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|Review Article|

Breeding Efforts for Increasing Genetic Gain in Sorghum and Bajra

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Abstract- Millets, also known as nutri-cereals, are nutritionally superior crops with sorghum and pearl millet accounting for the majority of millet production in India. Despite their importance for food, fodder and industry, yields are limited due to both abiotic and biotic stresses, producing significant gaps between potential and realised productivity. Increasing genetic gain through effective breeding is therefore critical, but traditional procedures are limited by long breeding cycles and low selection precision. CMS-based hybrid breeding has greatly enhanced productivity in both crops; yet, reliance on limited cytoplasmic sources has increased disease susceptibility, emphasising the importance of cytoplasmic diversification and integrated resistance breeding. Advances in molecular markers, QTL mapping and genome-assisted breeding have increased selection efficiency, while new methods like genomic selection, speed breeding, gene editing, MAGIC populations, and high-throughput phenotyping provide chances to accelerate genetic improvement. Integrating these approaches is critical for developing high-yielding, stress-resilient, and nutritionally superior sorghum and pearl millet cultivars.

Keywords: sorghum, pearl millet, bajra, genetic gain, hybrid breeding, marker-assisted selection, genomic selection, speed breeding

1. Introduction

Millets, classified as small-seeded cereals, are also known as nutricereals or miracle grains due to their exceptional nutritional properties. Anbukkani et al., 2017, Hemamalini et al., 2023. Majorly three millets, including Bajra, sorghum, finger millet and minor millets, including foxtail, proso, kodo, barnyard, and little, are grown in India Chaudhary et al., 2023; National Spectrum, n.d. Millets are good sources of minerals, including calcium, zinc, iron, magnesium, and phosphorus, as well as high protein and being gluten-free, which can help improve the micronutrient status of the general population. Bhatt et al., 2022, Anitha et al., 2024, Saini et al., 2021. They have also been shown to have a low glycemic index (GI), making them a valuable food source for individuals with diabetes. Bora et al., 2019. They can also be used as prebiotics and probiotics. Nithyanatham et al., 2019, Banerjee et al., 2012. In India, Sorghum and Bajra are grown majorly. These are considered as climate resilient cereal crop and are recognized for their extraordinary adaptability to drought, heat, and poor soil fertility. Millet productivity and adaptation are significantly constrained by both abiotic and biotic stresses, which prevent crops from reaching their full genetic potential. Among abiotic stresses, drought resulting from inadequate rainfall and non-irrigated conditions, along with heat stress, severely affects crop productivity, particularly when temperature stress coincides with critical stages of growth (Peacock, 1982; Prasad et al., 2021). These stresses are especially prominent in sorghum and bajra grown under rainfed and semi-arid environments. In addition to abiotic constraints, biotic stresses such as insect pests and diseases caused by fungal, bacterial, and viral pathogens play a major role in reducing yield and deteriorating grain quality, thereby leading to substantial economic losses (Kumar et al., 2014; Negi et al., 2025). A large number of insect pests have been reported in sorghum and bajra, including major pests such as stem borers, greenbugs, and aphids. Diseases occurring either alone or in combination further aggravate yield instability and cause significant annual economic losses (Li et al., 2008; Liu et al., 2016). Consequently, a considerable gap exists between the potential and realized yields of millets due to the combined effects of abiotic and biotic stresses such as drought, heat stress, stem borer infestation, grain mold, and the parasitic weed Striga (Das et al., 2019; Mola, 2021). Therefore, improving tolerance to abiotic stresses, particularly high temperature, along with resistance to major biotic stresses such as downy mildew and insect pests, remains a key objective of millet improvement programmes (Shivhare and Lata, 2017) Many studies have reported a decline in the area under millet cultivation, but maintaining a relatively stable or increasing trend in productivity. Globally, the area under millets declined by about 25.71% between 1961 and 2018, while productivity increased by nearly 36% during the same period (Meena et al., 2021). Similarily in India the cultivated area of sorghum and pearl millet has declined substantially over time due to multiple agronomic and socio-economic factors. The total sorghum area decreased from 155.71 lakh ha to 39.95 lakh ha (Indiastat, 2025) and bajra declined from 90.2 lakh ha to 68.35 lakh ha from 1950's to 2024-25. (Indiastat, 2025). In pearl millet, although the cultivation area and production declined after the 1970s due to downy mildew epidemics, productivity has shown a positive growth trend in recent decades (Nagraj et al., 2012; Kumar et al., 2024). Thus, overall studies stated negative growth rates for both sorghum and bajra area and production, while productivity has remained stable or increased. (Meena et al., 2021; Prabhu et al., 2022). This decrease in cultivation area coupled with increasing productivity emphasizes the importance of enhancing genetic gain in millet improvement programmes. Genetic gain is the improvement in average genetic or phenotypic performance achieved through selection over breeding cycles (Rutsoki et al., 2019; Krishnappa et al., 2021). Under shrinking land resources, accelerating genetic gain is the most sustainable strategy to improve productivity; therefore, this paper discusses breeding strategies for increasing genetic gain in sorghum and pearl millet under changing environmental conditions.

