Small Millets Breeding

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Abstract

Millets are small-grained ancient cereal crops and one of the earliest sources of food known in the prehistoric period. It is believed that they were under cultivation since 8000 BC. These crops adapted well to the marginal and dryland ecosystem due to their climate resilience, biotic stress tolerance and ability to grow in the wild besides providing nutritious grains. Among the millets, small millets form a distinct group and comprise of finger millet (*Eleusine coracana*), little millet (*Panicum sumatrense*), foxtail millet (*Setaria italica*), proso millet (*Panicum miliaceum*), kodo millet (*Paspalum scrobiculatum*), barnyard millet (*Echinochloa frumentacea*) and brown top millet (*Brachiaria ramosa* (L.)) in India along with a few more cereals like teff, fonio, job's tears and guinea millet in some other parts of the world. Except finger millet, other small millets received very limited attention with respect to crop improvement and crop husbandry. Early efforts in finger millet and other crops mainly concentrated on introduction and domestication of indigenous accessions and selection among the available variability. This led to release of some cultivars prior to independence which were major staples before green revolution. Post 1960s, the area and importance of these crops started declining with the emergence of fine cereals. Realizing the importance of small millets and lack of organized research efforts, the Indian Council of Agricultural Research established the All India Coordinated Small Millets Improvement Project in 1986 with its headquarters in University of Agricultural Sciences, Bangalore. Since then, concerted efforts in germplasm collection, recombination breeding and crop production and protection have

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resulted in development and release of many improved cultivars for commercial cultivation by the dryland farmers along with improved package of practices. Development of early maturing, high yielding and drought-resistant varieties with emphasis on both grain and biomass continue as important breeding objectives in all the small millets. Breeding methodologies aiming at recombination breeding slowly started gaining momentum in all the small millets though the progress is hampered by typical floral biology and anthesis behaviour. In the last three decades, more than 200 improved cultivars have been released by adopting different breeding approaches to suit the location-specific requirements of the farmers. This chapter describes the breeding efforts made in different small millets crops and progress so far in India in other countries.

Keywords

Little millet · Barnyard millet · Foxtail millet · Proso millet · Minor millets

8.1 Introduction

Millets and sorghum comprise of an important group of cereal crops known for their nutritional values. Small millets, also known as minor millets, are a group of small-seeded cereal crops of the grass family Poaceae. Small millets are hardy and climate resilient suitable for range of soil, environmental conditions and are prone to drought and high temperature. Small millets are adapted to a range of temperatures, moisture-regimes and input conditions and are perhaps the only cereal crops that can grow in arid lands with only 350–400 mm annual rainfall. Millets, with their ability to tolerate and survive under conditions of continuous or intermittent drought periods, are the major crops successfully cultivated in dry regions where fine cereals such as rice and wheat cannot be grown. The area under millet production has been on the decline since green revolution, more so in case of small millets (80% for small millets other than finger millet, 53% for finger millet). The period between 1961 and 2015 saw a dramatic decrease in cultivated area under millets. The area under all small millets other than finger millet has declined drastically in all states, and the total production of small millets has declined by more than 75% (Table 8.1). Low productivity under marginally grown conditions, declining support has significantly contributed to the fall of millets in Indian agriculture, which is gradually reversing. However, the production has increased over time through productivity improvement by crop breeding efforts (Ganapathy et al. 2021a, b).

Small millets are important crops of rainfed areas in semi-arid regions. Presently, they are cultivated on a limited area globally mainly due to the shift from traditional crops to more remunerative crops. Small millets serve as major food components in various traditional foods and are generally eaten as rice apart from its use in various value-added products and also for beverages and are ingredients in a variety of multigrain and gluten-free cereal products. Due to sedentary lifestyle conditions and its associated health concerns, there is a growing awareness among the consumers

Table 8.1 All India area, production and productivity of small millets

Year/crop	Element	1951–1952	1961–1962	1971–1972	1981–1982	1991–1992	2001–2002	2011–2012	2015–2016	2016–2017	2017–2018	2018–2019[a]
Ragi	Area	2.19	2.51	2.43	2.61	2.13	1.65	1.18	1.14	1.03	1.19	0.92
	Prodn.	1.31	2.03	2.21	2.96	2.58	2.37	1.93	1.82	1.39	1.99	1.22
	Yield	599	808	911	1134	1212	1442	1641	1601	1363	1662	1332
Other small millets	Area	4.76	4.87	4.48	3.79	2.09	1.31	0.80	0.65	0.62	0.55	0.50
	Prodn.	1.92	2.05	1.67	1.64	0.88	0.58	0.45	0.39	0.44	0.44	0.37
	Yield	402	421	373	433	423	440	565	601	714	804	747
Total millets	Area	32.41	36.91	35.44	34.78	26.61	22.28	17.01	15.01	14.26	14.24	12.25
	Prodn.	11.64	15.76	16.92	22.20	16.23	18.80	18.64	14.52	16.2	16.44	13.97
	Yield	359	427	491	638	610	844	1096	968	1136	1154	1140

Area, million ha; Prodn, million tonnes; Yield, kg/ha

Source: DMD, GoI and Agricultural Statistics at a glance 2018; https://eands.dacnet.nic.in/Advance_Estimates.htm

[a] Fourth Advance Estimates

and are seeking more diversified diets that are both tasty and healthy (Ganapathy et al. 2021a, b). Small millet fit in the diversified food system as a healthy food choice because they provide high energy, high dietary fibre, quality protein and balanced amino acid, essential minerals, vitamins and antioxidants, and many of them have low glycaemic index (GI). Due to these inherent features of small millets, they are popularly known as nutri-cereals. The nutrient content of grains varies among different small millets. Finger millet grains contain high calcium (~350 mg/100 g). Nutrient contents like grain iron, zinc, calcium, protein and crude fibre among small millets are presented in Table 8.2. Small millets play a strategic role as a staple food for the poor and, lately, as a healthy food for those in urban areas. It underlines the necessity of directing more research and development towards these crops.

8.2 Genetic Improvement in Small Millets

Diversity in crop cultivars is very important for sustaining global food production. Germplasm provides the required variability for genetic improvement of crops. Small millets germplasm possess larger genetic variation for morpho-agronomic traits, grain quality and stress tolerance traits, and promising germplasm sources have been reported and are being utilized in the improvement programmes. Various breeding methods such as pureline selection, pedigree selection, mass selection and mutation breeding, which are applicable to self-pollinating crops, are followed in small millets as well. Reports on small millets cultivars released over a period of time shown that a majority of them were released following selection from local landraces/cultivars, followed by pedigree selection in the early phase of crop improvement. Recombination breeding has not been exploited to its fullest extent as in other crops like sorghum, pearl millets and other fine cereals. The major reasons are difficulty in hybridization due to small sized florets and irregular flowering behaviour. Mutation breeding is one of the viable approach in different breeding crops and has been successfully demonstrated in finger millet (Ganapathy et al. 2021a, b). Hybridization to create variability followed by selection in segregating population has been an important breeding method in finger millet and comparatively less in other small millets like little millet, barnyard millet, foxtail millet and proso millet. The diversity in small millets in the form of genetic resources, floral biology, breeding methods, constraints and strategies for small improvement in each of the seven small millets are discussed hereunder.

8.3 Finger Millet

Finger millet (*Eleusine coracana* (L.) Gaertn.) is an important food staple of Africa and Southern Asia. Finger millet cropping area globally is estimated to be around 4.0–4.5 million ha. In India, the crop is estimated to be cultivated on an area of 1.2 million ha with an estimated production of 2.0 million tonnes. The major finger millet-growing countries in Africa are the sub-humid regions of Ethiopia, Malawi,

Table 8.2 Nutritive composition of millets vis-a-vis fine cereals (values per 100 g)

Crop	Protein (g)	Carbohydrate (g)	Fat (g)	Crude fibre (g)	Mineral Matter (g)	Calcium (mg)	Phosphorous (mg)
Sorghum	10.4	72.6	1.9	1.6	1.6	25	222
Pearl millet	11.6	67.5	5.0	1.2	2.3	42	296
Finger millet	7.3	72.0	1.3	3.6	2.7	344	283
Proso millet	12.5	70.4	1.1	2.2	1.9	14	206
Foxtail millet	12.3	60.9	4.3	8.0	3.3	31	290
Kodo millet	8.3	65.9	1.4	9.0	2.6	27	188
Little millet	8.7	75.7	5.3	8.6	1.7	17	220
Barnyard millet	11.6	74.3	5.8	14.7	4.7	14	121
Barley	11.5	69.6	1.3	3.9	1.2	26	215
Maize	11.5	66.2	3.6	2.7	1.5	20	348
Wheat	11.8	71.2	1.5	1.2	1.5	41	306
Rice	6.8	78.2	0.5	0.2	0.6	10	160

Source: National Institute of Nutrition (NIN), Hyderabad

Tanzania, Kenya, Uganda, Zambia, Zaire and Zimbabwe. Similarly, in South Asia, the crop is mainly grown in Southern India followed by Nepal and to a certain extent reported in Bhutan and Sri Lanka. In India, the crop is mostly grown in Karnataka followed by other states like Tamil Nadu, Uttarakhand, Orissa, Maharashtra and Andhra Pradesh. Cultivation of this crop extends from mean sea level to hilly regions of Himalayas and is adapted to wide range of soil and environmental conditions but performs well under well-drained, loamy or clay loamy soils. The grains of finger millet are known for its highest amount of calcium and also with contents of iron, zinc, dietary fibre and essential amino acids (Shobana et al. 2013). The grains are resistant to storage infestation by pests, and with minimum attention, the grain can be stored for up to 50 years (Iyengar et al. 1945). The stover after harvest of grains is a source of nutritive fodder to animals and is highly preferred due to sweet-smelled stalks. Comparing other small millets, genetic gain in yield is much pronounced in finger millet but not exploited to the extent observed in other major cereals. The reason is mainly due to irregular flowering behaviour, small-sized florets owing to difficulties in hybridization. However, the diversity existing for grain yield, nutritional superiority and its ability to tolerate range of environmental conditions makes it a promising crop for the future. Research efforts aims at using a combination of approaches for genetic improvement of grain and forage yield, nutritional parameters, biotic and abiotic stresses, identification of end-use specific genotypes and exploring possibilities of exploitation of heterosis.

8.3.1 Gene Pool of *Eleusine coracana*

The cultivated *Eleusine coracana* is highly variable in their centres of origin both in Africa and the Indian subcontinent. The species *E. coracana* is classified into subspecies *africana* and *coracana*. The subspecies *africana* is a wild type and consists of race *africana* and *spontanea*. The subspecies *coracana* is a cultivated type and are classified into four different races based on inflorescence morphology, viz. *elongata*, *plana*, *compacta* and *vulgaris* (Prasada Rao et al. 1993). Both wild (subspecies *africana*) and cultivated finger millet (subspecies *coracana*) are being collected conserved in various gene banks. *africana* subspecies occasionally crosses with the subspecies *coracana* to produce fertile hybrids. Derivatives of such crosses are aggressive colonizers and are grouped under the race *spontanea* (De Wet et al. 1984). Wild finger millet is native to Africa and believed to have been migrated to warmer parts of Asia and America. The diploid wild species *E. indica*, *E. floccifolia* and *E. tristachya* are believed to form the secondary gene pool, while the species *E. intermedia*, *E. jaegeri*, *E. kigeziensis*, *E. multiflora* and *E. semisterlis* (*E. compressa*) form the tertiary gene pool (Guarino 2012).

