonomy 20, 509–517.

Heap, I.M., Morrison, I.N., 1996. Resistance to aryloxyphenoxypropionate and cyclohexanedione herbicides in green foxtail (*Setaria viridis*). Weed Sci. 44, 25–30.

Hilu, K.W., 1988. Identification of the 'A' genome of finger millet using chloroplast DNA. Genetics 118, 163–167.

Hilu, K.W., de Wet, J.M.J., 1976. Domestication of *Eleusine coracana*. Econ. Bot. 30, 199–208.

Hilu, K.W., de Wet, J.M.J., Harlan, J.R., 1979. Archeobotany and the origin of finger millet. Am. J. Bot. 66, 330–333.

Hirano, R., Naito, K., Fukunaga, K., Watanabe, K.N., Ohsawa, R., Kawase, M., 2011. Genetic structure of landraces in foxtail millet (*Setaria italica* (L.) P. Beauv.) revealed with transposon display and interpretation to crop evolution of foxtail millet. Genome 54, 498–506.

Hiremath, S.C., Chennaveeraiah, M.S., 1982. Cytogeneticals studies in wild and cultivated species of *Eleusine* (Gramineae). Caryologia 35 (1), 57–69.

Hiremath, S.C., Salimath, S.S., 1992. The 'A' genome donor of *Eleusine coracana* (L.) Gaertn. (Gramineae). Theor. Appl. Genet. 84, 747–754.

Hu, H.K., Ma, S.Y., Shi, Y.H., 1986. The discovery of a dominant male-sterile gene in millet (*Setaria italica*). Acta Agron. Sin. 12, 73–78, (in Chinese).

Jain, A.K., Gupta, J.C., Yadava, H.S., 1991. Stability of resistance to blast in foxtail millet. Mysore J. Agric. Sci. 25, 221–223.

Jain, A.K., Joshi, R.P., Singh, G., 2014. Identification of host resistance against banded leaf and sheath blight of foxtail millet. JNKVV Res. J. 48, 170–174.

Jansen, P.C.M., Ong, H.C., 1996. *Eleusine coracana* (L.) Gaertn. In: Grubben, G.H.J., Partohardjono, S. (Eds.), Plant Resources of South-East Asia, No. 10 Cereals. Backhuys Publishers, Leiden, The Netherlands.

Jia, X., Shi, Y., Song, Y., Wang, G., Tian-yu, W., Li, Y., 2007. Development of EST–SSR in foxtail millet (*Setaria italica*). Genet. Resour. Crop Evol. 54, 233–236.

Jia, X., Zhang, Z., Liu, Y., Zhang, C., Shi, Y., Song, Y., et al., 2009. Development and genetic mapping of SSR markers in foxtail millet [*Setaria italica* (L.) P. Beauv.]. Theor. Appl. Genet. 118, 821–829.

Jia, G., Huang, X., Zhi, H., Zhao, Y., Zhao, Q., Li, W., et al., 2013a. A haplotype map of genomic variations and genome-wide association studies of agronomic traits in foxtail millet (*Setaria italica*). Nat. Genet. 45, 957–961.

Jia, G., Shi, S., Wang, C., Niu, Z., Chai, Y., Zhi, H., et al., 2013b. Molecular diversity and population structure of Chinese green foxtail [*Setaria viridis* (L.) Beauv.] revealed by microsatellite analysis. J. Exp. Bot. 64 (12), 3645–3656.

Jiyaju, C., 1989. Importance and genetic resources of small millets with emphasis on foxtail millet (*Setaria italica*) in China. In: Seetharam, A., Riley, K.W., Harinarayana, G. (Eds.), Small Millets in Global Agriculture. Oxford and IBH publishing, New Delhi, India, pp. 101–104.

Jiyaju, C., Yuzhi, Q., 1993. Recent developments in foxtail millet cultivation and research in China. In: Seetharam, A., Riley, K.W., Harinarayana, G. (Eds.), Small Millets in Global Agriculture. Oxford and IBH publishing, New Delhi, India, pp. 101–107.