2. Genetic Gain

Genetic gain represents the improvement achieved by selecting superior individuals whose performance exceeds a defined threshold. The rate of genetic gain (ΔG) is described by the breeder's equation, where genetic gain depends on selection intensity (i), selection accuracy (r), and additive genetic variance (σ_a), divided by the length of the breeding cycle (L), expressed as:

$$\Delta G = \frac{i \times r \times \sigma_a}{L} \tag{1}$$

(Lorenz et al., 2013, Williamson and Leonelli, 2022; Seck et al., 2023). Thus, increasing selection accuracy and reducing breeding cycle results in higher genetic gain. (cobb et al., 2019)

The integration of molecular tools with conventional breeding has enabled faster genetic improvement. Advanced Molecular techniques including as marker-assisted selection (MAS), marker-assisted backcrossing (MABC), marker-assisted recurrent selection (MARS), genomic selection (GS), mutant breeding, and genome editing have been proven to increase genetic gain per unit time (Gudi et al., 2022). Among these, Genomic selection is especially effective among these since even moderate prediction accuracies combined with shorter breeding cycles can lead to big increases in production. The use of high-throughput phenotyping and genotyping further enhances selection efficiency and accuracy in modern breeding programmes (Heffner et al., 2010; Anand et al., 2023).

3. Breeding Efforts

3.1. Early Phase of Breeding in Sorghum and Bajra

Sorghum improvement till 1960s focused on selections from local landraces. Notable examples include Saonar, Ramkel, Aispuri, PJ, Maldandi, and Dagdi selections from Maharashtra; Bilichigan, Fulgar White, Kanvi, Nandyal, Hagari, and Yanigar from Karnataka; Nandyal (N), Guntur (G), and the Anakapalle series from Andhra Pradesh; the CO series from Tamil Nadu; Budh Perio (BP-53), Sundhia, and Chasation from Gujarat; Gwalior and Indore selections from Madhya Pradesh; and RS selections from Rajasthan (Patil et al., 2014; Elangovan et al., 2009). Maldandi sorghum showed two variant types based on internode length, of which long-internode plants were early flowering, fast growing after the first month, better adapted to shallow soils, and had superior earhead emergence. Consequently, short-internode types were eliminated, leading to the selection of M 35-1, which proved superior in earliness, yield, grain size, and market price (PS Reddy & BVS Reddy, 2019; Patil et al., 2014). Similarly, in pearl millet, open-pollinated varieties were widely grown during the early phases, and mass selection from locally adapted germplasm led to the development of OPVs such as C1, C2, Co.2, Co.3, T5, T55, AKP1, AKP2, Baroda 5, RSJ, Bajra 1, and LM 38-39, among others (Yadav and Rai, 2013; Charyulu et al., 2014). Pusa Moti pearl millet, developed through selection from African cultivars (Improved Ghana), significantly outperformed several other improved varieties and recorded yield advantages of up to 63% over local varieties in Delhi (Ahluwalia, 1964; Andrews and Kumar, 1996). Following the establishment of ICRISAT in the 1970s, the development of high-yielding pearl millet cultivars progressed through population improvement and recurrent selection using diverse Asian and African germplasm, resulting in varieties such as WC-C75, ICMV 221, ICTP 8203, HC 4, Raj 171, JBV 2, JBV 3, HC 20, RCB 2, CZP 9802, and Pusa 266 (Nurgaliyev et al., 2024; Yadav and Rai, 2013). These breeding efforts which mainly used landrace selection and open-pollinated varieties, increased local adaptability and grain quality; however, genetic improvement was slow and gradual during this period. Limited selection intensity, narrow genetic base, and strong genotype × environment interactions restricted further yield enhancement, leaving non-additive gene action unexploited. These limits underlined the need for more efficient breeding strategies, prompting the use of hybrid breeding to accelerate genetic progress by exploiting heterosis.

