

INDUCED GENETIC VARIABILITY FOR GRAIN AND FODDER YIELD ARCHITECTURE IN M_s YELLOW-PERICARP SORGHUM MUTANTS

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ABSTRZACT

Yellow-pericarp sorghum landraces have value for food, feed and dryland production, but their breeding progress is constrained by limited selectable variability. This study quantified induced variability for 11 yield and yield-contributing traits in 39 M_s mutant derivatives of the *rabi* landrace Udgir Piwali, together with four commercial checks and the parental control. The entries originated from gamma irradiation (100–500 Gy), ethyl methanesulphonate (0.1–0.3% EMS) and selected combined treatments. They were evaluated during *rabi* 2025–26 at Parbhani, India, in a randomized block design with two replications. Analysis of variance detected genotype effects for every trait: nine traits were significant at $P < 0.01$, while days to 50% flowering and 100-seed weight were significant at $P < 0.05$. Grain yield ranged from 44.15 to 66.70 g plant⁻¹ and fodder yield from 72.85 to 139.50 g plant⁻¹. The leading mutant, 200Gy+0.2%EMS-1, yielded 66.70 g grain plant⁻¹, representing a 17.64% advantage over Udgir Piwali (56.70 g plant⁻¹) and a 0.23% numerical advantage over CSV-29R (66.55 g plant⁻¹). Phenotypic coefficients of variation exceeded genotypic coefficients for all traits. Moderate GCV occurred for panicle weight (15.67%), fodder yield (15.59%), panicle length (13.38%), plant height (12.71%) and panicle width (10.04%). High broad-sense heritability coupled with high genetic advance as a percentage of the mean was expressed by fodder yield (83.96%, 29.47%), plant height (79.76%, 23.42%), panicle weight (75.62%, 28.12%) and panicle length (70.60%, 23.19%). Grain yield showed moderate heritability (47.59%) and moderate genetic advance (11.18%). The results demonstrate useful, trait-specific induced variability in the M_s population. Direct phenotypic selection should be most effective for panicle weight, fodder yield, panicle length and plant height, whereas grain-yield gains should be confirmed across environments and supported by component-trait selection.

KEYWORDS: broad-sense heritability; EMS; gamma irradiation; genetic advance; mutation breeding; *rabi* sorghum; Sorghum bicolor

INTRODUCTION

Sorghum [*Sorghum bicolor* (L.) Moench] supports food, feed and industrial value chains in water-limited environments because of its adaptation to heat, intermittent drought and marginal soils. In India, post-rainy-season sorghum is especially important for grain quality and dry fodder. Yellow-pericarp types add specific value because their grain is generally low in condensed tannins and is suited to food, feed and starch-based uses. Nevertheless, locally adapted yellow-grained landraces often remain tall, heterogeneous and lower yielding than improved cultivars. Breeding progress therefore depends on creating and then accurately partitioning new variation for grain yield, fodder yield and the architectural traits that determine both.

Mutation breeding is useful when an adapted landrace lacks sufficient allelic diversity for a target phenotype. Gamma irradiation produces chromosomal and DNA lesions across a dose range, whereas ethyl methanesulphonate (EMS) mainly induces point mutations. Their single and combined use can broaden phenotypic variation without replacing the recurrent genetic background. In sorghum, induced-mutant populations have yielded early-flowering, high-yielding and morphologically distinct derivatives, but the magnitude of useful

variation depends on genotype, mutagen, generation and environment (Larik et al., 2009; Kalpande et al., 2022; Surashe et al., 2022).

Selection should not be based on range or mean performance alone. The genotypic coefficient of variation (GCV) estimates variability attributable to genetic differences relative to the trait mean, whereas the phenotypic coefficient of variation (PCV) includes both genetic and environmental components. Broad-sense heritability (H^2) quantifies the proportion of observed variance attributable to genotypic variance in the tested environment. Genetic advance as a percentage of the mean (GAM) adds an expected-response dimension. High H^2 coupled with high GAM generally supports efficient phenotypic selection, while high H^2 with low or moderate GAM may reflect restricted dispersion or non-additive contributions (Burton & DeVane, 1953; Johnson et al., 1955; Hanson et al., 1956).

Recent work confirms that sorghum populations differ markedly in these parameters. Broad germplasm panels can show high heritability for yield and biomass traits (Gebregergs & Mekbib, 2020; Ngidi et al., 2024; Somu et al., 2025), while mutant populations provide a more focused route to variation within elite or locally adapted backgrounds (Mirgude et al., 2024; Bhadange et al., 2025; Shinde et al., 2026). The M_5 stage is especially relevant because selected derivatives have undergone several generations of selfing and phenotypic screening; useful changes should be more stable, but prior selection may narrow the range relative to earlier generations.

Table 1. Positioning of the present M_5 evaluation within recent sorghum variability studies.

Study	Population	Mutation basis	Relevance to the present objective
Kalpande et al. (2022)	M_2 – M_3 ; two sorghum cultivars	Gamma rays, EMS and combinations	Early and 24–49% higher-yielding mutants; 100 Gy + 0.1% EMS showed high effectiveness and efficiency
Mirgude et al. (2024)	M_3 ; 60 TSV-32 mutants plus comparators	Gamma irradiation	Wide variability; high heritability with medium GCV, PCV and GAM for grain yield
Bhadange et al. (2025)	M_4 ; 30 Udgir Piwali mutants plus four comparators	Gamma irradiation	Significant variation across 14 traits and several multi-trait mutant candidates
Shinde et al. (2026)	M_4 ; 60 Udgir Piwali mutants plus four comparators	Gamma rays, EMS and combinations	High H^2 –GAM for panicle weight and fodder yield; moderate response parameters for grain yield
Present study	M_5 ; 39 selected mutants plus five comparators	Gamma rays, EMS and combinations	Stage-advanced quantification of mean performance, GCV, PCV, H^2 and GAM for 11 yield-related traits

EMS, ethyl methanesulphonate; GCV, genotypic coefficient of variation; PCV, phenotypic coefficient of variation; H^2 , broad-sense heritability; GAM, genetic advance as a percentage of the mean.

