Floral Biology, Pollination, Genetics, Origin, and Diversity in Proso Millet (*Panicum miliaceum* L.)

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D. S. Supritha Raj, Shridhar Ragi, Basavaraj M. Pattanashetti, and Isha Mendapera

Abstract

Proso millet is a diet crop that was domesticated about 10,000 years ago, and it has been rampant throughout the ancient civilization. At present, this crop is cultivated across Asia, Australia, North America, Europe, and Africa. In developed nations, it serves as both bird and livestock feed, while in certain Asian regions, it is consumed as a food source for humans. This marginal crop displays high variation in its morphological features and is appropriate for dry-land agriculture. It exhibits exceptional water-use efficiency, necessitating the minimum water requirement among all cereal crops. Furthermore, it boasts a nutritional profile abundant in protein, vitamins, minerals, and essential micronutrients like Fe, Zn, Cu, and Mn, in comparison to other primary cereal crops. Globally, plant breeders are employed to create upgraded cultivars using traditional and innovative breeding methodologies. The germplasm encompassing a broad range of crop genetic diversity is safeguarded by many countries in gene banks. Nonetheless, the absence of a linkage map information and sufficient genomic tools have impeded the progress of crop enhancement. Therefore, proso millet must receive extra consideration from the scientific community and superior advancement is essential in genetic improvement and associated research.

D. S. Supritha Raj · B. M. Pattanashetti
Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad, Karnataka, India

S. Ragi (✉)
Division of Genetics, ICAR-Indian Agricultural Research Institute, IARI, New Delhi, India

I. Mendapera
Department of Genetics and Plant Breeding, Navsari Agricultural University, Navsari, Gujarat, India

S. Mishra et al. (eds.), *Genetic Improvement of Small Millets*,
https://doi.org/10.1007/978-981-99-7232-6_18

Keywords

Proso millet · Germplasm · Origin

18.1 Introduction

Proso millet, scientifically known as *Panicum miliaceum* L., is tetraploid small millet with a chromosome count of $2n = 4x = 36$ and a basic chromosome count of $x = 9$. This ancient cereal crop has been cultivated by humans for centuries. The diversity of its names showcases its worldwide distribution. In the United States, it is known as common millet and hog millet, while in China, it is referred to as broomcorn millet. In Germany, it is called 'hersey', and across Asia Pacific nations, Korea, and Japan, it is recognized as common millet. In France, it is known as French white (Rajput et al. 2014). It goes by diverse names in different languages in India, such as, Panivaragu in Tamil, Cheena in Bengali, Baragu in Kannada, Variga in Telugu, Vari in Marathi, China Bachari-bagmu in Odia, and Cheno in Gujarati (Rajasekaran and Francis 2021). This exceptionally diverse crop possesses remarkable nutritional qualities and is poised to become a crucial element in enhancing food diversity. It is primarily utilized for human consumption across Asia. However, it finds use as both birdseed and livestock feed in the United States.

Proso millet is cultivated on marginal lands with less inputs as minor millet. It is a shallow-rooted, short-duration (70–90 days) growing crop with the lowest water and nourishment prerequisite making it adaptable for rising in warm and dry atmospheres. It displays remarkable drought tolerance and has the ability to emerge in dry, semi-arid areas, producing seeds with an annual precipitation as low as 330–350 mm (Baltensperger 2002; Lyon et al. 2008). From a nutritional standpoint, the grains represent a valuable carbohydrate source, and have abundant protein ($>14\%$), dietary fiber, minerals, vitamins, and a well-balanced profile of crucial amino acids.

18.2 Origin and Domestication of Proso Millet

Proso millet is a primeval identified cereal domesticated roughly 10,000 years ago in semi-arid parts of China (Lu et al. 2009a, b; Hunt et al. 2014). This crop has historical significance and possesses different theories about its origin. Vavilov (1926) stated that China serves as the focal point of variation for this millet, while Harlan (1975) suggested that both China and Europe are probable regions for the domestication of proso millet. Furthermore, instances of charred grains and grain impressions on pottery have been discovered at multiple locations in Eastern Europe dating back to periods before 7000 calibrated years before the present (cal BP), as noted by Hunt et al. (2008) and Zohary and Hopf (2000).