3.2. Hybrid Breeding

Heterosis, or hybrid vigor, refers to the superior performance of F_1 hybrids over their parents for traits such as yield, earliness, and stress tolerance. In millets, particularly pearl millet and sorghum, exploitation of heterosis has resulted in substantial genetic gains, making hybrid breeding a key strategy for productivity enhancement.

3.2.1. Sorghum

Hybrid breeding in sorghum became easy with the discovery of the A1 (milo) cytoplasm, which enabled cytoplasmic male sterility (CMS) based hybrid seed production (Stephens and Holland, 1954; Meng et al., 2025). In CMS systems, male-sterile lines are designated as A-lines, while their corresponding maintainer lines are referred to as B-lines. Subsequently, multiple CMS sources - A1, A2, A3, A4, A5, and A6 were identified, expanding the scope of hybrid breeding in sorghum (Reddy et al., 2008; Kibalnik and Elkonin, 2020). The utilization of A1 cytoplasm resulted in substantial heterosis, with 15–26% heterobeltiosis for grain yield reported in sorghum hybrids (Reddy et al., 2004). This led to the release of several successful hybrids such as CSH 1, CSH 25, CSH 27, and CSH 28, which significantly enhanced grain and fodder yields and demonstrated wide adaptation (Bohra et al., 2016). The adoption pattern of sorghum hybrids in India evolved over time. During the first phase CSH 1 replaced most of the traditional cultivars; in the middle phase (1976–1986), these earlier hybrids (CSH 1, CSH 2, and CSH 4) were replaced by CSH 5 and CSH 6. and which were again replaced by high yielding hybrids such as CSH 9, MSH 51, JKSH 22 and several private-sector hybrids (post 1986). (Deb et al., 2004; Choudhary et al., 2022). Grain yield, plant height, days to flowering, and micronutrient content are the main goals of hybrid sorghum breeding efforts; grain yield is given top emphasis because it directly affects economic returns. Several studies have shown that sorghum hybrids achieved significant yield advantages over local varieties, underscoring the role of hybrid breeding in accelerating genetic gain (Lv et al., 2024).

3.2.2. Pearl Millet

Hybrid parent research at ICRISAT, Patancheru has largely focused on developing downy mildew (DM) resistance, followed by resistance to smut and ergot, while maintaining early maturity (75–85 days) (Charyulu et al., 2014). The discovery of cytoplasmic male sterility and the release of the male-sterile line Tift 23A carrying the A_1 cytoplasm enabled commercial F_1 hybrid production in pearl millet in India and led to the development of five hybrids (HB 1–HB 5) between 1965 and 1969 using Indian-bred pollinators (Singh et al., 2014; Yadav et al., 2013). Although the frequently utilised A1 CMS source was not directly associated with DM susceptibility, the reliance on a single seed parent raised concerns over genetic vulnerability (Rai and Thakur, 1995; Yadav et al., 1993). From 1965 to 1972, HB 3 (23A × J104) was the most popular hybrid because to its greater performance (Kumar et al., 1983). To broaden the cytoplasmic base, several alternative CMS sources were identified from cultivated and wild germplasm, including A1, A2, A3, A5, Aegp, PT 732, DSA lines, and PMC lines (Hanna, 1989; Reddy et al., 2004). However, the A2 and A3 CMS systems were unstable, limiting their commercial use, whereas Aegp, A4, and A5 were found to be highly stable and suitable for hybrid breeding (Rai et al., 2009; Singh et al., 2021). The adoption of CMS-based hybrids eventually increased genetic gains in pearl millet, to the annual gain from 4.4 to 6.6 kg/ha/year (Yadav et al., 2021). Further efforts to diversify the A1 cytoplasmic system and add DM resistance led to the production of multiple resistant male-sterile lines at PAU, resulting in the release of PHB 10 and PHB 14, the first DM-resistant pearl millet hybrids in India. (Rai and Singh, 1987; Singh et al., 2014)

Overall, CMS-based hybrid breeding in sorghum and pearl millet has played a crucial role in accelerating genetic gain by enhancing yield potential, stability, and stress resilience. However, the hybrid's long-term viability was constrained by its dependence on a restricted cytoplasmic and parental genetic foundation, as well as vulnerability to developing biotic stresses. These constraints highlighted the need for more accurate and efficient breeding procedures, resulting in the integration of marker-assisted breeding strategies to further accelerate genetic gain and boost stress resilience.