Accordingly, the present study addressed one objective: to assess variability for yield and yield-contributing traits in M_5 yellow-pericarp sorghum mutants. The analysis tested whether the population retained significant genotype-level variation, identified trait-specific extremes and superior derivatives, and determined which traits combined useful genetic dispersion with high expected response to selection.

2. MATERIALS AND METHODS

2.1 Plant material and mutagenic origin

The base genotype was Udgir Piwali, a yellow-pericarp *rabi* sorghum landrace collected from Udgir in Latur District, Maharashtra, India. The parent is described as a tall, approximately 118-day landrace with a 100-seed weight of 2.62 g, grain productivity of 20–22 q ha⁻¹ and fodder productivity of 96–98 q ha⁻¹. Seed irradiation was undertaken at the Bhabha Atomic Research Centre, Trombay, Mumbai. The M_5 test panel comprised 39 mutant lines selected from selfed M_4 panicles. Their treatment histories represented gamma irradiation at 100, 200, 300, 400 and 500 Gy; EMS at 0.1, 0.2 and 0.3%; and the combined treatments 100 Gy + 0.1% EMS, 100 Gy + 0.2% EMS, 200 Gy + 0.1% EMS and 200 Gy + 0.2% EMS. The test also included Udgir Piwali as the parental control and four commercial checks: CSV-29R, CSV-60, Parbhani Moti and Parbhani Super Moti.

2.2 Experimental site, design and crop management

The field experiment was conducted during *rabi* 2025–26 at the Department of Genetics and Plant Breeding, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani, Maharashtra, India. The site lies in an assured-rainfall zone with a reported long-term annual rainfall of approximately 865.3 mm. Forty-four entries were evaluated in a randomized block design with two replications. Entries were hand-dibbled in 4-m rows at 45 cm × 15 cm spacing. Fertilizer was applied at 80:40:40 kg N:P:K ha⁻¹, and standard crop-management practices were followed uniformly.

Table 2. Experimental structure and measurement framework.

Item	Description
Genetic material	39 Ms mutants + 4 checks + Udgir Piwali parent = 44 entries
Experimental design	Randomized block design with two replications
Season and location	Rabi 2025–26; VNMKV, Parbhani, Maharashtra, India
Planting geometry	4-m entry rows; 45 cm between rows and 15 cm between plants
Plant sampling	Five competitive plants per entry for plant-based observations
Phenology	Days to 50% flowering; days to maturity
Plant and panicle architecture	Plant height; primaries panicle ⁻¹ ; grains primary ⁻¹ ; panicle length; panicle width
Productivity	Panicle weight; 100-seed weight; fodder yield plant ⁻¹ ; grain yield plant ⁻¹
Statistical parameters	RBD ANOVA; σ^2g , σ^2e and σ^2p ; GCV, PCV and ECV; broad-sense H ² ; GA and GAM

2.3 Trait measurement

Days to 50% flowering was the interval from sowing until half of the plants in an entry flowered. Plant height was measured at maturity from the plant base to the point of terminal-inflorescence initiation. Days to maturity was recorded from sowing to grain maturity. Primary branches on the panicle rachis and grains per primary branch were counted. Panicle length was measured from the lowest rachis node to the panicle tip, and panicle width was measured at the middle of the head. Dry panicle weight, 100-seed weight, threshed grain yield per plant and dry fodder yield per plant were expressed in grams. Five randomly selected competitive plants represented each entry for plant-based measurements.

2.4 Statistical analysis

Replication-wise means were analysed according to the randomized block model $Y_{ij} = \mu + g_i + r_j + e_{ij}$, where μ is the grand mean, g_i is the effect of the i th genotype, r_j is the effect of the j th replication and e_{ij} is random error. Analysis of variance followed Panse and Sukhatme (1985). Genotypic variance was estimated as $\sigma^2g = (MSg - MSe)/r$, environmental variance as $\sigma^2e = MSe$, and phenotypic variance as $\sigma^2p = \sigma^2g + \sigma^2e$ (Burton & DeVane, 1953).

Relative coefficients were calculated as $GCV = 100(\sqrt{\sigma^2g}/\bar{x})$, $PCV = 100(\sqrt{\sigma^2p}/\bar{x})$ and $ECV = 100(\sqrt{\sigma^2e}/\bar{x})$. GCV and PCV were classified as low (<10%), moderate (10–20%) or high (>20%) following Sivasubramaniam and Madhava Menon (1973). Broad-sense heritability was $H^2 = 100(\sigma^2g/\sigma^2p)$ and was classified as low (<30%), moderate (30–60%) or high (>60%) (Hanson et al., 1956; Johnson et al., 1955). Expected genetic advance at 5% selection intensity was $GA = 2.06 \times \sqrt{\sigma^2p} \times H^2$, with heritability used as a proportion. GAM was calculated as $100(GA/\bar{x})$ and classified as low (<10%), moderate (10–20%) or high (>20%). Descriptive ranking and visualizations were generated directly from the genotype means reported in the thesis tables. No correlation, path-coefficient or nutritional-quality result was included.

3. RESULTS

3.1 Genotype effects were detected for all 11 traits

Genotypes differed for every recorded trait (Table 3; Figure 1). Nine traits showed highly significant genotype effects ($P < 0.01$): plant height, days to maturity, primaries panicle⁻¹, grains primary⁻¹, panicle length, panicle width, panicle weight, fodder yield plant⁻¹ and grain yield plant⁻¹. Days to 50% flowering and 100-seed weight were significant at $P < 0.05$. The largest F ratio occurred for days to maturity (23.22), followed by fodder yield (11.47), plant height (8.88) and panicle weight (7.20). These results establish a selectable genotype component for phenology, architecture and productivity in the stage-advanced mutant panel.

Table 3. Analysis of variance for 11 quantitative traits in the Ms yellow-pericarp sorghum panel.