8.3.2 Floral Biology and Breeding Behaviour of Finger Millet

The floral biology has been described by Rachie and Peters (1977) and recently by Gupta et al. (2011). Finger millet is predominantly self-pollinated, and extent of outcrossing is reported to be less than 1%. The inflorescence consists of terminal digitate spikelets, borne on a long peduncle from the end of 4–5 spikes which radiate in a whorl called fingers with one finger a little lower the whorl referred to as thumb. Rachis of the spikes is flat. Spikelets are sessile arranged in two rows alternatively attached to one side of the rachis. Each spikelet consists of 3–7 flowers averaging to 5 florets and enclosed by common glumes. Androecium consists of three stamens with long filaments and short oblong anthers. Ovary has two styles with plumose stigma. The terminal floret is sterile. Anthesis proceeds from top spikelets and progresses downwards. The maximum number of flowers opens on the third to fourth day. Flower opening also depends on the earhead shape; the compact types open during 2–3 am, fisty 3–5 am and open types during 1–2 am. Flower opening varies from place to place depending upon the temperature and humidity. Flowering takes place simultaneously in all fingers. Pollen viability is short, 10–15 min. Complete opening of the inflorescence requires 7–8 days. Anthers require about 45 min for dehiscence after emergence. The stigma is receptive for about 5 min after emergence from the glumes. Self-pollination is the general rule because the period of anthesis is very short. Cross fertilization by wind and insects is not a rarity, but less than 1%.

8.3.3 Germplasm Conservation and Utilization of Finger Millet

Gene bank assumes greater role and serves as reservoirs of diversity and source of alleles for genetic enhancement of crop plants. In India, the National Active Germplasm Collection Site (NAGS) located at All India Coordinated Small Millets Improvement Project (AICSMIP), Bangalore, made efforts to assemble large collections of germplasm at the global level with a total collection of 7070 germplasm. Similarly, the National Bureau of Plant Genetic Resources based in New Delhi, India, maintains 11,170 accessions of finger millet under long-term conservation. Most of these collections are indigenous with about 117 accessions of exotic origin. These Indian collections include six wild relatives, 154 advanced improved varieties and 64 breeding/research materials. ICRISAT, Patancheru, India, maintain a total of 7519 accessions. The Agricultural Research Station, USDA, Griffin, Georgia, maintains about 766 accessions of which 17 are wild relatives belonging to *E. floccifolia*, *E. indica*, *E. jaegeri*, *E. multiflora* and *E. tristachya*. The major germplasm conservation centres in small millets are given in Table 8.3.

The Indian and African germplasm are highly diverse, and a very few systematic studies have been conducted to compare the diversity among the accessions available in the gene banks. In general, the Indian germplasm are reported to be diverse for grain and dry stover yield. Early maturing varieties combining high grain yield, quality and stover yield are ideally preferred by farmers. The African germplasm exhibited larger variation for plant height, stout plant stature, long narrow finger, higher number of spikelets, poor threshability, late maturing and poor harvest index.

Table 8.3 Major germplasm conservation centres in small millets

Crop	Gene bank	Number of germplasm (Approx)
Finger millet	National Active Germplasm Collection Site (NAGS), Bangalore. India	7070
	ICAR-National Bureau of Plant Genetic Resources, New Delhi	11,170
	International Crops Research Institute for Semi-Arid Tropics, Hyderabad	7519
Proso millet	Russian Federation	8778
	Chinese Academy of Agricultural Sciences	8451
	ICAR-National Bureau of Plant Genetic Resources, New Delhi	1005
	National Active Germplasm Collection Site (NAGS), Bangalore, India	920
	International Crops Research Institute for Semi-Arid Tropics, Hyderabad, India	842
Foxtail millet	Chinese National Gene Bank	26,670
	ICAR-National Bureau of Plant Genetic Resources, New Delhi	4667
	National Active Germplasm Collection Site (NAGS), Bangalore, India	2821
	ORSTOM-MONTP, France	3500
	Svalbard Global Seed Vault, Norway	2505
	International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru	1542
Little millet	National Active Germplasm Collection Site (NAGS), Bangalore, India	2000
	International Crops Research Institute for Semi-Arid Tropics, Hyderabad, India	1000
	ICAR-National Bureau of Plant Genetic Resources, New Delhi	1799
Barnyard millet	National Institute of Agro-Biological Sciences, Tsukuba, Japan	3671
	ICAR-National Bureau of Plant Genetic Resources, New Delhi	1953
	National Active Germplasm Collection Site (NAGS), Bangalore, India	2000
Kodo millet	ICAR-National Bureau of Plant Genetic Resources, New Delhi	2362
	National Active Germplasm Collection Site (NAGS), Bangalore, India	1537

The African germplasm are said to possess higher level of resistance to blast, the most devastating disease in finger millet (Kiran Babu et al. 2013).

For effective utilization of the germplasm for genetic improvement programme, Upadhyaya et al. (2006) established core collection of 622 genotypes representing geographical regions and biological races from the entire collection. The African (58.7%) and Asian (35.8%) collections were predominant, while those from America and Europe were represented by 0.8–1.1%, respectively. The cultivated subspecies *coracana* occupied 97.4% of the core, while African accessions represented only 2.6%. Among the *coracana* subspecies, race *vulgaris* were predominant (62.5%) followed by *plana* (16.8%) *compacta* (12.4%) and *elongata* (8.3%). The core collections were evaluated for 15 quantitative and five qualitative traits, and a mini-core collection of 80 accessions was constituted. Wide variability was reported among the mini-core collections for economically important traits like days to flowering (51.24–93.73), plant height (72.66–113.31 cm), length of longest finger (49.79–139.73 mm), finger per ear (6.13–9.41) and grain yield (691–2430 kg/ha). Upadhyaya et al. (2007) reported diversity in 909 accessions introduced from southern and eastern African region from ICRISAT gene bank and observed large variability for plant pigmentation, growth characters, flowering, plant height and inflorescence length and width and grain colour. Their study also characterized the variability among different finger millet races. Daba and Keneni (2010) reported little or low effect of geographical origin on the pattern of diversity studied from native and exotic collections in Ethiopia. Their study revealed biomass, earweight and grain weight contributing more towards the observed diversity.

8.3.4 Varietal Improvement of Finger Millet in India

Breeding methods such as pureline selection, recombination breeding and mutation breeding are the widely used approaches for genetic improvement in finger millet. Mass selection has been used for purification of the landraces and varieties developed by pureline or pedigree systems. Pureline selection has also been extensively used in finger millet improvement. Single plants selections were made from landraces (germplasm) and improved farmers' varieties, and the promising lines for earliness, pest and disease resistance and grain yield were evaluated under multilocational trials and released as varieties (Ganapathy 2017a).

Hybridization was used extensively in finger millet compared to other small millets. Until the 1950s, the improvement aimed at improving locally adapted lines by centres. Subsequently millet improvement took place after establishment of the Project for Intensification of Regional Research on Cotton, Oilseeds and Millets (PIRRCOM) during the late 1950s and later formulation of the All India Coordinated Millets Improvement Project during 1965. Genetic resources of finger millet and small millets were assembled during the 1960s. The exotic lines from Africa were introduced to India during the 1970s. The lines from Africa had greater vigour, high finger length and good grain filling ability and thick robust stems with broad dark green leaves (Seetharam 1982). Recombination breeding took place between indigenous, exotic and indigenous with exotic lines. Selections were followed from crosses involving Indian and exotic lines in various combinations for early, medium and late duration (more than 110 days).

Varieties developed from Indian × Indian crosses such as Udaya, K 7, Purna, Annapurna, Cauvery, Shakti and HPB 7-6 had moderate productivity. Hybridization among the Indian × exotic cross led to breakthrough in bringing greater variability and improving productivity of finger millet. This led to 50–60% increased productivity in Karnataka and Tamil Nadu (Seetharam 1982; Nagarajan and Raveendran 1985).

The period of finger millet improvement during 1964–1986 witnessed a revolution due to the introduction of Indo-African crosses of finger millet by the late Dr. CH Lakshmanaiah, who is known popularly as "Ragi Brahma" for his pioneering work that resulted in the release of 16 varieties designated as "Indaf" series. The yield levels of these varieties ranged from 3000 to 4000 kg/ha. In a significant move, the All India Coordinated Small Millets Improvement Project (AICSMIP) was launched in 1986 by the Indian Council of Agricultural Research with its headquarters in GKVK, UAS, Bangalore. Following this, during the period between 1986 and 2000, the yield potential has further improved ranging up to 4500 kg/ha with varieties which are resistant to blast disease. GPU 28 is one such medium-duration variety maturing in 110–115 days released during 1996. The variety is suited for delayed sowing under terminal drought conditions. It is also resistant to neck and finger blast which is a major constraint to finger millet production. The potential yield of the variety is 3500–4000 kg/ha. Presently the variety is grown on a larger area (about 70% area) in Karnataka. Joint efforts were made by the Department of Agriculture in each of the finger millet growing states, state seed corporation, state agricultural universities and private seed sectors for augmenting the availability of quality seed of GPU 28. During 2000–2012, upon establishment of AICSMIP, efforts were laid on developing productive lines with elite background through hybridization to improve high grain and straw yield suitable for *kharif* and also *rabi* seasons. The yield levels further increased subsequently ranging up to 5000 kg/ha. Currently, research efforts are underway to develop long-, medium- and short-duration varieties with high grain yield, resistant to blast disease, and to address the challenges like drought, saline and alkaline soils, cold season and hilly areas and mechanical harvesting. Some of the latest finger millet varieties released for cultivation are given in Annexure.

8.3.5 Strategies for Enhancing Productivity and Utilization of Finger Millet

8.3.5.1 Germplasm Evaluation

There is need for systematic evaluation of indigenous and exotic germplasm available with the national gene bank under multilocation germplasm for early maturity, photo insensitivity, drought tolerance, blast and other disease and pest resistance, nutritional (protein, calcium, iron, zinc and essential amino acids) and antioxidants of therapeutic value.

8.3.5.2 Participatory Selection and Varietal Development

Farmers grow finger millet under marginal fertile soil conditions, and the performance of these varieties largely depends upon edaphic and climatic conditions which is least represented in research stations. This warrants participation of the farmers in selection of desired genotypes/varieties. Appropriate selection and breeding efforts involving farmers participatory approach is required to be taken up to develop high yielding finger millet varieties for different production systems under varying environmental conditions.

8.3.5.3 Breeding for Blast Resistance and Other Pests

Blast disease is major problem in finger millet affecting the crop at all stages of crop growth, and number of varieties are susceptible. Understanding the pathogen diversity in the geographical area, screening germplasm collections, identification of resistant germplasm and development of blast resistant varieties based on knowledge of the strains are desirable for development of durable resistance.

8.3.5.4 Interspecific Hybridization and Search for Novel Traits

There is need for search of novel traits in wild species especially from primary and secondary gene pool for disease resistance, cytoplasmic genic male sterility and other novel traits. The search and discovery of genetic or cytoplasmic male sterility would be a substantial breakthrough in the improvement of this crop by opening up the possibilities for effective population improvement.

8.3.5.5 Development of Early Maturing Varieties

Development of early maturing superior genotypes which can fit in different cropping systems as well as provide substantial yield under water stress is one of the important breeding objectives.

8.3.5.6 Genetic Improvement for Drought Tolerance

Systematic research to identify diverse drought tolerant genotypes, understand mechanisms of drought tolerance from multilocational screening, as well as identify key surrogate/adaptive traits needs to initiated. The identified lines should be used in introgression breeding for development of improved drought tolerant finger millet genotypes.

8.3.5.7 Stover Yield and Quality Improvement

Although finger millet crop is predominantly grown for grain/food purpose, the stover after harvest of crop is an excellent source of nutritive fodder to cattle. There is need to identify superior non-lodging tall types with superior grain and fodder yield. The African types are known to possess more plant height, and there is need to utilize these types for improvement of fodder yield and quality.

8.3.5.8 High Yielding White Finger Millet Varieties

Few white grain types are rich in protein (~12%) compared to coloured types (~8%) but are low yielding. Therefore, there is need to develop improved white grained finger millet genotypes for malting purposes as well as other end uses such as weaning foods, infant foods and malted milk foods, etc.

8.3.5.9 Nutritional Improvement

Finger millet is highly nutritious and thus calls for intensive evaluation of germplasm to assess its nutritional qualities. Finger millet grains besides providing energy are also a rich source of calcium and iron, and its proteins are a good source of essential amino acids and can greatly contribute to micronutrient and protein malnutrition affecting women and children in African and south-east Asian countries. The most cost-effective approach for mitigating micronutrient and protein malnutrition is to introduce varieties bred for iron, zinc and protein content in grains. Attempts to breed finger millet for enhanced grain nutrients are still in its infancy. Evaluation of finger millet core germplasm for grain nutrients and agronomic traits revealed a substantial genetic variability for grain iron, zinc, calcium and protein contents. Therefore, there is need to use the identified accessions in strategic research for development of nutritionally rich cultivars of finger millet.