3.3. Marker-Assisted Selection

3.3.1. Sorghum

For drought Drought is a major abiotic constraint in sorghum, causing 50–60% yield loss when stress occurs at the vegetative stage. The stay-green trait is one of the resistance mechanisms, which refers to the delayed senescence of leaves under post-flowering drought, independent of genotype maturity. This trait is strongly associated with the prolonged photosynthesis and grain filling under water-limited conditions (Ejeta and Knoll, 2007; Bejiga et al., 2021).

Extensive QTL mapping studies have identified multiple genomic regions controlling stay-green and post-flowering drought tolerance. Using single marker analysis, twelve QTLs for post-flowering drought tolerance were identified, of which six QTLs associated with stay-green were mapped across five linkage groups. Notably, QTLs on three linkage groups were also seen positively associated with grain yield under irrigated conditions, suggesting a physiological link between stay-green expression under drought and yield performance under non-stress environments (Ejeta and Knoll, 2007). Further studies identified major stay-green QTLs, including Stg1, Stg2, Stg3, Stg4, Stg3A, and Stg3B, which have been widely used in sorghum breeding programs (Mwamwahonje et al., 2021; Subudhi et al., 1999).

To introgress major stay-green QTLs (Stg1, Stg3, Stg4, StgB) Marker-assisted backcrossing has been used from the drought-tolerant donor B35 into the senescent sorghum background R16, resulting in improved chlorophyll retention, green leaf area, and prolonged photosynthesis under post-flowering drought stress. These results confirm the stable expression of stay-green QTLs and proving the effectiveness of MAS in enhancing drought tolerance and genetic gain in sorghum (Kassahun et al., 2010; Galyuon et al., 2019).

For *Striga* *Striga hermonthica* or witch weed is considered as one of the most severe biotic restrictions in sorghum production. It causes yield losses ranging from 40% to full crop failure in Sub-Saharan Africa, particularly under low soil fertility and drought-prone circumstances. (Mbuvi et al., 2017; Begna, 2021; Tulu et al., 2024). Conventional control measures have shown limited effectiveness, making host plant resistance through marker-assisted selection (MAS) a sustainable strategy.

Several studies have successfully identified and introgressed Striga resistance QTLs into farmer-preferred sorghum cultivars. Five major Striga resistance QTLs on various sorghum chromosomes were identified through QTL mapping under field conditions using recombinant inbred line populations derived from IS9830 × E36-1 and N13 × E36-1 (Grenier et al., 2007; Ali et al., 2016). Three to four resistance QTLs for striga from donor line N13 were transferred into farmer-preferred varieties through backcrossing using MAS, which resulted in significantly lower Striga infestation tested under artificially inoculated field conditions (Ngugi et al., 2015; Yohannes et al., 2019).

Further validation of MAS-based introgression was reported by Afolayan et al., (2019), who successfully introgressed one to four Striga resistance QTLs into Nigerian sorghum varieties SAMSORG39 and DANYANA. Recently, Baloch et al., (2023) have revealed six Striga resistance QTLs distributed across five chromosomes A, B, I, J1 and J2, highlighting the importance of MAS for producing lasting Striga-resistant sorghum cultivars.

Across several chromosomes, QTL mapping in sorghum has identified genetic areas linked to resistance to serious diseases such ergot, rust, grain mould, and anthracnose. A main gene (Cg1) and a number of moderate-to-large-effect QTLs found on chromosomes 1, 5, 6, 8, 9, and 10 regulate anthracnose resistance. While rust resistance is primarily governed by a significant QTL on linkage group 10 and grain mould resistance involves several QTLs and candidate R2R3-MYB genes. Notably, resistance QTLs for a number of diseases are found on chromosome SBI-06, suggesting resistance gene clustering and offering useful targets for marker-assisted breeding.