Examining phytoliths discovered in ancient storage pits at the archeological site of Cishan, situated on the border between the Loess Plateau and the North China

Plain, was conducted by Lu et al. (2009a, b). By analyzing carbon-dating results from 47 archeological samples, they deduced that the earliest cultivation of this millet commenced around 10,000 years BC in the semi-arid regions of China. Proso millet was probably cultivated more rapidly than other grains during the early Holocene because of relatively arid conditions. As a result, the oldest records are from the Cishan site in the Yellow River basin in China, which dates to between 10,300 and 8700 cal years BP. Moreover, it was postulated by Lu et al. that proso millet was autonomously cultivated as a primary crop in the Northern Chinese region approximately 10,000 years ago. Over time, it subsequently spread to adjoining areas including Russia, India, the Middle East, and Europe. However, Zhao (2011) contended that due to the degraded state of samples obtained from the Cishan excavation, the actual domestication might have taken place between 7600 and 8100 years ago. Based on analyses of charred remnants of proso millet seeds discovered in Dadiwan, Northwestern China, it is conceivable that the domestication could have transpired around 5900 BC. The dispersal of proso millet to Europe and West Asia might have occurred by the close of initial millennium BC, influenced by alterations in agronomic practices in respective regions (Miller et al. 2016). With the aim of understanding the archeo-botanical evidence of millet discovered in Eastern Europe and exploring the possibility of several domestication locations, Hunt et al. (2011) performed genetic diversity and phylogeographic analyses on proso millet across Eurasia. These two earlier data points point to its separate domestication in central Asia or Eastern Europe, although they might possibly point to domestication within China that later moved across the Eurasian steppe in a westward trajectory (Jones 2004). One western and one eastern gene pool had been detected via their analyses, but further investigation and factual support would be obligatory to pinpoint the second domestication center (Eastern Europe or Central Asia).

18.3 Taxonomic Hierarchy and Botany

Proso millet is a member of the family *Poaceae*, tribe *Paniceae*, and order *Poales* (Christenhusz and Byng 2016; Gomashe 2017). The primary mode of pollination for proso millet is self-pollination, although a natural cross-pollination rate of over 10% has also been observed (Baltensperger 2002). It is generally considered as allotetraploid possessing $2n = 4x = 36$ chromosomes, even though there is insufficient genetic distinction. The ancestral lineages of proso millet remain ambiguous. Nonetheless, an attempt was made to identify potential progenitors that might have acted as paternal contributors to proso millet (Hunt et al. 2014). They utilized nuclear as well as chloroplast DNA sequences from *Panicum miliaceum* as well as various diploid and tetraploid relatives, to conduct an in situ hybridization analysis. Weedy forms of *P. miliaceum*, i.e., witch grass (*P.capillare*) and Torpedo grass (*P. repens*) have been identified to play a role in its origin as an allotetraploid. (Fig. 18.1). The *Panicum* species, especially those from the Old World, need to be studied further.

The *Panicum* genus contains two sub-species (subspp), namely *subspp. Miliaceum*, which has cultivated variants, and *subspp. Ruderale*, with weedy and

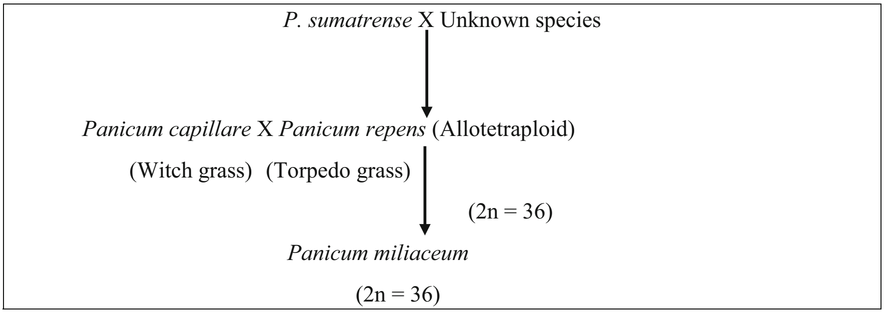

Fig. 18.1 Possible source of *Panicum miliaceum* origin. (Source: Conceptualised from Hunt et al. 2014)