8.4 Foxtail Millet

Foxtail millet [*Setaria italica* (L.) Beauv.] is one of the oldest of the cultivated millets in the world and is grown in about 23 countries in Asia, Africa and America. It is a self-pollinating species ($2n = 2x = 18$), belonging to family *Poaeceae* and subfamily *Panicoideae*. It is good as food, feed and fodder crop, which matures in a short duration. It is cultivated mainly on poor or marginal soils in southern Europe and in temperate, subtropical and tropical Asia (Marathee 1993). Its grain is used for human consumption and as feed for poultry and cage birds. The total world area is estimated to be about 10.5 lakh ha with a grain production of about 22.9 lakh tonnes. The major growing countries are China, the USA and India, with a contribution of only 2.4% to the total millets production in the world. In China, foxtail millet is next to rice and wheat in importance. In India, because of the drought tolerance, it was once an indispensable crop of vast rainfed areas in semi-arid regions, especially the Deccan plateau. But the area under foxtail millet has come down drastically during the 1990s mainly due to introduction of more remunerative crops like sunflower and soybean in blacksoils (Hariprasanna 2017). At present, foxtail millet is cultivated on a very limited area of about 70,000 ha mostly in Andhra Pradesh, Karnataka, Telangana, Tamil Nadu, Maharashtra, Rajasthan, Madhya Pradesh and north-eastern states.

Foxtail millet is adapted to a wide range of elevations, soils and temperatures and can grow from mean sea level to up to 2000 m altitude. It is drought tolerant and has a low water requirement, but does not recover well from drought conditions because of shallow root system. It is mostly grown to meet the domestic needs of the rural people and is widely used as an energy source for pregnant and lactating women and also for sick people and children, and especially for diabetics (Sema and Sarita 2002; Hariprasanna 2017). The grains are rich in protein (12.3%) and crude fibre (8%) and gaining importance as a diabetic food due to relatively low-to-medium glycaemic index (Janani et al. 2016; Dayakar Rao et al. 2017; Wahlang et al. 2018). It has been suggested that foxtail millet protein be used as a food component to fight type 2 diabetes and cardiovascular diseases (Choi et al. 2005).

8.4.1 Origin and Taxonomy of Foxtail Millet

Foxtail millet has originated in China and has the longest history of cultivation among the millets, having been grown in China since sixth millennium BC. Carbonized foxtail millet has been identified in archaeological sites in China. The cultivation has been mentioned in Chinese records as early as 2700 BC (Vinall 1924). Its domestication and cultivation were the earliest identifiable manifestation of neolithic culture, the beginning of which has been estimated at over 4000 years ago (Chang 1968). The principal centre of diversity for foxtail millet is East Asia, including China and Japan (Vavilov 1926). A multiple domestication hypothesis (de Wet et al. 1979) is widely accepted though several hypotheses concerning the origin and domestication of foxtail millet have been proposed. From Central Asia, it spread to India and European countries (Oelke et al. 1990).

The genus *Setaria* consists of approximately 125 species (Dwivedi et al. 2012), widely distributed in warm and temperate areas. The genus includes a large number of valuable perennial forage grasses and grain crops (Chennaveeraiah and Hiremath 1991). Foxtail millet is the most economically valuable of the genus (Baltensperger 1996). Malm and Rachie (1971) thoroughly reviewed the domestication of foxtail millets and the taxonomy. The geographical origin of foxtail millet based on cytological studies indicated that wild ancestor of foxtail millet is *S. viridis* (Li et al. 1945). Three main groups of cultivated foxtail millet gene pool were suggested, namely, Chinese (from China, Japan and Korea), tropical (from Taiwan, India and Kenya) and European group, on the basis of isozyme studies in accessions of *S. italica* and *S. viridis*, respectively (Jusuf and Pernes 1985; Panaud 2006).

On the basis of inflorescence morphology, foxtail millet is classified into two species, *S. pumila* and *S. italica*. The species *S. italica* is divided into two subspecies *viridis* and *italica*. The subspecies *italica* is classified into three races and ten sub-races (Prasada Rao et al. 1987). The race *moharia* (common in Europe, south-east Russia, Afghanistan and Pakistan) is divided into sub-races *aristata*, *fusiformis* and *glabra*; race *maxima* (common in eastern China, Georgia, Japan, Korea, Nepal and northern India) is divided into sub-races *compacta*, *spongiosa* and *assamense*; and race *indica* (remaining parts of India and Sri Lanka) is divided into sub-races *erecta*, *glabra*, *nana* and *profusa*. Race *maxima* has also been introduced in the USA.

8.4.2 Germplasm Resources and Utilization of Foxtail Millet

Wide genetic diversity is available in foxtail millet, and more than 44,000 germplasm have been conserved in different gene banks all over the world (Vetriventhan et al. 2020). Major collections include Chinese National Gene Bank (CNGB, 26,670 accessions); ICAR-National Bureau of Plant Genetic Resources, New Delhi (4667); ORSTOM-MONTP, France (3500); Svalbard Global Seed Vault, Norway (2505); International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru (1542); National Institute of Agro-biological Sciences (NIAS), Japan (1299); and North Central Regional Plant Introduction Station, USDA-ARS, USA (1000).

The ICAR-Indian Institute of Millets Research, Hyderabad, holds about 4554 accessions in its medium-term storage module. The National Active Germplasm Site (NAGS) for small millets was established at University of Agricultural Sciences, Bengaluru, in 1992. It holds about 2559 accessions, most of which have been characterized and catalogued. At Tamil Nadu Agricultural University, Coimbatore, considerable diversity was observed among 741 accessions maintained for all the agronomic characters (Nirmalakumari and Vetriventhan 2010). The Regional Agricultural Research Station, Acharya NG Ranga Agricultural University, Nandyal, Andhra Pradesh, also maintains an active collection of more than 1000 accessions, which has been used in varietal development programmes. The ICRISAT has constituted a core collection comprising 155 accessions using the taxonomic and qualitative traits data (Upadhyaya et al. 2008). Multi-location evaluation of core collection has resulted in identification of a number of diverse germplasm accessions with agronomically and nutritionally (high seed protein, calcium, iron and zinc) superior traits. Further, a mini core comprising of 35 accessions has been developed (Upadhyaya et al. 2011), which is an ideal resource for studying population structure and diversity and identifying new sources of variation for use in breeding and genomics studies in foxtail millet.

8.4.3 Genetics and Cytogenetics of Foxtail Millet

The most common basic chromosome number in genus *Setaria* is $x = 9$ (Singh and Gupta 1977), although numbers like $x = 7$, 8 and 10 are also found rarely. Cultivated millet *S. italica* (L.) Beauv. and closely related species *S. viridis* L. are both diploids with $2n = 2x = 18$. Different levels of polyploidy ($3x$, $4x$, $5x$, $6x$, $7x$, $8x$ and $12x$) are also known in different species of *Setaria*. Intraspecific polyploidy has been reported in many *Setaria* species like *S. sphacelata* showing $2x$, $4x$ and $6x$ (Singh and Gupta 1977). Studies on chromosome structure revealed four pairs of metacentric, four pairs of submetacentric and one pair of acrocentric chromosomes in foxtail millet (Chandola 1959). Chikara and Gupta (1979) observed one pair of SAT-chromosomes each in six varieties, which differed in the number of metacentric, submetacentric and acrocentric chromosomes. These differences were attributed to structural changes. However, meiosis was normal showing nine bivalents

(Chandola 1959; Singh and Gupta 1977). A complete set of nine primary trisomics ($2n + 1$) (cv. Yugu No. 1) of foxtail millet was identified cytologically from progenies derived from crosses between autotriploids ($2n = 2x = 27$) and their diploid counterparts (Wang et al. 1999). In a *S. italica* × *S. viridis* cross regular nine bivalent formation was noticed. Regular chromosome pairing in the hybrid and its partial fertility suggests that genomes of foxtail millet (*S. italica*) and *S. viridis* are similar and that foxtail millet originated from wild *S. viridis* through selection and further cultivation (Li et al. 1945).

Genetic studies in foxtail millet have been conducted mostly on morphological characters and disease response (Malm and Rachie 1971). Most of the previous works have focused on estimating heritability and realized genetic gains, with little attention directed to measuring levels of heterosis or to assessing the relative importance of different types of gene action due to highly self-pollinated nature (Athwal and Singh 1966; Gill and Randhawa 1975; Vishwanatha et al. 1981; Gurunadha Rao et al. 1984; Prasada Rao et al. 1985; Nirmalakumari and Vetriventhan 2010). Agronomic traits like days to 50% flowering, plant height, total number of tillers, number of productive tillers, panicle length and days to maturity exhibited highly significant positive correlations with grain yield. Characters such as flag leaf area and 1000-grain weight were also observed to influence yield. High heritability was observed for all the quantitative traits like flowering duration, plant height, inflorescence length and test weight (Hariprasanna et al. 2015, 2017, 2018, 2019). Negative association of protein content and calcium content with grain yield has been reported along with negative association of carotene with grain yield (Prasanna et al. 2013). So simultaneous improvement of these traits along with grain yield may not be possible.

8.4.4 Reproductive Biology of Foxtail Millet

Foxtail millet matures in 60–90 days depending on genotype. It forms a slender, erect, leafy stem varying in height from 40 to 150 cm. The stem produces an inflorescence terminally. There is a very quick transition period from vegetative growth to flower development (Baltensperger 1996). The inflorescence is a dense, cylindrical terminal spike borne on a thin and very short pedicel (Sundararaj and Thulasidas 1976) with short side branches bearing spikelets and bristles. The shortened side branches are called secondary clusters or lobes. The compressed hairy panicle 5–30 cm long resembles yellow foxtail, green foxtail or giant foxtail. Each spikelet consists of a pair of glumes that embrace two minute flowers (about 1 mm in length), the lower one sterile and the upper one bisexual, with three stamens and a long oval smooth ovary with two long styles, which terminate in a brush-like stigma (Hector 1936). The spikelets are glabrous, elliptic to obovate and about 2 cm long. One to three bristles develop at the base of each spikelet (Vinall 1924). Anthesis in foxtail millet generally takes place near midnight and in the morning, but varies significantly with the environment (Malm and Rachie 1971). The rate of anthesis is generally favoured by low temperature and high humidity.

The small seeds, around 2 mm in diameter, are encased in a thin, papery hull which is easily removed after threshing. The seed coat and husk of foxtail are generally of single entity with glossy appearance. The grains are very similar to paddy rice in grain structure with outer husk, which needs to be removed in order to be used. Seed colour varies greatly between genotypes and is usually yellowish, cream to orange or yellow brown to black in colour (Seetharam et al. 2003). Seed colour varies greatly between genotypes and is usually yellowish in colour. Morphology and anthesis behaviour make foxtail millet one of the most difficult species to cross pollinate.

8.4.5 Breeding Objectives of Foxtail Millet

The principal breeding objectives in foxtail millet include development of early maturing, high yielding and drought-resistant varieties like any other small millets. Maximization of biomass and the harvest index are also the target traits. Genotypes have to be tailored for early, mid-late or late maturity, depending on the location-specific requirements of soil, rainfall, temperature, humidity, day length and cropping patterns (Harinarayana 1989). Dwarf plant stature to reduce lodging, water-use efficiency and nitrogen-use efficiency, uniform maturity, etc. are other breeding objectives.

8.4.6 Breeding Methods of Foxtail Millet

Pureline selection from the local germplasm remained the prime breeding method for improving performance, particularly grain yield of foxtail millet. As foxtail millet is largely self-pollinated and out-crossing is very much limited, and because of the anthesis behaviour, hybridization followed by selection was a difficult breeding procedure to adopt and could not gather much research efforts. Difficulties in emasculation and pollination in small millets in general, identification of true hybrids, limited heterosis in inter-varietal crosses (Srivastava and Yadava 1977) and the non-availability of diverse germplasm resources to the breeders acted as major constraints in varietal improvement in foxtail millet (Hariprasanna 2017). Some of the latest foxtail millet varieties released for cultivation are given in Annexure.

