

10. Crop Breeding Strategies to Enhance Inherent Adaptability and Productivity of Millets

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Abstract:

In the developing world, particularly in the arid regions of Africa and Asia, millets are a staple meal. The majority of millets are native to Africa and were domesticated there before spreading to other regions of the world. Millets are also known as nutricereals because they provide more nutrients overall than traditional food grain crops like paddy and wheat. A range of small-seeded cereal crops belonging to the Poaceae grass family are referred to as small millets. These contains millet varieties like kodo, proso, foxtail, finger, and barnyard. Little millets ability to withstand climate change and consumers growing interest in healthy diets highlight the need for greater research and development on these crops. Proso millet and other small millets, with the exception of finger millet and foxtail millet, have gotten very little attention from researchers in terms of developing genetic and breeding for yield enhancement.

There have been significant breeding efforts in foxtail millet, finger millet, and proso millet in China, India, and the United States of America, respectively. In order to improve small millets, recent developments in phenotyping and genomics technology as well as the diversity of available germplasm can be used. To create drought or heat-tolerant lines, breeding operations have taken advantage of limited features with limited genetic and genomic resources.

Keywords:

Small millets, Nutricereals, Genetics, Breeding

10.1 Introduction:

Millets is a collective term referring to a number of small-seeded annual grasses that are cultivated as grain crops and represented by sorghum (jowar), pearl millet (bajra), finger millet (ragi) and minor millets like banyard millet, proso millet, kodo millet and foxtail millet. Being excellent source of essential nutrients to the millions of rural poor in India, they are also called as 'nutritious cereals'. Millets are the staple food for the world's poorest and most food insecure populations across the semi-arid tropics. The crop development initiatives on Millets and Directorate of Sorghum Research, under the umbrella of Indian Council of Agricultural Research, and other institutions in both public and private sector are aiming to enhance livelihood of dryland farmers through improvement of millet yield.

Millets are better adapted to dry, infertile soils than most other crops, and are therefore often cultivated under extremely harsh conditions - for example, high temperatures, low and erratic precipitation, short growing seasons and acidic and infertile soils with poor water-holding capacity. The majority of millets have short life cycles, robust, deep root systems, and can expand quickly when moisture is present. As a result, they can survive and reliably produce small quantities of grain in areas where mean annual precipitation is as low as 300 mm.

This compares with a minimum water requirement of 400 mm for sorghum and 500-600 mm for maize. Despite not tolerating prolonged drought, some species (such as pearl and proso millets) appear to tolerate temperatures that are higher than those of sorghum and maize.

In developing countries, millet cropping systems tend to be extensive, with limited application of improved technologies, except in some of the more commercialised farming regions in India. In Asia, millet is restricted almost exclusively to two countries, India and China, although Myanmar, Nepal and Pakistan also produce small quantities. India is the world's largest producer, harvesting about 170 lakh tons, nearly 20 percent of the world's output (FAO Stat, 2021).

Pearl millet, which accounts for about two-thirds of India's millet production, is grown in the drier areas of the country, mainly in the states of Rajasthan, Maharashtra, Gujarat, Uttar Pradesh and Haryana. Finger millet is produced mainly in the state of Karnataka, but also in Orissa, Uttar Pradesh and Tamil Nadu.

Crop improvement is generally more difficult in millet than in most other crops, largely because of the nature of the environment in which they are grown. Hybrid breeding programmes have traditionally targeted the relatively better environments, although even these environments are harsher than those for most other crops. Hybrid grain cultivars have been developed for pearl millet in India and the United States, but perform best in areas where rainfall is reliable.

10.2 Global Scenario of Millets:

Table 10.1: Global Scenario of Millets

Regions	Area (lakh ha)	Production (lakh ton)
Africa	489	423
Asia	162	215
India	138	173
World	718	863

(Source: FAO Stat 2021)

Crop genetic improvement and breeding aim to increase genetic gain, which is defined as the amount of increase in performance achieved over generations through artificial selection [1]. Since the invention of DNA technologies, plant breeding has transformed, from conventional breeding which primarily relies on visual phenotypical selection and experience, into the era of molecular breeding [2].

Crop genetic improvement and breeding have been greatly advanced by harnessing and integrating the theories and technologies of DNA markers, marker-assistant selections (MAS) and genetic engineering, as envisaged by more precise foreground and background selection, discovery and utilisation of more diverse genetic stocks and shortening of breeding cycles [3,4]. Yet, agronomically important traits are often so-called complex traits controlled by poly- and/or oligo-genic loci.

So far, the success of molecular plant breeding is restricted to limited traits governed by major effect genes due to the intrinsic downsides of low genome coverage of molecular markers, difficulties in exploring a wider range of genetic resources and unavoidable linkage drag associated with selection of large segments of chromosomal regions [5].

Hence, breakthroughs in theoretic framework and technologies are required to further speed up breeding practice. Since 2005, the invention of next generation (massively parallel) and third generation (single molecular) sequencing technologies, genome-wide association studies (GWAS), genome editing (GE), molecular modules (MMs), genome selection (GS), as well as non-invasive high throughput phenomics, has revolutionised the scope and toolkits of crop breeding, allowing much more effective exploitation of historically preserved natural and/or artificially generated variation, minor effects of poly- and oligo-genic genes/alleles, and phenotyping and selection of large scale breeding populations in an unprecedented manner[6,7,8,9,10].

