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Evaluation of Multi-Parent Cross Derivatives for Important Yield and Related Traits in Post-Rainy Season Sorghum (*Sorghum bicolor* L. Moench)

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Abstract

The study evaluates the agro-morphological performance of F_4 Multi-parent Advanced Generation Inter-cross derivatives in post-rainy season sorghum (*Sorghum bicolor* L. Moench) at the regional station, Solapur, Maharashtra, during 2023-24. Utilizing a Randomized Block Design, 25 successful multi-parent cross combinations derived from 18 diverse founder lines were assessed for 11 quantitative traits. Analysis of variance revealed highly significant genetic differences ($P<0.01$) across all traits, including substantial selection potential within the population. The F_4 population achieved remarkable genetic gains over parental means, specifically in grain weight (97.25%), panicle weight (89.54%), and fodder weight (63.40%), while successfully maintaining the early maturity essential for moisture stressed rabi environments. High broad-sense heritability ($h^2>80\%$) was observed for all traits, with grain weight (72.34%) and fodder yield (73.23%) showing exceptional genetic advance as a percentage of mean, suggesting that these yield traits are primarily governed by additive gene action and are highly responsive to selection. Pearson correlation analysis demonstrated that grain weight has strong positive associations with panicle weight (0.96) and panicle width (0.80). Principle Component Analysis indicated that the first three components accounted for 74.13% of total variation, with PC1 (42.89%) primarily driven by yield-contributing traits, effectively clustering superior genotypes such as G12 and G14. Ultimately, the MAGIC strategy successfully broadened the genetic base, enabling the recombination of favourable alleles to develop high yielding, climate resilient sorghum varieties in post-rainy sorghum.

Key words: Sorghum, MAGIC population, Genetic variability, Heritability, Principal component analysis, Yield potential

Multi-parent Advanced Generation Inter-cross is a highly innovative approach to the plant breeding field, created with the highly specific aim of intensive inter-crossing of genomes and the combination of ancestral alleles [1-2]. Compared to traditional biparental populations, MAGIC populations are crossed with more than two founder lines (typically eight or more parents), the outcome of which, alone, saturates the allelic diversity of the ensuing recombinant inbred lines [2-3]. Repeated cycles of inter-crossing gradually break down the genomes of the founder lines and rebuild them into fine-scale mosaics. This process creates many more recombination events than conventional crossing methods, which increases genetic diversity and improves the chances of identifying useful trait combinations. This level of genetic fragmentation is capable of creating a far greater level of resolution of complex traits, making it possible to discover new alleles and genetic interactions, which would be lost in more simplistic breeding designs [3-4]. MAGIC populations have already been demonstrated to be effective in a variety of valuable cereal species, including rice, where they have been used to unravel the complicated genetic basis of grain yield and seed quality, and in barley, bread wheat, and maize to enhance resistance to numerous biotic and abiotic stressors [4-5]. The breeders have been able to isolate a high diversity of a variety of gene pools, with the assistance of the multi-parent resources developed in sorghum, which has uncovered valuable genetic variations, which will lead to high-quality agro-morphological performance.

The current study is targeted at a systematic investigation of the F_4 MAGIC derivatives to optimize the productivity of sorghum in a specific ecological niche of the post-rainy (rabi) season through this developed genetic platform. The post-rainy season in India has a set of environmental constraints unique to it, and crops generally have to rely on the declining moisture content of the soil, and a challenging balance between possible yields and drought tolerance needs to be achieved [6]. To cope with these challenges, a breeder must be very knowledgeable regarding the genetic background of the most significant traits,

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including the type and extent of genetic variability, heritability, and genetic advancement [7]. A major measure of the degree to which phenotypic selection is precise is heritability, and some prior sorghum MAGIC research has found that the broad-sense heritability of height and maturity in plants is often large, whereas grain yield/plant largely has more intermediate levels of heritability due to its sensitivity to environmental changes [8]. In addition, genotypic correlation and path analysis must be integrated to determine both direct and indirect effects of various characters on the final yield that can provide the transparency required to determine the most effective selection indices [1]. This study expands the genetic foundation of experimental lines well beyond the reach of conventional breeding approaches. By broadening the allelic diversity through multi-parental recombination, it enables the identification of progenies that express desirable agro-morphological traits while maintaining strong adaptation to the post-rainy environment. Such an enriched genetic base not only strengthens resilience against climatic constraints but also provides a more reliable platform for selecting superior lines that can contribute to sustainable sorghum improvement [2], [4]. This multi-parent derivatives test will ultimately be applied in the creation of the fundamental genetic data, which may be used to create effective breeding approaches that will generate high-yielding and resistant sorghum varieties that can support the nutritional and economic needs of the growing world population [6], [9].

MATERIALS AND METHODS

Study area and experimental design

The research experiment was conducted at the Regional Station, Centre on Rabi Sorghum, ICAR- Indian Institute of Millets Research (IIMR), located in Shelgi, Solapur, Maharashtra, during the Rabi season of 2023-24. The cultivation period spanned from November 2023 to April 2024, with temperatures ranging from approximately 30°C to 40°C. Cultivation occurred in deep, black soil, and the crop was mainly cultivated using residual moisture and with supplemental irrigation. A Randomized Block Design (RBD) with three replications was used for sowing. The seeds were sown at a spacing of 3m × 3rows × 0.45m (plot size: 4.05 m^2). For sowing, 45 cm (row to row) and 15 cm (plant to plant) spacing were followed.

Experimental materials

Initially, 18 MAGIC founder lines were selected and utilized in a "funnel mating design" to generate 41 multi-parent cross combinations. From these combinations, 668 F_2 progenies were obtained and subsequently advanced through self-pollination to the F_4 generation. Rigorous evaluation and selection were conducted, resulting in the identification of 25 successful multiparent cross combinations in the F_4 generation (Table 2). The selected F_4 progenies were comprehensively assessed for various agronomic traits during the Rabi season of 2023-24. This systematic approach allowed the development and evaluation of promising sorghum genotypes with enhanced genetic diversity and the potential for improved agronomic traits.