Kono, Y., Yamauchi, A., Kawamura, N., Tatsumi, J., Nonoyama, T., Inagaki, N., 1987. Interspecific differences of the capacities of waterlogging and drought tolerances among summer cereals. Japan J. Crop Sci. 56, 115–129.

Kono, Y., Yamauchi, A., Nonoyama, T., 1988. Comparison of growth response to waterlogging of summer cereals with special reference to rooting ability. Japan J. Crop Sci. 57, 321–331.

Krishnamurthy, L., Upadhyaya, H.D., Gowda, C.L.L., Kashiwagi, J., Purushothaman, R., Singh, S., et al., 2014a. Large variation for salinity tolerance in the core collection of foxtail millet (*Setaria italica* (L.) P. Beauv.) germplasm. Crop Pasture Sci. 65, 353–361.

Krishnamurthy, L., Upadhyaya, H.D., Purushothaman, R., Gowda, C.L.L., Kashiwagi, J., Dwivedi, S.L., et al., 2014b. The extent of variation in salinity tolerance of the mini core collection of finger millet (*Eleusine coracana* L. Gaertn.) germplasm. Plant Sci. 227, 51–59.

Kumar, B., Kumar, J., 2009. Evaluation of small millet genotypes against endemic diseases in mid-western Himalayas. Indian Phytopathol. 62 (4), 518–521.

Kumari, K., Muthamilarasan, M., Misra, G., Gupta, S., Subramanian, A., Parida, S.K., et al., 2013. Development of eSSR-Markers in *Setaria italica* and their applicability in studying genetic diversity, cross-transferability and comparative mapping in millet and non-millet species. PloS ONE 8 (6), e67742.

Lata, C., Bhutty, S., Bahadur, R.P., Majee, M., Prasad, M., 2011. Association of an SNP in a novel DREB2-like gene SiDREB2 with stress tolerance in foxtail millet [*Setaria italica* (L.)]. J. Exp. Bot. 62 (10), 3387–3401.

Li, Y.M., 1997. Breeding for foxtail millet drought tolerant cultivars (in Chinese). In: Li, Y. (Ed.), Foxtail Millet Breeding. Chinese Agriculture Press, Beijing, China, pp. 421–446.

Li, H., Meng, W.J., Liu, T.M., 1935. Problems in the breeding of millet [*Setaria italica* (L.) Beauv.]. J. Am. Soc. Agron. 27, 426–438.

Li, C.H., Pao, W.K., Li, H.W., 1942. Interspecific crosses in *Setaria*. II. Cytological studies of interspecific hybrids involving 1, *S. faberii* and *S. italica*, and 2. A three way cross, F_2 of *S. italica* × *S. viridis* and *S. faberii*. J. Hered. 33, 351–355.

Li, Y., Wu, S., Cao, Y., 1995. Cluster analysis of an international collection of foxtail millet (*Setaria italica* (L.) P. Beauv.). Euphytica 83, 79–85.

Li, G.Y., Fan, Z.Y., Liu, F., Zhang, P., Li, W.X., Liu, Q.S., et al., 2009. Studies on vitamin E in foxtail millet determined by HPLC method. J. Agric. Sci. Technol. 11 (1), 129–133.

Lin, H., Chiang, C., Chang, S., Kuoh, C., 2011. Development of simple sequence repeats (SSR) markers in *Setaria italica* (Poaceae) and cross-amplification in related species. Int. J. Mol. Sci. 12, 7835–7845.

Liu, Z.L., Cheng, R.H., Li, X.Y., 1996. The pedigree analysis and evaluation of north China summer millets. Crops 5, 24, (in Chinese).

Liu, Z.L., Cheng, R.H., Zhang, F.L., Xia, X.Y., Shi, Z.G., Hou, S.L., 2006. Millet variety in boreali-sinica summer millets region and its pedigree evolution and analysis on genetic foundation. Acta Agric. Boreali-Sin. Suppl. 21, 103–109, (in Chinese).