Crop scientists at ICRISAT are striving to achieve disease resistance, stress tolerance and nutritional improvement in our mandate crops. Modernization of the breeding programs includes rapid generation advancement methods, utilization of data-driven decision making digital platforms, molecular tools and advanced phenotyping technologies. These are the key areas of focus for enhancing productivity and boosting varietal development in a demand-driven approach.

10.3 Why Millets Are Called as Nutri-Cereals?

Because millets are exceptionally nutrient-dense cereals that significantly contribute to consumers' food and nutritional security, millets are known as Nutri-cereals. Because they are a natural source of iron, zinc, calcium, and other nutrients essential for easing India's malnutrition epidemic, millets are a nutritional powerhouse. Millets are not only more nutrient-dense than traditional cereal crops (wheat and rice), but they are also good sources of carbohydrates, minerals, and phytochemicals with nutraceutical advantages. Dietary fibre (15–20%), protein (7–12%), fat (2–5%), and carbohydrates (65–75%) are all abundant in millets. Anemia affects 40% of preschoolers, according to estimates, because of an iron deficiency in their bodies. Moreover, 250–500 thousand kids are thought to lose their vision each year as a result of vitamin A insufficiency. The world's anaemia problem can be efficiently solved by consuming millets (NIN, 2019). In addition, they are essential components of numerous multigrain and gluten-free cereal products, as well as conventional meals and drinks. Moreover, millets are consumed as fermented beverages, improving their digestibility, increasing the availability of nutrients like protein and minerals, and reducing antinutritional effects. Because of the rising prevalence of sedentary lifestyles and the resulting health issues, consumers are seeking out foods that are more nutrient-rich, flavourful, and healthy [11]. Little millets are an ideal choice for a nutritious food since they provide considerable amounts of calories, dietary fibre, protein with a balanced amino acid profile, various essential minerals, vitamins, antioxidants, and a low glycemic index (GI). [12, 13, 14, 15]. They are referred to as "Smart-Food Crops" and "Nutri-Cereals," respectively, because of these qualities. There are various varieties of millets, each having a unique nutritional profile. Regardless of variety, however, finger millet grains have exceptionally high calcium content (>350 mg per 100 g), followed by tef (159 mg per 100 g); proso millet, job's tears, foxtail millet, and barnyard millet are rich in protein (>10%); foxtail millet, little millet, and job's tears are rich in fat (>4.0%); barnyard millet, little millet, foxtail millet and fonio are rich in crude fibre (6.7–13.6%), little and barnyard millets are rich in iron (9.3–18.6 mg per 100 g) compared to other major cereals such as rice, wheat and sorghum[16, 15].

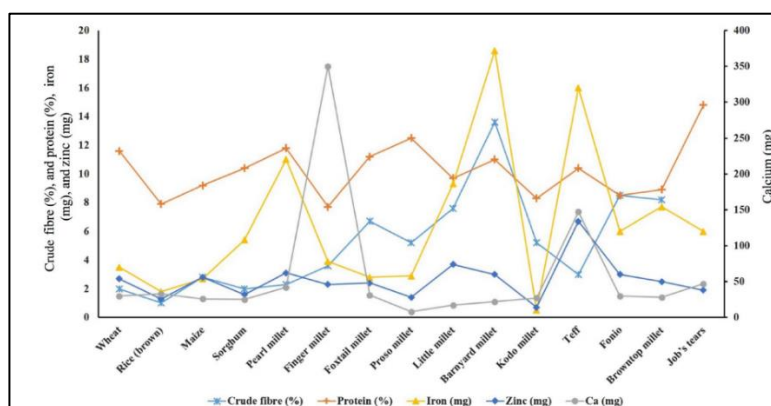


Figure 10.1 displays the protein, crude fibre, iron, zinc and calcium content of small millets. Small millets serve as a strategic food source for the impoverished and, more recently, as a nutritious diet for people living in cities, underscoring the need to focus more research and development on these crops.

10.4 Conventional Breeding Strategies in Millets:

Millets also use a variety of breeding techniques, including pure line selection, pedigree selection, mass selection, and mutation breeding, which are relevant to crops that self-pollinate. According to reports on millets cultivars issued over time, the majority of them were released following pedigree selection, then selection from local landraces and cultivars (hybridization and selection).

For instance, in India, out of the 248 varieties of six millets (finger millet—121, foxtail millet—32, proso millet—24, kodo millet—33, barnyard millet—18, and little millet—20), approximately 65% were released after selection from landraces, approximately 30% through pedigree selection, and 5% through mutation breeding. [17]. 11 proso millet cultivars were released in the USA by landrace selection, and 8 through pedigree selection. [18,19].

