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Genetic variability studies in M₄ generation of mutagenized population of yellow pericarp sorghum for yield and yield contributing traits (*Sorghum bicolor* (L.) Moench)

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Abstract

The experiment comprised of 30 yellow pericarp sorghum mutants of M₄ generation derived from selfed seed of individual panicles of M₃ generation from each gamma irradiation-treatment i.e. 6 mutants from each treatment viz., 100 Gy, 200 Gy, 300 Gy, 400 Gy and 500 Gy along with a parental control 'Udgir Piwali' and 3 checks, was conducted at Parbhani (M.S.) during *rabi*, 2024-25 towards understanding the extent of variability, heritability and genetic advance for yield and its associated traits. The analysis of variance indicated significant differences among the mutants for all the traits examined. Results indicated relatively higher mean performance in checks for most of the characters studied including grain production. The GCV and PCV estimates showed wide variation for most of the characters studied in segregating M₄ generation. High heritability, medium GCV, PCV and GA were observed for grain yield per plant and its most of the component-traits. Among the fourteen characters evaluated, several yellow sorghum mutant genotypes namely, 100Gy-4, 200Gy-3, 200Gy-2, 300Gy-5, 300Gy-6, 400Gy-1, 400Gy-2 and 500Gy-6; consistently exhibited superior performance over multiple agromorphological traits. In addition, mutants viz., 300Gy-5, 200Gy-1, 200Gy-6, 400Gy-2, 400Gy-3 and 200Gy-5 demonstrated specific promise for drought tolerance-related physiological attributes. Such genotypes can be effectively utilized as potential donor parents in empirical breeding programs aimed at developing improved yellow pericarp sorghum varieties or hybrids with better nutritional and agronomical potential.

Keywords: *Sorghum bicolor* (L.) Moench, mutants, yellow pericarp, heritability, variability, genetic advance

Introduction

Sorghum (*Sorghum bicolor* (L.) Moench.) is cultivated predominantly in USA, China, India and Africa for both human and livestock consumption. Sorghum is cultivated over 42 million ha with an annual production of 62 thousand metric tonnes of grain with a productivity of 1435 kg/ha. In India, Sorghum is cultivated over of 4.11 million ha with an annual production of 4.70 million tonnes of grain. Top sorghum producing states are Maharashtra which contributes 49.14% of area and 47% production, Karnataka and Madhya Pradesh (Anonymous, 2025). The industrial demand for the grain sorghum as a raw material has been increasing. In recent years, due to climate change the length of rainy season and the corresponding growing season have reduced. In this scenario, water deficit leads to a shift in cropping pattern towards drought tolerant food crops which is unavoidable. When compared to other crops, low productivity is the main issue with grain sorghum production. The composition of sorghum grains includes proteins (11.6%), minerals (1.6%), fibers (1.6%), starch (72.6%) and other vital nutrients, such as pyridoxine, niacin and riboflavin. Among cereals, yellow pericarp sorghum contains high levels of carotenoids, specifically lutein and zeaxanthin that are important for eye health and prevention of macular degeneration with high antioxidant-property. Further, low rainfall and marginal soils are ideal growing conditions for yellow pericarp sorghum cultivars. Which serves as a source of carbohydrates and animal feed.

The yellow pericarp sorghum variety has low tannin levels (Gualtieri and Rappaccini, 1990) [11], unlike high-tannin brown-seeded sorghum, which inhibits digestive enzymes and dietary proteins. When used to replace up to 75% of maize in broiler diets, yellow pericarp sorghum resulted in improved dressing percentage and pancreas weight; while reducing abdominal fat pad and caeca weights, leading to optimal weight gain and feed conversion ratios (Adamu *et al.*, 2012) [1]. This yellow sorghum variety 'Udgir Piwali', is also a rich source of bioactive phenolic compounds, known for their antioxidant, anti-inflammatory, antiproliferative and antidiabetic properties. The modified yellow pericarp sorghum starch, with its lower protein content, is valuable in syrup production and the confectionery industry due to its higher glucose content compared to native starch. Additionally, yellow pericarp sorghum contains beta-carotene, an essential nutrient for eye health (Kshirsagar, 2021) [15]. The yield of yellow sorghum starch (78.5%) is higher than the 68-75% yields reported for white and dark sorghum starches (Elevina *et al.*, 1997) [12].