Table 18.1 Various races of proso millet

Race	Inflorescence morphology	Characteristics
Miliaceum	The "inflorescences" are sizeable and open, featuring slightly upright branches that are minimally divided. The form of the inflorescence morphology bears resemblance to wild *P. miliaceum*	These two races befall across the range of broomcorn millet cultivation, from Eastern Europe to Japan
Patentissimum	Its having slender and diffused panicle branches, which are quite similar to race *miliaceum* and is difficult to distinguish	
Contractum	Compact and drooping inflorescences	
Compactum	Cylindrical-shaped erect inflorescences	Highly evolved cultivars of "broomcorn" millet, which are generally have compact inflorescences
Ovatum	Compacted and a little curved inflorescences with ovate shape	

Source: Gomashe (2017)

natural forms (Gomashe 2017; Zhang et al. 2018). Cultivated *P. miliaceum* are further classified into five different races (*miliaceum, patentissimum, contractum, compactum,* and *ovatum*) as per the inflorescence morphology (Lyssov 1975) without any taxonomic validity (see Table 18.1).

The wild proso types have lax panicles, narrow lemmas and spikelet stalks are jointed, and true wild proso types are native to central China from where cultivated ones are aroused. Whereas, cultivated types are characterized by lax or compressed panicles, jointless spikelet stalks and broader lemmas. Yet, the wild variations present in the temperate regions of Europe, Asia, and the United States exhibit distinctions from the wild variant found in China. It is probable that these wild variations originated from cultivated types that have regained the ability for seeds to disperse naturally, subsequently spreading as unwanted plants.

18.4 Botany and Genetic Features

Proso millet is categorized as a short-day C_4 plant that completes its life cycle within a year. It typically grows upright, reaches up to a height of 30 to 100 cm. Its stem and leaves can be hollow, covered in hair, or smooth. The plant displays swollen spaces between its nodes and possesses a shallow root system. It can withstand drought but is vulnerable to frostbite and water-logging conditions. It is usually harvested at physiological maturity to avoid seed-shattering (Kaume 2006). The young plants produce seminal roots that are eventually replaced by adventitious roots. The stem, also known as a culm, is often hollow and cylindrical. At the lower internodes, axillary buds develop into tillers and lateral branches.

Proso millet is primarily self-pollinated, although there is more than 10% of spontaneous cross-pollination (Baltensperger 2002). The inflorescence is a drooping panicle that are typically 10–45 cm long, open or compact and appears like broom with basipetal pattern (from top to bottom) of florets opening (Gomashe 2017; Changmei and Dorothy 2014; Habiyaremye et al. 2017a, b).

The primary branches conclude in spikelets with zero bristles below them. The proso spikelets are solitary, nearly 0.5 cm long and comprises two glumes (lower and upper glume) and two lemmas (lower and upper lemmas), and a single palea (Lu et al. 2009b). The outer and inner glumes are of different lengths, with the inner glume being the same length as the spikelet and shorter outer glume. The lower lemma possess a sterile floret without stamen; however, upper lemma encompasses fertile floret (Gupta et al. 2011) and is shorter than lower lemma. The palea of lower lemma (sterile floret) is very much reduced, while the palea of upper lemma is well present (Seetharam et al. 2003). Upper lemma has three stamen and two feathery stigmas. These anthers are blackish or dark brown in color. The ovary has bifid style and has plumose stigmas (Nanda and Agrawal 2008).

Proso normally blooms between 10:00 and 12:00. The window of time between the blooming and closure of flowers is about 7 min. Cloudy days may delay blossoming, while intense sunshine and reduced humidity may rush the process. From the beginning of anthesis to the end of the last floret on the panicle, it takes around 12–15 days. The anther dehiscence overlaps with stigma receptivity and anthers dehydrate within a few minutes of floral opening (Fig. 18.2).

Achieving successful crossbreeding in proso millet presents a challenge due to a 10% potential for cross-pollination. This poses difficulty in carrying out crossing without causing harm to the stigma and preventing premature pollen shedding before emasculation. A method for emasculation and crossing in proso millet, as outlined by Nandini et al. (2019), involves a cold spray technique. In addition, Nelson et al. (1984) provide a description of crossing procedures utilizing manual emasculation. The conventional approach to emasculation in proso millet includes the use of hot water with temperature of 50 °C for a duration of 5 min to inactivate anthers and pollen grains. By customizing the treatment's temperature and time, this approach may be utilized successfully anywhere. The tiny caryopsis seeds are oval in form which measure around 3 mm in length and 2 mm in breadth. The seeds of proso millet show a range of colors, spanning from white, cream, and yellow to orange, red, black, and brown (Fig. 18.3).