An essential breeding technique for millets, particularly for finger millet, foxtail millet, and proso millet, involves hybridization to promote variety followed by selection in a population that is segregating. Whereas 22% of foxtail millet cultivars and 29% of proso millet cultivars followed the hybridization and selection breeding strategy, 45% of the finger millet cultivars released in India [17]. Millets floral shape and anthesis behaviour, on the other hand, make them difficult to hybridise.

Due of difficulties in hybridization, there is a limited amount of hybrid vigour that can be utilised in small millets. Hence, creating male sterile lines would be a practical way to exploit heterosis, which is effectively used in important crops for the generation of commercial hybrid seeds. In finger millet, just one male sterile line (INFM 95001), with a GMS system created from the source parental line IE 3318 (germplasm), has so far been recorded (EMS) [20]. In foxtail millet, various types of male sterile lines have been created in China [21]. However only partially genetic male sterility lines have been effective in producing hybrid seed. [22].

In general, self-pollinated crops where hybridization is exceedingly difficult to induce variety have benefited greatly from mutant breeding. 13 millet cultivars (including Finger Millet 8, Kodo Millet 3, and Little Millet 2) have been released in India as a result of mutation breeding.

It is necessary to investigate the use of chemical hybridising agents (CHAs) to cause male sterility in small millets. In finger millet, the early-maturing mutant lines with high yield and yield component characters were found to be responsive to 500 Gy and 600 Gy. [23], and the treatments using 0.30% and 0.45% EMS [24], 0.03% nitroso guanidine (NG), and a combination of 300 Gy gamma ray and 0.30% EMS were shown to be more successful at causing beneficial mutations. For barnyard millet, 500 Gy and 600 Gy of gamma irradiation produce good variability, and 0.3% of EMS was identified as the LD50 value. A dose of 0.4% EMS was found to be ideal for the best recovery of viable mutants in kodo millet. [25]. The characterization of small millets germplasm and their usage in creating and releasing a number of cultivars, especially for resistance/tolerance to biotic and abiotic stresses, have both been successful using traditional breeding methods.

10.5 Current Breeding Strategies in Millets:

10.5.1 Sorghum- Jowar (*Sorghum Bicolor*):

Two product categories are the focus of sorghum breeding programmes: variety (using a population enhancement strategy) and hybrid (using a heterosis breeding approach). The type of product also depends on the additive and non-additive trait inheritance patterns, the homogeneity or heterogeneity of the growing environment, and the accessibility of agricultural inputs like irrigation and nutrients. A long-term breeding objective for sorghum has been to increase its tolerance to drought. Because to the shifting climate in sorghum-growing countries, breeding for HT tolerance is a new focus in sorghum research. As a result, comprehension of drought tolerance (staying green and producing under stress) is somewhat better than that of HT tolerance. Yet, in order to address the necessary tolerance levels in cultivated sorghum varieties or hybrids, there are genetic as well as breeding gaps in both stresses.

A. Genetic Analysis of Important Agronomical and Adaptive Traits in Sorghum:



Figure 10.2: Sorghum- Jowar (*Sorghum Bicolor*)

In the past few decades, a number of significant genetic loci and genes affecting sorghum agronomical and adaptive qualities have been discovered, mostly by GWAS, QTL mapping, and mutant analysis. This has been made possible by the rapid development of sequencing and phenotyping technologies. Despite the fact that the control mechanism of these genes is still largely unknown, the knowledge amassed to date and the genetic resources produced are sufficient to permit the development of super sorghum for a variety of end purposes. The sorghum breeding team at ICRISAT conducts research to improve precision and genetic gain. All market sectors (post-rain, rain, forage, sweet sorghum/high biomass sorghum) have unique breeding strategies, and hybridity testing (QC) is routinely carried out in F1s, which aids in the early identification of bogus hybrids. In order to anticipate the performance in isolation as well as the values in hybrid combinations (GCA, SCA) of the future fixed inbred lines, testcross, early yield trial, disease, and pest screening are routinely carried out in F6. For GCA, yield potential is the main attribute of interest. "Testing GCA in early generations assists in creating superior hybrids while saving time and money," said

Dr. Ephrem Habyarimana, principal scientist-sorghum breeding team, of ICRISAT. Using heterosis is yet another critical element in the production of sorghum. It is well-known breeding for drought and high temperature stress tolerance. The two primary methods used to screen and generate genetic material for drought tolerance are direct and indirect traits-based selective breeding. The most favoured form of selection based on developmental features or monitoring the water status and function of plants is indirect selection breeding. [26]. Sorghum cultivars that are evolving and carrying several productivity features can also be more drought tolerant. For instance, under field conditions, the presence of epicuticle wax on leaf and stalk may inhibit evapotranspiration in sorghum. [27]. In the sorghum drought-tolerant breeding programme, which is helpful for post-rainy breeding pipelines in India, the "Physiological Breeding" approach is gaining ground. The remain green phenotype of sorghum is the most important drought tolerance characteristic. [28,29,30]. Many sorghum hybrids with the stay green trait introgressed have been developed and are being successfully grown all over the world. While keeping an eye on sterility, grain quality, and heterosis, a breeding strategy with other important agronomic traits is needed to increase the rate of genetic gain in remain green and drought resistance traits. The proposed fast-track varietal and hybrid breeding approaches for drought tolerance in sorghum are depicted in Figure 10.3.