Mutation breeding is considered a key driver of evolution and offers a relatively fast method for improving various crops, particularly self-pollinated ones. Genetic variability in quantitatively inherited traits is crucial for breeders to make selections, and mutation breeding serves as an alternative approach to enhance this variability. It is often used to address defects in cultivars that already possess good agronomic traits. Among the different physical mutagens, such as x-rays, fast neutrons, thermal neutrons, ultraviolet and beta radiation, gamma rays and electron beams are particularly well-known for their effects on plant growth and development. These mutagens induce cytological, physiological and morphological changes in both somatic and germ line cells. Numerous studies have demonstrated the use of gamma radiation to induce genetic variability in quantitative traits, aiming to improve yield and yield-contributing characteristics. Recently, high-power linear electron accelerators, with energy ranges from 500 KeV to 10 MeV, have gained attention for various applications. These accelerators operate with a switch-on-off mechanism, similar to X-ray facilities and produce electron beams that can irradiate materials in a high-throughput manner. Electron beam radiation has thus become a crucial tool for inducing genetic variability and enhancing yield and yield-contributing traits. Hence, the aim of this work was also to determine how much extent the electron beams can produce the desired variability needed to create high-yielding sorghum mutants.

Materials and Methods

The present investigation was carried out at the Research Farm of the Department of Agricultural Botany, Vasantrao

Naik Marathwada Krishi Vidyapeeth, Parbhani (M.S.) utilizing a set of 30 sorghum mutants developed through gamma irradiation at doses of 100 Gy, 200 Gy, 300 Gy, 400 Gy and 500 Gy (six mutants per treatment group) from the M₃ generation. These mutants were evaluated alongside four standard checks: CSV-29R, Parbhani Moti, Parbhani Supermoti and Udgir Piwali (Parental genotype Table 1). The material was advanced to the M₄ generation using the ear-to-row method. Sowing was done in the last week of October using a Randomized Block Design (RBD) with two replications, maintaining inter-row and intra-row spacing of 45 cm and 15 cm, respectively. All recommended agronomic practices and plant protection measures were followed throughout the crop season. In each replication, five plants were randomly selected and tagged for data collection and their average values were used for statistical analysis.

Table 1: Salient features of sorghum landrace used in the study

Features	Yellow pericarp sorghum landrace 'Udgir Piwali'
Season	<i>Rabi</i>
Plant height (cm)	227
Days to 50% flowering	72
Maturity duration (days)	118
100 seed weight (g)	2.62
Grain yield (q/ha)	20-22
Fodder yield (q/ha)	96-98

Observations were recorded for yield, yield-contributing traits and drought-related physiological parameters. The recorded traits included days to 50% flowering, plant height, days to maturity, number of primaries per panicle, number of grains per primary branch, panicle length, panicle width, grain yield per plant, 100-seed weight, fodder yield per plant, relative water content, chlorophyll content (SPAD value), total leaf area and flag leaf area. The data were analyzed for variance following the method described by Panse and Sukhatme (1967) [16]. Coefficients of variation were calculated as per Burton (1952) [8], while broad-sense heritability and genetic advance were estimated following the procedures of Johnson *et al.* (1955) [13] and Allard (1960) [4], respectively.

Results and Discussion

Analysis of variance

The results of analysis of variance for evaluation of sixty-four mutant genotypes in *Rabi* sorghum are furnished in Table 2. Highly significant differences among the genotypes were observed for all the fourteen characters indicating presence of sufficient amount of variability in all the characters studied.