Liu, Z., Bai, G., Zhang, D., Zhu, C., Xia, X., Cheng, R., et al., 2011a. Genetic diversity and population structure of elite foxtail millet [*Setaria italica* (L.) P. Beauv.] germplasm in China. Crop Sci. 51, 1655–1663.

Liu, Q., Triplett, J.K., Wen, J., Peterson, P.M., 2011b. Allotetraploid origin and divergence in *Eleusine* (Chloridoideae, Poaceae): evidence from low-copy nuclear gene phylogenies and a plastid gene chronogram. Ann. Bot. 108 (7), 1287–1298.

Liu, Q., Iang, B., Wen, J., Peterson, P.M., 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.

Mallikharjun, D.R., Hiremath, S.C., Rao, S.R., Kumar, A., Sheelavanthmath, S.S., 2005. Genome interrelationship in the genus *Eleusine* (Poaceae) as revealed through heteroploid crosses. Caryologia 58 (4), 300–307.

Maloo, S.R., Saini, D.P., Paliwal, R.V., 2001. Meera (SR 16) – a dual purpose variety of foxtail millet. Int. Sorghum Millets Newsl. 42, 75–76.

Mantur, S.G., Viswanath, S., Kumar, T.B.A., 2001. Evaluation of finger millet genotypes for resistance to blast. Indian Phytopathol. 54 (3), 387.

Maqsood, M., Ali, S.N.A., 2007. Effects of environmental stress on growth, radiation use efficiency and yield of finger millet (*Eleusine coracana*). Pak. J. Bot. 39 (2), 463–474.

Mauro-Herrera, M., Wang, X., Barbier, H., Brutnell, T.P., Devos, K.M., Doust, A.N., 2013. Genetic control and comparative genomic analysis of flowering time in *Setaria* (Poaceae). Genes Genome Genet. 3, 283–295.

Mbabwine, Y., Sabiiti, E.N., Kiambi, D., 2005. Assessment of the status of plant genetic resources in Kabale highlands, Uganda: a case of cultivated crop species. Commissioned by GMP to IPGRI, p. 71.

Mehra, K.K., 1962. Natural hybridization between *Eleusine coracana* and *E. africana* in Uganda. J. Indian Bot. Soc. 41, 531–539.

Musia, G.D., 2013. Identification of microsatellite markers for finger millet (*Eleusine coracana*) by analysis of roche 454 gs-flx titanium sequence data. MSc Thesis. School of Pure and Applied Sciences of Kenyatta University, Nairobi.

Muthamilarasan, M.E., Suresh, B.V., Pandey, G.A., Kumari, K.A., Parida, S.W.K.U., Prasad, M.A., 2014. Development of 5123 intron-length polymorphic markers for large-scale genotyping applications in foxtail millet. DNA Res. 21, 41–52.

Muza, F.R., Lee, D.J., Andrews, D.J., Gupta, S.C., 1995. Mitochondrial DNA variation in finger millet (*Eleusine coracana*). Euphytica 81, 199–205.

Naciri, Y., Darmency, H., Belliard, J., Dessaint, F., Pernès, J., 1992. Breeding strategy in foxtail millet, *Setaria italica* (L. P. Beauv.) following interspecific hybridization. Euphytica 60 (*2*), 97–103.

Naga, B.L.R.I., Mangamoori, L.N., Subramanyam, S., 2012. Identification and characterization of EST–SSRs in finger millet (*Eleusine coracana* (L.) Gaertn.). J. Crop Sci. Biotechnol. 15 (1), 9–16.

Nagaraja, A., Jagadish, P.S., Ashok, E.G., Gowda, K.T.K., 2007. Avoidance of finger millet blast by ideal sowing time and assessment of varietal performance under rain fed production situation in Karnataka. J. Mycopathol. Res. 45 (2), 237–240.

Neshamba, S.M., 2010. Variability for drought tolerance in finger millet (*Eleusine coracana* (L.) Gaertn.] accessions from Zambia. MSc Thesis. School of Agricultural Science of the University of Zambia, Lusaka.