Data collection

Growth parameters such as yield and yield-related components were recorded according to standard procedures. Plant-based data were collected from five randomly selected plants per plot, and plot-based data were obtained from the entire harvestable area. DF- Days to 50% flowering, DM- Days to maturity, PH-Plant height (cm), PE- Panicle exertion (cm), Ped L- Peduncle length (cm), PL- Panicle length (cm), PWdt- Panicle width (cm), PWt- Panicle weight/plot (kg), GWt-Grain weight/plot (kg), FWt- Fodder weight plot (kg), and 100 SWt- 100 seed weight (g) are among the 11 quantitative traits that were recorded and collected data in the study.

Table 1 List of 18 founder lines used for the crossing programme under study

S. No.	Parents	Specific characteristics
1.	Sel. 3	Earliness, tolerant to shoot fly, charcoal rot, and drought
2.	Parbhani Moti	Bold and pearly white grains, Tolerant to shoot fly and charcoal rot
3.	Solapur Dagadi	Bold grain size
4.	Phule Revati	Round bold grain and pearly white, tolerant to shoot fly, foliar diseases, and stem borer
5.	CRS 4	Resistance to foliar diseases, grain mold, and high fodder yield
6.	DSV 4	High yielding
7.	DSV 5	High yielding
8.	PKV Kranti	Aphid and shoot bug resistant
9.	Phule Suchitra	Round bold grain, tolerant to shoot fly, charcoal rot, and drought
10.	CSV 14 R	Round bold seed, better resistance to shoot fly, charcoal rot, and drought
11.	Phule Anuradha	Earliness, bold & pearly white grain, tolerant to shoot fly, charcoal rot, and drought
12.	CSV 216 R	High-yielding, tolerant to shoot fly and charcoal rot
13.	CRS 20	Drought tolerant
14.	CSV 22	Round bold grain, tolerant to shoot fly and charcoal rot
15.	Phule Chitra	Medium bold grain, tolerant to shoot fly, charcoal rot, and drought
16.	CSV 29 R	Lustrous seed, tolerant to charcoal rot, shoot fly, stem borer, shoot bug, and sugarcane aphid
17.	CSV 26	Tolerant to charcoal rot, shoot fly, stem borer, shoot bug
18.	M 35-1	Earliness, drought-tolerant, grain and fodder quality

Statistical analysis

The recorded data were subjected to a comprehensive statistical evaluation using R studio software with specialized packages ("*psych*", "*performance Analytics*", "*ggplot2*", "*factoextra*", "*dplyr*", "*FactoMineR*", "*reshape2*", "*pheatmap*", and "*patchwork*"). Mean performance values were computed to provide an initial overview of trait expression across genotypes, while analysis of variance (ANOVA) was employed to detect significant differences among treatments. Distributional characteristics were examined through skewness and kurtosis, thereby assessing the symmetry and peakness of trait distributions. Genetic variability was quantified using phenotypic and genotypic coefficients of variance (PCV and GCV), and the efficiency of selection was further evaluated through estimates of broad-sense heritability (H^2), genetic advance (GA), and genetic advance as a percentage of mean

(GAM). Trait associations were explored using Pearson's correlation coefficients, enabling the identification of direct and indirect selection pathways. To capture the underlying structure of multivariate variation, principal component analysis (PCA) was performed, with biplots and loading scores providing a clear visualization of trait clustering and genotype differentiation. Collectively, these analyses facilitated a robust characterization of genetic diversity and highlighted traits with greater potential for targeted improvement.

In the present study, eighteen (18) founder lines (Table 1) were selected based on diverse agronomic attributes to generate through possible eight-parent cross combinations. Comparative evaluation of progeny performance against parental lines revealed considerable variation across key agronomic traits, underscoring the effectiveness of multi-parental crossing in enhancing genetic diversity. Superior progenies exhibiting improved trait expression were identified, thereby facilitating the selection of promising cross combinations for further advancement. Through this approach, twenty-five successful multi-parent cross combinations were developed (Table 2), representing a valuable genetic resource for subsequent evaluation and breeding programs aimed at improving sorghum productivity and resilience.

Table 2 Pedigree structure of multi-parent cross combinations developed under study

S. No.	Pedigree
1.	[(Sel.3 × CRS4) × (Solapur Dagdi × Phule Revati)] × [(Sel.3 × Parbhani Moti) × (Sel.3 × Solapur Dagadi)]
2.	[(CSV 216R × CRS 4) × (M 35-1 × CSV 29R)] × [(Sel.3 × Solapur Dagadi) × (Sel.3 × CRS 4)]
3.	[(M 35-1 × CSV 29R) × (CSV 216R × CRS 4)] × [(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)]
4.	[(DSV 5 × Sel.3) × (Parbhani Moti × CRS 20)] × [(Sel.3 × CRS 4) × (Solapur Dagadi × Phule Revati)]
5.	[(CSV 14R × DSV 4) × (CSV 26 × PKV Kranti)] × [(CSV 29R × PKV Kranti) × (Parbhani Moti × DSV 5)]
6.	[(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)] × [(CSV 14R × PKV Kranti) × (CSV 14R × Phule Revati)]
7.	[(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)] × [(DSV 5 × Sel.3) × (Parbhani Moti × CRS 20)]
8.	[(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)] × [(M 35-1 × CSV 22) × (Phule Chitra × CSV 22)]
9.	[(M 35-1 × CSV 22) × (Phule Chitra × CSV 22)] × [(DSV 5 × Sel.3) × (Parbhani Moti × CRS 20)]
10.	[(M 35-1 × CSV 29R) × (CSV 216R × CRS 4)] × [(CRS 14R × Solapur Dagadi) × (CRS 4 × Phule Revati)]
11.	[(Phule Revati × Parbhani Moti) × (DSV 5 × Phule Suchitra)] × [(CSV 26 × Phule Suchitra) × (DSV 5 × Phule Revati)]
12.	[(Phule Revati × Parbhani Moti) × (DSV 5 × Phule Suchitra)] × [(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)]
13.	[(DSV 5 × Phule Revati) × (CSV 216R × CSV 29R)] × [(CSV 29R × PKV Kranti) × (Parbhani Moti × DSV 5)]
14.	[(CSV 14R × Phule Revati) × (CSV 26 × Phule Revati)] × [(Phule Chitra × CSV 22) × (M 35-1 × CSV 22)]
15.	[(Phule Chitra × CSV 22) × (M 35-1 × CSV 22)] × [(CSV 14R × Phule Revati) × (CSV 26 × Phule Revati)]
16.	[(Phule Anuradha × Parbhani Moti) × (CSV 216R × CRS 4)] × [(PKV Kranti × Solapur Dagadi) × (Phule Suchitra × CSV 14R)]
17.	[(Phule Anuradha × Parbhani Moti) × (CSV 216R × CRS 4)] × [(CSV 26 × Phule Suchitra) × (DSV 5 × Phule Revati)]
18.	[(CRS 4 × Sel.3) × (DSV 5 × Sel.3)] × [(DSV 5 × Phule Revati) × (CSV 216R × CSV 29R)]
19.	[(CSV 14R × Phule Revati) × (CSV 26 × Phule Revati)] × [(Phule Revati × Parbhani Moti) × (DSV 5 × Phule Suchitra)]
20.	[(DSV 5 × Sel.3) × (Parbhani Moti × CRS 20)] × [(CSV 29R × PKV Kranti) × (Parbhani Moti × DSV 5)]
21.	[(PKV Kranti × Solapur Dagadi) × (Phule Suchitra × CSV 14R)] × [(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)]
22.	[(CSV 26 × Phule Suchitra) × (DSV 5 × Phule Revati)] × [(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)]
23.	[(CSV 14R × PKV Kranti) × (CSV 14R × Phule Revati)] × [(CSV 26 × DSV 4) × (CSV 14R × Phule Revati)]
24.	[(CSV 26 × DSV 4) × (CSV 14R × Phule Revati)] × [(Parbhani Moti × CRS 20) × (M 35-1 × CSV 29R)]
25.	[(CSV 29R × PKV Kranti) × (Parbhani Moti × DSV 5)] × [(CRS 4 × Phule Revati) × (PKV Kranti × Phule Revati)]