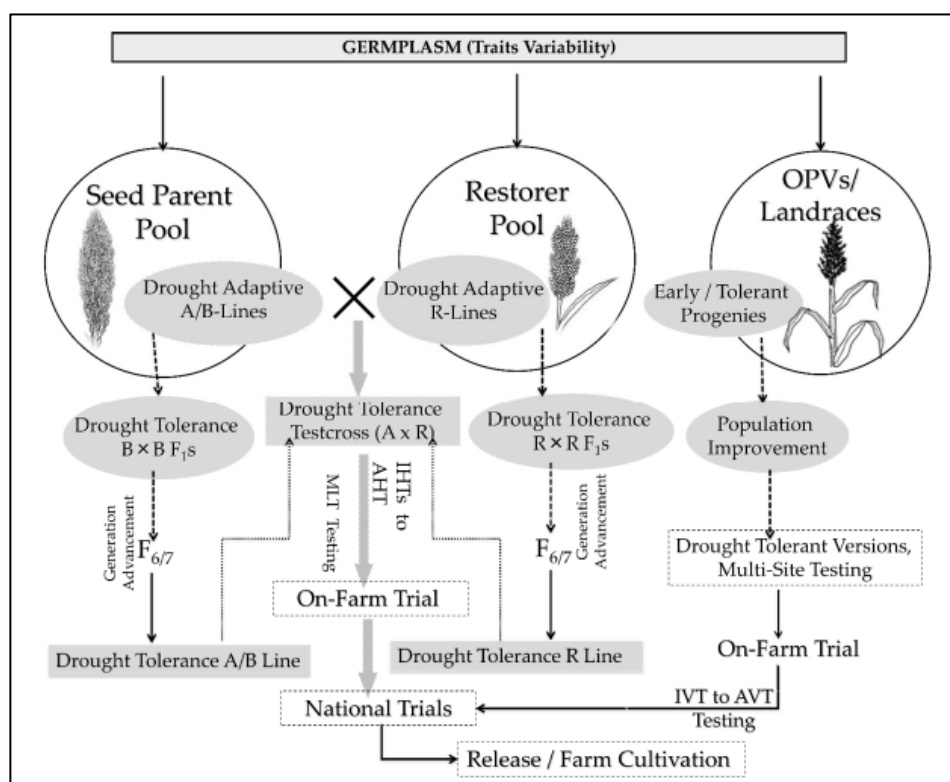


Figure 10.3: Fast-track breeding approaches for developing variety and hybrids for drought tolerance in sorghum. Briefly, genetic variation for drought tolerance in sorghum is sourced from elite breeding populations or germplasm. In sorghum, development of hybrid requires a male sterile line (A-line), a maintainer line (B-line), and a restorer line (R-line). A-line is male sterile and used as female; B-line is an isogenetic line of A-line and serves as

maintainer line, and R-line is a male fertile line used as pollen parent. Identified tolerant lines will be crossed within gene pool (B-lines/R-lines) of sorghum (without interrupt maintainer or restoration genes) to produce recombinants to select and fix in subsequent generations (i.e., F2–F7). At $\geq F7$ stage, crosses between two gene pool rewards the hybrids population to test in target sites to release a candidate hybrid with tolerance and on parallel, respective B lines to be converted to its male sterile version (A-line) for commercial production. Various test crosses between A and R lines go through testing at initial hybrid trials (IHTs) to advanced hybrid trials (AHTs) in on-farm tests, whereas in open pollinated varieties (OPVs) breeding, the selected intra-population progenies crosses were recommended to be released as a final product after sequential testing at multiple locations under initial variety trials (IVT) and advanced variety trials (AVT). There are around five different cytoplasmic male sterility (CMS) lines in sorghum; A1 CMS are widely used in commercial hybrid breeding and are being examined for other CMS lines' potential uses. Variations have considerable masking epistasis effects when researching the genetics of HT tolerance features since HT effects are thought to be of a geographical and temporal nature. Generally speaking, low to moderate heritability, such as that found in sorghum or other comparable crops, implies the viability of genetic modification, such as open-pollinated varieties or broad-based hybrids (top-cross and three-way cross) that depend on characteristics gene effects. In sorghum improvement projects, two lines, B35 and BTx3197, were used as HT tolerant sources. [31,32]. The proposed breeding plan (Figure 10.4) can be enhanced with further understanding of linked traits and their effective screening techniques. However, it is still in the early phases of comprehending the crop variability spectrum to HT. [33].