Neves, S.S., Swire-Clark, G., Hilu, K.W., Baird, W.V., 2005. Phylogeny of *Eleusine* (Poaceae: Chloridoideae) based on nuclear *ITS* and plastid *trnT-trnF* sequences. Mol. Phylogenet. Evol. 35, 395–419.

Nirgude, M., Babu, B.K., Shambhavi, Y., Singh, U.M., Upadhyaya, H.D., Kumar, A., 2014. Development and molecular characterization of genic molecular markers for grain protein and calcium content in finger millet (*Eleusine coracana* (L.) Gaertn.). Mol. Biol. Rep. 41 (3), 1189–1200.

Nirmalakumari, A., Vetriventhan, M., 2010. Characterization of foxtail millet germplasm collections for yield contributing traits. Electron. J. Plant Breed. 1, 140–147.

Obidiegwu, O.N., Obidiegwu, J.E., Parzies, H., 2013. Development of SSR for foxtail millet (*Setaria italica* (L.) P. Beauv.) and its utility in genetic discrimination of a core set. Genes Genomics 35, 609–615.

Opole, R., Prasad, P.V.V., Kirkham, M.B., 2010. Effect of high temperature stress on growth, development and yield of finger millet. In: ASA, CSSA, and SSSA 2010 International Annual Meetings. Oct 31 – Nov 4. Long Beach, CA.

Pandey, G., Misra, G., Kumari, K., Gupta, S., Parida, S.K., Chattopadhyay, D., et al., 2013. Genome-wide development and use of microsatellite markers for large-scale genotyping applications in foxtail millet [*Setaria italica* (L.)]. DNA Res. 20 (2), 197–207.

Panwar, P., Jha, A.K., Pandey, P.K., Gupta, A.K., Kumar, A., 2011. Functional markers based molecular characterization and cloning of resistance gene analogs encoding NBS-LRR disease resistance proteins in finger millet (*Eleusine coracana*). Mol. Biol. Rep. 38 (5), 3427–3436.

Philip, J., Maloo, S.R., 1996. An evaluation of *Setaria italica* for seed iron content. Int. Sorghum Millets Newsl. 82, 82–83.

Prasada Rao, K.E., de Wet, J.M.J., 1997. Small millets. In: Fuccilo, D., Sears, L., Stapleton, P. (Eds.), Biodiversity in Trust. Cambridge University Press, UK, pp. 259–272.

Prasada Rao, K.E., de Wet, J.M.J., Brink, D.K., Mengesha, M.H., 1987. Intraspecific variation and systematics of cultivated *Setaria italica*, foxtail millet (Poaceae). Econ. Bot. 41, 108–116.

Prasada Rao, K.E., de Wet, J.M.J., Reddy, V.G., Mengesha, M.H., 1993. Diversity in the small millets collection at ICRISAT. In: Riley, K.W., Gupta, S.C., Seetharam, A., Mushonga, J.N. (Eds.), Advances in Small Millets. Oxford & IBH Publishing Co, New Delhi, India, pp. 331–346.

Purseglove, J.W., 1972. *Eleusine coracana* (L.) Gaertn. Tropical Crops. Monocotyledons. Longman Group Limited, London, UK, pp. 147–156.

Qie, L., Jia, G., Zhang, W., Schnable, J., Shang, Z., Li, W., et al., 2014. Mapping of quantitative trait locus (QTLs) that contribute to germination and early seedling drought tolerance in the interspecific cross *Setaria italica* × *Setaria viridis*. PloS ONE 9 (7), e101868.

Rao, A.N.S., 1990. Estimates of losses in finger millet (*Eleusine coracana*) due to blast disease (*Pyricularia grisea*). J. Agric. Sci. 24, 57–60.

Reddy, V.G., Upadhyaya, H.D., Gowda, C.L.L., 2006. Characterization of world's foxtail millet germplasm collections. SAT eJ. 2, 1–3.