RESULTS AND DISCUSSION

Analysis of variance (ANOVA)

The analysis of variance study reveals interesting insights into the genetic variability and potential for improvement in the studied crop. The ANOVA for 11 quantitative characters showed highly significant differences among the tested genotypes for days to flowering (DF), days to maturity (DM), plant height (PH), panicle exertion (PE), peduncle length (Ped L), panicle length (PL), panicle width (PWdt), panicle weight (PWt), grain weight (GWt), fodder weight (FWt) and 100 seed weight (100 SWt) at ($P < 0.01$) level of significance (Table 3). These differences indicated genotypes differ strongly for these agronomic traits, offering good selection potential for the improvement of yield and yield-related traits via selection. The replication effects were significant for days to flowering (DF), days to maturity (DM), plant height (PH), panicle length (PL), fodder weight (FWt), while non-significant for panicle exertion (PE), peduncle length (Ped L), panicle width (PWdt), panicle weight (PWt), grain weight (GWt), and 100 seed weight (100 SWt). In general, traits with significant genotype difference and non-significant Replication effects panicle exertion (PE), peduncle length (Ped L), panicle width (PWdt), panicle weight (PWt), grain weight (GWt), and 100 seed weight (100 SWt) are the most robust for selecting superior lines because genetic signals are strong and not confounded by block variability.

Variability and frequency distribution

Descriptive statistics play a central role in the process of generalizing the large amounts of data into comprehensive data, effectively simplifying the complex data of biology [10]. These parameters give invaluable information on central tendency, variability, and distribution, and help in determining outliers [11]. They also allow to come up with strong hypotheses about the genetic basis of quantitative traits by laying the groundwork for inferential statistics [10], [12]. In the present investigation of an F_4 MAGIC sorghum population, many minor-effect genes are usually grouped together in quantitative trait loci to affect quantitative traits [13]. Higher-order statistics, such as skewness and kurtosis, also helped to explain the genetic behaviour of these traits by giving valuable insights into the nature of action of the genes and the approximate number of genes in segregating the generations [14-15].

F_4 population analysis demonstrated that there is considerable genetic variation, and the coefficient of variation (CV) is lower than 7% on all traits assessed. Such a low CV means that there is not a significant environmental impact, and the observed deviation could be mostly genetic in nature. Peduncle length (6.68%), panicle exertion (5.82%), and grain weight (4.78%) showed great differences. Frequency distributions were further elucidated; leptokurtic distributions were observed in days to 50% flowering (0.666), plant height (1.235), panicle length (1.747), and fodder weight (2.881). Days to maturity, panicle length, and fodder weight showed positive skewness (0.051, 0.127, and 1.702, respectively), which is a complementary interaction between genes. Characteristics with large skewness or kurtosis, especially fodder weight, suggest that there are rare but valuable recombinants that require intensive selection in order to maximize genetic gain.

Comparison between progeny and parental averages revealed substantial genetic gains mentioned in (Table 4). Grain yield per hectare increased by approximately 97.25%, panicle weight by 89.54%, and fodder weight by 63.40%, highlighting strong additive effects. Morphological traits also improved, with peduncle length and panicle width increasing by 90% and 56%, respectively, confirming inheritance of larger panicles. Plant height moderately (7.9%), maintaining a favourable architecture that reduces lodging risk. Importantly, yield gains were achieved without delaying crop maturity; flowering and maturity times decreased slightly (-1.2% and -0.6%), preserving earliness essential for post-rainy season cultivation. Overall. Progeny performance surpassed parental means, with panicle weight (7593.45 kg/ha) and grain weight (6015.17 kg/ha). And fodder weight (9023.79 kg/ha) showed the greatest improvements. These findings demonstrated the effectiveness of multi-parent crosses in broadening genetic diversity and accelerating the development of superior sorghum lines.