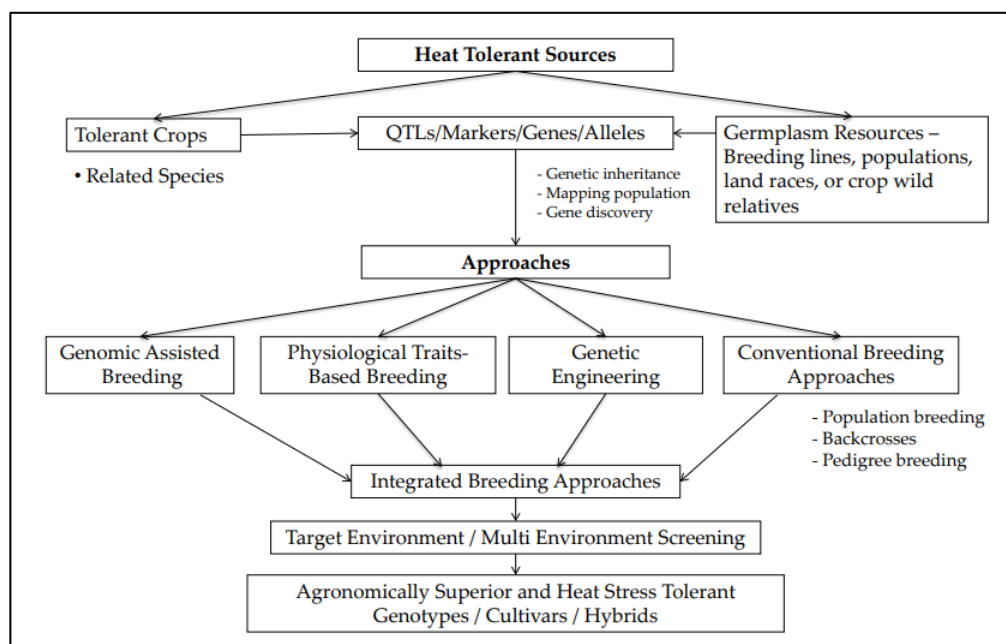


Figure 10.4: Proposed breeding approaches for development of sorghum heat (high) temperature (HT) stress tolerant cultivar. Briefly, HT breeding requires HT sources from the breeding lines or germplasm collections from the source; dissecting HT trait genetics and inheritance in the future will guide the discovery of the candidate genes and loci (QTLs)

in future. Identified sources/QTLs/genes can be transferred to elite cultivars that require HT for wider cultivation. To date, no straightforward breeding approach is available for HT. The proposed model is a combination of pre-breeding to product development. Breeding approaches will depend on the mode of trait inheritance (few/major genes or many/minor genes) in conventional breeding or physiological traits-based breeding methods. Genomic approaches will assist the breeding HT sorghum through advanced markers association studies, diagnostic markers, whereas, genetic engineering method helps in gene editing, provided a key candidate gene is identified for HT in sorghum.

The reported 26 QTLs for HT in sorghum can be validated and used in regular breeding with support of diagnostic markers (for screening), and forward through genomic selection in breeding pipelines is recommended. Integrated breeding approaches with appropriate testing and screening in target and multi-environments are needed to identify and develop agronomically superior heat tolerant cultivars or hybrids. Approximately 1000 breeding lines (600 B-lines, 300 R-lines, and 100 variations) are evaluated at ICRISAT for seed set and blooming. Just eight of the 1000 lines (ICSR 14001, ICSR 8, ICSR 21, ICSB 55, ICSB 84, ICSB 603, ICSV 162, ICSV 376) maintain their flowering times throughout the rainy and post-rainy seasons with 100% seed set, suggesting that these lines may be HT-tolerant [34]. In order to attain a greater rate of seed set under HT, HT tolerance breeding involves systematic relevant features discovery more than pollen germination and its viability. The proposed breeding plan and selection procedures can make significant use of the primary (directly contributing to HT tolerance) and secondary (indirectly contributing to HT tolerance) features.

The incorporation and validation of the reported 26 QTLs for five phenotypes claimed for HT tolerance in breeding pipelines may be made possible by the integrated breeding of phenomics and genomics, which could result in a wider range of HT tolerance progenies with improved agronomic features. In order to evaluate the co-segregation pattern of several QTLs to pyramid HT tolerance traits in breeding pipelines, the maximal QTLs found for leaf firing as an HT tolerance trait may attract rapid validation in various genetic backgrounds. In comparison to conventional breeding pipelines, HT tolerance breeding pipelines are probably smaller. In order to comprehend the desired level of HT (average higher temperature prevalence in the target growing crop ecosystem), they can be managed independently during the early phases of breeding.

To estimate the potential advantages of changing the crop cycle, improving yield potential characteristics, and incorporating drought and HT tolerance in India and Mali [35], a simulation study was carried out using a sorghum model. Several locations saw increased grain yield as a result of drought and HT tolerance. Overall, they came to the conclusion that a variety of features would need to be combined in order to boost and maintain sorghum output in both current and future climates.

B. Population Breeding Approach for Development of Sorghum Genotypes for Improved Yield and Resistance to Grain Mold:

Infected sorghum grown during the rainy season suffers from physical and chemical quality problems that result in smaller grains, blackening, and unfitness for human consumption. Hence it has become essential to breed for grain mold resistance. Grain mold is a problem

that has been extensively addressed by pedigree breeding all across the world. To create genotypes resistant to grain mold, a population breeding strategy was used in the current study. Finding stable grain mold-resistant lines with good grain yield (GY) is difficult due to the complicated genotype environment interactions (GEIs). Assessment of the efficacy in 33 population breeding derivatives chosen from the 2017 evaluation of 150 genotypes across four locations.