Table 2: Analysis of variance for yield and yield contributing characters in yellow pericarp sorghum

Source of Variation	DF	Days to 50% flowering	Days to maturity	Plant height (cm)	No. of primaries/panicle	No. of grains/primary	Panicle length (cm)	Panicle width (cm)
Replications	1	3.30882	0.36765	406.212	0.24721	3.13471	0.04979	0.21392
Treatments	33	7.8115**	14.1858**	616.2**	115.957**	14.5785**	3.22629**	1.0279**
Error	33	1.18761	5.39795	284.285	13.3963	2.75228	0.43724	0.06111
Source of Variation	DF	100-seed weight (g)	Fodder yield/Plant (g)	Relative water Content (%)	Chlorophyll content (SPAD values)	Leaf area (cm ²)	Flag leaf area (cm ²)	Grain yield/ plant (g)
Replications	1	0.04765	0.84941	7.56164	8.79121	225.644	36.6986	8.0868
Treatments	33	1.3785**	555.97**	17.0846**	23.9364**	2405.1**	1210.65**	350.416**
Error	33	0.07613	50.4312	9.06209	8.38683	430.274	117.983	10.7059

* and ** Significant at 5 % and 1% level of significance, respectively.

Genetic variability study

The effectiveness of a breeder in enhancing the genetic potential of a species largely depends on the availability and extent of variability in quantitative traits, such as grain or fodder yield. These traits are typically governed by multiple genes and are influenced by complex genetic interactions. Induced mutagenesis serves as a valuable tool to broaden the genetic variability for such traits, potentially resulting in both favourable and unfavourable outcomes. Evaluating the degree of variation in quantitative traits is essential to determine the suitability of mutation breeding for trait improvement. When a mutant exhibits an increased mean performance for a targeted trait, it indicates the potential for genetic advancement through selection, thereby supporting the use of mutation breeding as an effective strategy for crop

improvement. In the present study, the influence of polygenic mutations on quantitative traits in the M₄ generation was evaluated using parameters, such as mean performance, genotypic variance, phenotypic variance, heritability and genetic advance.

The observations on mean performances across 14 agromorpho-physiological traits highlighted the potential of several advanced yellow pericarp sorghum mutants – particularly, 400Gy-2, 300Gy-6, 200Gy-2, 200Gy-3, 200Gy-1, 200Gy-5, 400Gy-6, 500Gy-5, 100Gy-4, 300Gy-4 and 400Gy-1 for use as parent lines or donors in breeding programmes aimed at enhancing yellow pericarp sorghum yield. Similar patterns in yield performance, have also been reported at large in the previous studies on *Sorghum bicolor* (L.) Moench (Table 2).

Table 2: Trait-wise promising yellow sorghum mutant lines in the present investigation

SN.	Characters	Promising mutant genotypes
1.	Days to 50% flowering	100Gy-5, 100Gy-6, 100Gy-1, 100Gy-2, 400Gy-3
2.	Days to maturity	100Gy-1, 100Gy-3, 100Gy-5, 200Gy-2, 500Gy-3
3.	Plant height (cm)	200Gy-2, 300Gy-4, 300Gy-5, 400Gy-2, 400Gy-4, 500Gy-3, 500Gy-6
4.	Number of primaries/ panicle	300Gy-4, 300Gy-6, 400Gy-2, 100Gy-4, 500Gy-6
5.	Number of grains/ primary	400Gy-2, 400Gy-4, 400Gy-6, 200Gy-5, 300Gy-6
6.	Panicle length (cm)	100Gy-1, 100Gy-2, 100Gy-3, 300Gy-2, 300Gy-4, 400Gy-2, 400Gy-1
7.	Panicle width (cm)	100Gy-1, 100Gy-2, 300Gy-3, 300Gy-4, 300Gy-6, 400Gy-2, 400Gy-3
8.	100-seed weight (g)	100Gy-1, 100Gy-4, 100Gy-5, 200Gy-1, 300Gy-3, 300Gy-6, 400Gy-2
9.	Grain yield per plant (g)	100Gy-1, 100Gy-2, 100Gy-4, 200Gy-1, 200Gy-2, 200Gy-3, 200Gy-5, 300Gy-4, 300Gy-5, 300Gy-6, 400Gy-3, 400Gy-1, 400Gy-2, 400Gy-6, 500Gy-1, 500Gy-2, 500Gy-4, 500Gy-6
10.	Fodder yield per plant (g)	300Gy-6, 400Gy-2, 200Gy-3, 200Gy-2, 300Gy-5, 400Gy-1
11.	Relative water content (g)	200Gy-1, 200Gy-5, 200Gy-6, 300Gy-5, 300Gy-6, 400Gy-3, 400Gy-2, 500Gy-6
12.	Chlorophyll content [SPAD values]	100Gy-6, 300Gy-2, 300Gy-4, 400Gy-1, 500Gy-2
13.	Leaf area (cm ²)	100Gy-2, 100Gy-3, 200Gy-5, 300Gy-1, 300Gy-6, 400Gy-1, 400Gy-2, 500Gy-1
14.	Flag leaf area (cm ²)	100Gy-1, 100Gy-3, 200Gy-3, 300Gy-1, 300Gy-2, 400Gy-2, 400Gy-1, 500Gy-2, 500Gy-6