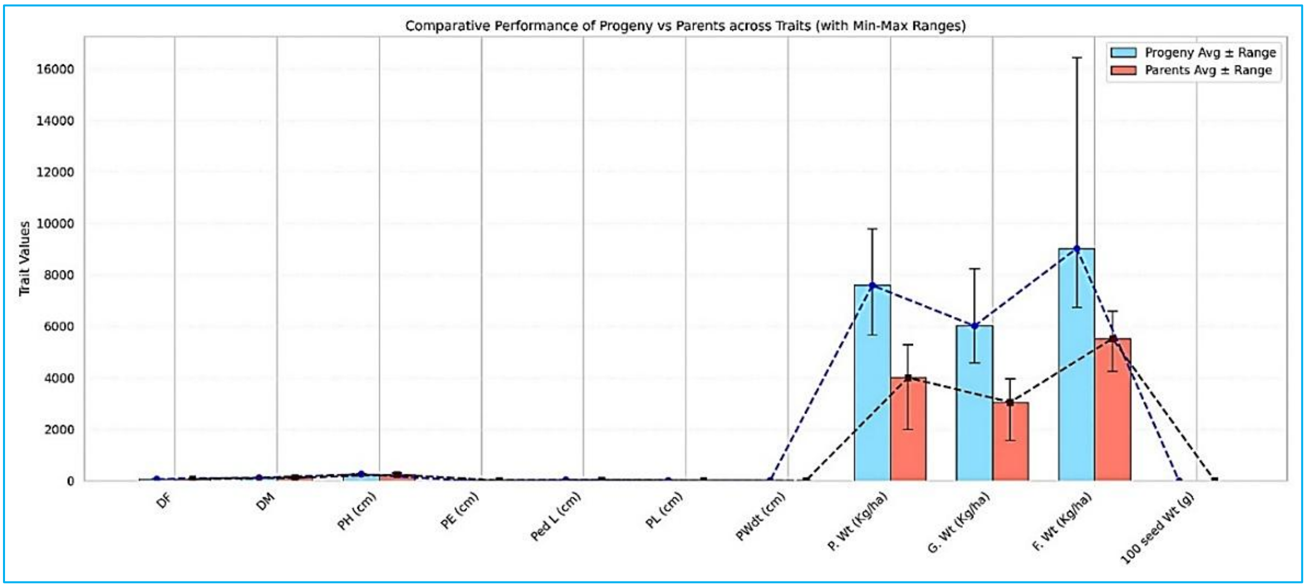


Fig 1 Comparative performance of progeny vs parents across all quantitative and qualitative trait

Table 3 ANOVA analysis of variance of advanced lines of multi-parent derived progenies along with its parents

Traits	DF	DM	PH (cm)	PE (cm)	Ped L (cm)	PL (cm)	PWdt (cm)	P.Wt (Kg/ha)	G.Wt (Kg/ha)	F.Wt (Kg/ha)	100 SWt (g)
No. of replication	3	3	3	3	3	3	3	3	3	3	3
No. of treatment	43	43	43	43	43	43	43	43	43	43	43
Treatment mean sum of square	69.98 ***	74.55 ***	1955.77 ***	23.50 ***	370.42 ***	20.30 ***	3.68 ***	12780332.64 ***	8637255.25 ***	22158830.44***	0.564 ***
Replication mean sum of squares	63.1***	16.7*	394.47*	0.41 ns	2.72 ns	2.42*	0.086 ns	42484.21 ns	143221.0 ns	919115.6**	0 ns
Error mean sum of squares	2.08	4.92	111.39	0.36	5.04	0.62	0.04	65235.12	52173.62	126088.05	0.00
Trait mean	68.53	118.9	249.36	10.34	33.59	18.07	4.63	6091.79	4773.72	7558.17	3.59
Minimum	52.00	99.00	161.00	4.20	14.00	10.50	2.50	1636.78	1366.20	3950.62	2.56
Maximum	81.00	130.0	333.00	15.60	50.40	27.50	6.42	9876.54	8659.26	16913.58	4.64
Std. Error (m)	0.83	1.28	6.09	0.35	1.30	0.46	0.12	147.46	131.88	205.01	0.02
Std. Error (d)	1.18	1.81	8.62	0.49	1.83	0.65	0.17	208.54	186.50	289.93	0.02

***= significant at <0.01 level of significance; ** = highly significant at <0.01 level of significance; *= significant at 0.05 level of significance; ns = non-significant) DF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PE- Panicle exertion, Ped L- Peduncle length, PL- Panicle length, PWdt- Panicle width, P.Wt- Panicle weight, G.Wt- Grain weight, F.Wt-Fodder weight, and 100 SWt- 100 seed weight

Heritability and genetic advance

The magnitude of genetic variation within the breeding population is essentially crucial to the success of any crop improvement program. Selection is the main way of determining and isolating the best genotypes, though its effectiveness is confined to the range of genotypic variation at hand [16]. The intensive assessment of genetic parameters such as the phenotypic coefficient variation, genotypic coefficient of variation, broad-sense heritability (h^2), and genetic advance as a percentage of mean makes a strict condition of successful use of variability in the breeding of sorghum [17-18]. The phenotypic and the genetic components of variance of eleven quantitative traits were determined in the present study of the F_4 MAGIC population. These analyses showed that there was more phenotypic variance than genotypic variance (8.248), and phenotypic variance increased with all assessed characters, which is also reflected in PCV being slightly greater than the corresponding genotypic coefficients of variance (GCV). This variation portrays that environmental factors are able to affect the expression of the traits, but since the differences are marginal, it is possible to conclude that there is a strong genetic foundation for the observed variability. In particular, the fact that disparities between the phenotypic and genotypic variances are very low, and that the estimates of heritability are very high (more than 80% in all instances), proves that the environment had a minimal impact on phenotypic performance of the F_4 population. Such a significant degree of genetic influences suggests that selecting based on phenotypic traits will reliably reflect genotypic value.

The GCV of the various traits showed significant variation, indicating the potential for genetic enhancement. Most importantly, high GCV values were found for panicle exertion (26.85%), peduncle length (32.85%), panicle width (23.78%), panicle weight (33.79%), grain weight (35.43%), and fodder weight (35.85%). Such high values suggest that there is a high genetic variability in traits contributing to yield, which is necessary to attain high genetic gains in subsequent breeding generations. The values of GCV were low at days to 50% flowering (6.94%), days to maturity (4.05%), and plant height (9.94%), indicating that there was little opportunity to select directly in these particular traits in this population. Moderate GCV values, on the other hand, were obtained in panicle length (14.17%) and 100 seed weight (12.06%), shown in (Table 5).

Although high heritability is an important parameter, it does not solely imply high genetic gain unless it is coupled with substantial genetic progress [16]. Heritability refers to the proportion of observable variation that is attributed to genetic influences, while genetic advance indicates the expected improvement that can be achieved through selective breeding. In this study, a combined analysis of H^2 and GAM indicated that both are expected to be strongly in a number of important traits. Traits panicle weight (98.48%, 69.08%), grain weight (98.20%, 72.34%), and fodder weight (98.31%, 73.23%) exhibited exceptionally high values. Similarly, high heritability and Gam were recorded for panicle exertion (95.50%, 54.06%), peduncle length (96.02%, 66.32%), and panicle width (96.62%, 48.16%), H^2 and GAM, respectively. The high heritability and high genetic advance are also highly indicative of an additive gene action governing these traits, and thus make them highly sensitive to direct selection [17-18].