A substantial genotype-environment interaction (GEI) was found for grain mold resistance, GY, and all other associated variables. This GEI was examined using the genotype plus genotype-by-environment interaction (GGE) biplot approach. Compared to genotype (G) location (L), which accounted for 21.9% of the variation in GY, the location explained 51.7% of the variation, while the genotype accounted for 11.2%. G and L were more significant (30.7%) contributors to variance in grain mould resistance. The identification of promising genotypes for GY and grain mould resistance was aided using a graphical biplot technique. Dharwad proved to be the best test site for both GY and grain mould resistance.

During a "which-won-where" investigation, the test areas were divided into three clusters for GY and two clusters for grain mould resistance. optimal genotypes for each The Genotype plus genotype-by-environment interaction (GGE) biplot analysis was used to analyze a significant GEI observed for GY, grain mold resistance, and all other associated traits. For GY, the location explained a higher proportion of variation (51.7%) while genotype (G) \times location (L) contributed to 21.9% and the genotype contributed to 11.2% of the total variation. For grain mold resistance, G \times L contributed to a higher proportion of variation (30.7%). A graphical biplot approach helped in identifying promising genotypes for GY and grain mold resistance. Among the test locations, Dharwad was an ideal location for both GY and grain mold resistance. During a "which-won-where" investigation, the test areas were divided into three clusters for GY and two clusters for grain mould resistance. In each of these clusters, the top genotypes were chosen. It is advised to breed for a certain cluster. GY is regulated by blooming time, 100-grain weight (HGW), and plant height (PH), whereas grain mould resistance is influenced by glume coverage and PH, according to genotype-by-trait biplots. There is potential to increase both yield and resistance at the same time because GY and grain mould score were independent of one another.

C. ICRISAT Work on Sorghum with Different Countries:

Two stay-green QTLs (stg3A and stg3B encoding transpiration efficiency and Water Usage Efficiency) were backcrossed into three genetic backgrounds using marker assistance at ARI-Makutupora in Tanzania. In Senegal, similar efforts are being made to introduce stg3A and stg3B QTLs in three genetic backgrounds. The markers used in each of these introgression systems were created by ICRISAT. In the ICRISAT Kiboko station, 44 landraces and their wild relatives were tested for drought resistance under both well-watered and drought-stressed situations. In the ICRISAT Alupe station, 64 genotypes, including 17 wild relatives, 8 landraces, 13 improved varieties, and 26 F4 offspring of chosen parents, were screened for striga resistance. Particularly among the F4 crosses, more resistant and high-yielding genotypes were discovered than the standard checks. Future research must search for more varied sources of Striga resistance and pyramid several resistance mechanisms into farmer-favored cultivars.

10.4.1 Pearl Millet- Bajra (*Pennisetum Glacum*):

The Indian Prime Minister on September 28, 35 new crop varieties and hybrids were presented to the country by Mr. Narendra Modi, of which three were the result of the work with ICRISAT. Two chickpea types and a hybrid of pearl millet were created by genomic-assisted breeding. The cultivars are climatically adaptable, mature earlier, produce more, and are immune to serious illnesses.

A. Extra-Early Pearl Millet with Increased Disease Resistance and Higher Yield:

Because to HHB 67 Improved, more than two million people in India have access to food security. Out of the 7–7.5 million hectares that are used to cultivate pearl millet each year, more than 800,000 ha are planted with this extra-early (76 days to maturity), Downy mildew-resistant, farmer and consumer–preferred variety. This well-liked hybrid has assisted in preventing the annual losses of US\$ 8 million that mildew might bring about in Rajasthan and Haryana.



Figure 10.5: Pearl Millet- Bajra

However, before the illness takes hold, the lifespan of any pearl millet hybrid is often no longer than 4-5 years. The second cycle of this hybrid, known as HHB 67 Improved 2, was created by Chaudhary Charan Singh Haryana Agricultural University (CCSHAU) and ICRISAT and recently released by the Indian Government. It has 12% more blast resistance, 15% more grain yield, and 21% more dry fodder yield while still maintaining its early-maturity trait. In India's parched north and northwest, this hybrid has the potential to improve food, fodder, nutritional, and economic security. HHB 67 Improved 2 was created through translational genomics and cooperation between the ICRISAT, Chaudhary Charan Singh Haryana Agricultural University, and the Indian Council of Agricultural Research (ICAR).

10.5.2 Finger Millet (*Eleusine Coracana*):

Eleusine coracana (L.) Gaertn., often known as ragi, is crucial to the dryland agricultural system. It is a crop that is grown in some regions of the world for both food and forage. It is grown in Africa, as well as in Uganda, Tanzania, Kenya, Ethiopia, Rwanda, Zaire, Eritrea,

and Somalia, as well as in Asia's India, Burma, Nepal, Sri Lanka, China, and Japan. The primary main meal for the people of South Karnataka in India is finger millet. It offers a wide range of nutritional advantages and contains roughly 30 times as much calcium as rice. The cattle industry makes substantial use of finger millet straw as feed. Depending on the moisture available, finger millet can be grown all year round. Crop improvement and management tactics require fresh attention due to changes in climatic conditions, biotic and abiotic yield limiting factors, and other considerations.