Flag leaf area is a critical factor in sorghum's grain production, as it is the final leaf to develop before flowering and plays a major role in photosynthesis. Its size and efficiency contribute significantly to the accumulation of carbohydrates and nutrients required for grain filling. Traits like flag leaf area, relative water content and chlorophyll content are often used to identify drought-tolerant genotypes. As a result, breeding for drought resistance has increasingly focused on selecting plants that maintain grain yield under stress conditions. Successful grain filling under drought depends on the flag leaf's ability to maintain or adapt its function. Despite its importance, comprehensive studies on the structural, physiological and biochemical characteristics of flag leaves under drought are limited and scattered, with most research focusing on wheat (Biswal and Kohli, 2013) [7].

Heritability (h^2), genetic advance (GA) and genetic advance as % of mean (GA %) in yellow pericarp sorghum mutant lines are graphically depicted in Figure 1. Further, the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) for yield and yield contributing character in yellow pericarp sorghum are also graphically exhibited in Figure 2.

Days to 50 % flowering: For the trait 'days to 50% flowering', the genotypic and phenotypic variances were recorded as 3.312 and 3.906, respectively. The corresponding Genotypic Coefficient of Variation (GCV) and Phenotypic Coefficient of Variation (PCV) were calculated at 2.661% and 2.889%. Although, heritability in the broad sense was high (84.8%), the trait showed a relatively low genetic advance of 3.45. Additionally, the

genetic advance as a percentage of the mean was found to be 5.05%, indicating limited expected improvement through selection. The higher PCV compared to GCV suggests the influence of environmental factors on the expression of this trait (Table 3).

- **Days to maturity:** The analysis of this earliness trait revealed a genotypic variance of 4.394 and a phenotypic variance of 7.093. The corresponding Genotypic Coefficient of Variation (GCV) was estimated at 1.832%; while the Phenotypic Coefficient of Variation (PCV) was slightly higher at 2.327%. A moderate level of heritability (61.9%) in conjunction with a low genetic advance (3.39) indicated limited potential for genetic improvement through direct selection. The greater PCV relative to GCV further suggests that environmental factors significantly influence the expression of this trait.
- **Plant height (cm):** Plant height exhibited considerable genetic variability, with genotypic and phenotypic variances estimated at 165.96 and 308.10, respectively. The genotypic coefficient of variation (GCV) was 5.296%, while the phenotypic coefficient of variation (PCV) was marginally higher at 7.216%, indicating a minor influence of environmental factors. Medium heritability (53.9%) coupled with a substantial genetic advance (19.47) suggests the predominance of additive gene action and the potential effectiveness of selection for this trait.
- **Number of primaries per panicle:** The trait under investigation showed a genotypic variance of 51.88 and a phenotypic variance of 57.97. Both the genotypic coefficient of variation (GCV) and phenotypic