Trait	MS replication	MS genotype	MS error	F genotype	Sig.	df genotype, error
Days to 50% Flowering	7.68	21.57	11.75	1.84	*	43, 43
Plant height	337.36	2161.11	243.35	8.88	**	43, 43
Days to Maturity	5.50	92.60	3.99	23.22	**	43, 43
Number of Primaries per Panicle	10.64	63.29	11.74	5.39	**	43, 43

Trait	MS replication	MS genotype	MS error	F genotype	Sig.	df genotype, error
Number of Grains per Primary	0.07	12.00	3.78	3.17	**	43, 43
Panicle length	0.01	11.51	1.98	5.80	**	43, 43
Panicle width	0.11	1.46	0.55	2.64	**	43, 43
Panicle weight	73.60	303.60	42.15	7.20	**	43, 43
100-seed weight	0.26	0.13	0.07	1.69	*	43, 43
Fodder Yield per Plant	26.18	576.79	50.28	11.47	**	43, 43
Grain Yield per Plant	9.36	66.10	23.47	2.82	**	43, 43

Replication $df = 1$. * $P < 0.05$; ** $P < 0.01$, as reported in the source ANOVA. MS, mean square.

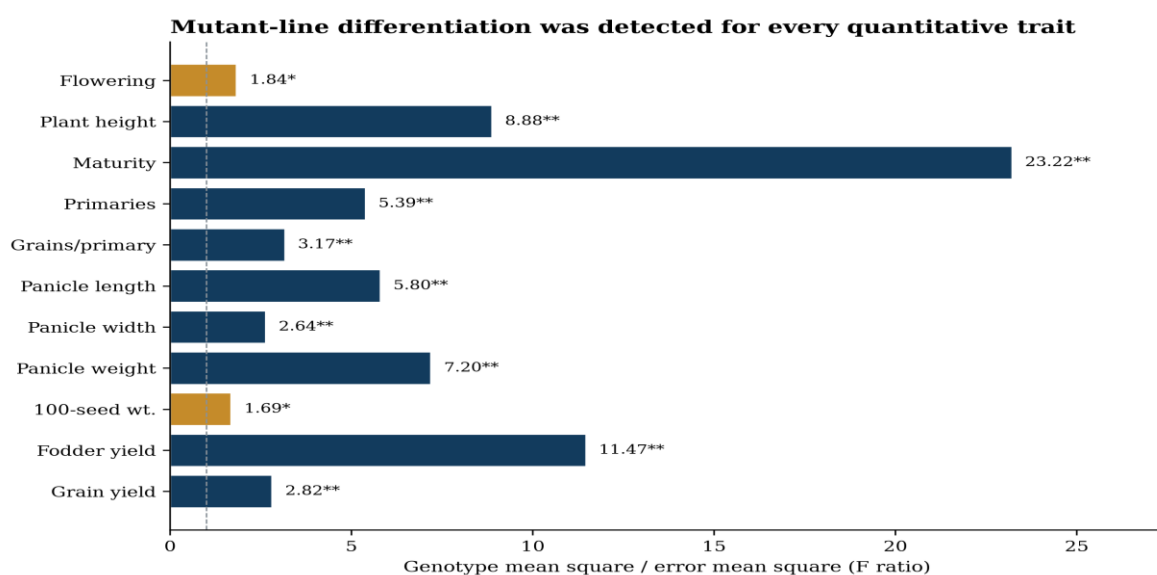


Figure 1. Trait-specific genotype F ratios. Bar colour distinguishes $P < 0.01$ (navy) from $P < 0.05$ (ochre); significance levels reproduce the source ANOVA.

3.2 Mutagenesis generated wide phenotypic ranges and distinct trait leaders

The population displayed broad, biologically meaningful ranges (Table 4; Figure 2). Flowering occurred between 68.0 and 86.0 days, maturity between 102.5 and 134.5 days, and plant height between 162.35 and 289.55 cm. Panicle weight spanned 41.87–103.77 g, fodder yield 72.85–139.50 g plant⁻¹ and grain yield 44.15–66.70 g plant⁻¹. Relative to Udgir Piwali, the population extremes extended in both directions for every trait. The dispersion was especially large for panicle weight, panicle width, panicle length, fodder yield and plant height.

Table 4. Population range and leading mutant for each trait.

Trait	Mean	Range	Minimum genotype	Maximum genotype	Leading mutant	Value	Selection meaning
Days to 50% flowering	78.20	68.00–86.00	100Gy+0.2%EMS-4	100Gy-1	100Gy+0.2%EMS-4	68.00	Earliness
Plant height	243.65	162.35–289.55	400Gy-3	100Gy+0.1%EMS-3	100Gy+0.1%EMS-3	289.55	Reduced or increased stature
Days to maturity	119.75	102.50–134.50	0.3%EMS-2	100Gy+0.1%EMS-2	0.3%EMS-2	102.50	Earliness

Trait	Mean	Range	Minimum genotype	Maximum genotype	Leading mutant	Value	Selection meaning
Primaries panicle ⁻¹	54.18	36.35–67.70	200Gy-3	0.2%EMS-4	0.2%EMS-4	67.70	Higher value
Grains primary ⁻¹	26.15	20.20–30.65	300Gy-5	200Gy+0.2%EMS-4	200Gy+0.2%EMS-4	30.65	Higher value
Panicle length	16.32	10.14–23.30	0.3%EMS-5	CSV-60(Ch)	400Gy-4	19.40	Higher value
Panicle width	6.69	5.02–8.51	0.1%EMS-2	CSV-60(Ch)	0.1%EMS-5	8.34	Higher value
Panicle weight	72.95	41.87–103.77	0.1%EMS-2	500Gy-5	500Gy-5	103.77	Higher value
100-seed weight	3.096	2.380–3.560	CSV-29R(Ch)	100Gy+0.2%EMS-5	100Gy+0.2%EMS-5	3.560	Higher value
Fodder yield plant ⁻¹	104.09	72.85–139.50	100Gy+0.1%EMS-2	Parbhani Super-moti(Ch)	400Gy-2	139.15	Higher value
Grain yield plant ⁻¹	58.79	44.15–66.70	0.3%EMS-5	200Gy+0.2%EMS-1	200Gy+0.2%EMS-1	66.70	Higher value

For flowering and maturity, the leading value is the minimum. Plant height is direction-dependent: shorter plants may reduce lodging, while taller plants may increase fodder. For all other traits the leading value is the maximum.