Fig. 18.2 (**a**, **b**) Proso millet crop in field, (**c**) inflorescence, (**d**) panicle, (**e**) seeds, (**f**) seed enclosed in glumes and clasping lemma and palea

Fig. 18.3 Proso millet inflorescence and its parts. (**a**) Inflorescence; (**b**) Opened spikelet; (**c**) Outer glume; (**d**) Inner glume; (**e**) Inner lemma; (**f**) Palea; (**g**) Inner glume; (**h**) Outer glume; (**i**) Upper lemma; (**j**) Anther; (**k**) Grain enclosed in lemma and palea; (**l**) Grain. (Source- Gupta et al. 2011)

18.5 Germplasm Conservation and Utilization

The success of every breeding program hinges on the germplasm variability. Improvement through conventional plant breeding has decreased both intraspecific variation and interspecific variability among farmed crops by creating and encouraging genetically homogeneous cultivars (Haussmann et al. 2004). Such as, the six cultivars of proso millet that are most often cultivated in the United States were all derived by classical breeding and selection from landraces. As a result, they all have a limited genetic base (Rajput et al. 2014). Thus, creating and maintaining a collection of plant genetic resources, or germplasm, for all cultivated crops is crucial, especially for underused and understudied crops like millets (Upadhyaya et al. 2014) (Table 18.2).

Study of proso millet has been overlooked because of the priority given to primary crops. Currently, a global inventory of 29,308 proso millet accessions has been compiled and preserved. The most extensive germplasm collection is maintained by Russia, housing 8778 accessions, with China following closely at 8451. Other significant repositories of the crop's genetic diversity can be found in Ukraine, India, and the United States as well (Upadhyaya et al. 2016). The future progress of proso millet genetics will heavily rely on effectively harnessing this genetic variation through breeding. Within India, approximately 3000 accessions are safeguarded across two national institutions: the All India Coordinated Research Project on Small Millets (AICRP-small millets) and the National Bureau of Plant Genetic Resources (NBPGR). In addition, the International Crop Research Institute for the Semi-Arid Tropics (ICRISAT) is also involved in the maintenance of plant genetic resources. In 1976, AICRP established a specialized center in Bengaluru (Rajasekaran and Francis 2021), where ongoing endeavors encompass the gathering, examination, and documentation of germplasm for small millets. Remarkably, AICRP oversees 920 accessions of Proso millet, while NBPGR, India's primary institution for managing plant genetic resources of agri-horticultural crops, supervises around 994 proso millet accessions. In addition, ICRISAT, which possesses 849 accessions, is engaged in categorizing and evaluating proso millet germplasm. Using 20 different qualitative and quantitative characteristics, ICRISAT has established a central collection comprising 106 accessions from the 833 proso millet accessions procured from 30 distinct countries. The process of forming this core collection involved randomly selecting 10% of accessions from each of the 101 clusters (Upadhyaya et al. 2011). ICRISAT has disseminated a total of 6047 proso germplasm accessions to 25–37 countries, including two sets of core collections. It is imperative to subject these accessions to thorough evaluation for variability, a crucial step toward the development of high-yielding varieties.

18.6 Germplasm Resource Evaluation and Management

Managing germplasm resources is crucial for enhancing the genetic traits of crop species, as highlighted in Table 18.3. The diverse collection of Proso millet germplasm accessions at the ICRISAT Genebank showcases significant variation in important agronomic and nutritional attributes, as well as resilience against both biotic and abiotic stresses. A study by Wang et al. (2007) evaluated the agronomic viability, disease resistance, and nutritional significance of Proso millet germplasm accessions held at the National Centre for Crop Germplasm Conservation in Beijing,

Table 18.2 Prominent genetic repositories safeguarding proso millet germplasm on a global scale