- coefficient of variation (PCV) were relatively moderate, recorded at 13.94% and 14.82%, respectively. Heritability in the broad sense was high (88.4%), the trait showed a relatively higher genetic advance of 13.87. Additionally, the genetic advance as a percentage of the mean was found to be 27%,
- **Number of grains per primary:** The number of grains per primary branch exhibited a genotypic variance of 5.91 and a phenotypic variance of 7.28. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded at 11.6% and 12.88%, respectively, indicating a moderate level of variability. Although the trait showed high heritability (81.1%), it was associated with a low genetic advance of 4.512 and a genetic advance as percent of mean (GAM) of 21.53%.
 - **Panicle length (cm):** Panicle length showed a relatively low genotypic variance (1.39) and a slightly higher phenotypic variance (1.61). The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated at 7.72% and 8.31%, respectively, indicating a narrow difference between the two. Although this trait exhibited high heritability (86%), it was associated with a low genetic advance (2.26), suggesting limited scope for improvement through selection. The higher PCV compared to GCV reflects minor environmental influence (Table 3).
 - **Panicle width (cm):** Among all the traits studied, panicle number recorded the lowest estimates of genotypic and phenotypic variances, measured at 0.48 and 0.51, respectively. The genotypic coefficient of variation (GCV) was 12.83%, while the phenotypic coefficient of variation (PCV) was slightly higher at 13.23%. Despite the low genetic advance (1.38), the trait exhibited high heritability (94.1%), indicating that genetic factors play a significant role in its expression, though the potential for improvement through selection remains limited.
 - **100-seed weight (g):** This trait recorded the second lowest genotypic and phenotypic variances among all characters studied, with values of 0.65 and 0.68, respectively. The genotypic coefficient of variation (GCV) was 20.62%, while the phenotypic coefficient of variation (PCV) was slightly higher at 21.22%, indicating moderate variability with minor environmental influence. The trait exhibited high heritability (94.5%) along with a low genetic advance of 1.61, suggesting limited improvement through selection despite strong genetic control (Table 3).
 - **Grain yield per plant (g):** Grain yield per plant exhibited a lower genotypic variance (169.85) and a slightly higher phenotypic variance (175.20) among the evaluated sorghum mutant lines and check varieties. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were estimated at 26.94% and 27.36%, respectively, indicating high variability with minimal environmental influence. This trait showed high heritability (96.9%) along with a moderate genetic advance (26.434), and a genetic advance as a percentage of mean (GAM) of 32.68%. The observation that PCV slightly exceeded GCV suggests some environmental effect on trait expression (Table 3).
 - **Fodder yield per plant (g):** For this trait, the genotypic variance was estimated at 252.78, while the phenotypic variance was slightly higher at 277.98. The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded at 16.63% and 17.44%, respectively, indicating moderate variability with limited environmental influence. The trait demonstrated high heritability (90.9%) along with a moderate genetic advance of 31.23 and a genetic advance as a percentage of mean (GAM) of 32.68%.
 - **Relative water content (%):** The genotypic and phenotypic variances for relative water content (RWC) were calculated as 4.01 and 8.54, respectively. The genotypic coefficient of variation (GCV) was 2.27%, while the phenotypic coefficient of variation (PCV) was slightly higher at 3.32%, indicating minimal environmental influence. RWC showed high heritability (82.1%) combined with a low genetic advance of 2.82, suggesting limited potential for improvement through selection.
 - **Chlorophyll content (SPAD values):** Chlorophyll content, measured as SPAD values, exhibited a genotypic variance of 7.77 and a phenotypic variance of 11.98. The genotypic coefficient of variation (GCV) was estimated at 5.02%, while the phenotypic coefficient of variation (PCV) was slightly higher at 6.24%, indicating a modest influence of environmental factors. This trait recorded moderate heritability (65%) along with a low genetic advance of 4.6, suggesting limited scope for improvement through selection.
 - **Leaf area (cm²):** The genotypic and phenotypic variances for leaf area were estimated at 987.41 and 1202.54, respectively. The genotypic coefficient of variation (GCV) was calculated as 10.06%, while the phenotypic coefficient of variation (PCV) was slightly higher at 11.10%, indicating moderate environmental influence. This trait showed moderate heritability (58.65%) in conjunction with a high genetic advance of 58.65, suggesting good potential for improvement through selection.
 - **Flag leaf area (cm²):** Flag leaf area showed a genotypic variance of 546.33 and a phenotypic variance of 605.32. The genotypic coefficient of variation (GCV) was recorded at 14.85%, while the phenotypic coefficient of variation (PCV) was slightly higher at 15.63%, indicating a modest environmental effect. This drought-related trait exhibited high heritability (90%) along with a substantial genetic advance of 45.74, suggesting strong genetic control and good potential for selection (Table 3).
- The findings of the present investigation are consistent with the earlier observations of Abraha *et al.* (2015) [2]. Therefore, as shown in Table 3, the genetic variability parameters observed across the different agromorphological and physiological traits evaluated in the present study are discussed under the following sub-headings:
- Genotypic and phenotypic variance**
- The genotypic coefficient of variation (GCV) was consistently slightly lower than the phenotypic coefficient of variation (PCV) across all traits studied. The higher PCV values compared to GCV indicate that the observed