8.4.7 Production Constraints of Foxtail Millet

Though foxtail millet is not severely affected by any major biotic stress factors, blast disease caused by pathogenic fungus, *Magnaporthe grisea*, is one of the major diseases affecting the production, especially in northern China and India (Nakayama et al. 2005). Blast affects both grain and forage production in foxtail millet. Symptoms of the disease appear as circular spots with straw-coloured centres on leafblades. Other frequently occurring diseases are sheath blight, downy mildew and rust. Among the insect pests, shoot fly (*Atherigona atripalpis* Wiede) is one of the important pests in foxtail millet. Shoot fly do not prefer the foxtail millet genotypes possessing lower moisture, crude protein and total sugar content for its oviposition and dead heart infestation (Sanjeev et al. 2011).

Drought stress and high temperature are important abiotic factors affecting grain yield and biomass. Prolonged moisture stress severely affects crop establishment and biomass yield. High temperature above 35 °C coinciding with flowering affects seed set. Lodging is another important yield and quality-reducing factor depending on the environmental conditions. Thin stem, tall plant height and poor root anchoring due to light soils often lead to lodging during maturity.

8.4.8 Future Prospects of Foxtail Millet

The foxtail millet genome has been sequenced, and the first assembled reference genome of foxtail millet and green foxtail was released in the year 2012 by two independent groups (Zhang et al. 2012; Bennetzen et al. 2012). The Joint Genome Institute of the US Department of Energy and the Center for Integrative Genomics had constructed a public domain database PHYTOZOME (http://phytozome.jgi.doe.gov/pz/portal.html) to provide online resources for foxtail millet genomics with unrestricted public access. The genome data generated by Beijing Genomics Institute (Zhang et al. 2012) are available in Foxtail millet Database (http://foxtailmillet.genomics.org.cn/). A large volume of information on genomic, genic and ILP marker resources are available in the Foxtail Millet Marker Database developed by National Institute for Plant Genome Research, New Delhi (https://59.163.192.91/foxtail/markers.html). Availability of genomic information and resources has now provided numerous scientific leads to proceed further towards crop improvement of millets, cereals and bioenergy grasses. The major research areas that need to be further explored are structural genomics, genome-wide studies of gene families involved in abiotic stress tolerance, epigenetics and gene expression regulation and understanding the genetics and genomics of nutritional traits (Muthamilarasan and Prasad 2015). More high yielding and nutritious varieties need to be developed to popularize the crop and regain the lost area. Promotion of foxtail millet cultivation through appropriate policy interventions can ensure food, nutrition, fodder and livelihood security in the dryland agriculture.

8.5 Barnyard Millet

Barnyard millet (*Echinochloa frumentacea* (RoxB). Link), being a climate-resilient crop, also produces multiple securities like food, nutrition, fodder, fibre, health, livelihood and ecology. Globally, India is the largest producer of barnyard millet, both in terms of area (0.146 million ha) and production (0.147 million tonnes) with average productivity of 1034 kg/ha during the last 3 years (IIMR 2018). It is widely cultivated as minor cereal for food as well as fodder in India, China, Japan, Korea, Pakistan, Nepal and Africa. Due to its remarkable ability to withstand erratic rainfall and varying weather conditions, it has been classified as one of the drought stresses, hardy crops which is largely cultivated in harsh and fragile environments. It is a regular crop up to 2700 m above MSL during *kharif* season in Uttarakhand and Tamil Nadu and forms a mainstay of agricultural diet and cultural system of hill people. Diversity in this crop is eroded fast due to several reasons like cultivation on poor, shallow and marginal soils under rainfed conditions, reduction in area under cultivation and changing social, economic and cultural dimensions of farming community in India (Maikhuri et al. 2001). Barnyard millet with rich nutritional profile is one of the best choices for patients with dietary-based health defects like diabetics, heart-related diseases and celiac diseases. Millets are free from gluten; hence, gluten-allergic patients require these minor millets for health improvement. Traditional foods prepared from barnyard millet such as roti, payasam, pongal, pulav, idli, dosa and muruku are very popular in southern India. In addition to human food, it has an important place in dairy due to high palatability of its fodder, which can also be used for making hay or silage.

8.5.1 Origin and Taxonomy of Barnyard Millet

The barnyard millet belongs to the genus *Echinochloa*, the family *Poaceae* and subfamily *Panicoideae* (Clayton and Renvoize 2006). The genus *Echinochloa* comprises about 250 related species of annual or perennial grasses widely distributed in temperate and warmer parts of the world (Bajwa et al. 2015). Xiaoyan et al. (2015) conducted microfossil studies on both lithic implements and sediment samples from previously studied levels of occupation, and they found evidence for the exploitation of nuts, such as acorns (*Lithocarpus*/*Quercus sensulato*), and water chestnuts (*Trapa*), as well as extensive evidence for the processing of another wetland grass, barnyard grass (*Echinochloa* spp.), indicating that this wild millet was an important resource harvested and processed alongside rice and only abandoned in favour of rice at a later stage of the domestication process. The two species of barnyard millet are grown as cereals. *Echinochloa crus-galli* is native to temperate Eurasia and was domesticated in Japan some 4000 years ago. *E. oryzoides*, the most aggressive weed, is recognized taxonomically as *E. crus-galli* var. *oryzicola*. It differs from *E. crus-galli* in having $2n = 36$ rather than $2n = 54$ chromosomes (De Wet et al. 1983). *Echinochloa colona* is widely distributed in the tropics and subtropics of the Old World. It was domesticated in India. *Echinochloa colona* is morphologically allied to *E. crus-galli*. Four morphological races are recognized, although these do not have geographical, ecological or ethnological unity. Race *laxa* is confined to Sikkim, while races *robusta*, *intermedia* and *stolonifera* are also grown in India (De Wet et al. 1983). The two cultivated species under genus *Echinochloa*, *E. frumentacea* (Indian barnyard millet) and *E. esculenta* (Japanese barnyard millet) are cultivated for food and fodder by hilly and tribal communities in Asia particularly in India, China, Africa and Japan.

8.5.2 Germplasm Resources and Utilization of Barnyard Millet

The most of the germplasm accessions of barnyard millet are housed in India and Japan. ICAR-Vivekananda Parvatiya Krishi Anusandhan Sansthan (VPKAS), Almora, India; ICAR-National Bureau of Plant Genetic Resources, New Delhi; ICAR-Indian Institute of Millets Research (IIMR), India; National Institute of Agrobiological Sciences (NIAS), Japan; and International Crop Research Institute for the Semi-Arid Tropics (ICRISAT), India, are actively involved in collection, conservation and utilization of germplasm lines in barnyard millet. Germplasm characterization for morphological traits is the preliminary step; this not only provides information on heritability of the traits but also increases the germplasm utilization. Gowda et al. (2008) evaluated 729 germplasm accessions of barnyard millet for yield and related traits over the years. Correlation and path coefficient analysis for morphological traits in barnyard millet showed significant direct effect of heat units at maturity, photothermal units at 50% flowering, plant height, days to 50% flowering and weight of panicle on grain yield, and they could serve as a useful criterion in the development of short high yielding cultivars (Mehta et al. 2007).

Wallace et al. (2015) have genotyped the core collection (89 accessions) following genotyping-by-sequencing (GBS) approach and identified several thousand SNPs and found four populations within *E. colona* and three in *E. crus-galli*, which match with phylogenetic relationships. ISSR (Nozawa et al. 2004) and RAPD (Deepti et al. 2012) markers were identified and used in the diversity analysis in the germplasm accessions of Indian and Japanese barnyard millet accessions. Lal and Maloo (2006) studied the path coefficient analysis in Indian barnyard millet and found that main panicle weight, plant height and primaries had high effect on seed yield. The 95 germplasm lines representing the global collection were evaluated for qualitative and quantitative traits, and cluster analysis showed that Indian and origin unknown accessions grouped in *E. frumentacea* group, Japanese accessions grouped in *E. esculenta* group and third group contained the accessions from Russia, Japan, Cameroon and Egypt (Sood et al. 2015). Gupta et al. (2009) evaluated 194 accessions collected from different eco-geographical regions of India for 14 quantitative traits. Five groups were formed based on location of collection; group C with unknown origin exhibited maximum diversity with 17.67% coefficient of variation. The other groups recorded mean coefficient of variation between 12% and 13%. Correlation studies showed leaf width and number of racemes are useful to carry out selections in segregating populations.

8.5.3 Reproductive Biology of Barnyard Millet

In barnyard millet, the inflorescence is seen in varying shapes (pyramidal, cylindrical, globose and elliptic), colours (green, light green, light purple and dark purple) and compactness (open, intermediate and compact) (Gupta et al. 2009; Sood et al. 2015). Raceme number varies from 22 to 64 per inflorescence (Renganathan et al. 2017) and varies in arrangement from one side, two sides or around the rachis. The position of florets varies from one side of raceme to around the rachis in which spikelets will be arranged in 3–4 rows (florets positioned on one side of raceme) and irregularly arranged (florets positioned around the raceme). Each spikelet contains two florets; upper fertile floret contains two unequal glumes, lemma and palea, three stamens (white, yellow and dark purple coloured) and plumose type of bifid stigma (white, pink and purple coloured). Anthesis and pollination are basipetal in nature where flower opening which starts at 5 am reaches maximum at 7–8 am and closes by 10 am (Sundararaj and Thulasidas 1976: Jayaraman et al. 1997).

8.5.4 Breeding Objectives of Barnyard Millet

Barnyard millet is known for its high biomass production apart from grain yield; hence, it is cultivated as a dual-purpose crop. The breeding goal is to improve its biomass yielding ability (green fodder and dry fodder yield) along with grain yield. The quality of the fodder for its easy digestibility and preference by the cattle is also good in barnyard millet when compared to other millets. Breeding methodologies focussing on the use of physiological traits-based phenotyping in millets will be one of the potential areas to exploit for crop improvement. Development of cultivars with dual-purpose types (early maturing quick growing and high biomass yielding lines) is another breeding objective. The grain size in the developed cultivars is small, and dehulling efficiency directly depends upon the grain size of the crop. Hence, increasing the grain size in barnyard millet is another area of research to increase the grain yield as well as dehulling percentage. The length of the panicle and number of productive tillers are having high correlation with grain yield. Developing lines with more spikes and long panicles is another targeted area. Grain smut is the major biotic constraint causing yield loss up to 60%. Japanese barnyard millet and *E. colona* are immune to the disease. Japanese type and Indian type are not easily crossable because of hybrid sterility. However, *E. colona*, wild relative of Indian barnyard millets, is crossable with cultivated type and may be used as a donor source for resistant genes to grain smut. In barnyard millet, male sterile lines are not available and hand emasculation and pollination are very difficult because of the large number of tiny flowers in single inflorescence. Identification/development of male sterile lines is of prime importance for recombination breeding. Barnyard millet is rich in dietary fibre, iron and zinc minerals; targeting the nutritional traits and developing varieties with high nutrient content are of great advantage in developing naturally fortified cultivars.

8.5.5 Breeding Methods of Barnyard Millet

Barnyard millet is a self-pollinated crop with 5–10% of outcrossing. In kharif season because of high relative humidity and less difference between day and night temperatures, the flowers will open in less number, and pollination is mostly cleistogamous. In rabi season because of low relative humidity, more difference between day and night temperature (night cold temperature followed by early morning exposure of florets to sunlight) leads to opening of a greater number of florets and pollination after opening of the floret. Hence, in rabi season, the outcrossing percentage is higher than in kharif season. The breeding objectives are based upon the pollination type in the crop. Barnyard millet being a self-pollinated crop uses breeding methods like selection, pedigree method, single seed descent method and mutation breeding. Most of the varieties released in barnyard millet are based on selection method from germplasm lines. In recent years, pedigree method is in practice to combine the favourable traits of two parents with more understanding of the traits and emasculation and pollination techniques.