Table 1. Different QTLs identified for shootfly resistance Reddy et al 2025

SBI	QTLs for shoot fly resistance traits
SBI-01	QEg28.dsr-1.1 (oviposition non-preference), QSv (seedling vigour), QTdl.dsr-1.1 (trichome density), QGs.dsr-1, QSv.dsr-1.1 (glossiness)
SBI-05	QGs.dsr-5 (glossiness), QTdl.dsr-5 (trichome density), QEg.dsr-5 (oviposition non-preference), Qdh.dsr-5 (dead hearts)
SBI-07	QGs.dsr-7 (glossiness), QEg21.dsr-7, QEg28.dsr-7 (oviposition non-preference), Qdh.dsr-7.1, Qdh.dsr-7.2 (dead hearts)
SBI-10	QGs.dsr-10 (glossiness), QEg21.dsr-10, QEg28.dsr-10 (oviposition non-preference), Qdh.dsr-10.1–Qdh.dsr-10.4 (dead hearts), QTdu.dsr-10.1, QTdl.dsr-10.1, QTdu.dsr-10.2, QTdl.dsr-10.2 (trichome density), QSv.dsr-10 (seedling vigour)

3.3.2. Pearl Millet (Bajra)

Early QTL mapping studies by Yadav et al., (1999a, 1999b) identified several genomic regions associated with terminal drought tolerance for grain yield in pearl millet. Some QTLs were consistent across different water-stress environments and genetic backgrounds of the two mapping populations studied, while others were population or environment-specific, indicating complex genetic control of drought tolerance. Genomic regions on linkage groups (LG) 1 and 2 were associated with superior grain yield and better yield maintenance under terminal drought stress (Yadav et al., 2011; Serraj et al., 2005).

For downy mildew major QTLs offering resistance were discovered on LG1 against Indian pathogen populations, LG4 against Nigerian and Niger populations, and LG2 against the Senegalese population, accounting for significant phenotypic variance (Jones et al., 1995). Additionally, several pathogen populations –specific downy mildew resistance QTLs were detected on LG1, LG2, LG4, and LG7, which, although these loci may not confer durable resistance across environments, they are valuable for region- and population-specific breeding programmes (Gulia et al., 2007). Rust resistance mapping indicated linkage group 3 connected with isolate 93-3 and linkage group 4 with isolate 92-1, and resistance to pyricularia leaf spot was acquired from the same Pennisetum glaucum ssp. monodii accession harbouring the Rr1 rust resistance gene (Morgan et al., 1998).

Beyond stress resistance, extensive efforts have also focused on identifying markers and QTLs for key agronomic and developmental traits. Grain yield was associated with markers SNP101, Xibmsp11/AP6.1, Xibmsp09/AP10.2, and Xibmcp09/AP10.1, while spike length was linked to SNP101. Plant height and tillering were associated with PgAAO1 and PgHK4, respectively. QTLs governing the stay-green trait were mapped to AP10.2 (Xibmsp09) and AP10.1 (Xibmcp09). In addition, several genes controlling flowering and photoperiod response—such as PgEMF2, PgFY, PgGI, PgHD1, PgHD3a, PgHD6, PgLFL1, PgMADS11, PgPHYA, PgPHYB, PgPHYC, PgPHTC, PgPIPK1, PgPRR73, PgPRR95, PgTFL1, Pg7830, Pg7840, and PgDwarf8—have been identified (Singh and Nara, 2023).

Nutritional quality improvement through MAS has also been demonstrated. Anuradha et al., (2017) identified three markers—Xpsmp2261 (R^2 = 13.34%), Xipes0180 (R^2 = 11.40%), and Xipes0096 (R^2 = 11.38%) associated with grain iron and zinc concentration. Singhal et al., 2021 has also observed phenotypic variance (R^2) explained by different QTLs for grain Fe and Zn content ranged from 2.85 (QGFe.E3.2014-2016Q3) to 19.66% (QGFe.E1.2014-2016Q3) and from 2.93 (QGZn.E3.2014-2016Q3) to 25. 95% (QGZn.E1.2014-2016Q1). The validated LG3 QTLs for high grain iron and zinc density have subsequently been targeted for marker-assisted breeding at ICRISAT (Ashok Kumar et al., 2019).