variability is influenced not only by genetic factors but also by environmental conditions. Analysing both PCV and GCV provides valuable insight into the relative contributions of genetic and environmental components to trait variability. This comparison is particularly important in identifying stable and heritable traits for use in breeding programs. The effectiveness of selection largely depends on the magnitude of these coefficients especially GCV as most economically important traits, such as grain yield, are complex in inheritance and significantly affected by gene-environment interactions. In this study, the genotypic coefficient of variation was lower than the phenotypic coefficient for all traits. Although the phenotypic variance was higher than the genotypic variance, the small difference between them suggests that the environment had little effect on these traits. For the traits plant height, fodder yield per plant, grain yield per plant, high estimates of genotypic and phenotypic variance have been observed. These findings are consistent with the results reported by Singh and Makne (1980) [19] for plant height, Seetharama *et al.* (1990) [18] for plant height, Ali *et al.* (2009) for grain yield per plant and Tariq *et al.* (2012) [20] for panicle length and forage yield.

Genotypic and phenotypic coefficient of variation

The genotypic coefficient of variation estimates for all the characters studied were found lower than the phenotypic coefficients of variation, and the variations between them were of lower magnitude.

As per the classification by Deshmukh *et al.* (1986) [9], the genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) can be categorized as low (<10%), moderate (10–20%), and high (>20%). In the present study, moderate levels of both GCV and PCV were observed for traits such as fodder yield per plant (GCV:

16.63%, PCV: 17.44%), number of primaries per panicle (GCV: 13.94%, PCV: 14.82%), number of grains per primary (GCV: 11.60%, PCV: 12.88%), panicle width (GCV: 12.83%, PCV: 13.23%), leaf area (GCV: 10.06%, PCV: 11.10%), and flag leaf area (GCV: 14.85%, PCV: 15.63%); Traits showing low GCV and PCV included days to 50% flowering (GCV: 2.66%, PCV: 2.88%), plant height (GCV: 2.27%, PCV: 3.31%), days to maturity (GCV: 1.83%, PCV: 2.32%), panicle length (GCV: 7.72%, PCV: 7.85%), and chlorophyll content (GCV: 5.02%, PCV: 6.24%); High estimates of GCV and PCV were recorded for 100-seed weight (GCV: 20.62%, PCV: 21.22%) and grain yield per plant (GCV: 26.94%, PCV: 27.36%), indicating substantial genetic variability for these traits in the present investigation.

For traits where the phenotypic coefficient of variation (PCV) was slightly higher than the genotypic coefficient of variation (GCV), the small difference between the two suggests minimal environmental influence on the expression of these traits. This implies that selection based on phenotypic performance would be effective for improving these characteristics. The narrow gap between PCV and GCV indicates that these traits are relatively stable and less affected by environmental fluctuations.

Furthermore, the absence of high GCV and PCV values for most traits, except for 100-seed weight and flag leaf area—suggests that direct selection may be more beneficial for improving specific traits, such as grain yield per plant. These findings align with those of earlier researchers, including Veerabhadhiran and Kennedy (2001) [22], Arunkumar *et al.* (2004) [5], Tesfamichael *et al.* (2015) [21], Dhutmal *et al.* (2015) [10], Khandelwal *et al.* (2015) [14] and Ravali *et al.* (2021) [17].