		Germplasm		
Country	Institution	Cultivated	Wild	Total
Russia federation	N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry (VIR)	8778	–	8878
China	Institute of Crop Science, Chinese Academy of Agricultural Sciences (ICS-CAAS)	8451	–	8451
Ukraine	Plant Production Institute nd. a. V. Ya. Yuryev of NAAS (IR)	1046	–	5022
	Ustymivka Experimental Station of Plant Production (UDS)	3975	1	
India	AICRP on Small Millets (AICRP- Small Millets)	920	–	2767
	International Crop Research Institute for the Semi-Arid Tropics (ICRISAT)	849	–	
	National Bureau of Plant Genetic Resources (NBPGR)	994	4	
USA	United State Department of Agriculture-Agricultural Research Service, North Central Regional Plant Introduction Station, (USDA-ARS, NCRPIS)	717	4	721
Japan	Department of Genetic Resources I, National Institute of Agrobiological Sciences (NIAS)	516	–	516
Bulgaria	Institute for Plant Genetic Resources "K. Malkov" (IPGR)	489	–	489
Mexico	Estación de Iguala, Instituto Nacional de InvestigacionesAgrícolas (INIA-Iguala)	400	–	400
Poland	Plant Breeding and Acclimatization Institute (IHAR)	354	–	354
	Botanical Garden of Plant Breeding and Acclimatization Institute (BYDG)	359	–	359
Hungary	Institute for Agrobotany (RCA)	243	1	244
Australia	Australian Tropical Crops and Forages Genetic Resources Centre (ATCFC)	228	–	228
Bangladesh	Plant Genetic Resources Centre, BARI (PGRC, BARI)	198	–	198
Czech Republic	GenBank Department, Division of Genetics and Plant Breeding, Research Institute of Crop Production (RICP)	171	–	171
Germany	GenBank, Leibniz Institute of Plant Genetics and Crop Plant Research	165	–	165

Source: Upadhyaya et al. (2016)

China. This assessment led to the identification of superior accessions exhibiting single or multiple advantageous traits. Regarding the germplasm maintained within the ICRISAT collection, it was observed that the majority of early-flowering genotyes were originated from Syria, whereas late-flowering types were traced back to India. In addition, dwarf plant height accessions were found to have roots in Mexico, in contrast to tall plant height accessions that were linked to Sri Lanka.

Table 18.3 Genetic assets pinpointed for diverse characteristics within the Indian program

Character	Promising genotypes	Reference
Days to flower	IC345024, JPM 44,IPM 40, IPM 2125, IPM 2589, IPM 84, IPM 273, IPM-982	NBPGR- Annual Report, (1986, 1987)
Panicle length	Shai Local, Rampur Local	NBPGR- Annual Report, (2011)
Blast, sheath blight, leaf blight, grain smut	TNAU 218, TNAU 164, DHPRMV 2769, TNAU 148	Anonymous (2014)
Rust	TNAU 145, TNAU 204, 218, 220 and CO 5	AICSMIP (2014)
Grain yield (g)	EC 24114,IPM 364, IC 41847, IPM 36, IPM 33, IC 52792, IC 28829, EC 24113	NBPGR- Annual Report (2012)

Source: Gomashe (2017)

The origins of shorter panicle exertion accessions could be traced to the former USSR, whereas longer panicle variants were sourced from Nepal. Notably, accessions demonstrating favorable exertion tendencies were predominantly associated with Australia and China (Reddy et al. 2007).

Graybosch and Baltensperger (2009) assessed 650 different accessions of proso millet to identify instances of endosperm starch with a waxy (amylase free) characteristic. They came to the conclusion that this waxy trait was controlled by duplicate recessive alleles at two distinct loci. Dikshit and Sivaraj (2013) identified accessions with elevated protein content and a wide range of morpho-agronomical attributes. Other investigations, such as those by Natarajan et al. (1978), Manoharan and Sivasubramanian (1982), Hawlader (1991), Prasad et al. (1995), Panwar and Kapila (1992), Reddy et al. (2007), Salini et al. (2010), and Sasamala et al. (2011), have also underscored significant diversity in proso millet concerning both its morphological traits and attributes linked to yield.

In proso millet, only a few diseases have been documented, with the main ones being head smut, sheath blight, bacterial spot, and others. Researchers have focused on enhancing proso millet's resistance to head smut and melanosis (Konstantinov and Grigorashchenko 1987; Maslenkova and Resh 1990; Konstantinov et al. 1989, 1991; Soldatov and Agafonov 1980; Shailaja et al. 2009). Some proso millet germplasm varieties and accessions that show promise in resisting shoot fly and rice moth have also been identified (Shailaja et al. 2009; Murthi and Harinarayana 1989). Abiotic stresses also affect proso millet. Breeding efforts in the United States have given priority to developing strains resistant to lodging (Baltensperger et al. 1995a, b, 2004). In addition, some sources have been reported for demonstrating salinity tolerance (Accession no. 008211, 008214, and 008226) (Sabir et al. 2011).