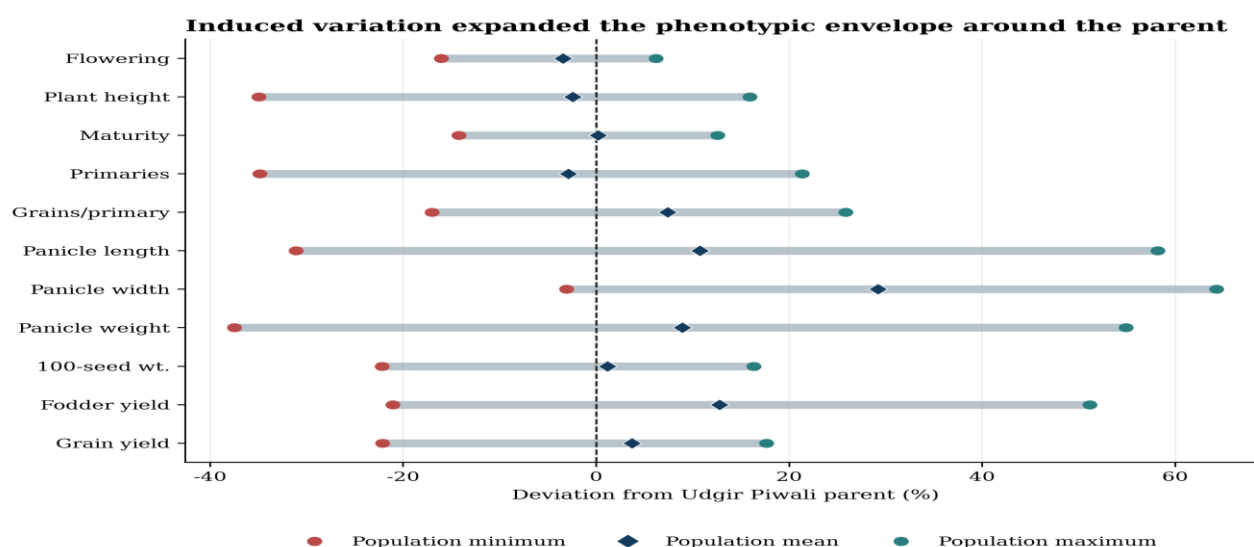


Figure 2. Phenotypic variability envelope expressed as deviation from the Udgir Piwali parent. The figure displays dispersion, not a universal superiority direction: lower values are desirable for earliness, while height depends on breeding purpose.

3.3 Grain-yield superiority was concentrated in a small group of multi-trait mutants

The mean grain yield was 58.79 g plant⁻¹. Twenty-three entries exceeded this mean. The highest-yielding mutant, 200Gy+0.2%EMS-1, produced 66.70 g plant⁻¹, 17.64% more than the parent and 0.23% more than the best check, CSV-29R. The 10.00-g advantage over the parent slightly exceeded the reported 5% critical difference of 9.77 g; its 0.15-g numerical advantage over CSV-29R did not. The line 100Gy+0.2%EMS-1 yielded 66.50 g plant⁻¹ and also exceeded the parent by more than the 5% critical difference. Several other mutants approached the best check while offering contrasting architectures.

The most balanced early, high-yielding phenotype was 0.3%EMS-2. It flowered in 73.0 days, matured in 102.5 days, carried 101.87-g panicles and yielded 66.10 g grain plant⁻¹. The semi-dwarf line 300Gy-2 combined a height of 190.50 cm, maturity at 113.0 days and 65.70 g grain plant⁻¹. Conversely, 400Gy-2 expressed dual-purpose potential through 139.15 g fodder and 62.80 g grain plant⁻¹. The heaviest panicles occurred in 500Gy-5 (103.77 g), whereas 100Gy+0.2%EMS-5 had the highest 100-seed weight (3.560 g).

Table 5. Ten highest-yielding M_s mutants and selected component traits.

Mutant	Grain yield (g plant ⁻¹)	Advantage over parent (%)	Flowering (d)	Maturity (d)	Panicle wt. (g)	100-seed wt. (g)	Fodder (g plant ⁻¹)
200Gy+0.2%EMS-1	66.70	17.6	76.5	122.5	68.45	3.070	94.30
100Gy+0.2%EMS-1	66.50	17.3	76.0	118.5	93.93	3.050	86.95
0.3%EMS-2	66.10	16.6	73.0	102.5	101.87	3.060	121.45
100Gy+0.1%EMS-5	66.00	16.4	79.5	123.5	80.27	3.200	104.90
300Gy-2	65.70	15.9	78.0	113.0	81.93	3.220	93.90
100Gy+0.1%EMS-2	65.65	15.8	79.5	134.5	74.50	2.900	72.85
400Gy-4	64.70	14.1	82.0	131.5	86.43	3.545	115.95
300Gy-5	64.45	13.7	81.0	119.5	84.59	3.335	121.65
100Gy-1	63.05	11.2	86.0	121.0	67.43	2.665	120.95
400Gy-2	62.80	10.8	82.0	129.0	77.75	3.215	139.15

Parent grain yield = 56.70 g plant⁻¹; best-check grain yield (CSV-29R) = 66.55 g plant⁻¹; 5% critical difference for grain yield = 9.77 g.