On the other hand, the study revealed that the days to maturity had a relatively low GAM (7.58%), even though the heritability was high (82.51%). This implies that non-additive gene effects might be involved in such a trait and limits the possibility of rapid improvement by simple phenotypic selection, and may instead involve breeding heterosis or more advanced selection methods. Overall, the considerable heritability and significant genetic advancement observed in grain and fodder yield components demonstrate the F_4 MAGIC population's high selection efficiency [19]. These findings confirm that the multi-parent crossing strategy was effective in increasing the genetic base, allowing for the identification of superior lines with significantly higher yield potential through future breeding cycles.

Table 4 Descriptive statistics for eleven quantitative traits of an F_4 MAGIC population

Traits	CV%	Skewness	Kurtosis	Progeny			Parents			Gain %
				Min	Max	Aver.	Min	Max	Aver.	
DF	2.10	-0.275	0.666	63.33	79.00	68.20	54.33	76.67	69.00	-1.16
DM	1.86	0.051	-0.486	112.33	127.67	118.60	106.33	128.00	119.35	-0.63
PH (cm)	4.23	-0.778	1.235	214.00	288.33	257.25	173.67	307.00	238.41	7.90
PE (cm)	5.82	-0.447	-0.610	4.26	15.28	9.61	8.00	13.90	11.36	-15.40
Ped L (cm)	6.68	-0.211	-1.481	28.82	50.36	41.93	16.67	33.00	22.01	90.50
PL (cm)	4.37	0.127	1.747	15.24	22.72	18.53	11.07	25.87	17.44	6.25
PWdt (cm)	4.45	-0.147	-1.448	4.53	6.40	5.45	2.97	5.17	3.50	55.71
P. Wt (Kg/ha)	4.19	-0.084	-1.130	5670.78	9800.82	7593.45	2007.20	5300.41	4006.16	89.54
G. Wt (Kg/ha)	4.78	-0.012	-1.083	4584.77	8236.21	6015.17	1583.58	3969.82	3049.48	97.25
F. Wt (Kg/ha)	4.70	1.702	2.881	6740.74	16444.44	9023.79	4258.44	6599.18	5522.59	63.40
100 SWt (g)	0.72	-0.154	-0.054	3.18	4.62	3.78	2.58	3.99	3.34	13.17

Table 5 Estimation of genetic parameters for yield and its attributing characters of the Sorghum MAGIC population

Traits	DF	DM	PH (cm)	PE (cm)	Ped L (cm)	PL (cm)	PWdt (cm)	P. Wt (Kg/ha)	G. Wt (Kg/ha)	F. Wt (Kg/ha)	100 SWt (g)
σ^2 g	22.63	23.21	614.79	7.71	121.79	6.56	1.21	4238365.84	2861693.87	7344247.46	0.187
σ^2 p	24.71	28.13	726.18	8.07	126.83	7.18	1.25	4303600.96	2913867.49	7470335.51	0.188
GCV	6.94	4.05	9.94	26.85	32.85	14.17	23.78	33.79	35.43	35.85	12.06
PCV	7.25	4.46	10.8	27.47	33.52	14.83	24.19	34.05	35.75	36.16	12.08
h^2 (%)	91.6	82.51	84.66	95.5	96.02	91.3	96.62	98.48	98.2	98.31	99.64
GA	9.38	9.01	46.99	5.59	22.27	5.04	2.23	4208.71	3453.46	5535.34	0.89
GAM (%)	13.68	7.58	18.84	54.06	66.32	27.9	48.16	69.08	72.34	73.23	24.8

(Variation array for GCV, PCV, $h^{2,}$ and GAM ░ Low ▒ Moderate ▓ High)

σ 2 g-genotypic variance; σ 2 p-phenotypic variance, DF- Days to 50% flowering, DM- Days to maturity, PH- Plant height, PE- Panicle exertion, Ped L- Peduncle length, PL-Panicle length, PWdt- Panicle width, P.Wt-Panicle weight, G.Wt-Grain weight, and F.Wt-Fodder weight

Pearson correlation

In a breeding program, the correlation between yield, yield components, and other economic traits is important for selection, especially when the breeder needs to improve several traits simultaneously. Pearson's correlation coefficient is commonly used in linear regression to measure the strength of the relationship between two traits. A positive correlation increases the selectivity for both traits, whereas a negative correlation decreases the selectivity. Therefore, it is important for breeders to identify correlations that have a genetic basis or reflect environmental factors that affect the traits. The Pearson correlations were shown in (Fig 2) for the studied traits were analyzed by using *"psych"* package in R software.

The present investigation revealed that trait grain weight (Kg/ha) had a positive and significant association with panicle weight (Kg/ha) (0.96***), panicle width (cm) (0.80***), peduncle length (cm) (0.78***), stover weight (Kg/ha) (0.67***), 100 seed weight (g) (0.57***) and plant height (cm) (0.40***). Furthermore, a positive yet statistically non-significant correlation was observed with panicle length (cm) (0.17 NS). Grain weight (Kg/ha) showed a non-significant and negative association with Panicle exertion (cm) (-0.24 NS) and days to maturity (-0.017 NS). Therefore, increasing yield should be accomplished with the help of direct and indirect selection of the yield-boosting features [20-22].

Days to 50% flowering had a positive correlation with Days to maturity (0.82***), and both traits showed a non-significant association with other traits. Panicle weight (Kg/ha) had a significant and positive correlation with plant height (0.46***), Peduncle length (0.73***), Panicle width (0.79***), grain weight (0.96***), fodder weight (0.67***), and 100-seed weight (0.57***). Fodder weight (Kg/ha) showed a positive association with peduncle length (0.52***), panicle width (0.47***), panicle weight (0.66***), and grain weight (0.67***), as shown in the matrix, ensuring that the selection for higher grain productivity will simultaneously enhance fodder yield. Traits that significantly contributed to grain yield also exhibited positive intercorrelations, indicating coordinated expression and potential for simultaneous selection [23-24].

These results reinforce the effectiveness of the MAGIC breeding strategy, which promotes high recombination and breaks undesirable linkages. The significant positive correlations among yield-related traits suggest that recombination has successfully aligned favourable alleles, enabling simultaneous improvement of grain yield, biomass, and panicle architecture. Collectively, these findings suggest that focusing selection on panicle architecture in these F4 derivatives will effectively produce high-yielding and dual-purpose sorghum varieties [25].