Use of chemical hybridizing agents and mutation with physical and chemical means are the other methods of creating variation for selection and also to identify male sterile lines if any produced in the population. Improvement/modification over the SSD method is single panicle descent method which is in practice in barnyard millet for the development of improved cultivars. The information on molecular marker development and use in breeding programs is lacking in this crop. Recently, the Japanese barnyard millet *E. crus-galli* (STB08) genome is sequenced (Guo et al. 2017), and the draft genome sequence is available for use in development of markers and identification of candidate genes for particular traits. Availability of the molecular markers (SSRs, SNPs) and the genome sequence information boosts the breeding work through the application of advanced breeding tools like MABB and MARS for the development of cultivars with specific defect correction or for multiple trait improvement.

8.5.6 Production Constraints of Barnyard Millet

The developed cultivars in barnyard millet are based on selection from germplasm collections without much intervention of advanced breeding methodologies. Lack of clear information on physiological traits, biochemical traits and nutritional traits in barnyard millet is hindering the progress in improving the crop for high yield other end specific cultivar development. Negative correlation of earliness, high grain yield and biomass yield is also limiting the development of superior varieties. Fodder yield is one of the most important components nowadays along with grain yield; development of high biomass lines hinders high grain production as photosynthates translocate more to biomass production and less to reproductive parts hence lowering the grain yield. Recombination breeding combines the favourable traits of two or more parents and releases the variation in the segregating populations, but recombination breeding is difficult in barnyard millet because of many tiny flowers arranged closely in the inflorescence. Emasculation and hybridization are difficult in this millet like other millets because of early hours of flower opening, non-abundance of pollen grains, short viability of pollens, short opening time of flowers and tightly attached lemma and palea around the stigma and anthers (Sood et al. 2015). Genomic resources are helpful for the progress of any crop species, and they assist in effective characterization of germplasm resources and subsequent use in the discovery of

QTL/gene(s) for the crop improvement program. However, genome research in barnyard millet is still in the early stage and far behind the other minor millets (Renganathan et al. 2020). Very limited attempts have been made to discover the genomic structure and associated downstream processes due to its genome complexity and lack of research funding on this orphan crop. Some of the latest barnyard millet varieties released for cultivation are given in Annexure.

8.5.7 Future Prospects of Barnyard Millet

Understanding the genetic base and inheritance pattern of traits governing the yield and biomass is of prime importance in this crop. Usefulness of physiological trait-based phenotyping to unravel the stress tolerance mechanisms and to identify the suitable cultivars for stress-prone areas is urgently required to combat the changing climatic conditions. The nutritional superiority available in barnyard millet germplasm will help the breeders to develop suitable cultivarsnaturally enriched with nutrients and minerals gives added advantage for popularization and also for nutritional security. Widening the genetic base specifically for the traits like grain size, panicle length, high biomass and number of productive tillers through recombination breeding and mutational breeding is the way forward to bring improvement in both pre-harvest and post-harvest processing aspects in barnyard millet. Use of wild relatives and progenitor species for transferring the resistant genes for biotic stresses may fetch rewards in the near future by avoiding the yield losses both in grain and fodder.

The fertility barriers between Indian and Japanese types may be analysed, and advanced biotechnological tools may be used to overcome the barriers. Overcoming the barriers will help in many ways of combining the favourable traits of both types in one background. Molecular sequence data generation and its use in breeding are completely lacking in barnyard millet specifically in Indian barnyard millet when compared to other millets like foxtail millet, proso millet, finger millet, pearl millet and sorghum. Generation of genome sequence data, genome structure studies, evolution pattern of the genome and relatedness of barnyard millet genome with other millets, unraveling of nutrient accumulation pathways, identification of genes/QTLs and tagging of genes with particular traits on particular linkage groups are the niche areas of research in barnyard millet to bring suitable improvement in the development of high yielding cultivars.

8.6 Little Millet

Little millet (*Panicum sumatrense* Roth. ex. Roem and Schultz) is indigenous to the Indian subcontinent and also has wild ancestor *Panicum psilopodium* present throughout India. It is widely cultivated as minor cereal across India and to a certain extent in Nepal and western Burma. In India, the crop is majorly grown in Madhya Pradesh, Chhattisgarh, Karnataka, Tamil Nadu, Orissa, Andhra Pradesh, Jharkhand

and Bihar. The crop is hardy and moisture stress tolerant and provides reasonable harvest even in degraded soils and unfavourable weather conditions (Selvi et al. 2014). The crop is cultivated both in the tropics and subtropics even up to an altitude of 2000 m above mean sea level. The crop is known for its drought tolerance and is considered as one of the least water demanding crops. Other advantage is that the grains can be stored for up to 10 years or more without much loss due to deterioration (Selvi et al. 2014). Consequently, it has traditionally played an important role as a reserve food crop. The crop is also grown in the eastern parts of India where it formed part of tribal agriculture. Cultivated area under crop has drastically declined from about 5 lakh ha during 2001–2002 to presently about 2–2.5 lakh ha and production of about 1 lakh tonnes. However, exact figures on current area, production and productivity are not available. Madhya Pradesh state occupies about 40–50% of the area under little millet followed by Chhattisgarh, Tamil Nadu, Karnataka, Maharashtra, Orissa, Andhra Pradesh and Jharkhand. The average productivity of the crop is around 500–600 kg/ha.

Nutritionally the grain of little millet is comparable or even superior to some of the major cereals. In general, little millet is a disease-free crop, but occurrence of grain smut (*Macalpino mycessharmae*) can lead to economic losses at times. Among insect pests, incidence of shoot fly is widely reported and known to cause economic losses. The crop is known for high content of crude fibre in its grains. It is also rich source of protein (~7.7%) and fat (~4.8%), minerals and vitamins and requires consideration as essential food for nutritional security. The crop matures in 80–120 days depending on the type of cultivar grown. Yield levels in this crop may reach close to 3 tonnes/ha under favourable conditions.

8.6.1 Morphological Variation in Little Millet

Panicum sumatrense subsp. *sumatrense* is a morphological variable cereal largely cultivated in India followed by Sri Lanka, Nepal and Burma. The species include wild and cultivated forms. The species is divided into *P. sumatrense* subsp. *sumatrense* to include cultivated one and subsp. *psilopodium* (Trin.) de Wet comb. nov. to include the wild progenitor. These two subspecies cross where they are sympatric to produce fertile hybrids, derivatives of which are often weedy in little millet fields. Weedy types are derived between wild and cultivated types and escape from cultivation due to the ability of efficient natural seed dispersal. *P. sumatrense* is extensively variable with regard to growth habit and inflorescence morphology. Based on the morphological variation and distribution, two races of cultivated little millet are recognized, namely, *nana* and *robusta* (de Wet et al. 1983). Race *nana* resemble wild subspecies of *P. sumatrense* with regard to inflorescence morphology. Race *nana* includes plants with decumbent to almost prostrate culms that become erect at time of flowering. Inflorescences are large and open with the upper branches sometimes clumped and curved at time of maturity. Height of the plants ranges from 50 to 100 cm. Terminal inflorescences size range from 14 to 50 cm long and are erect, open and strongly branched, and sometimes branches get clumped at time of maturity. Race *robusta* are erect plants with large strongly branched open or compact inflorescence. Flowering culms grow tall and range between 120 and 190 cm and robust. Terminal inflorescence is in range of 20–46 cm long, open or compact and strongly branched. Open inflorescences are essentially erect, while compact inflorescences are curved at maturity. This race is grown in northwestern Andhra Pradesh and adjacent Orissa where it crosses with race *nana* (de Wet et al. 1983).

8.6.2 Genetic Improvement of Little Millet

Major work reported so far is on screening of the germplasm for improved genotypes for yield and other important traits, germplasm diversity studies, identification of resistant sources for smut resistance, testing association among different traits influencing yield, proximate and mineral composition in grains, mutation studies and creation of new variation and identification of surrogate/adaptive traits and genotypes for drought tolerance (Ganapathy 2017b). The race *nana* matures faster and generates less biomass than *robusta* (de Wet et al. 1983). In the tribal area of the Indian Kolli Hills, diversity among locally grown landraces of little millet was found to be high for all morphological traits measured both within and between landraces (Arunachalam et al. 2005). High diversity and heritability and genetic advancement was reported for yield and productive tillers in 109 landraces indicating selections for varietal development (Nirmalakumari et al. 2010). Evaluation of about 460 collections of little millet held by ICRISAT revealed high genetic variation for most of the quantitative traits tested (Upadhyaya et al. 2014). A core collection of 56 genotypes was constituted which represents seed bank collections. Increased heritable lodging resistance has been introduced to a population of little millet with γ-ray mutational breeding (Nirmalakumari et al. 2007). Channappagoudar et al. (2007) identified traits influencing grain yield in the crop. Taller genotypes were found to be high yielding, and shorter genotypes are medium to low yielding. Other parameters are number of leaves and tillers per plant positively contributing towards higher grain yield. Leaf area index and leaf area duration were also important growth parameters for improving the yield and total dry matter as it indicates the efficiency of the photosynthetic system. Overall, the study reported TNAU 63 (20.2 q/ha) and DPI 1869 (18.3 q/ha) and TNAU 18 (16.9 q/ha) were high yielding with high values for most morpho-physiological parameters. Gollagi et al. (2013) analysed the biophysical basis of yield enhancement in little millet and observed high transpiration rate in low yielding genotypes and low rate in high yielding genotypes. They also observed that higher yielding types had higher stomatal conductance (60 DAS) which could be because of higher stomatal frequency on abaxial surface leading to enhanced canopy photosynthesis. Nirmalakumari and Ulaganathan (2013) followed farmers' participatory approach to identify trait-specific genotypes. Twelve genotypes were evaluated by farmers on community plots managed by them at several sites in agro-ecological areas. Farmers evaluated for panicle type, yield traits, seed size and lodging resistance and rated the varieties based on their preferences. Farmers showed more interests towards compact panicles possessing bold seeds, pest and disease-free genotypes and non-lodging characteristics.

Salini et al. (2014) evaluated 105 germplasm of little millet for various traits and selected 12 promising lines as parents and reported several cross combinations. Gene action was studied for 11 characters, and they reported non-additive gene action for all the characters except plant height where additive and non-additive played equal role. High coefficient of variation was observed for grain yield per plant and number of basal tillers per plant. Heritability estimates were high for all the characters except flag leaf sheath length. Inheritance of qualitative characters indicated monogenic simple dominance inheritance for most traits except grain colour. Stability analysis was carried out for 12 parents in four environments for eight characters and identified IPmr 1046 and IPmr 889 as stable genotypes for grain yield.

Girish et al. (2013) evaluated six improved types, RLM 40, BL 4, RLM 186, DLM 14, GV-2-1 and RLM 141, to identify high yielding types with checks JK 8 and OLM 203. They identified two lines, BL 4 (1141 kg/ha grain yield and 5 tonnes/ha fodder yield) and DLM 14 (grain yield of 1292 kg/ha and fodder yield of 5 tonnes/ha), as promising compared to check JK 8 which yielded 994 kg/ha with 6 tonnes/ha fodder yield. DLM 44 was reported to be early with height of about 100 cm and suited for intercrop with redgram. Sasamala et al. (2012) studied the genetic diversity among 22 little millet lines evaluated over 12 environments. The study identified KCM 42, KCM 102D, Sabar and Co 2 most divergent with KCM 594 and RCM 4 indicating that hybridization between these genotypes likely to give better recombinants in segregating generations.

M.S. Swaminathan Research Foundation (MSSRF), Chennai, has taken initiatives to collect, evaluate and conserve little millet in Tamil Nadu to improve cultivation of the crop. In Kolli Hills of Tamil Nadu, little millets were preferred by tribal farmers as they provided sustainable benefits. MSSRF attempted to bring back cultivation of the small millets and also to revitalize their conservation of local landraces and cultivars. The participatory rural appraisal conducted with farmers of the regions revealed interest of the farmers in millets but are getting eroded due to low productivity of landraces that are under traditional cultivation. Ideal approaches are to introduce scientific steps to optimize their cultivation practices under site-specific constraints. Arunachalam et al. (2005) from MSSRF studied the stability of genetic diversity among landraces of little millet in south India at the ecological level. Genetic divergence studies revealed high diversity among set of landraces analysed at two locations for two seasons. Days to maturity and flowering contributed most to the genetic differentiation. The study confirmed the sustained availability of the divergence in little millet in Kolli Hills of Tamil Nadu. They observed location specific expression of traits among the landraces and further suggested that breeding and selection to be followed as per the needs of the region.