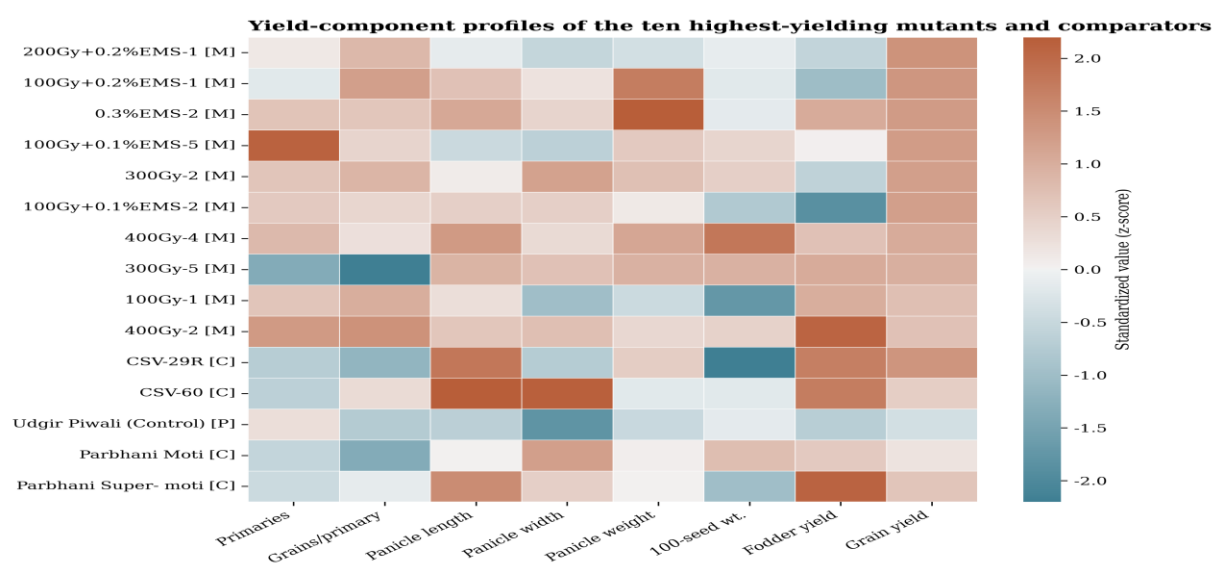


Figure 3. Standardized yield-component profiles of the ten highest-yielding mutants and five comparators. Values are z-scores calculated across all 44 entries. [M], mutant; [C], commercial check; [P], parental control.

3.4 Genetic parameters identified four high-response selection targets

PCV exceeded GCV for all traits, as expected when environmental variance contributes to phenotype (Table 6). The difference was narrowest for days to maturity (0.28 percentage points), fodder yield (1.42), plant height (1.52), primaries panicle⁻¹ (1.94) and panicle weight (2.35). Moderate GCV was recorded for panicle weight (15.67%), fodder yield (15.59%), panicle length (13.38%), plant height (12.71%) and panicle width (10.04%). No trait reached the high-GCV category. Grain yield had low GCV (7.85%) but moderate PCV (11.38%), indicating that the observed yield range contained a meaningful environmental component.

Heritability ranged from 25.68% for 100-seed weight to 90.93% for days to maturity. Fodder yield, plant height, panicle weight and panicle length combined high H² with high GAM and therefore offered the strongest expected response to phenotypic selection. Days to maturity had the highest H² but only moderate GAM, indicating reliable ranking but a smaller proportional gain under the specified selection intensity. Grain yield exhibited moderate H² (47.59%) and GAM (11.18%). Days to 50% flowering and 100-seed weight had low H² and low GAM, suggesting that single-environment phenotypic ranking for these traits should be interpreted cautiously.

Table 6. Variance components, coefficients of variation, broad-sense heritability and expected genetic advance.

Trait	$\sigma^2_g / \sigma^2_e / \sigma^2_p$	GCV (%)	PCV (%)	PCV-GCV	H ² (%)	GA	GAM (%)
Days to 50% flowering	4.91 / 11.75 / 16.66	2.83	5.22	2.39	29.46 (Low)	2.48	3.17 (Low)
Plant height	958.88 / 243.35 / 1202.23	12.71	14.23	1.52	79.76 (High)	57.05	23.42 (High)
Days to maturity	45.17 / 4.51 / 49.68	5.61	5.89	0.28	90.93 (High)	13.22	11.04 (Moderate)

Trait	$\sigma^2_g / \sigma^2_e / \sigma^2_p$	GCV (%)	PCV (%)	PCV–GCV	H ² (%)	GA	GAM (%)
Primaries panicle ⁻¹	25.77 / 11.74 / 37.52	9.37	11.31	1.94	68.70 (High)	8.68	16.02 (Moderate)
Grains primary ⁻¹	4.11 / 3.78 / 7.89	7.75	10.74	2.99	52.07 (Moderate)	3.02	11.54 (Moderate)
Panicle length	4.76 / 1.98 / 6.75	13.38	15.92	2.54	70.60 (High)	3.78	23.19 (High)
Panicle width	0.45 / 0.55 / 1.00	10.04	14.97	4.93	45.00 (Moderate)	0.93	13.90 (Moderate)
Panicle weight	130.73 / 42.15 / 172.87	15.67	18.02	2.35	75.62 (High)	20.51	28.12 (High)
100-seed weight	0.026 / 0.075 / 0.101	5.19	10.25	5.06	25.68 (Low)	0.17	5.43 (Low)
Fodder yield plant ⁻¹	263.26 / 50.28 / 313.54	15.59	17.01	1.42	83.96 (High)	30.67	29.47 (High)
Grain yield plant ⁻¹	21.31 / 23.47 / 44.79	7.85	11.38	3.53	47.59 (Moderate)	6.57	11.18 (Moderate)

H², broad-sense heritability. Classification: GCV/PCV and GAM—low <10%, moderate 10–20%, high >20%; H²—low <30%, moderate 30–60%, high >60%. Seed-weight variance components are shown to three decimals because rounding to two decimals obscures the reported H² estimate.