Reddy, V.G., Upadhyaya, H.D., Gowda, C.L.L., Singh, S., 2009. Characterization of eastern African finger millet germplasm for qualitative and quantitative characters at ICRISAT. SAT eJ. 7, 1–9.

Reddy, I.N.B.L., Reddy, D.S., Reddy, V.P., Narasu, M.L., Sivaramakrishnan, S., 2011. Efficient microsatellite enrichment in finger millet (*Eleusine coracana* (L.) Gaertn.) – an improved procedure to develop microsatellite markers. Asian Austral. J. Plant Sci. Biotechnol. 5 (1), 47–51.

Richardson, W.L., 1958. A technique of emasculating small grass florets. J. Genet. 18, 69–73.

Saleh, A.S.M., Zhang, Q., Chen, J., Shen, Q., 2013. Millet grains: nutritional quality, processing, and potential health benefits. Compr. Rev. Food Sci. Food Saf. 12 (3), 281–295.

Salimath, S.S., de Oliveira, A.C., Godwin, I.D., Bennetzen, J.L., 1995a. Assessment of genome origins and genetic diversity in the genus *Eleusine* with DNA markers. Genome 38, 757–763.

Salimath, S.S., Hiremath, S.C., Murthy, H.N., 1995b. Genome differentiation patterns in diploid species of *Eleusine* (Poaceae). Hereditas 122, 189–195.

Sato, K., Mukainari, Y., Naito, K., Fukunaga, K., 2013. Construction of a foxtail millet linkage map and mapping of spikelet-tipped bristles 1 (*stb1*) by using transposon display markers and simple sequence repeat markers with genome sequence information. Mol. Breed. 31 (3), 675–684.

Shailaja, H.B., Thirumeni, S., 2007. Evaluation of salt-tolerance in finger millet (*Eleusine coracana*) genotypes at seedling stage. Indian J. Agric. Sci. 77, 672–674.

Shao, L.H., Wang, L., Bai, W.W., Liu, Y.J., 2014. Evaluation and analysis of folic acid content in millet from different ecological regions in Shanxi province. Sci. Agric. Sin. 47 (7), 1265–1272.

Sharma, R., Girish, A.G., Upadhyaya, H.D., Humayun, P., Babu, T.K., Rao, V.P., et al., 2014. Identification of blast resistance in a core collection of foxtail millet germplasm. Plant Dis. 98 (4), 519–524.

Shet, R.M., Gireesh, C., Jagadeesha, N., Lokesh, G.Y., Gowda, J., 2009. Genetic variability in segregating generation of interspecific hybrids of finger millet (*Eleusine coracana* (L.) Gaertn.). Environ. Evol. 27, 1013–1016.

Shet, R.M., Jagadeesha, N., Lokesh, G.Y., Gireesh, C., Gowda, J., 2010a. Genetic variability, association and path coefficient studies in two interspecific crosses of finger millet [*Eleusine coracana* (L.) Gaertn.]. Int. J. Plant Sci. 5 (1), 24–29.

Shet, R.M., Mallikarjuna, N.M., Kumar, K.S.N., Gowda, J., Kumar, M.V.M., 2010b. Cytomorphological studies in interspecific hybrids of finger millet. Gregor Mendel Found. J. 1, 68–72.

Siles, M.M., Nelson, L.A., Baltensperger, D.D., 2001. Technique for artificial hybridization of foxtail millet [*Setaria italica* (L.) Beauv.]. Crop Sci. 41 (5), 1408–1412.

Srinivasachary, S., Dida, M.M., Gale, M.D., Devos, K.M., 2007. Comparative analyses reveal high levels of conserved colinearity between the finger millet and rice genomes. Theor. Appl. Genet. 115, 489–499.

Suryanarayana, L., Sekhar, D., Rao, N.V., 2014. Genetic variability and divergence studies in finger millet. Int. J. Curr. Microbiol. Appl. Sci. 3 (4), 931–936.

Tian, R.Z., Quan, J.Z., 1995. Niangu 1, a new summer millet cultivar. Crop Genet. Res. 1, 53–54.