8.6.3 Varietal Development of Little Millet

Varietal development has received less attention as the case in other small millets. Most of the varieties released were developed through mass selection or pureline selection methods. Breeding for new varieties using hybridization techniques is limited owing to difficulties encountered in crossing due to tiny spikelets on brittle pedicels (Nirmalakumari et al. 2007). Mutation breeding was used as complement to conventional breeding methods for genetic improvement of little millet. A number of high yielding varieties have been developed and released for cultivation in different little millet-growing states. The improved varieties are able to meet the specific requirements of different regions. Although yield has been the main criterion for development of new varieties, the varieties OLM 20 possess drought tolerance, OLM 36 for brown spot and sheath blight and OLM 203 blast and grain smut. Birsa Gundli 1, selection from local developed from BAU, Ranchi, is very early and matures in 55–60 days with reasonable grain yield. The latest varieties released in different states and popular in different little millet growing states are given in Annexure.

8.6.4 Future Prospects of Little Millet

For valuing the genetic diversity in the germplasm, systematic evaluation and unlocking the genetic diversity in the germplasm should be the major objective for genetic improvement. Grain yield has always been an important trait for genetic improvement. Efforts towards improvement for yield have led to marginal improvement. Selection for component traits such as compact panicle types and large seed size should be done. Knowledge on floral biology and hybridization techniques requires attention. Moreover, the small-sized florets in this crop have hindered in the genetic improvement of this crop through hybridization techniques. Although millets are grown on poor soils under dry conditions, genotypes/cultivars responsive to high input conditions should also be identified. Little millet is well-known for its drought tolerance and is considered as one of the least water-demanding crops. Few isolated studies have indicated less loss in grain yield under water stress compared to proso millet and foxtail millet.

Cultivars possessing drought tolerance and better regenerative capacity on reversal of dry spell for harsh conditions should be focus of genetic improvement. Farmers' participatory approach should be followed for deriving improved varieties. The dry fodder after harvest of the crop is source of nutritious fodder to animals. It is possible that the variability in the quality stover could be exploited to develop improved varieties with better nutritive value. Pests and diseases infecting little millet are less. However, earlier studies have indicated shoot fly and grain smut causing economic losses. Host plant resistance should be a major strategy for pest and disease resistance. Lodging and grain shattering are the other important agronomic traits which should receive due attention while improving for grain yield. Breeding for specific end uses should receive priority as this attracts the private sector industries to invest in millets. Little millet is known to mature in 60–80 days. However, early maturing genotypes with substantial high yield and photo-insensitive genotypes suiting different cropping systems should be developed.

8.7 Kodo Millet

Kodo millet (*Paspalum scrobiculatum* L.) is widely distributed in damp habitats in the tropics and subtropics. It is grown in arid regions of Asia, New Zealand and the USA as a pasture crop. It is an indigenous cereal of India largely grown in Madhya Pradesh, Chhattisgarh, Uttar Pradesh, Tamil Nadu, Maharashtra, Karnataka and some parts of Andhra Pradesh (Yadava and Jain 2006). It is popularly known as kodo (Hindi), Varagu (Tamil), Arika (Telugu), Harka (Kannada), Kodra (Gujarati, Marathi and Punjab) and Kodua (Oriya) in India (Ayyangar and Rao 1934; Deshpande et al. 2015). It has several names in different parts of the world like bastard millet, creeping paspalum, ditch millet, Indian paspalum, koda grass, scrobic, water couch and Kodohirse (German) (Knees and Gupta 2013). In India, kodo millet is widespread and grown in about 1.5–2.0 lakh ha with a productivity of about 400–500 kg/ha depending on environmental conditions. Madhya Pradesh and Chhattisgarh account for nearly 70–80% area under this crop, and other important states are Tamil Nadu, Maharashtra, Uttar Pradesh and Gujarat.

8.7.1 Floral Biology of Kodo Millet

Kodo millet is a highly self-pollinated crop with cleistogamous flowers, but several researchers observed opening of the flowers at varying time between 2:30 am and 11:30 am at various growing regions and also protogynous lines (Youngman and Roy 1923; Ayyangar and Rao 1934; Verma 1989; Yadava 1997). Inflorescences are composed of 3–5 racemes alternately arranged on a short to elongated primary axis. Racemes are up to 13 cm long, with sub-sessile spikelets arranged in 2–3 rows along one side of flattened rachis. Spikelets are glabrous, orbicular or broadly elliptic, conspicuously plano-convex, 1.8–3.5 mm long. The lower glume is absent and upper glume is as long as the spikelet. The lower lemma is flat more or less membranaceous and without palea. The upper lemma is crustaceous, often brown and shiny when grains are mature and embraces the crustaceous palea. The grain is elliptic-orbicular in outline and 1.5–2.5 mm long (de Wet et al. 1983). Gynoecium is monocarpellary, ovary is superior, one cell with one ovule, two stigmas, feathery with distinct style. The grains are elliptic, convex in front and flat on back of palea; scutellum is up to half the length of the grain. The grain is enclosed in hard, corneous, persistent husks that are difficult to remove.

Three races of kodo millet were recognized based on arrangement of spikelets on the raceme. They are *regularis*, where the spikelets arranged in the two rows on the one side of flattened rachis; *irregularis*, where the spikelets are arranged in 2–4 irregular rows along the rachis; *variabilis*, where spikelets in the lower part are irregularly arranged and in the upper part the spikelets are in two regular rows on the raceme. In all three types of racemes, spikelets are arranged on flattened rachis. The grain may vary in colour from light red to dark grey (de Wet et al. 1983). The crop matures in 3–4 months with average yield varying from 250 to 1000 kg/ha (Hulse et al. 1980), and crop has a potential yield of 2000 kg/ha (Harinarayana 1989).

8.7.2 Germplasm and Core Collection Status

About 8000 accessions of kodo millet have been conserved in main ex situ gene banks around the world. In Indian gene banks, around 3956 accessions have been conserved at AICSMIP, Bangalore (1537); ICSRISAT, Hyderabad (665); and NBPGR, New Delhi (2362) (Upadhyaya et al. 2014). National Active Germplasm Site (NAGS), AICSMIP, published a catalogue on evaluation of 1038 accessions for 16 and 11 qualitative and quantitative descriptors, respectively, and at TNAU, Coimbatore, 427 accessions have been maintained. ICRISAT established a core collection comprising 75 accessions belonging to 53 distinct clusters of 656 kodo millet germplasm collections (Upadhyaya et al. 2014). These genotypes could be utilized in breeding programme aimed at development of new genetic variants and recombinants.

8.7.3 Varietal Development of Kodo Millet

Kodo millet has received very less priority like other small millets in the agricultural research though the genetic improvement work started before the independence in the country. Some of the early efforts in crop improvement of kodo millet have resulted in the release of improved varieties as early as the 1940s. The first improved variety PLR 1 was released in 1942 for the rainfed areas of Tamil Nadu. Another improved variety, T2, was released in 1949, and Co 1 was released from TNAU, Coimbatore, during 1953. Post independence, the genetic improvement work was initiated in Madhya Pradesh during 1964 with the financial assistance from the state government. Niwas 1, another improved variety, was released in 1971 as the outcome of this work for general cultivation in Madhya Pradesh (Yadava and Jain 2006). Since 1978, the centre of excellence for the improvement of small millets established at Dindori (JNKVV) by ICAR with the assistance of International Development Research Centre (IDRC), Canada, is devotedly working towards the improvement of kodo millet.

With the establishment of AICSMIP in 1986, the IDRC centre became part of AICSMIP, and varietal development gained momentum. The AICSMIP centres located at Tribal Agricultural Research Station, JNKVV, Dindori, and Agricultural College, JNKVV, Rewa, are exclusively working on kodo and little millets. Presently emphasis is being given to the development of high yielding varieties with resistance to biotic and abiotic stresses; enrichment of germplasm; their critical evaluation for morphological, physiological and biotic and abiotic resistance traits;

and enhancement in available genetic variability through hybridization/mutagenesis for identification of ideotypes suitable for different farming situations (Yadava and Jain 2006; Hariprasanna 2017).

8.7.3.1 Pureline Selection in Kodo Millet

The varieties released in kodo millet so far are mainly developed through selection from landraces or germplasm. Some of the kodo millet varieties, namely, APK 1, GK 2 and KMV 20, were the product of selection from germplasm introduced in different agro-ecosystem. The pureline selection remained the prime breeding method for improving performance, particularly grain yield. Single plant selection from landraces and cultivated varieties and their evaluation for economic characters like earliness, resistance to biotic stresses and high yield have resulted in the development and release of many varieties in kodo millet. During the period from 1942 to 2020, about 36 varieties have been released, of which 11 were released before establishment of AICSMIP (1986) and rest after 1986. Among these, pureline selection has resulted in the development and release of 22 varieties of kodo millet.

8.7.3.2 Recombination Breeding

The difficulties in emasculation and pollination due to small and delicate spikelets combined with brittleness of flattened rachis have resulted in a slow progress in recombination breeding in kodo millet. However, the methods of hybridization and selection have been standardized and extensively used in the recent past for the creation of variability and selection of transgressive segregants from advanced generations. The hand emasculation technique developed by Verma (1989) and modified by Yadava (1997) has been found effective in kodo millet. The controlled pollination just after the emasculation helps in development of hybrids. The contact method as suggested for finger millet is successfully used in kodo millet with slight modifications. In this method, the panicles of selected plants are tied to other panicle in which crossing is to be attempted before flowering to enhance the chances of natural cross pollination. It resulted in low frequency of true hybrids which can be identified with the help of marker characteristics of the parents.

8.7.3.3 Mutation Breeding

In kodo millet, Mishra et al. (1985) were first to introduce quantitative variation through gamma irradiation. The sensitivity to gamma irradiation varied from genotype to genotype. Yadava (1997) found maximum mutation frequency and effectiveness at 25 kR dose of gamma irradiation. The mutants having auricle pigmentation, late maturity, complete panicle emergence and dark brown seed have been developed (Yadava et al. 2003). A protogynous mutant having two rows of spikelets on rachis was also identified from 5 kR dose of gamma irradiation in JK 76. Among the mutants identified, KM 86 and KM 99 have high yield potential coupled with early maturity. There is thus ample possibility for improvement following physical and chemical mutagenesis in kodo millet (Yadava and Jain

2006). Some of the latest kodo millet varieties released for cultivation are given in Annexure.

8.8 Proso Millet

Proso millet (*Panicum miliaceum*) is an important minor millet belonging to the family Gramineae. The crop is a short-duration millet variety and grown in India, the USA and other countries. It is specially adapted to tropics and high altitudes, where the growing season is short and the soil is marginal and poor in fertility. Among grain crops, proso millet requires less soil moisture. The crop is well adapted to high elevations and cultivated even in the Himalayan region up to an altitude of 2700 m. The dehusked grain (about 70% of the whole grain) is nutritious and is generally cooked like rice. Sometimes, it is ground to make roti and eaten. Green plants are fodder for cattle and horses, also used as hay. The crop is ready for harvest in 70–80 days. The average grain yield in India varies between 500 and 700 kg/ha in drylands and 1500 and 2000 kg/ha under irrigated/favourable conditions. The dry stover is normally three times higher than grain yield and is used as cattle feed.

8.8.1 Morphology and Reproductive Biology

The plant grows to a height of 30–100 cm, and stem is hollow, hairy or glabrous with swollen internodes and a shallow root system. It is a short-day, short-duration (60–90 days) crop. The crop is harvested at its physiological maturity to avoid shattering of grain. The flowering takes place usually between 10:00 am and 12:00 noon. However, flowering is influenced by environmental conditions especially humidity and temperature. The inflorescence is a drooping panicle and looks like a broom with basipetal opening of florets, i.e., from top to bottom. The spikelet consists of two glumes and two lemmas. The lower lemma has a sterile floret, and upper lemma has a fertile floret. The stamen possesses three anthers and two feathery stigmas. The anther dehiscence coincides with stigma receptivity, and anthers appear dry within a few minutes of flower opening. It usually takes 10–12 days for complete flowering within an inflorescence. Though self-pollination is the rule, up to 10% cross-pollination may occur (Popov 1970). Nelson (1984) reported crossing techniques in proso millet using hand emasculation. Cold spray technique for emasculation and crossing was reported by Nandini et al. in 2019. Seeds of proso millet are oval and 3 mm long, and colour varies from white, golden yellow, orange, red, brown to black (Baltensperger 2002).