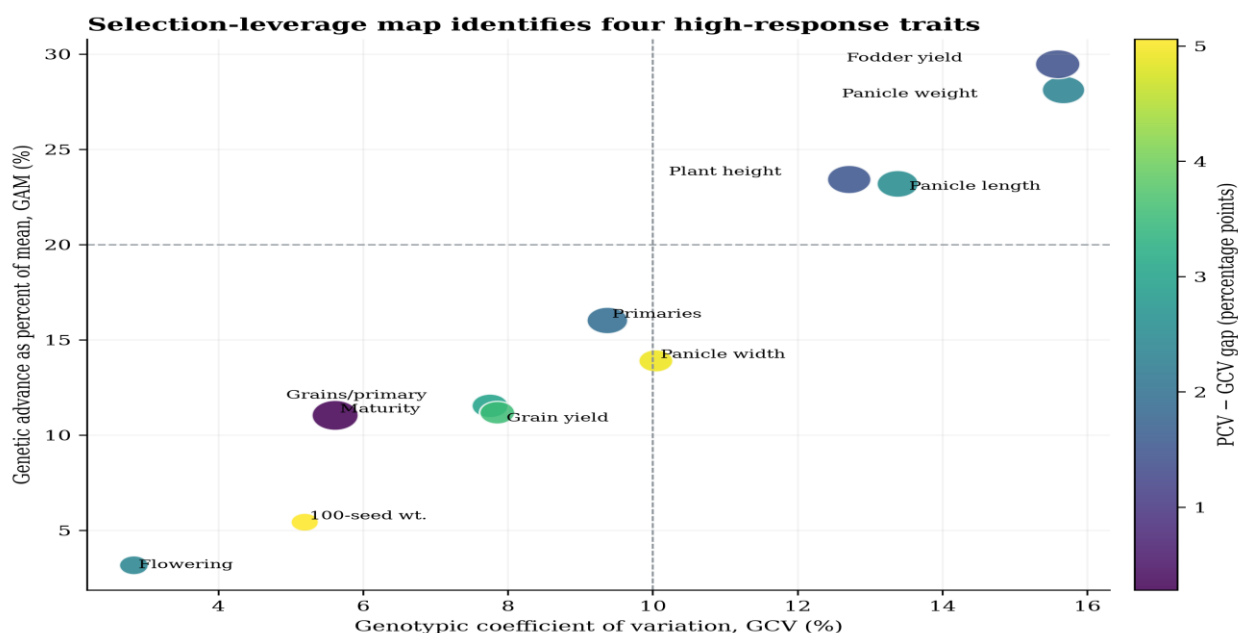


Figure 4. Selection-leverage map based on GCV, GAM and broad-sense heritability. Bubble area is proportional to H², and colour indicates the PCV–GCV gap. The upper-right quadrant (GCV ≥10%, GAM ≥20%) identifies the four strongest direct-selection targets: plant height, panicle length, panicle weight and fodder yield.

4. DISCUSSION

4.1 The M_s panel retained useful variation after generation advancement

Significant genotype effects for all 11 traits demonstrate that advancing selected Udgir Piwali derivatives to M_s did not eliminate useful diversity. The range was not restricted to one trait class: phenology, stature, panicle architecture, seed mass, grain yield and fodder yield all responded. This broad response is consistent with the capacity of gamma rays and EMS to perturb different genetic targets and with earlier sorghum studies that recovered induced polygenic variation (Larik et al., 2009; Kalpande et al., 2022; Surashe et al., 2022). It also supports the practical value of maintaining multiple treatment histories during mutant-line advancement rather than relying on a single mutagen dose.

The strongest F ratio occurred for maturity, while the largest economically relevant GCV values occurred for panicle weight and fodder yield. These statistics answer different questions. A large F ratio indicates precise discrimination among genotype means relative to experimental error. GCV describes the proportional breadth of genetic variation. Thus, maturity was highly repeatable but proportionally less dispersed, whereas panicle weight and fodder yield combined appreciable dispersion with reliable genetic control.

4.2 Selection response should be trait-specific

The joint interpretation of GCV, H² and GAM places panicle weight, fodder yield, panicle length and plant height in the highest-priority class. Their moderate GCV indicates usable dispersion; high H² indicates that much of the

observed variation was genotypic; and high GAM predicts a substantial response at 5% selection intensity. Similar combinations have been reported in sorghum mutant and germplasm populations, although the absolute magnitudes vary with population breadth and environment (Gebregergs & Mekbib, 2020; Mirgude et al., 2024; Somu et al., 2025).

Days to maturity illustrates why heritability should not be interpreted alone. Its H^2 of 90.93% was the highest in the experiment, but GCV was only 5.61% and GAM 11.04%. Selection can therefore rank maturity reliably, but the expected proportional shift is moderate. Grain yield presented the opposite challenge: a useful phenotypic range and several superior means, but only moderate H^2 and GAM. Direct yield selection is still possible, yet confirmation across environments and simultaneous attention to panicle weight, panicle length and grain number should improve stability.

The low H^2 and GAM for days to flowering and 100-seed weight imply a larger role for experimental error and micro-environmental heterogeneity in this single trial. Their genotype effects were significant only at the 5% level. Consequently, extreme values such as 68-day flowering in 100Gy+0.2%EMS-4 and 3.560-g 100-seed weight in 100Gy+0.2%EMS-5 are valuable leads, but should not be treated as fixed breeding values until repeated.

4.3 Stage-advanced comparison suggests selective retention rather than uniform variability

A closely related M₄ Udgir Piwali panel reported by Shinde et al. (2026) provides a useful, though not experimentally paired, generational benchmark. Panicle weight and fodder yield remained the strongest selection targets in both generations. Their M₅ estimates were somewhat lower than the M₄ values, as were the grain-yield estimates (Table 7). This pattern is compatible with prior selection and line loss narrowing the distribution during advancement, although differences in the entries and season prevent a causal generational inference. The important result is that the trait hierarchy persisted: panicle and biomass traits retained greater selection leverage than grain yield itself.

Table 7. Descriptive comparison with a closely related M₄ Udgir Piwali mutant panel.

Trait or feature	M ₄ : H ² (%) / GAM (%)	Present M ₅ : H ² (%) / GAM (%)	Interpretation
Panicle weight	80.0 / 37.72	75.62 / 28.12	High-response target persisted; proportional variation was lower in M ₅
Fodder yield plant ⁻¹	88.0 / 37.27	83.96 / 29.47	Highest M ₅ GAM and strong direct-selection opportunity
Grain yield plant ⁻¹	55.0 / 15.59	47.59 / 11.18	Moderate response in both stages; multi-environment confirmation is important
Population context	60 M ₄ mutants + 4 comparators	39 M ₅ mutants + 5 comparators	Panels are related in origin but not identical, so comparisons are descriptive

M₄ values are from Shinde et al. (2026). The populations and seasons are not identical; the comparison indicates continuity of trait ranking, not a formal generation effect.