Tian, B.H., Wang, S.Y., Li, Y.J., Wang, J.G., Zhang, L.X., Liang, F., et al., 2008. Response to sodium chloride stress at germination and seedling and identification of salinity tolerant genotypes in foxtail millet landraces originated from China. Acta Agron. Sin. 34 (12), 2218–2222.

Tian, B., Wang, J., Zhang, L., Li, Y., Wang, S., Li, H., 2010. Assessment of resistance to lodging of landrace and improved cultivars in foxtail millet. Euphytica 172, 295–302.

Upadhyaya, H.D., 2008a. Genotyping of composite collection of finger millet [*Eleusine coracana* (L.) Gaertn.]. Generation Challenge Program: Cultivating Plant Diversity for the Resource Poor (Abstract). CIMMYT, Mexico, pp. 64–65.

Upadhyaya, H.D., 2008b. Genotyping of composite collection of foxtail millet [*Setaria italica* (L). P. Beauv.]. Generation Challenge Program: Cultivating Plant Diversity for the Resource Poor (Abstract). CIMMYT, Mexico, pp. 66–67.

Upadhyaya, H.D., Pundir, R.P.S., Hash, C.T., Hoisington, D., Chandra, S., Gowda, C.L.L., et al., 2005. Genotyping finger millet germplasm – developing composite collection. Generation Challenge Program Review Meeting, September 2005, Rome, Italy.

Upadhyaya, H.D., Gowda, C.L.L., Pundir, R.P.S., Reddy, V.G., Singh, S., 2006a. Development of core subset of finger millet germplasm using geographical origin and data on 14 quantitative traits. Genet. Resour. Crop Evol. 53, 679–685.

Upadhyaya, H.D., Varshney, R.K., Hash, C.T., Hoisington, D.A., Gowda, C.L.L., Reddy V.G., et al., 2006b. Development of composite collection and genotyping of foxtail millet (*Setaria italica* (L.) Beauv.) composite collection, Generation Challenge Program Annual Research Meeting, September 2006, Sao Paulo, Brazil.

Upadhyaya, H.D., Gowda, C.L.L., Reddy, V.G., 2007. Morphological diversity in finger millet germplasm introduced from Southern and Eastern Africa. SAT eJ. 3 (1), 1–3.

Upadhyaya, H.D., Pundir, R.P.S., Gowda, C.L.L., Reddy, V.G., Singh, S., 2008. Establishing a core collection of foxtail millet to enhance the utilization of germplasm of an underutilized crop. Plant Genet. Resour. 7 (2), 177–184.

Upadhyaya, H.D., Sarma, N.D.R.K., Ravishankar, C.R., Albrecht, T., Narasimhudu, Y., Singh, S.K., et al., 2010. Developing a mini-core collection in finger millet using multilocation data. Crop Sci. 50, 1924–1931.

Upadhyaya, H.D., Ramesh, S., Sharma, S., Singh, S.K., Varshney, S.K., Sarma, N.D.R.K., et al., 2011a. Genetic diversity for grain nutrients contents in a core collection of finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm. Field Crops Res. 121, 42–52.

Upadhyaya, H.D., Ravishankar, C.R., Narasimhudu, Y., Sarma, N.D.R.K., Singh, S.K., Varshney, S.K., et al., 2011b. Identification of trait-specific germplasm and developing a mini core collection for efficient use of foxtail millet genetic resources in crop improvement. Field Crops Res. 124, 459–467.

Vadivoo, A.S., Joseph, R., Ganesan, N.M., 1998. Genetic variability and diversity for protein and calcium contents in finger millet (*Eleusine coracana* (L.) Gaertn.) in relation to grain color. Plant Foods Hum. Nutr. 52 (4), 353–364.

Vetriventhan, M., 2011. Phenotypic and genetic diversity in the foxtail millet (*Setaria italica* (L.) P. Beauv.) core collection. PhD Thesis. Agricultural College and Research Institute, Tamil Nadu Agricultural University, Madurai, Tamil Nadu, India.