18.6.1 Core Collection Development

A core collection, which is made up of a small proportion (about 10%) of accessions from an existing germplasm collection, aids in capturing all of the variability for use in breeding operations. At ICRISAT, 833 accessions were classified into five groups based on race, and Ward's approach was used to cluster the data using information on 20 morpho-agronomic variables (Upadhyaya et al. 2011). A core collection of 106 accessions was generated by randomly selecting 10% (or at least one accession) from each of the 101 clusters. These core collections serve as excellent genetic resources for discovering novel sources of variation and to conduct genomic research.

18.7 Germplasm Molecular Characterization

The extent of exploration has been limited for genetic diversity for proso millet (Goron and Raizada 2015). The genetic diversity analysis presents challenges due to its tetraploid nature and the absence of sequencing data (Hunt et al. 2011). Molecular markers have significantly aided studies concerning genetic diversity, taxonomic relationships, and population structure across various species. Nevertheless, marker information for proso millet remains scarce (Rajput et al. 2014). Research focusing on proso millet's genetic diversity has employed molecular markers like random amplified polymorphic DNA (RAPD), amplified fragment length polymorphism (AFLP), and simple sequence repeat (SSR) markers (Habiyaremye et al. 2017a).

Using RAPD molecular markers, the diversity of four *Panicum* species and individual accessions of proso millet was assessed (M'Ribu and Hilu 1996). Their research proved that molecular markers might be a useful tool for preserving genetic variation. More than ten years afterward, AFLP markers were employed to examine the genetic variation among three cultivated and nine untamed biotypes from the United States and Canada (Karam et al. 2004). In another study, Lágler et al. (2005) contrasted a medieval millet landrace with 20 prevalent proso millet cultivars using markers like inter simple sequence repeat (ISSR), simple sequence repeat (SSR), and cleaved amplified polymorphic DNA (CAP).

SSR markers, also known as microsatellites, are highly utilized for diversity studies due to their plentiful presence. The scarcity of proper proso millet genomic resources has led researchers to derive SSR markers from genomic sequences of related plant species for proso millet (Habiyaremye et al. 2017a). In a study by Hu et al. (2009), a total of 46 SSR markers sourced from rice, wheat, oat, and barley were employed to study the genetic diversity of 118 Chinese germplasms originating from diverse ecological regions. Similarly, Rajput et al. (2014) evaluated 8 proso millet genotypes using 548 SSR markers derived from switch grass, given that switch grass is the closest genetic relative to proso millet. The initial proso genome SSR markers were introduced by Cho et al. (2010). As a result, numerous researchers have effectively harnessed SSR markers for probing genetic diversity in distinct sets of proso millet germplasm (Hunt et al. 2011; Rajput et al. 2016; Liu et al. 2016).The exploration of proso millet's genetic diversity encompasses various approaches, including DNA markers and additional genomic tools such as polymerase chain reaction (PCR) involving 6 intron splice junctions (ISJ) and long random primers, as demonstrated by Hu et al. (2008) and Araki et al. (2012). Furthermore, genotyping methodologies (Hunt et al. 2011, 2013) and the utilization of Illumina sequencing along with de novo transcriptome assemblies for generating short-read sequences have also contributed to understanding proso millet's genetic makeup (Hou et al. 2017).

18.8 Genetic Improvement of Proso Millet: Achievements and Status

18.8.1 India

Since the beginning of the study, the All India Coordinated Small Millets Improvement Project (AICSMIP) and SAUs have investigated the germplasm lines for yield and other trait improvement. However, very few improved varieties of proso millet (Table 18.3 and 18.4) have been generated using traditional plant breeding methods.