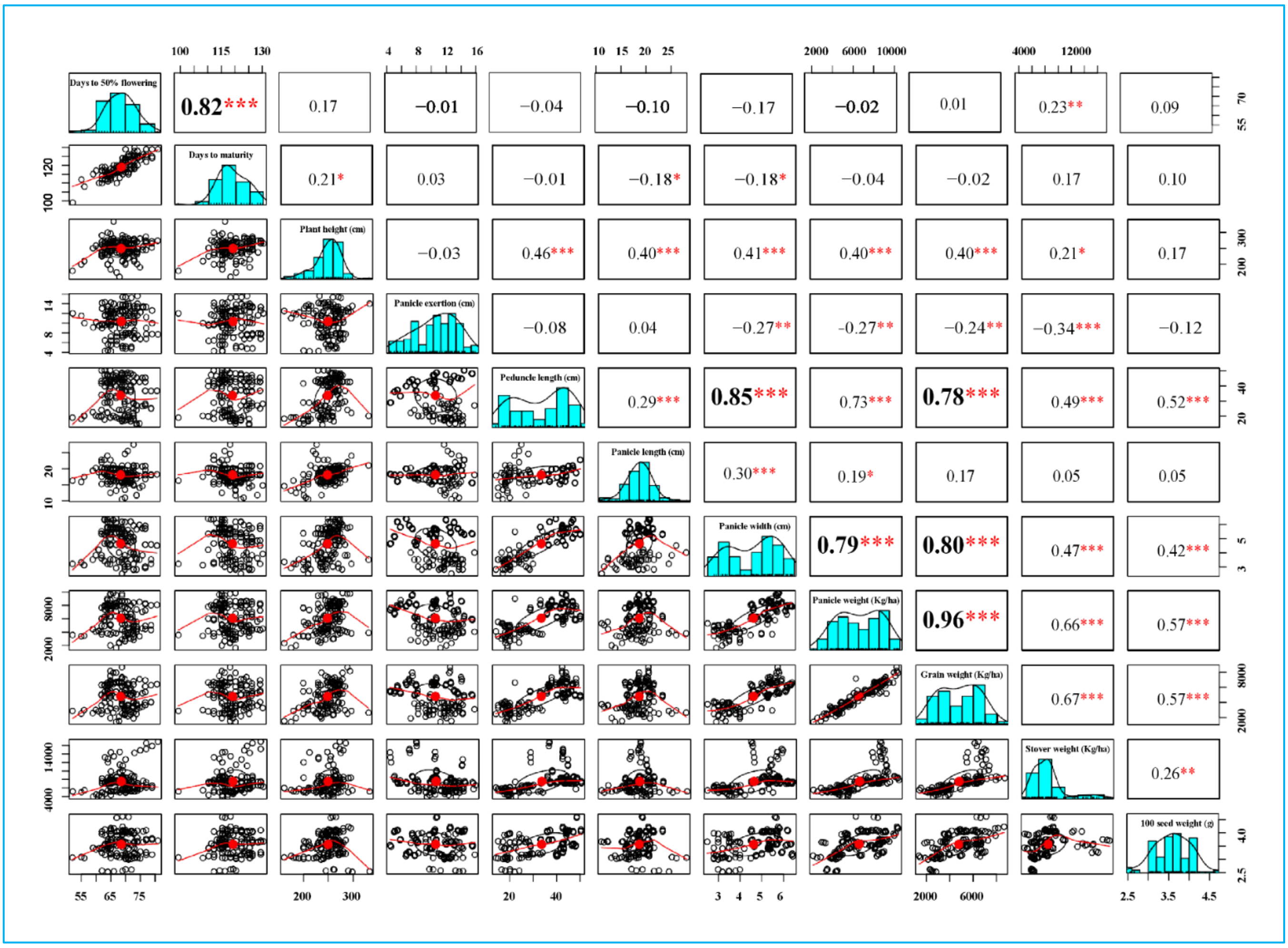


Fig 2 Pairwise scatter plot matrix (lower triangle boxes), histograms (in the diagonal boxes), and Pearson correlation coefficients among variables (upper triangle boxes). (*), (**) and (***) denote that the corresponding variable is significant at 10%, 5%, and 1% level, respectively. Absence of a star denotes no significant variable

Principal component analysis (PCA)

The grouping of points on the PCA plot indicates genetic relationships and population structure within the MAGIC lines, showing how they relate to the genetic diversity of their founders. The spread of the points reflects the overall genetic diversity within the population, with distinct clusters suggesting subgroups with different genetic contributions from the founders. Data visualization for multivariate analyses was performed using specialized R packages "factoextra" and "FactoMineR", designed for principal component analysis (PCA).

Inference from the variance distribution in principal components

The Principal Component Analysis was done using 11 traits. The singular value decomposition approach was used for analysis. A total of 11 Principal Components were computed in the analysis, out of which 3 had eigenvalues greater than 1 (As per Kaiser's rule, the principal components with eigenvalues greater than 1 should be considered for further analysis). The highest variation was explained by PC1 (42.89%) with an eigenvalue of 2.17. The principal components PC2 and PC3 explained 19.06% and 12.18% of the variation, respectively which shown in (Table 6).

Table 6 Proportion of variance and cumulative proportion of variance for the principal components of eleven quantitative traits in MAGIC population

Principal component	Standard deviation	Proportion of variance	Cumulative proportion
PC1	2.17	42.89	42.89
PC2	1.45	19.06	61.95
PC3	1.16	12.18	74.13
PC4	0.97	8.55	82.68
PC5	0.81	5.91	88.59
PC6	0.71	4.58	93.16
PC7	0.59	3.16	96.32
PC8	0.45	1.88	98.20
PC9	0.32	0.91	99.11
PC10	0.27	0.66	99.77
PC11	0.16	0.23	100.00