Figure 10.6: Finger Millet (*Eleusine Coracana*)

At Hebbal School (now University of Agricultural Sciences, Bangalore), Dr. Leslie Coleman started a finger millet development effort that led to the introduction of the first finger millet variety H22 in India. The All India Coordinated Small Millets Improvement Project (AICSMIP), which has its headquarters at the University of Agricultural Sciences, GKVK, Bengaluru, was subsequently started in 1986. The primary goal of breeding was to create strains with high grain production and blast resistance that would work in habitats that were both rainfed and irrigated. There are currently 135 different types of finger millet available. Indaf (like Indaf 7 and Indaf 9) and KMR (like KMR-301, KMR 630, KMR-316, KMR-204 & KMR 340) series varieties from ZARS, Mandya and GPU series varieties (like GPU-28, GPU-45, GPU-48, GPU-66) from PC unit, AICRP on Small Millets, UAS, Bangalore were identified as a result of the groundbreaking work on finger millet.

10.5.3 Foxtail Millet (*Setaria Italica*):

One of the oldest crops in the world, foxtail millet ranks second in overall millet production and provides six million tonnes of grain to populations in southern Europe and Asia. [36,37]. The hardy weed *Setaria viridis*, which is thought to be the progenitor of foxtail millet, is closely related to this plant. With several reports of herbicide resistance, *S. viridis*, or green foxtail, is a problem throughout Eurasia and North America where it frequently coexists with its domesticated cousin [38,39,40]. The global distribution of two phenotypically distinct kinds of foxtail millet-the waxy grain type and the non-waxy grain type-is an intriguing aspect of the variety of modern foxtail millet [41]. Low amounts of amylose in the grain endosperm, which results in waxiness in cereal grains, giving the grain

a sticky texture when cooked [41]. Due to its significance in China, the Chinese National Genebank (CNGB), which as of 2012 had 26,670 accessions, appears to preserve the largest collection [65]. Genebanks in Japan (National Institute of Agrobiological Sciences, NIAS) and the USA (USDA, Plant Genetic Resources Conservation Unit, PGRCU) provide access to a wide range of foxtail millet variation. ICRISAT maintains germplasm from 26 different nations. There have been some core and mini-core collections put together [43,44].



Figure 107: Foxtail Millet (*Setaria Italica*)

The foxtail millet molecular genomics field is advancing quickly as a result of the recently made sequence data available. In order to create maps, examine DNA polymorphisms, evolutionary origins, and relatedness to other cereals for future crop development initiatives, numerous genetic markers have been identified and used in foxtail millet [45,46,47,48]. It has become possible to create a huge library of markers made up of intron-length polymorphisms (ILPs) thanks in part to the amount of EST data that can be utilised to create flanking primers [49]. Marker-based, high-throughput genotype identification has made some early advances [50,51]. One study found an association between stress tolerance and an allele-specific single nucleotide polymorphism (SNP) encoding for the dehydration responsive element binding (DREB) gene [52]. The SNP was validated in a foxtail millet core collection, where it was discovered that the allele accounted for 27% of the overall variation of stress-induced lipid peroxidation. The SNP shows potential in marker-assisted breeding selection [53]. Both callus bombardment reported [55,56,57] and agrobacterium methods [53] have been discussed for foxtail millet transgenic protocols enabling some potentially useful molecular analyses. A pollen-specific gene has been modified in one study [58] to impair anther function through a co-suppression mechanism. This modification may have been made to enable the creation of male-sterile plants, which are useful for breeding foxtail millet hybrid variants.

10.5.4 Kodo Millet (*Paspalum Scrobiculatum*):

The only nation where it is being harvested as a grain in substantial amounts, primarily on the Deccan plateau, is India. India is where kodo millet was domesticated approximately 3000 years ago [59]. The grain has a wide variety of high-quality proteins [60,61] and,

especially when compared to other millets, has a high antioxidant activity (anti-cancer) [62,63,64]. Kodo is high in fibre and, like finger millet, may be beneficial for diabetes [60]. It may be grown in a range of poor soil types, from gravelly to clay, and is drought-tolerant [65,66].

Kodo is high in fibre and, like finger millet, may be beneficial for diabetes [60]. It may be grown in a range of poor soil types, from gravelly to clay, and is drought-tolerant [59,66]. There has been significant variation reported in numerous phenotypic measures, including time till blooming, tiller number, and yield, indicating that general morphological variability is substantial [67,68].



Figure 10.8: Kodo Millet (*Paspalum Scrobiculatum*)

Kodo millet's genome does not appear to have any genetic or molecular maps, which is unfortunate [13]. This is probably because of the issue of recurrent cross-hybridization with its wild relatives. Kodo millet has a limited number of molecular markers, yet these markers have been used to characterise diversity and phylogeny [66,70]. There has been some preliminary work in miRNA target site prediction using ESTs from kodo [71]. Using ESTs from kodo, there has been some preliminary work on predicting the miRNA target site [71]. Target genes were discovered to be involved in the metabolism of carbohydrates, cellular transport, and the production of structural proteins, but this study was severely constrained due to a severe lack of kodo DNA information; instead, the closely related rice genomic sequence was used for binding-site prediction. The media conditions for callus regeneration protocols have been studied with regard to transgenic methods for kodo, and regenerated plantlets were successfully raised from seed to maturity in soil [72]. Kodo millet is a species that ICRISAT conserves, and a core collection that captures the phenotypic diversity of the entire collection has been formed [68].