18.8.2 United States

In 1972, the United States initiated a dedicated breeding initiative for proso millet at the Panhandle Research and Extension Center (PHREC). At Scottsbluff, Lenis Nelson established the inaugural proso millet center for research and breeding, resulting in the release of four cultivars: Sunup, Dawn, Cerise, and Rise. Notably, Dawn emerged as the primary parent in different varietal development endeavors. In 1988, David Baltensperger earned significant recognition for his varieties, namely Early Bird, Hutsman, Sunrise, and Horizon, which remain widely cultivated to this day. More recently, Dipak Santra has embraced breeding programs for alternative crops, aiming to accelerate breeding efforts through genomic tools and enhance genomic resources for marker-aided selection (MAS) applications.

18.8.3 Russia

Russians employed mainly intra-specific hybridization for proso improvement. The remarkable cultivars such as 'Bistrove' and 'Krupnoskoroe' (*ssp. Subcoccineum*), with more than 5 tha^{-1} grain yield and shorter life cycles were released (Kurzeva et al. 2012). The value-added varieties like 'Sputnik' (*ssp. coccineum*), Sojuz (selection line 1.1980), and 'Slavjanskoe' (spp. *subflavum*) containing resistance for smut disease were developed in 2006. The new variety 'Regent' was developed using anther-culture technique in 2011. Mutant forms serve as the foundation for novel selection technologies, alongside the production of dihaploid plants, genotype documentation utilizing storage protein electrophoresis, and PCR-based DNA markers. The Proso millet genetic resources from Russia and USA are given in Table 18.5.

Table 18.4 Improved varieties released in proso millet in India

Sl. No.	Variety	Pedigree	Development center	Year	Salient features
1	Shyamcheena	A pure-line selection	–	1960	
2	Ram cheena	A pure-line selection	–	1960	
3	V-306	–	Andhra Pradesh	1965	
4	V-27	–	Andhra Pradesh	1965	
5	K2	A pure-line selection from PV-1685	Tamil Nadu Agricultural University, Coimbatore	1980	Tolerant to major pests and diseases
6	K1	Selection from local	Tamil Nadu Agricultural University, Coimbatore	1982	
7	BR-7	A pure-line selection	–	1982	Moderately resistant to Helminthosporium and shoot fly
8	CO-2	Pure-line selection from a local collection from Manjanaikanur in Annamalai block Coimbatore	TNAU, Coimbatore	1985	Shining yellow bold grain; densely pubescent
9	CO-3	Pure-line selection from the local collection maintained at TNAU	TNAU, Coimbatore	1985	Shining golden yellow grain drought tolerant, leaf pubescent
10	CO-4	Pure-line selection	TNAU, Coimbatore	1989	
11	Nagarjuna	Pure-line selection	ANGRAU, Hyderabad	1989	Early maturity
12	Sagar	Selection from local	ANGRAU, Hyderabad	1989	High seed yield
13	Bhawna	Pure-line selection	CSAUAT, Kanpur	1992	Early maturity
14	GPUP 8	S 7 × L 111	CSAUAT, Kanpur	2001	Resistant to brown spot
15	GPUP 21	GPUP 14 × K 1	PC unit, UAS, Bangalore	2003	High yield, moderately tolerant to shoot fly
16	Pratap chenna-1 (PR-18)	Pure-line selection	MPUA&T, Udaipur	2006	For sub-marginal/ shallow, undulating and hilly agro-ecological

(continued)

Table 18.4 (continued)

Sl. No.	Variety	Pedigree	Development center	Year	Salient features
					situations in Rajasthan
17	CO (PV) 5	Cross derivative of PV 1403 × GPUP 21	TNAU, Coimbatore	2007	Resistant to brown spot and tolerant to rust and grain smut
18	PRC-1	Selection from GPMS 519	GBPUA&T, Pantnagar	2008	Resistant to helminthosporium
19	TNAU 145	Cross-derivate of PV 1454 × TNAU 96	TNAU, Coimbatore	2009	Tolerant to rust and shoot fly
20	TNAU 151	TNAU 96 × PV 1673	TNAU, Coimbatore	2009	Tolerant to rust and shoot fly
21	TNAU 164	Derivate of TNAU 137 × CO4	TNAU, Coimbatore	2010	Resistant to rust and grain smut disease incidence
22	TNAU 202	PV 1453 × GPUP 16	TNAU, Coimbatore	2011	Recommended for cultivation in dry lands of India
23	TNPm-230	TNAU-164 × IPM-19	TNAU, Coimbatore	2017	Short duration, drought tolerant variety
24	DHPM-2769	Selection from IPM-2769	ARS, Hanumanamatti, UAS, Dharwad	2018	Suitable for contingency planting
24	PMV-442	GPMS 109 × GPMS 908	Project Coordinating Unit, UAS, Bengaluru	2019	