Vetriventhan, M., Upadhyaya, H.D., Anandakumar, C.R., Senthilvel, S., Parzies, H.K., Bharathi, A., et al., 2012. Assessing genetic diversity, allelic richness and genetic relationship among races in ICRISAT foxtail millet core collection. Plant Genet. Resour. 10 (03), 214–223.

Vijayalakshmi, D., Ashok, S.K., Raveendran, M., 2014. Screening for salinity stress tolerance in rice and finger millet genotypes using shoot Na+/K+ ratio and leaf carbohydrate contents as key physiological traits. Indian J. Plant Physiol. 19, 156–160.

Vishwanath, S., Gowda, S.S., Seetharam, A., Gowda, B.T.S., 1986. Reaction to blast disease of released and pre-released varieties of finger millet from different states. Millet Newsl. 5, 31.

Wang, T.Y., Darmency, H., 1997. Inheritance of sethoxydim resistance in foxtail millet, *Setaria italica* (L.) Beauv. Euphytica 94, 69–73.

Wang, T.Y., Du, R.H., Hao, F., 1993. Studies and utilization of highly male sterility of summer millet (*Setaria italica*). Sci. Agric. Sin. 26, 88, (in Chinese).

Wang, Y.R., Chu, J.H., Cao, X.J., Liu, H.X., Duan, C.L., Song, Y.C., 1997. Studies on resistance of foxtail millets (*Setaria italica*) to downy mildew (*Sclerospora graminicola*). Int. Sorghum Millets Newsl. 38, 133–134.

Wang, X., Yan, T., Zhou, H., 1998a. New millet cultivar Tie Gu 7. Crop Genet. Resour. 1, 55–56.

Wang, Y.W., Li, H.X., Wang, G.H., Tian, G., 1998b. Breeding of foxtail millet highly sterile line "Chang10A". Gansu Agric. Sci. Technol. 12, 12–13, (in Chinese).

Wang, Z.M., Devos, K.M., Liu, C.J., Wang, R.Q., Gale, M.D., 1998c. Construction of RFLP-based maps of foxtail millet. Theor. Appl. Genet. 96, 31–36.

Wang, R.Q., Gao, J.H., Mao, L.P., Du, R.H., Diao, X.M., Sun, J.S., 2002. Chromosome location of the male-sterility and yellow seedling gene in line 1066A of foxtail millet. Acta Bot. Sin. 44, 1209–1212, (in Chinese).

Wang, C., Chen, J., Zhi, H., Yang, L., Li, W., Wang, Y., et al., 2010a. Population genetics of foxtail millet and its wild ancestor. BMC Genet. 11 (1), 90.

Wang, Y.W., Li, H.X., Tian, G., Shi, Q.X., 2010b. Study on innovation and application of highly-male-sterile line with high outcrossing rate in millet. Sci. Agric. Sin. 43, 680–689, (in Chinese).

Wang, C., Jia, G., Zhi, H., Niu, Z., Chai, Y., Li, W., et al., 2012. Genetic diversity and population structure of Chinese foxtail millet [*Setaria italica* (L.) Beauv.] landraces. Genes Genomes Genet. 2 (7), 769–777.

Wang, J., Wang, Z., Yang, H., Yuan, F., Guo, E., Tian, G., et al., 2013. Genetic analysis and preliminary mapping of a highly male-sterile gene in foxtail millet (*Setaria italica* L. Beauv.) using SSR markers. J. Integr. Agric. 12, 2143–2148.

Werth, C.R., Hilu, K.W., Langner, C.A., 1994. Isozymes of *Eleusine* (Gramineae) and the origin of finger millet. Am. J. Bot. 81, 1186–1197.

Xu, J., Li, Y., Ma, X., Ding, J., Wang, K., Wang, S., et al., 2013. Whole transcriptome analysis using next-generation sequencing of model species *Setaria viridis* to support C4 photosynthesis research. Plant Mol. Biol. 83, 77–87.