A successful example of marker-assisted backcrossing in pearl millet is the introgression of downy mildew resistance into the elite male parent H 77/833-2 using ICMP 451 as the donor. This effort resulted in HHB 67 Improved, the first pearl millet hybrid developed through marker-assisted breeding and proposed for release in India (Hash et al., 2006). Similarly, introgression of LG4 blast resistance QTL from 863B-P2 was in improving susceptible hybrid HHB 146. (Bollam et al., 2018)

Overall, marker-assisted selection has played a significant role in accelerating genetic improvement in pearl millet by enabling precise introgression of QTLs governing stress tolerance, yield components, and nutritional quality. Despite these successes, the polygenic nature of complex traits and strong genotype × environment interactions limit the efficiency of MAS alone, highlighting the need for integration with genomic selection and high-throughput phenotyping in future breeding programs.

Table 2. QTLs and genes associated with disease resistance in sorghum.

Disease	Gene / QTL	Chromosome / Linkage Group	Mapping Population / Material	Phenotypic Variance (%)	Reference
Anthracnose	Multiple QTLs	Chr 1, 6, 8, 10	Minicore (association mapping)	-	Upadhyaya et al., 2013
Anthracnose	QTLs	Chr 9 (SC155-14E)	SC155-14E genome	19–62%	Patil et al., 2017
Anthracnose	QTLs	Chr 5 (C414-12E)	C414-12E genome	20–39%	Patil et al., 2017
Anthracnose	Cg1 (dominant gene)	LG 5	Cultivar SC748-5	-	Ramaswamy et al., 2008
Grain mold	Y1, Y3 (R2R3-MYB genes)	Not specified	RTx430 × RTx2911	-	Nida et al., 2019
Grain mold	Multiple QTLs	Multiple LGs	Mapping population	10–23%	Klein et al., 2001
Rust	Major QTL	LG 10	Mapping population	~40%	Tao et al., 1998
Rust	Multiple QTLs	All chromosomes (SBI-01 major)	Minicore, QL39/QL41, 296B/IS18551	-	Wang et al., 2014
Multiple diseases*	Disease QTL cluster	SBI-06	Various populations	-	Klein et al., 2001
Ergot	Five QTLs	SBI-01, 02, 06, 07, 08	Mapping population	High LOD	Parh et al., 2008

Table 3. Key high-iron and zinc pearl millet genotypes.

Category	Genotype	Year	Fe (mg/kg)	Zn (mg/kg)	Reference
OPV	ICTP 8203	1988	67	52	Singhal et al., 2022
OPV	ICMV 221	1993	61	45	Singhal et al., 2022; Velu et al., 2007
OPV	Dhanashakti	2014	71	—	Govindaraj et al., 2020
Hybrid	AHB 1200 Fe, HHB 299	2018	73–77	39–41	Govindaraj et al., 2020
Hybrid	RHB 233, RHB 234, AHB 1269, HHB 311	2019–20	83–91	39–46	Govindaraj et al., 2020