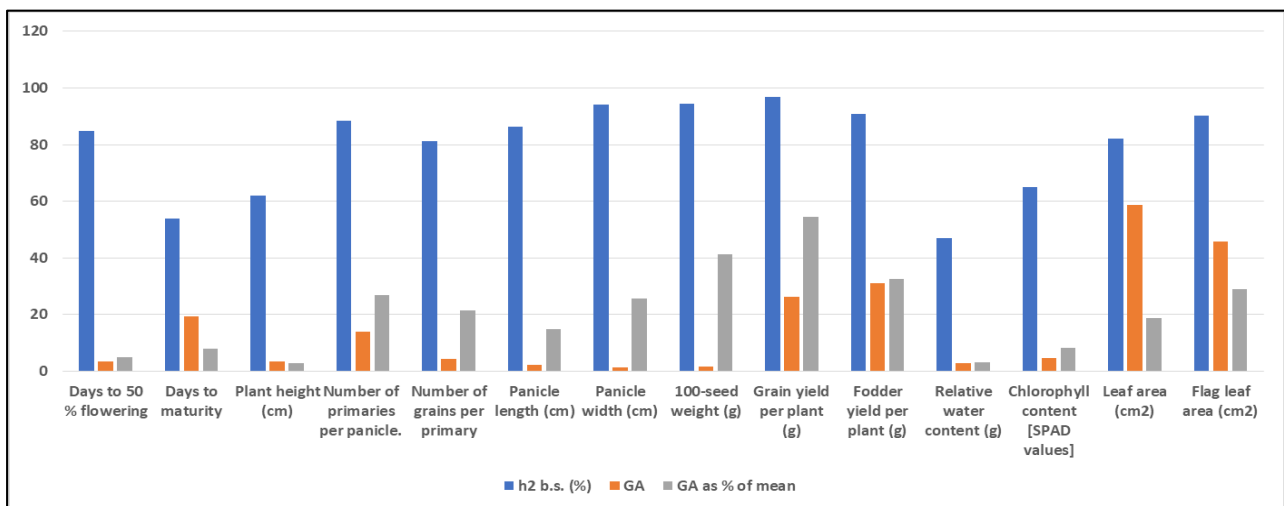
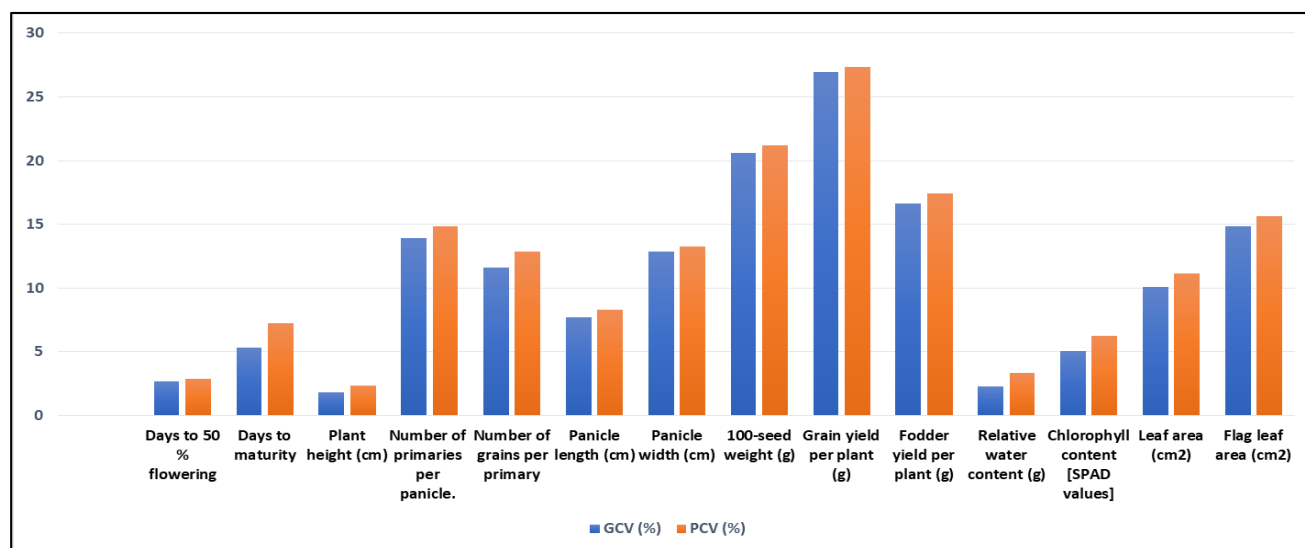