Several universities also maintain sizable kodo millet seed banks; the University of Agricultural Sciences in Bangalore is an excellent example of this [72]. Few reports of other banks with considerable numbers of accessions exist because the crop is not significant outside of India. To research the plant as a weed, certain agencies do maintain collections;

the US Department of Agriculture, for instance, has 336 accessions in its National Plant Germplasm System (GRIN)². Although some of these sources do contain seed with an African provenance, it is uncommon. Improved ecological research and coverage of the African continent would aid in revealing and preserving a variety of important features that international scientists might otherwise overlook.

10.5.5 Proso Millet (*Panicum Miliaceum*):

Proso millet, also known as broomcorn and common millet, was cultivated as early as 10,000 years ago in Neolithic China [73]. Proso has several advantages, including a high protein content that ranges from 11.3 to 17% of the dry matter of the grains [74]. Protein composition and amino acid profile exhibit genotypic variability [74]. The grain's potential for avoiding cancer, heart disease, managing liver disease, and controlling diabetes has been researched, and the findings are encouraging [75,76,77,78]. Five races of proso millet are grown in cultivation [79]. Race *miliaceum* has sub-erect branches with few subdivisions and big, open inflorescences that resemble wild proso. *Miliaceum* and *patentissimum* both have slender, spreading panicle branches. These two races, which are thought to be primitive, are present over the whole Eurasian range of proso. More compact inflorescences with drooping, cylindrical, and curving shapes can be seen on *contractum*, *compactum*, and *ovatum*, respectively [79].



Figure 10.9: Proso Millet (*Panicum Miliaceum*)

The 842 accessions that ICRISAT has from the five races [79]. Inflorescence length, plant height, panicle exertion, and flowering period have all been used to describe the collection's diversity [79]. The list of more noteworthy proso collections is in Table 2. The N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry in St. Petersburg is home to what is likely the largest collection of proso, with over 8778 accessions as of 2012[13]. There don't seem to be many core collections of proso millet for breeding outside of ICRISAT [68]. For the goal of SSR-based characterization, preliminary diversity clustering based on agronomic parameters was carried out on the Chinese collection [80]. It might be possible to repurpose and slightly alter the 118 landraces from China that make up the subset to create a true core collection.

10.5.6 Barnyard Millet (*Echinochloa* Spp.):

Barnyard millet is made up of two distinct species that belong to the genus *Echinochloa*, despite the fact that it is commonly referred to as a single taxonomic group. Whereas *Echinochloa frumentacea* (syn. *Echinochloa colona*) is found in Pakistan, India, Nepal, and central Africa, *Echinochloa esculenta* (syn. *Echinochloa utilis*, *Echinochloa crusgalli*) is grown in Japan, Korea, and the north-eastern region of China [81,82]. Differentiation is difficult since the morphological characteristics of the two species coincide. Only the presence or absence of an awn and minute variations in spikelet and glume shape allow for visual identification [83]. Thus, to facilitate research and analysis of their phylogeny, the common names Japanese and Indian barnyard millet have been proposed [81].



Figure 10.10: Barnyard Millet (*Echinochloa* Spp.)

The two millets are genetically separate despite sharing such striking morphological resemblance, as demonstrated by cytology and marker research; F1 hybrids of the two species are sterile [84,85]. Both species are well known for their rapid maturation, superior storage ability, and inclination to flourish in poor soil [81]. ICRISAT presently has 743 accessions of these barnyard millets from nine different countries, including a core collection of 89 varieties that was just recently produced [68].

The NIAS and the USDA both have more important collections [85]. Both millets have relatively limited availability of genetic maps and sequence data [13]. Callus regeneration procedures have been described for both species, but initial transgenic work has only been published on the Japanese version [86,55].

10.6 Future Prospects:

Farmers in drylands and tribal populations with less resources who live in unstable ecosystems produce millets. Millets, however, have experienced a revival as a result of rising public awareness of their potential health advantages and commercial use. Because of their similarity in usage and preparation, variety in their resistance to adversity, and nutritional value, small millets have the potential to replace or supplement major cereal mainstays. Small millets can be included into a variety of cropping systems both in irrigated

and rainfed environments. To speed up the improvement of small millets, genomic assisted breeding will make it easier to identify novel alleles and genes with higher agronomic performance and resilience to biotic and abiotic challenges. In order to increase and maintain sorghum output in both present and future climates, a number of traits would need to be combined and improved. It would be ideal to examine current finger millet advancements both nationally and internationally, pinpoint any gaps, and sketch out a strategy for crop improvement in the face of climate change. In the future, transgenic work can be investigated to published explant regeneration procedures for proso millet.

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