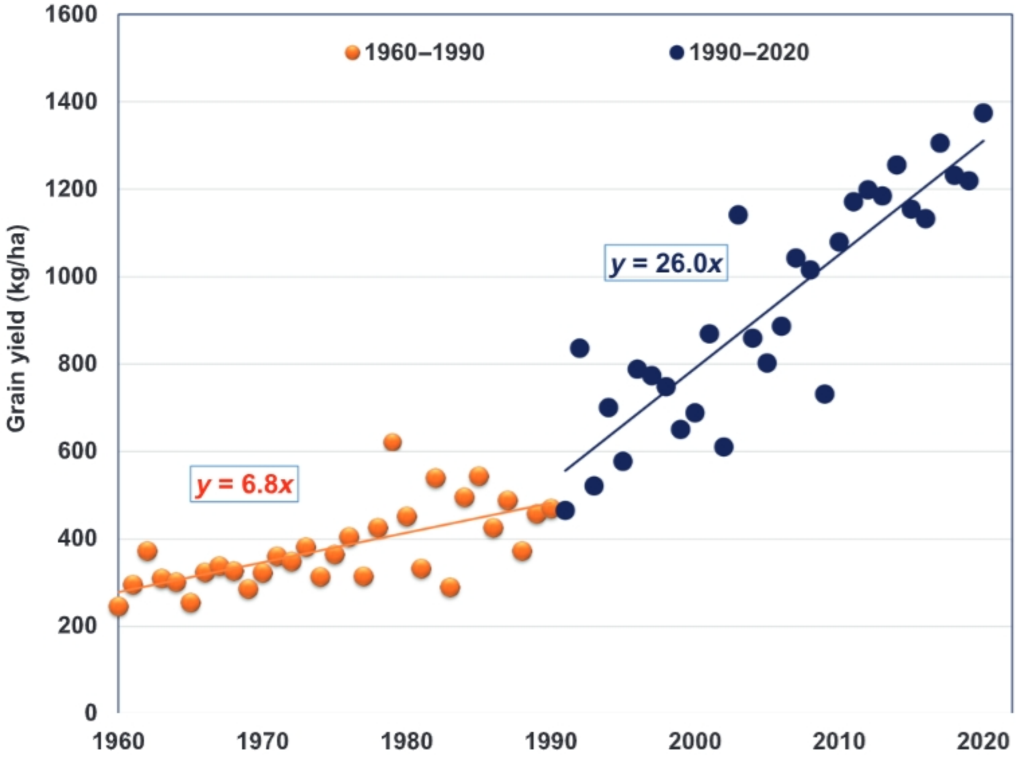

Fig. 1. (Image taken from Yadav et al., 2025)

3.4. Other Advanced Breeding Techniques

Other advanced breeding techniques have also been employed in sorghum and pearl millet improvement. Marker-assisted backcross breeding (MABC) has been successfully used in sorghum for shoot fly resistance, where six introgression lines were developed by crossing Parbhani Moti with J2614 (Gorthy et al., 2017).

Improvements in breeding efficiency have also been achieved through speed breeding approaches. In sorghum, the breeding cycle duration was reduced from 119 days under field conditions to 77 days using speed breeding (Sharma et al., 2024). Similarly, in pearl millet, genotypes with high iron and zinc content that typically require 10–11 generations under conventional field breeding were developed within only six to seven generations using speed breeding (Yadav et al., 2024; Sharma et al., 2024).

In addition, gene editing approaches have been explored for enhancing yield and quality traits. For quality improvement, protein digestibility and lysine content were targeted through editing of the KIC gene, achieving an editing efficiency of 92.4% (Li et al., 2018). For yield improvement, flowering time was modified by targeting the SbGA20ox5 (Sb09G230800) gene, with an editing efficiency of 83.3% (Char et al., 2019).

Productivity of pearl millet during 1960–1990 and 1991–2020. The figures inside graph indicate increase in grain yield (kg/ha/year).

Similarly, Nagesh et al., 2022 evaluated 24 sorghum varieties released between 1990 and 2020 across six locations over three years reported a substantial genetic gain in grain yield and disease resistance. The absolute genetic gain in grain yield was 44.93 kg ha/yr relative to the base variety CSV 15, with mean yield increasing from 2658 kg/ha in the 1990s to 4069 kg/ha in varieties released in the 2020s. Grain mold resistance also improved, showing an absolute genetic gain of -0.11 per year and a relative gain of 1.46% over CSV 15. The yield gains observed during last three decades for sorghum and bajra are 36% and 161% respectively. (Yadav et al., 2024)

4. Conclusion

Thus, enhancing genetic gain in sorghum and pearl millet requires an integrated breeding approach that combines conventional selection with modern genomic and biotechnological tools. Marker-assisted selection and backcross breeding have allowed for the accurate introgression of major-effect QTLs for abiotic and biotic stress tolerance, whilst genomic resources and QTL mapping have increased trait dissection efficiency and selection accuracy. The use of speed breeding has significantly reduced generation time, resulting in faster varietal development cycles. In parallel, gene editing technologies offer new opportunities for targeted improvement of yield, stress adaptation, and nutritional quality. The integration of these approaches, together with advanced phenotyping and multi-environment testing, has the potential to accomplish long-term genetic gain and generate climate-resilient, high-yielding, and nutritionally enhanced cultivars.

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Conflict of Interest

The authors declare no conflict of interest.

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