4.4 The best mutants represent contrasting breeding ideotypes

No single line maximized every trait, which is expected because grain and fodder productivity arise from different resource-allocation patterns. The top-yielding line 200Gy+0.2%EMS-1 provides a direct grain-yield candidate. The line 0.3%EMS-2 offers a stronger drought-escape ideotype because it combines very early maturity with heavy panicles and near-maximum grain yield. The line 300Gy-2 combines semi-dwarf stature, early maturity and high grain yield, which may improve lodging resistance without severe yield penalty. The line 400Gy-2 is a dual-purpose biomass candidate. The line 400Gy-4 combines high grain yield, long panicles and the second-highest seed weight. These contrasting profiles are more useful for parent selection than a single rank based only on grain yield.

The 200Gy+0.2%EMS treatment contributed the highest-yielding line and the line with the highest grains per primary. Combined treatments have previously produced high mutagenic effectiveness in sorghum (Kalpande et al., 2022). However, the current panel was selected rather than a balanced dose-response population. Treatment-level means, effectiveness and efficiency cannot therefore be inferred from the frequency of leading entries. The unit of inference is the individual mutant line.

4.5 Limitations and validation needs

The experiment was conducted in one season and location with two replications. Broad-sense heritability is therefore specific to this testing environment and includes all genetic variance components; it does not estimate additive heritability directly. Genotype-by-environment interaction could not be separated. Multi-location, multi-season trials are required before varietal nomination or stable donor designation. Replication-level observations were not included in the supplied chapters, so the article reproduces the reported ANOVA and variance estimates rather than independently refitting the trial.

One source-table inconsistency requires author verification before journal submission: for days to maturity, the ANOVA table reports genotype and error mean squares of 92.60 and 3.99 ($F = 23.22$), whereas the variability narrative/table reports $\sigma^2_g = 45.17$ and $\sigma^2_e = 4.51$. These two sets do not derive from the same rounded ANOVA

components. The manuscript retains each value in its original analytical context rather than silently altering either. Raw-data reanalysis should resolve the discrepancy and provide residual diagnostics.

5. CONCLUSIONS

The Ms Udgir Piwali mutant panel contained statistically detectable and practically useful variability for all 11 yield-related traits. The strongest direct-selection opportunities were panicle weight, fodder yield, panicle length and plant height because each combined moderate GCV with high broad-sense heritability and high GAM. Days to maturity was highly heritable but less variable, making it suitable for reliable phenological classification rather than large proportional gains. Grain yield showed moderate heritability and GAM; therefore, promising means should be advanced with component-trait information and verified across environments.

Among the entries, 200Gy+0.2%EMS-1 was the highest-yielding mutant, while 0.3%EMS-2 offered the most compelling early, heavy-panicle, high-yield ideotype. The semi-dwarf 300Gy-2, the dual-purpose 400Gy-2 and the long-panicle, bold-seeded 400Gy-4 represent complementary breeding resources. These lines warrant replicated multi-environment testing, within-line purification and stability analysis before release or use as donors.

Table 8. Evidence-to-action summary for breeding use of the Ms panel.

Decision tier	Trait or genotype focus	Evidence	Recommended next step
Immediate phenotypic selection	Panicle weight, fodder yield, panicle length, plant height	Moderate GCV + high H^2 + high GAM	Advance top families and confirm within-line uniformity
Phenology-based selection	Days to maturity	Low GCV + very high H^2 + moderate GAM	Use for reliable early/late classification; verify drought escape
Yield confirmation	Grain yield plant ⁻¹	Low GCV + moderate H^2 + moderate GAM	Test top lines across locations and seasons with component traits
Cautious single-trial selection	Days to flowering; 100-seed weight	Low H^2 + low GAM	Repeat measurements before fixation or donor designation
Priority mutant set	200Gy+0.2%EMS-1; 0.3%EMS-2; 300Gy-2; 400Gy-2; 400Gy-4	Complementary grain, earliness, stature, fodder and seed profiles	Enter multi-environment preliminary yield trials

Acknowledgements

The experimental material was irradiated at the Bhabha Atomic Research Centre, Trombay, Mumbai, and evaluated at Vasant Rao Naik Marathwada Krishi Vidyapeeth, Parbhani, India. Author-approved acknowledgements should be inserted before submission.

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Supplementary material

Table S1. Mean performance of 44 genotypes for 11 quantitative traits.

F50, days to 50% flowering; PH, plant height (cm); DM, days to maturity; NPPP, primaries panicle⁻¹; NGPP, grains primary⁻¹; PL, panicle length (cm); PWi, panicle width (cm); PWg, panicle weight (g); SW100, 100-seed weight (g); FYPP, fodder yield plant⁻¹ (g); GYPP, grain yield plant⁻¹ (g).

Genotype	F50	PH	DM	NPP P	NGP P	PL	PW i	PWg	SW10 0	FYP P	GYP P
0.1%EMS-1	81.0	178.25	124.0	58.2 5	25.50	16.70 0	5.4 6	67.30	3.035	120.0 5	58.55
0.1%EMS-2	76.0	240.45	115.0	57.3 5	25.20	11.47 0	5.0 2	41.87	3.050	88.20	44.95
0.1%EMS-5	78.5	209.80	117.0	63.1 0	29.05	17.97 0	8.3 4	57.40	3.205	95.30	60.25
0.2%EMS-3	80.0	232.15	119.5	57.8 0	30.00	17.10 0	8.1 7	69.36	2.955	86.25	60.65
0.2%EMS-4	78.0	281.40	124.0	67.7 0	30.15	18.20 0	8.3 2	77.41	2.820	100.5 5	57.60
0.2%EMS-5	78.0	269.05	122.0	52.7 5	27.55	14.66 0	7.9 1	65.89	2.930	115.7 0	59.30
0.3%EMS-1	77.0	240.15	108.5	53.8 5	25.90	16.55 0	6.2 6	67.35	2.515	105.6 5	58.25
0.3%EMS-2	73.0	282.60	102.5	58.0 0	27.70	18.90 0	7.0 7	101.8 7	3.060	121.4 5	66.10
0.3%EMS-4	78.0	260.65	115.0	53.1 0	25.45	13.90 0	6.3 2	64.48	2.650	111.6 0	53.40
0.3%EMS-5	77.0	197.50	116.5	52.1 5	25.10	10.14 5	5.9 7	64.79	3.185	87.00	44.15
100Gy-1	86.0	253.15	121.0	57.9 0	28.60	17.00 0	5.8 6	67.43	2.665	120.9 5	63.05
100Gy-4	79.0	243.50	115.0	51.3 0	27.80	15.20 5	6.2 0	76.73	3.285	107.0 0	55.40