Yadav, C.B., Bonthala, V.S., Muthamilarasan, M., Pandey, G., Khan, Y., Prasad, M., 2014a. Genome-wide development of transposable elements-based markers in foxtail millet and construction of an integrated database. DNA Res. 22, 79–90.

Yadav, C.B., Muthamilarasan, M., Pandey, G., Khan, Y., Prasad, M., 2014b. Development of novel microRNA-based genetic markers in foxtail millet for genotyping applications in related grass species. Mol. Breed. 34 (4), 2219–2224.

Yang, X., Wan, Z., Perry, L., Lu, H., Wang, Q., Zhao, C., et al., 2012. Early millet use in northern China. Proc. Natl. Acad. Sci. USA 109 (10), 3726–3730.

Yang, X.S., Wang, L.L., Zhou, X.R., Shuang, S.M., Zhu, Z.H., Li, N., et al., 2013. Determination of protein, fat, starch, and amino acids in foxtail millet [*Setaria italica* (L.) Beauv.] by Fourier transform near-infrared reflectance spectroscopy. Food Sci. Biotechnol. 22 (6), 1495–1500.

Zangre, G.R., Darmency, H., 1993. Potential for selection in the progeny of an interspecific hybrid in foxtail millet. Plant Breed. 110, 172–175.

Zegada-Lizarazu, W., Iijima, M., 2005. Deep root water uptake ability and water use efficiency of pearl millet in comparison to other millet species. Plant Prod. Sci. 8, 454–460.

Zhang, W.L., Guan, Y.A., 1995. Summer millet Jinan 8337 with high yield and quality. Crop Genet. Resour. 3, 28.

Zhang, J.P., Wang, M.Y., Bai, Y.F., Jia, J.P., Wang, G.Y., 2005. Rapid evaluation on drought tolerance of foxtail millet at seedling stage. J. Plant Genet. Resour. 6, 59–62, (in Chinese, English abstract).

Zhang, Y., Wang, J., Wang, W., Zeng, P., Han, C., Quan, Z., et al., 2012a. Genome sequence of foxtail millet (*Setaria italica*) provides insights into grass evolution and biofuel potential. Nat. Biotechnol. 30, 549–554.

Zhang, W., Zhi, H., Liu, B.-H., Xie, J., Li, J., Li, W., et al., 2012b. Screening of indexes for drought tolerance test at booting stage in foxtail millet. J. Plant Genet. Resour. 13 (5), 765–772.

Zhang, S., Tang, C., Zhao, Q., Li, J., Yang, L., Qie, L., et al., 2014. Development of highly polymorphic simple sequence repeat markers using genome-wide microsatellite variant analysis in foxtail millet [*Setaria italica* (L.) P. Beauv.]. BMC Genomics 15, 78.

Zhao, Z.H., Cui, W.S., Du, G., Yang, S.Q., 1996. The selection of millet photo- (thermo-) sensitive line 821 and study on the relation of sterility to illumination and temperature. Sci. Agric. Sin. 29, 23–31, (in Chinese).

Zhao, W., Lee, G.A., Kwon, S.W., Ma, K.H., Lee, M.C., Park, Y.J., 2012. Development and use of novel SSR markers for molecular genetic diversity in Italian millet (*Setaria italica* L.). Genes Genomics 34, 51–57.

Zhi, H., Wang, Y.Q., Li, W., Wang, Y.F., Li, H.Q., Lu, P., et al., 2007. Development of CMS material from intra-species hybridization between green foxtail and foxtail millet. J. Plant Genet. Resour. 8, 261–264.

Zhu, G.Q., Wu, Q.M., Ma, Y.T., 1991. Breeding of Ve type CMS in foxtail millet. Shaanxi Agric. Sci. 1, 7, (in Chinese).

Zhu, X.-H., Song, Y.-C., Zhao, Z.-H., Shi, Y.-S., Liu, Y.-H., Li, Y., et al., 2008. Methods for identification of drought tolerance at germination period of foxtail millet by osmotic stress. J. Plant Genet. Resour. 9, 62–67, (in Chinese, English abstract).