Inference from correlation between principal components and variables

The principal component PC1 had positive correlation with variables GW (0.437), PW (0.4334), PWdt (0.4108), Ped L (0.408), FWt (0.3179), 100 SWt (0.281), PH (0.2549), PL (0.1455), DF (0.0107) and DM (0.004), while negative correlation with variables PE (-0.1403). The principal component PC2 had positive correlation with variables DM (0.6629), DF (0.6575), F.Wt (0.1819), PH (0.125) and 100 SWt (0.0821), while negative correlation with variables G.Wt (-0.0024), PE (-0.0134), PW (- 0.0165), Ped L (-0.0457), PWdt (-0.1634) and PL (-0.2087). The principal component PC3 had positive correlation with variables PL (0.5859), PH (0.5313), PE (0.4831), Ped L (0.1268), DM (0.1024), DF (0.088) and PWdt (0.0147), while negative correlation with variables G.Wt (-0.1051), P.Wt (-0.1132), 100 SWt (-0.1213) and F.Wt (-0.2608) (Table 7). The PCA results confirm that yield-related traits cluster together and contribute strongly to PC1, making it a valuable axis for selecting high-performing genotypes. The separation of phenological traits in PC2 and structural traits in PC3 allows breeders to target specific trait combinations, such as early maturity with high biomass or compact architecture with enhanced grain yield. The observed clustering and trait associations validate the MAGIC strategy’s ability to break undesirable linkages and recombine favourable alleles. These insights can guide multi-trait selection and help prioritize genotypes for further evaluation under diverse agro-climatic conditions [26].

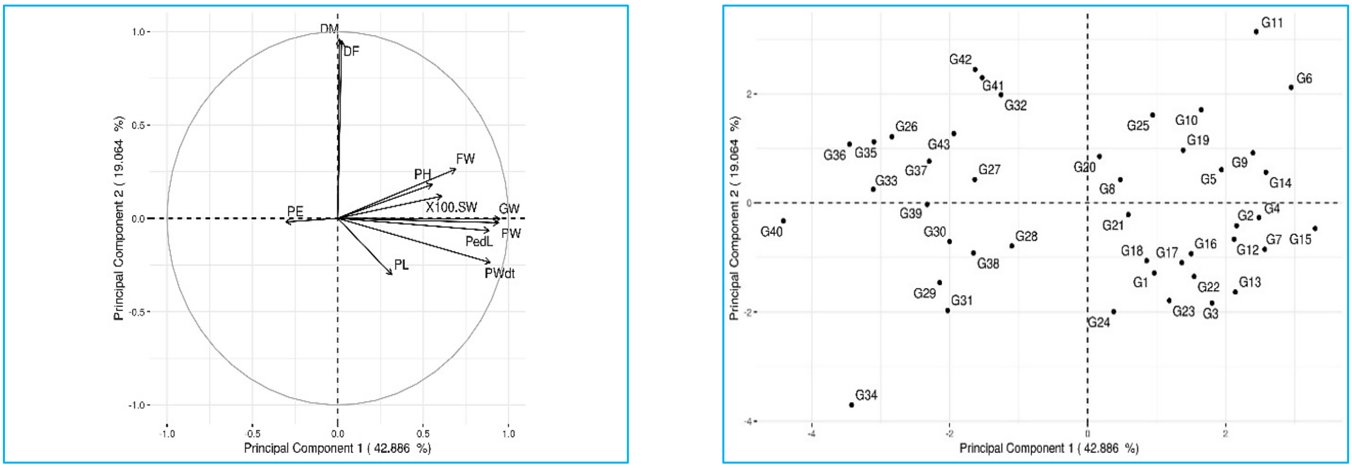
Table 7 Correlations of variables studied in the MAGIC population with principal components

Traits	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
DF	0.011	0.658	0.088	0.062	-0.052	0.144	0.180	0.235	0.657	-0.098	-0.059
DM	0.004	0.663	0.102	-0.018	-0.036	-0.065	0.172	0.040	-0.696	0.155	0.065
PH	0.255	0.125	0.531	0.223	-0.035	-0.526	-0.486	-0.244	0.114	0.022	-0.002
PE	-0.140	-0.013	0.483	-0.671	0.481	0.180	-0.080	0.025	0.050	0.153	0.010
Ped L	0.408	-0.046	0.127	-0.172	0.085	-0.115	0.530	-0.369	-0.043	-0.555	-0.195
PL	0.146	-0.209	0.586	0.352	-0.261	0.597	0.106	0.122	-0.125	0.001	0.039
PWdt	0.411	-0.163	0.015	0.020	0.055	-0.244	0.468	0.115	0.155	0.685	0.129
P. Wt	0.433	-0.017	-0.113	-0.066	0.093	0.042	-0.257	0.489	-0.136	-0.001	-0.679
G. Wt	0.437	-0.002	-0.105	-0.100	0.134	0.010	-0.180	0.395	-0.051	-0.326	0.688
F. Wt	0.318	0.182	-0.261	0.244	0.462	0.443	-0.207	-0.499	0.029	0.187	0.021
100 SWt	0.281	0.082	-0.121	-0.518	-0.667	0.196	-0.206	-0.274	0.064	0.157	0.037

The principal component analysis (PCA) offered a comprehensive view of trait relationships, genotype distribution, and component-wise variance within the dataset (Fig 3 a-d). Panel (a) presented a variable biplot, where each vector represented a trait such as plant height (PH), grain weight (GW), or dry matter (DM), projected onto the first two principal components PC1 and PC2 which together explained over 60% of the total variance. The direction and length of these vectors revealed how strongly each trait contributed to the components and how traits correlated with one another; traits pointing in similar directions were positively associated, while those pointing in opposite directions suggested trade-offs. Panel (b) mapped genotypes (G1-G42) in the same principal component analysis (PCA) space, showing how individual entries clustered based on their trait profiles. This helped identify promising genotypes with similar or unique combinations of traits, which was valuable for selection and classification in breeding programs. For instance, specific genotypes such as G12, G24, and G35 that align closely with high-yield vectors are prioritized as elite genotypes for further breeding. Panels (c) and (d) showed scree plots that visualized the proportion of variance explained by each principal component. The steep drop after the first few components and the flattening of the curve indicated that most of the meaningful variation was captured by the first two or three components, justifying their use for dimensionality reduction [27].