8.8.2 Germplasm Resources of Proso Millet

The extensive collection of proso millet germplasm (8778) is maintained in Russia followed by Chinese academy of agricultural sciences (8451). Other major gene banks conserving the crop's genetic variability are in Ukraine, India, and the USA (Upadhyaya et al. 2014). In India, the AICSMIP, NBPGR and ICRISAT are involved in plant genetic resource in collection, distribution and utilization. AICSMIP is a national active germplasm site and maintains a collection of about 920 accessions of proso millet. NBPGR is maintaining about 1005 germplasm accessions. ICRISAT with about 842 accessions is involved in germplasm characterization and evaluation of proso millet. ICRISAT developed a core collection of 106 accessions from 842 proso millet accessions of 30 countries based on 20 qualitative and quantitative traits.

8.8.3 Genetic Improvement of Proso Millet

In India, AICSMIP centres located in different states are involved in screening the germplasm lines since inception for grain yield and components. In proso millet, crop improvement programmes are focused on improving traits like yield, lodging resistance, non-shattering, early maturity, panicle type, waxiness, etc. Through conventional methods like pureline selection and pedigree breeding, improved varieties have been developed in proso millet in China, India, the USA, Russia and Kenya. In India, K2 is a variety developed through pureline selection, which is non-lodging and non-shattering (http://agritech.tnau.ac.in). The varieties TNAU 202 and ATL 1 are high yielding varieties developed by hybridization. Genetics and inheritance of waxy traits have been carried out. Waxy trait is reported to be controlled by duplicate recessive alleles. GBSSI gene (with two loci—S, L) mutations are identified to result in waxiness, while the GBSSI-S locus mainly contributes to the trait (Graybosch and Baltensperger 2009; Hunt et al. 2013; Rose and Santra 2013; Santra et al. 2015). Rajput et al. (2014) used molecular breeding tools to identify 18 quantitative trait loci (QTL) for phenotypic traits like heading date, test weight, grains per panicle, lodging, plant height, peduncle length, grain shattering and panicle length which may be validated and used for marker-assisted selection. Waxy forms of grains are preferred in the food industry for glutinous nature suited for beverage industry for their high fermentation efficiency.

Increasing proso millet production with declining area was the major challenge and was overcome with the development of modern varieties with greater adaptability to soil and environmental conditions and high yield potential of more than 4 tonnes/ha. Proso millet breeding programmes in Russia aimed at increasing productivity, smut disease resistance and grain quality like uniform size and shape and yellow endosperm with high carotenoid content. The major breeding method employed in Russia is intra-specific hybridization. A number of varieties were developed, and the notable cultivars are "Bistrove" and "Krupnoskoroe" (ssp. subcoccineum), which recorded up to 5 tonnes/ha grain yield with very short duration. Identification of genes for resistance, the improved varieties "Sputnik" (ssp. coccineum) and "Slavjanskoe" (spp. subflavum) were developed during 2006. The varieties were medium maturing and gave grain yield as high as 7 tonnes/ha. Russian variety Alba is reported as non-shattering grain variety. During 2006–2010, the new selection technologies based on mutant forms, dihaploid plants production, genotype identification with the use of storage proteins electrophoresis and DNA markers were developed. As an outcome of this, a new variety "Regent" was developed during 2011 using anther culture technique, and selection was done keeping in mind the productivity and grain quality parameters. The variety had high yield, medium maturity (95–105 days) and resistance to lodging and shattering.

8.8.4 Future Prospects of Proso Millet

The genetic and genomic resources development in proso millet lags behind most cereals. There is a need for an extensive trait-specific germplasm evaluation or donors for traits like biotic and abiotic stress tolerance, non-lodging, non-shattering, yield, compact panicle, bold grains and genetic male sterility systems. Precision phenotyping for major traits is a prerequisite. The identified germplasm can be used for introgression of genes into popular cultivars using modern breeding methods like genomics assisted breeding (marker assisted selection, marker assisted backcrossing, haplotype breeding, speed breeding, etc.) and transgenic approaches. Functional markers and gene introgression for traits like genetic male sterility, non-lodging, etc. can also be attempted from the model grass species foxtail millet in which genetic dissection of traits occurs at a faster pace.

8.9 Browntop Millet

Browntop millet (*Brachiaria ramosa* (L.) Stapf Nguyen) is an annual/perennial warm-season grass originated in Southeast Asia, often used in forage/pasture management systems. It is a minor millet mostly confined to a few thousands of hectares in South East Asia and parts of the USA. In India, it is grown mostly in southern India (Bhat et al. 2018) where it is locally known as pedda sama or korle. Though presently it is restricted to remote parts of Andhra Pradesh, Karnataka and Tamil Nadu states in southern India, it appears to have been a major staple crop in the late prehistory of the wider region of the Deccan. Domestic and wild/weedy forms of browntop millet are found in agricultural systems, often within the same field. Browntop millet grows in rocky, shallow soils from sea level up to 8000 ft above MSL. It is adaptable to almost all upland soil (Mitchell and Tomlinson 1989), but does not grow well in water-restricted, drought conditions. It will not survive in temperature less than 52 °F.

Browntop millet is used as both a human food crop and fodder. In some parts of the USA, it is grown as a fodder crop and bird feed and was introduced from India around 1915. Morphotypes or races are not known in browntop millet. Mulay and Leelamma (1956) have reported $2n = 36$ chromosomes in this species from India. The somatic chromosomes are small in size ranging in length between 1 and 2.5μ. This species was found to show two cytological races, which are morphologically indistinguishable. Diploid, tetraploid and hexaploid status has been reported in browntop millet with basic chromosome number of 9 ($2n = 2x = 18$; $2n = 4x = 36$, 72) (Vetriventhan et al. 2020).

Very limited genetic variability has been observed among the accessions assembled at ICAR-Indian Institute of Millets Research, Hyderabad. Two different panicle types have been found—open and bunchy. The florets are very minute, 1–2 mm in size. There are few reports on floral characteristics and anthesis behaviour. Artificial hybridization through hand emasculation and pollination has not been standardized so far, and hence, recombination breeding has not taken up shape as a breeding methodology. ICAR-Indian Institute of Millets Research maintains about 30 germplasm of browntop millet which are used for assessing the variability and for its use in further improvement programme. Pureline selection from the available germplasm appears to be a feasible strategy for improvement and release of cultivars in this crop as a short-term measure.

Annexure: Improved Varieties Developed and Released in Small Millets in India (2005–2020)

S. No.	Variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Avg. yield (q/ha)	Area of adaptation
Finger millet							
1	GPU 48	GPU 26 × L 5	PC Unit, Bengaluru	2005	95–100	28–30	Karnataka
2	PRM 1	Selection from Ekeshwar of Pauri Garhwal Region	Hill Campus, GBPUA&T, Ranichauri	2006	110–115	20–25	Hills of Uttarakhand
3	Bharathi (VR 762)	Pureline selection from VMEC 134	ANGRAU, Vizianagaram	2006	110–115	26–30	Andhra Pradesh
4	GPU 66	PR 202 × GPU 28	PC Unit, Bengaluru	2009	112–115	35–40	Karnataka
5	GPU 67	Selection from germplasm accession GE 5331	PC Unit, Bengaluru	2009	114–118	30–35	National
6	Srichaitanya (VR 847)	GPU 26 × L 5	ANGRAU, Vizianagaram	2009	110–115	26–28	Andhra Pradesh
7	KMR 301	MR 1 × GE 1409	VC Farm, Mandya, UAS, Bengaluru	2009	120–125	35–40	Southern Dry zone of Karnataka
8	KOPN 235	Selection from local germplasm	MPKVV, Rahuri	2011	115–120	25–26	Sub-mountain and Ghat zone of Maharashtra
9	OEB 526	SDFM 30 × PE 244	OAUT, Bhubaneswar	2011	110–115	25–26	Odisha, Bihar, Chhattisgarh, Karnataka, Tamil Nadu
10	OEB 532	GPU-26 × L-5	OAUT, Bhubaneswar	2012	110–115	22–25	Odisha, Bihar, Chhattisgarh, Karnataka, Tamil Nadu
11	KMR 204	GPU 26 × GE-1409	VC Farm, Mandya, UAS, Bengaluru	2012	95–100	30–35	Karnataka
12	VR 936	IE 2695 × PR 202	ANGRAU, Vizianagaram	2012	115–120	28–30	Andhra Pradesh

13	PPR 2700 (Vakula)	KM 55 × U22/B	ARS Perumallapalle, A.P.	2012	105–110	25–30	Andhra Pradesh
14	Indira Ragi 1	HR 911 × GE 669	Jagdalpur, IGKVV	2012	120–125	25–26	Chhattisgarh
15	VL 352	VR 708 × VL-149	ICAR-VPKAS, Almora	2012	95–100	33–35	All Ragi growing areas of country
16	Chhattisgarh Ragi-2	PR 202 × GE 669	Jagdalpur, IGKVV	2012	115–118	32–35	Chhattisgarh
17	VL 376	GE 4172 × VL Ragi 149	ICAR-VPKAS, Almora	2016	103–109	29–31	All Ragi growing areas of country
18	GNN-6	Selection from local germplasm WN-259	Navsari Agricultural University, Navsari	2016	120–130	28–30	Gujarat
19	GN-5	Selection from local germplasm WWN-20	Navsari Agricultural University, Navsari	2016	120–130	25–27	Gujarat
20	VL Mandua-348	VL Ragi 146 × VL Ragi 149	ICAR-VPKAS, Almora	2016	104–112	18–20	Uttarakhand
21	KMR 340	OUAT-2 × WRT-4	VC Farm, Mandya, UAS, Bengaluru	2016	90–95	35–40	Karnataka
22	Dapoli-2 (SCN-6)	Soma-clone of Dapoli-1	Dr. BSKKV, Dapoli	2017	118–120	25–27	Konkan region of Maharashtra
23	CO 15	CO 11 × PR 202	Centre on Excellence of Millets, TNAU, Athiyandal, Tamil Nadu	2017	115–120	29.0 under rainfed and 34.0 under irrigated	Tamil Nadu
24	GNN-7	Pureline selection from white type landrace of Nagli collected from Ahwa-Dang District, State: Gujarat	NavsariAgril. Univ., Gujarat	2017	123–128	25.0 q/ha	Gujarat

(continued)

S. No.	Variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Avg. yield (q/ha)	Area of adaptation
25	VL-379	GE-440 × VL-149	ICAR-VPKAS, Almora	2017	105–107	30–32	Recommended for Uttarakhand, Bihar, Jharkhand, Madhya Pradesh and North eastern states
26	Chhattisgarh Ragi-2 (BR-36)	PR-202 × GE-669	ZARS, Jagdalpur, IGKVV	2018	115–118	34–36	Chhattisgarh
27	DHFM-78-3	GE 1219 × Indaf 8	ARS, Hanumanamatti, UAS, Dharwad	2018	114–116		Recommended for cultivation in agro-climatic Zone—3 and 8 of Karnataka state
28	VL Mandua-380	GEC 440 × VL 149	ICAR-VPKAS, Almora	2019	115–116	18–19	Uttarakhand
29	Vegavathi (VR 929)	GE-3076 × VR-854	ARS, ANGRAU, Vizianagaram	2019	115–120	Grain yield is 36.1 q/ha and fodder yield is 7.2 tonnes/ha	National
30	Tirumala (PPR 1012)	AE 3077 × Ratnagiri	ARS, Perumallapalle, ANGRAU, Guntur	2019	115–120	Grain 35–37 q/ha fodder yield 7–8 tonnes/ha	Andhra Pradesh
31	GN 8	Pureline selection from local collection of Waghai Tal. Dist. Dang.	Navsari Agricultural University, Navsari	2019	105–110	31–32	Gujarat
32	FMV-1102	VR-708 × GPU-48	ZARS, Jagdalpur, IGKVV	2019	110–115	30–32 q/ha (grain) and 11–12 tonnes/ha (fodder)	Assam, Bihar, Chhattisgarh, Jharkhand,