Genotype	F50	PH	DM	NPP P	NGP P	PL	PW i	PWg	SW10 0	FYP P	GYP P
100Gy+0.1 %EMS-2	79.5	278.25	134.5	57.5 0	27.15	17.50 0	7.1 2	74.50	2.900	72.85	65.65
100Gy+0.1 %EMS-3	76.0	289.55	122.0	56.8 0	24.95	15.60 0	7.0 3	69.89	2.935	126.4 5	58.15
100Gy+0.1 %EMS-4	79.0	248.80	132.5	50.9 0	24.75	15.60 0	6.5 5	64.33	3.190	94.75	61.45
100Gy+0.1 %EMS-5	79.5	277.35	123.5	65.9 5	27.20	15.20 0	6.1 5	80.27	3.200	104.9 0	66.00
100Gy+0.2 %EMS-1	76.0	263.25	118.5	53.2 0	29.10	18.00 0	6.8 9	93.93	3.050	86.95	66.50
100Gy+0.2 %EMS-3	74.5	275.85	124.5	54.7 5	27.00	17.49 0	5.8 9	80.69	3.065	105.9 5	58.00
100Gy+0.2 %EMS-4	68.0	268.15	113.5	48.3 5	23.55	12.74 0	6.2 4	57.97	3.050	86.60	48.80
100Gy+0.2 %EMS-5	78.5	274.45	118.5	55.3 0	23.90	13.38 0	6.2 4	57.61	3.560	77.15	49.95
200Gy-1	80.0	248.70	119.0	50.3 0	25.05	16.15 5	6.4 5	75.94	3.230	86.45	62.15
200Gy-3	79.0	193.85	128.0	36.3 5	24.15	17.13 0	7.0 3	82.60	3.485	102.9 0	61.55
200Gy-4	73.5	190.50	109.0	43.5 0	20.90	14.28 5	6.5 0	61.96	3.395	120.9 0	48.75
200Gy-5	77.0	236.25	113.5	49.5 5	20.55	17.53 0	6.9 2	80.48	3.210	90.80	57.05
200Gy+0.1 %EMS-1	73.5	269.10	112.5	49.6 5	25.80	16.04 0	6.8 1	65.52	2.990	85.00	57.15
200Gy+0.1 %EMS-2	76.0	261.30	115.5	46.7 5	25.50	13.15 0	6.1 3	51.45	3.050	78.55	50.70
200Gy+0.1 %EMS-3	75.5	210.45	117.5	48.4 5	27.15	14.24 0	6.2 7	67.58	3.020	113.8 0	51.20
200Gy+0.2 %EMS-1	76.5	264.40	122.5	54.9 5	28.20	16.00 0	6.2 4	68.45	3.070	94.30	66.70
200Gy+0.2 %EMS-2	74.0	238.65	124.0	56.3 0	24.20	14.72 0	6.2 7	81.76	3.070	109.2 0	57.50
200Gy+0.2 %EMS-4	76.5	195.25	116.5	58.0 5	30.65	15.20 0	6.1 6	68.69	3.005	89.10	59.70
300Gy-2	78.0	190.50	113.0	57.8 5	28.35	16.55 5	7.6 8	81.93	3.220	93.90	65.70
300Gy-3	85.0	201.25	123.5	55.4 0	27.20	15.73 0	8.0 0	71.00	3.205	93.65	58.40
300Gy-5	81.0	263.80	119.5	46.7 0	20.20	18.48 0	7.3 0	84.59	3.335	121.6 5	64.45
400Gy-2	82.0	277.75	129.0	61.3 5	29.60	17.86 0	7.3 2	77.75	3.215	139.1 5	62.80
400Gy-3	80.0	162.35	120.0	57.5 5	26.75	16.77 0	6.5 9	74.23	3.255	98.80	61.35
400Gy-4	82.0	259.10	131.5	58.8 0	26.80	19.40 0	6.9 9	86.43	3.545	115.9 5	64.70
500Gy-2	80.0	281.55	120.5	54.1 0	28.50	15.00 0	5.4 5	63.52	3.425	116.4 0	55.65
500Gy-3	80.0	233.10	124.5	57.0 0	25.95	16.60 0	5.9 5	96.65	3.075	95.85	59.50
500Gy-5	84.0	272.45	127.5	56.0 0	26.25	18.87 0	6.8 3	103.7 7	3.495	106.8 5	57.85
CSV- 29R(Ch)	77.0	242.35	120.5	50.2 0	23.35	20.60 0	6.0 7	79.63	2.380	132.6 0	66.55
CSV-60(Ch)	78.0	222.05	112.5	50.6 0	26.95	23.30 0	8.5 1	70.66	3.050	132.9 5	61.75
Udgir Piwali (Control)	81.0	249.75	119.5	55.8 0	24.35	14.73 0	5.1 8	66.98	3.060	92.30	56.70
Parbhani	79.0	221.65	109.5	51.1	22.90	16.37	7.7	73.67	3.285	114.0	60.05

Genotype	F50	PH	DM	NPP P	NGP P	PL	PW i	PWg	SW10 0	FYP P	GYP P
Moti(Ch)				0		0	2			5	
Parbhani Super- moti(Ch)	80.0	270.15	132.5	51.6 0	25.85	19.90 0	7.1 2	73.31	2.850	139.5 0	62.50
Grand mean	78.20	243.65	119.7 5	54.1 8	26.15	16.32	6.6 9	72.95	3.10	104.0 9	58.79
SEm ±	2.42	11.03	1.50	2.42	1.38	1.00	0.5 3	4.59	0.19	5.01	3.43
CD (5%)	6.91	31.46	4.28	6.91	3.92	2.84	1.5 0	13.09	0.55	14.30	9.77

Values reproduce the source genotype-mean table. "Ch" denotes commercial check. The source table did not provide a 1% critical difference