Fig 1: Heritability (h²), genetic advance (GA) and genetic advance as% of mean (GA%) in M₄ generation of yellow pericarp sorghum

Table 3: Genetic variability parameters for yield and yield contributing characters in M₄ generation of yellow pericarp sorghum

Sr. No.	Characters	Range		Mean	$\sigma^2(g)$ (Genotypic variance)	$\sigma^2(p)$ (Phenotypic variance)	GCV (%)	PCV (%)	h ² b.s. (%)	GA	GA as% of mean
		Minimum	Maximum								
1.	Days to 50% flowering	63.50	71.50	68.39	3.312	3.906	2.661	2.889	84.8	3.452	5.05
2.	Days to maturity	110.0	121.50	114.42	165.96	308.1	5.296	7.216	53.9	19.48	8.01
3.	Plant height (cm)	201.0	279.10	243.25	4.394	7.093	1.832	2.327	61.9	3.399	2.97
4.	Number of primaries per panicle	34.80	68.70	51.37	51.28	57.98	13.94	14.82	88.4	13.87	27.01
5.	Number of grains per primary	13.00	26.30	20.94	5.913	7.289	11.61	12.89	81.1	4.512	21.54
6.	Panicle length (cm)	12.35	17.70	15.28	1.395	1.613	7.73	8.31	86.4	2.262	14.79
7.	Panicle width (cm)	3.67	7.04	5.42	0.483	0.514	12.83	13.232	94.1	1.389	25.64
8.	100-seed weight (g)	2.85	6.70	3.91	0.651	0.689	20.63	21.223	94.5	1.616	41.31
9.	Grain yield per plant (g)	18.74	87.69	48.36	169.85	175.21	26.95	27.37	96.9	26.43	54.66
10.	Fodder yield per plant (g)	68.30	130.80	95.56	252.77	277.98	16.64	17.45	90.9	31.231	32.68
11.	Relative water content (g)	78.86	92.36	88.04	4.011	8.542	2.275	3.319	47.0	2.827	3.211
12.	Chlorophyll content [SPAD values]	46.90	63.65	55.11	7.775	11.968	5.029	6.24	65.0	4.63	8.35
13.	Leaf area (cm ²)	251.31	372.9	312.21	987.41	1202.55	10.06	11.107	82.1	58.65	18.79
14.	Flag leaf area (cm ²)	104.74	221.67	157.34	546.33	605.32	14.85	15.63	90.3	45.744	29.07

**Fig 2:** Genotypic and phenotypic coefficients of variation for yield and yield contributing characters in M₄ generation of yellow pericarp sorghum

Conclusion

Several of the identified promising mutant lines demonstrated significantly superior or above-average performance across key agro-morphological and physiological traits, including grain and fodder yield per plant. Among the 14 traits evaluated, genotypes such as 300Gy-6, 400Gy-2, 200Gy-3, 100Gy-1, 300Gy-4, 400Gy-1 and 500Gy-6 consistently exhibited strong performance across multiple parameters. Furthermore, mutants such as 300Gy-5, 200Gy-1, 200Gy-6, 400Gy-2, 400Gy-3 and 200Gy-5 showed marked improvement in drought tolerance-related physiological traits. These findings offer valuable insights for sorghum breeding programmes by identifying promising genotypes with favourable agronomic and physiological trait combinations, providing a strong foundation for varietal improvement and genetic enhancement aimed at developing high-yielding and drought-tolerant sorghum cultivars.

Thus, the estimation of genetic parameters, such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance provided valuable insights into the extent and nature of variability among the genotypes. Traits such as Number of primaries per panicle, Number of grains per primary, grain yield per plant, Leaf area (cm²), Flag leaf area (cm²) and fodder yield per plant exhibited high values

for GCV, PCV, heritability and genetic advance, indicating the predominance of additive gene action and the potential effectiveness of selection for these traits. Therefore, these attributes are considered most important for yield improvement in sorghum. Furthermore, the variability analysis effectively differentiated the genotypes, reinforcing its utility in identifying superior lines for breeding programs.

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