18.8.4 China

The Agricultural Experiment Farms of the former Suyuan province (now located in Langshan town, Linhe District, Inner Mongolia) and the Guanghua Farm (which later became the Yan'an Research Institute of Agricultural Sciences) in the Shan-Gan-Ning Region were both engaged in proso millet breeding around 1940. Notably, the initial Agricultural Experiment Farm identified the Langshan 462 and Micang 155 varieties. These two varieties, Langshan 462 and Micang 155, gained prominence as the earliest proso millet types cultivated in the Qianshan region and Tumochuan Plain of Bayan Nur and Ulan Qab, Inner Mongolia, prior to 1965.

Between 1940 and 1970, there was a proliferation of 10 research organizations dedicated to enhancing proso millet varieties. This collective effort resulted in the successful development of 42 distinct varieties, constituting approximately 31% of all varieties bred in China. An influential contribution came from the Crop Breeding Institute of the Helongjiang Academy of Agricultural Sciences, which pioneered

Table 18.5 Proso millet genetic resources in different countries

Cultivar	Important traits	Cultivation location
Dawn	Maturing at an extremely early stage; uniform ripening; large seed	USA
Rise	Demonstrates stability across diverse cultivation conditions; characterized by small seeds and compact panicles.	USA
Sunup	Exhibits resilience across a broad spectrum of cultivation conditions.	USA
Earlybird	Strong straw durability, compact panicle; exceptionally large seed size, maturing at an early stage.	USA
Huntsman	Compact form of panicle, significant seed size, maturing at a later stage.	USA
Sunrise	Significant seed size, densely packed panicle.	USA
Horizon	Significant seed size; panicle with a closed structure.	USA
Bistroye	Produces abundant yield at an early stage of maturity.	Russia
Kruppnoskoroe	High-yielding early maturing, large grain	Russia
Sputnik, Slavjanskoe	Generates substantial harvest, maturing in the mid-early range, resilient against smut, and boasting superb groat quality.	Russia
Alba	Yields a significant harvest, matures in the mid-early phase, exhibits strong and rapid ripening, resistant to lodging and shattering, easily hulled, and delivers a substantial great output.	Russia

varietal improvement through hybridization techniques. This pioneering work set the foundation of hybridization-based breeding, ultimately yielding 10 new varieties. Among these, ‘Longshu 16’ stood out as the first broomcorn millet variety to be bred through hybridization in China.

18.8.5 Kenya

The team at Kenya Agricultural Research Institute (KARI) initiated an initial enhancement initiative by making a limited number of choices from local and ICRISAT-associated lineages. One notable outcome of this effort is the ‘KAT/PRO-1’ cultivar, which was created through mass selection and is recommended for farming in Kenya. Developed by KARI, this cultivar exhibits a 50% higher yield compared to indigenous variants. Its origins trace back to ‘N40101,’ a plant introduced from the former Soviet Union via ICRISAT. The other institutes working on proso millet genetic resources are in brief reviewd by Santra et al. (2019).

18.9 Conclusion and Future Perspectives

Proso millet stands as a neglected crop, often overlooked. Its remarkable ability to thrive under varying climates due to its minimal water requirements sets it apart from other cereal crops. This hardy crop displays resilience in the face of challenging conditions, particularly in arid regions and nutrient-depleted soils. Despite its potential benefits, proso millet's significance has waned against more prominent cereals such as rice, wheat, and maize. Nevertheless, the tide is turning, as more people are expressing interest in exploring these traditional crops. Considering the existing scenario of climate change, constrained resources, and escalating food insecurity, there is an urgent requirement to revitalize resilient and nutritionally dense crops such as proso millet. This underscores the importance of enhancing proso millet's genetics to create improved cultivars that offer not only enhanced yields but also enriched protein and mineral content. As we look ahead, initiatives aimed at advancing proso millet should embrace technological progress. This involves the development of innovative varieties, novel cultivation techniques, effective agronomic approaches, plant protection strategies, and the mechanization of farming practices.

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