(a) PCA-Biplot for variables

(b) PCA-Biplot for genotypes



(c) Screeplot explained proportion of variation

(d) Screeplot explained eigen values

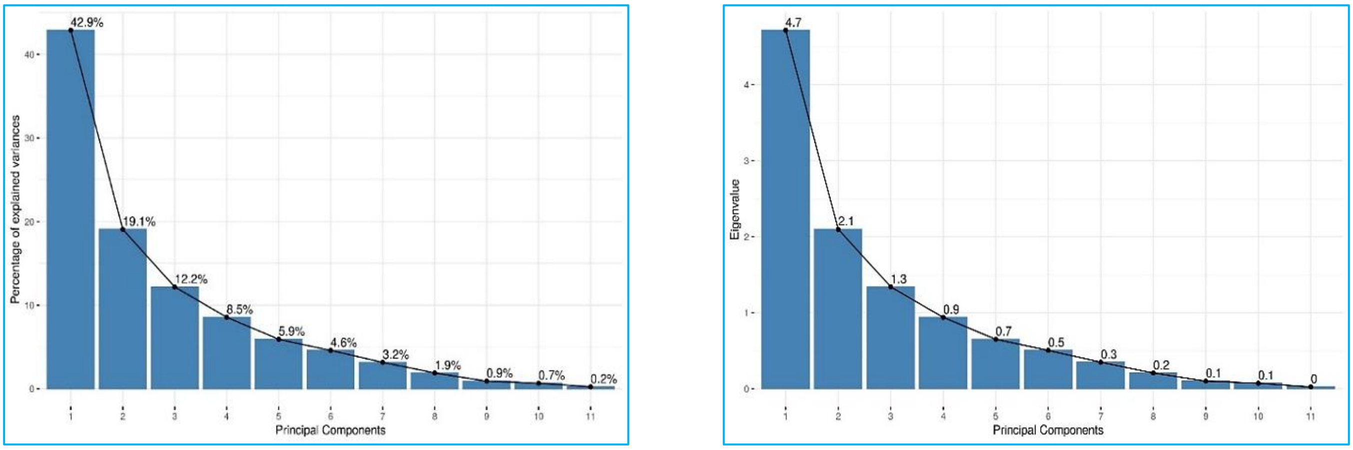


Fig 3 Multivariate characterization of the MAGIC sorghum population. (a) PCA variable biplot illustrating the correlations and contributions of eleven quantitative traits to the first two principal components. (b) PCA genotype biplot showing the distribution and clustering of individual entries (G1-G42) based on phenotypic profiles. (c) Scree plot depicting the percentage of total variance explained by each successive principal component. (d) Scree plot visualizing the eigenvalues associated with each component, highlighting the primary factors driving population diversity

The variable biplot

This plot (Figure 3a) shows how each trait contributes to the variation in sorghum population.

Principal components (PC1 & PC2)

PC1 (42.886%): This is the most important axis. The vectors for grain weight, panicle weight, fodder weight, peduncle length, and panicle width are all aligned along the positive side of this axis. This indicates that PC1 primarily represents yield and biomass productivity.

PC2 (19.064%): The vectors for days to 50% flowering and days to maturity point straight up along this axis. This indicates that PC2 represents phenology (maturity duration).

Trait correlations

Positive correlation: Vectors with small angles between them (like GWt, PWt, and FWt) are strongly positively correlated. Selecting for one will likely improve the others.

Independence: The vectors for maturity (DF/DM) are almost at a 90 °angle to the yield traits (GWt/PWt). This is a crucial finding, as it suggests that selecting for higher yield without necessarily increasing the time to maturity is essential for rabi season sorghum, where moisture is limited.

Negative correlation: Panicle exertion points in the opposite direction of the yield traits, suggesting a negative relationship between the two in this specific population.

The individual / Score plot

This plot (Fig 3b) maps 43 genotypes (G1-G43) based on the 11 traits.

Yield performance: Genotypes located on the far right of the plot (positive PC1) are the top performers for yield-contributing traits. For example, G11, G6, G14, and G15 are likely your highest-yielding lines.

Maturity: Genotypes at the top (positive PC2), such as G11 and G42, are late-maturing. Genotypes at the bottom (negative PC2), such as G34 and G24, are earlier-maturing.

Selection interpretation

Top right quadrant: The lines such as G6, G10, G11 have high yield but may be late-maturing.

Bottom right quadrant: These lines genotypes G12, G13, G15, G3 are the "sweet spot" for rabi sorghum; they show high yield potential (positive PC1) while being relatively earlier or average in maturity (negative PC2), which is ideal for escaping terminal drought.

The first two PC1 and PC2 components explain approximately 61.95% of the total genetic variation. The PCA (principal component analysis) successfully separated yield-contributing traits from phenological traits, allowing for the identification of superior F_4 derivatives (notably those in the bottom-right quadrant) that combine high grain and fodder productivity with the early-to-medium maturity required for post-rainy season environments [28]. Overall, the integrated analysis of PCA biplots and scree plots provided a robust multivariate framework for interpreting trait associations, genotype diversity, and dimensionality reduction within the dataset. The variable biplot revealed key correlations and trade-offs among agronomic traits, while the genotype distribution plot enabled the identification of distinct clusters and outlier genotypes with unique trait combinations. The scree plots further validated that the first two principal components captured the majority of meaningful variation, justifying their use for simplified yet informative visualization. Collectively, these graphical outputs supported strategic trait selection and genotype classification, offering valuable insights for targeted crop improvement and breeding decisions [29].

CONCLUSION

The evaluation of F_4 MAGIC derivatives highlights the significant potential of multi-parent populations in enhancing the genetic architecture of post-rainy (rabi) season sorghum. The study successfully identified substantial genetic variability and high heritability for Research all critical agronomic traits, demonstrating that the MAGIC approach provides a robust platform for genetic improvement. Notably, the F_4 population exhibited massive genetic gains over parental averages, particularly for grain and fodder yields, with several derivatives outperforming established checks in the various stressed environments in Solapur. The principal component analysis effectively separated productivity-related variables from phenological traits, identifying a “selection sweet spot” in the bottom-right quadrant of the biplot. Genotypes such as G12 and G14 emerged as superior ideotypes, combining exceptional grain yields (exceeding 3700 kg/ha) with optimal panicle characteristics and the early-to-medium maturity required for rabi adaptation. These genotypes represent elite breeding materials that can be directly advanced for multi-location trials or used as parents in future crossing programs to enhance climate resilience. In conclusion, the integration of MAGIC populations into sorghum breeding strategies facilitates the recombination of diverse traits, enabling the development of high-yielding, stable varieties that can sustain productivity under the challenging conditions of terminal drought and receding soil moisture.

Conflict of interest

The authors declare no competing financial or non-financial interests.

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