							Uttarakhand, Madhya Pradesh
33	KMR-630	PR-202X GE1409	VC Farm, Mandya, UAS, Bangalore	2020	95–100	28–30	Karnataka
34	VR-988	GE 3076 × VR 855	ARS, ANGRAU, Vizianagaram	2020	110–115	28–30	Andhra Pradesh
35	PR-10-45 (Gowthami)	GPU 28 × GE 4931	ARS, ANGRAU, Peddapuram	2020	122–125	35–37	Andhra Pradesh
36	CFMV-1 (Indravathi)	VL 330 × GE 532	ARS, ANGRAU, Vizianagaram	2020	110–115	30–32	Andhra Pradesh, Karnataka, Tamil Nadu, Puducherry, and Odisha
37	CFMV-2	Pureline selection from local collections made under Dang District of Gujarat	Navsari Agricultural University, Navsari	2020	119–121	29–31	Andhra Pradesh, Chhattisgarh, Gujarat, Maharashtra and Odisha
38	VL-378	GEC 440 × VL 149	ICAR-VPKAS, Almora	2020	110–114	22–24	Rainfed organic conditions of Uttarakhand hills
39	VL-382	WR 2 × VL 201	ICAR-VPKAS, Almora	2020	106–108	11–13	Rainfed organic conditions of Uttarakhand hills
Foxtail millet							
1	Co 7 (TNAU 196)	Co 6 × ISe 247	TNAU, Coimbatore	2005	85–90	18–19	Tamil Nadu
2	HMT 100-1	RS 118 × PS 3	ARS, Hanumanamatti, UAS, Dharwad	2008	90–95	20–25	Karnataka
3	SiA 3085	Pure line from SiA 2644	RARS, Nandyal, ANRAU	2011	80–85	20–30	All foxtail millet growing areas of the country

(continued)

S. No.	Variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Avg. yield (q/ha)	Area of adaptation
4	Surya Nandi (SiA 3088)	Pure line from SiA 1244	RARS, Nandyal, ANRAU	2012	70–75	20–25	All foxtail millet growing areas of the country
5	SiA 3156	Pure line from 2871	RARS, Nandyal, ANRAU	2012	85–90	20–25	Andhra Pradesh, Bihar, Gujarat, Karnataka, Madhya Pradesh, Tamil Nadu and Uttarakhand
6	RAU (Rajendra Kauni 1-2)	Selection from Local germplasm of Laukaria, Raxaul, East Champaran	Rajendra Agricultural University, Bihar, Pusa, Samastipur	2017	80–83	23–25	Irrigated and rainfed upland of Bihar
7	DHFt-109-3	Co-5 × GPUS-30	ARS, Hanumanamatti, UAS, Dharwad	2018	86–88	Grain yield 29 q/ha Fodder yield 5.23 tonnes/ha	Recommended for cultivation in agro-climatic Zone 3 and 8 of Karnataka state
8	Hagari Navane-46	Sia 2644 × PS-4	Agricultural Research Station, Hagari, Ballari, University of Agricultural Sciences, Raichur	2019	85–90	16–20 q/ha (rainfed) 20–25 q/ha (irrigated)	Zones 1, 2 and 3 of Karnataka
9	SiA 3222 (Garuda)	SiA 3075 × SiA 326	Agricultural Research Station, ANGRAU, Nandyal, AP	2020	60	19–20	Andhra Pradesh
10	SiA 3223 (Renadu)	Developed from GS 96 population through MDPLS breeding	Agricultural Research Station, ANGRAU, Nandyal, AP	2020	86–90	34–35	Andhra Pradesh
11	ATL-1 (TNSi-331)	PS 4 × Ise 198	Centre for Excellence in Millets, Athiyandal, Tiruvannamalai, TNAU	2020	80–85	20–22	Tamil Nadu

Kodo millet							
1	JK 13	Selection from mutant JK 76	Rewa, JNKVV, Jabalpur	2007	95–100	22–23	National
2	JK 106	Selection from Sidhi dist. germplasm	Rewa, JNKVV, Jabalpur	2009	100–105	19–20	M.P. State
3	JK 65	Selection from Sidhi dist. germplasm	Rewa, JNKVV, Jabalpur	2009	105–110	23–25	National
4	JK 98	Selection from GPLM 317	Rewa, JNKVV, Jabalpur	2010	100–105	25–30	National
5	DPS 9-1	Selection from local land race	Dindori, JNKVV, Jabalpur	2011	105–110	27–30	National
6	Indira Kodo 1	Pureline selection	Jagdalpur IGKVV	2012	100–105	22–25	Chhattisgarh
7	Chhattisgarh kodo-2	Mutant Line of CO 3	Jagdalpur IGKVV	2014	95–100 days	25–26	Chhattisgarh
8	TNAU-86	Pureline selection from IPS 85	TNAU Coimbatore	2012	95–110	27–30	National
9	RK 390-25	Mutant of RK-390	Rewa, JNKVV	2012	100–105	25–28	National
10	Jawahar Kodo 137	Mutant of RK-390	Rewa, JNKVV	2016	100–105	26–29	Rainfed areas of Madhya Pradesh
11	KMV-543	Mutant of CO-3	ZARS, Jagdalpur, IGKVV	2019	105–110	25–27	Andhra Pradesh, Chhattisgarh, Gujarat, Jharkhand, Karnataka, Madhya Pradesh and Tamil Nadu
12	Kodo millet variety KMV 545 (TNPsc 262)	Pureline selection from DPS 63/58	Centre for Excellence in Millets, Athiyandal, Tiruvannamalai, TNAU	2020	105–110	28–30	Andhra Pradesh, Chhattisgarh, Gujarat, Jharkhand, Karnataka, Madhya Pradesh, Tamil Nadu and Telangana

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S. No.	Variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Avg. yield (q/ha)	Area of adaptation
14	GAK-3	Pureline selection from locally collected germplasm of Hilly regions of Rewa district of Madhya Pradesh	Hill Millet Research Station Anand Agricultural University Dahod 389 151	2020	105–110	23–25	Dry lands, hilly and tribal region of Dahod and Panchmahal districts of Gujarat
Barnyard millet							
1	CO(KV) 2	Pureline selection from EF 79	TNAU, Coimbatore	2008	95–100	21–22	Tamil Nadu state
2	DHBM 93-3	VL-13XIEC-566	ARS, Hanumanamatti, UAS, Dharwad	2016	90–95	22–24	National
3	DHB-93-2	EF-8 × IEC-566	ARS, Hanumanamatti, UAS, Dharwad	2018	86–88	Grain yield 27.6 q/ha and fodder yield 6.19 tonnes/ha	Recommended for cultivation in agro-climatic Zone—3 and 8 of Karnataka state
4	MDU-1	Pureline selection from Aruppukottai local	Agricultural Engineering College and Research Institute, TNAU, Madurai	2018	95–100	Grain yield of 15–17 q/ha (rainfed) and 22–25 q/ha (irrigated)	Suitable for southern districts of Tamil Nadu
						Fodder yield of 30–33 q/ha	
5	DHBM-23-3	VL-13 × IEC-566	ARS, Hanumanamatti, UAS, Dharwad	2019	88–100	20–21	Andhra Pradesh, Karnataka, Madhya Pradesh and Tamil Nadu

Little millet							
1	OLM 208	Selection from Lajigada local	OUAT, Berhampur	2009	100–105	12–15	National
2	OLM 217	Selection from Udayagiri local	OUAT, Berhampur	2009	105–110	15–16	National
3	Co 4	Co 2 × MS 1684	TNAU, Coimbatore	2005	75–80	16–20	Tamil Nadu
4	JK 36	Selection from local Shahdol germplasm	Rewa, JNKVV, Jabalpur	2009	75–80	10–12	M.P. state
5	BL 6	Paiyur 1 × OLM 29	Jagdalpur, IGKVV, Raipur	2016	90–95	12–14	National
6	DHLM 36-3	Co-4 × Paiyur—2	ARS, Hanumanamatti, UAS, Dharwad	2018	95–100	14–16	Karnataka
7	Chhattisgarh Kutki-2 (BL-4)	CO-2 × TNAU 97	Jagdalpur, IGKVV, Raipur	2016	90–95	10–12	Chhattisgarh
8	GV-2	Derivative from mutant of released variety ‘Gujarat Vari-1’	Waghai, NAU, Navsari	2016	115–125	26–28	Gujarat
9	Phule Ekadashi (KOPLM 83)	Selection from local germplasm	ZARS, Kolhapur, MPKV Rahuri	2016	120–130	12–14	Sub-montane and Ghat zone of Maharashtra
10	Jawahar Kutki 4 (JK 4)	DLM 42 × Kutki1	Rewa JNKVV Jabalpur	2016	75–80	13–15	Rainfed areas of Madhya Pradesh
11	DHLM-14-1	CO-2 × TNAU-110	ARS, Hanumanamatti, UAS, Dharwad	2018	97–99	Grain yield 16.0 q/ha and fodder yield 6.10 tonnes/ha	Recommended for Tamil Nadu, Karnataka, Gujarat, Maharashtra and Orissa

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S. No.	Variety	Pedigree	Institute where developed	Year of release	Maturity (days)	Avg. yield (q/ha)	Area of adaptation
12	GNV-3	Pureline selection from local land races collected from the Dang district of Gujarat	Waghai, NAU, Navsari	2018	110–115	28–29	Gujarat agro-climatic Zone I, II and III (dry lands/hilly/tribal region of Dang, Valsad, Navsari and Panchmahal districts of Gujarat)
13	ATL-1 (TNPsu 177)	CO (Samai) 4 × TNAU 141	Agriculture Research Station, Tamil Nadu Agricultural University	2019	85–90		Tamil Nadu
14	LMV513	CO-2 × TNAU-26	ARS, Hanumanamatti, UAS, Dharwad	2019	93–96	17–19	Andhra Pradesh, Karnataka, Madhya Pradesh, Maharashtra, Chhattisgarh, Odisha and Jharkhand.
15	BL-41-3	Paiyur 2 × TNAU 97.	ZARS, Jagdalpur, IGKVV	2019	95–100	16–19	Chhattisgarh
16	Jaicar Sama 1 (LMV-518)	Pureline selection from indigenous germplasm collection GPmr-1153	Indian Institute of Millets Research, Hyderabad	2020	98–102	15–17	Maharashtra, Andhra Pradesh, Telangana, Tamil Nadu, Puducherry
Proso millet							
1	TNAU 145	PV 1454 × TNAU 96	TNAU, Coimbatore	2007	70–72	18–20	Tamil Nadu
2	CO(PV) 5 (TNAU 143)	PV 1403 × GPUP 21	TNAU, Coimbatore	2007	70–75	23–25	National
3	TNAU 151	TNAU 96 × PV 1673	TNAU, Coimbatore	2008	72–75	18–20	National

4	TNAU 164	TNAU 137 × CO 4	TNAU, Coimbatore	2009	70–75	18–20	National
5	PratapCheena-1 (PR-18)	Pure line selection	MPUA&T, Udaipur	2006	65–70	15–17	National
6	PRC 1	Selection from GPMS 519	Ranichauri, GBPUA&T, Pantnagar	2008	70–75	10–12	Uttarakhand hills
7	TNAU 202	PV 1453 × GPUP 16	TNAU, Coimbatore	2011	70–75	18–20	National
8	TNPm-230	TNAU-164 × IPM-19	TNAU, Coimbatore	2017	70–75	21–23	National
9	DHPM-2769	Selection from IPM-2769	ARS, Hanumanamatti, UAS, Dharwad	2018	70–72	Grain yield 24.6 q/ha and fodder yield 4.16 tonnes/ha	Recommended for cultivation in agro-climatic Zone—3 and 8 of Karnataka state
10	PMV-442	GPMS 109 × GPMS 908	Project Coordinating Unit, UAS, Bengaluru	2019	70–75	14–16	Andhra Pradesh, Karnataka, Madhya Pradesh and Tamil Nadu, Bihar, Telangana, Puducherry

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