

Electronic Journal of Plant Breeding



Research Article

Induced polygenic variability for identification of high yielding mutants in M_3 - M_4 generations of finger millet (*Eleusine coracana* L. Gaertn)

Prashant Vasisth^{1*}, S. Rangaiah², Mohit Sharma¹, Vidyut Balar³ and Vaibhav Chittora⁴

¹Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India, 110012

²Department of Genetics and Plant Breeding, University of Agricultural Sciences, Bangalore, (KA) India, 560065

¹Division of Genetics, ICAR-Indian Agricultural Research Institute, New Delhi, India, 110012

³Department of Genetics and Plant Breeding, Anand Agricultural University, Anand, (GJ) India, 388110

⁴Department of Basic Science, Dr. Y. S. Parmar University of Horticulture and Forestry, Nauni, Solan (H. P.) India, 17323

*E-Mail: pvasisth555777@gmail.com

Abstract

The present investigation was undertaken for identification of high yielding desirable mutants from M_3 seeds of two gamma rays irradiated genotypes; GPU 28 with 3 doses (300,400,500 Gy) and KMR 204 with 2 doses (300,400 Gy). A total of 152 mutant lines (102 of GPU 28 and 50 of KMR 204) of finger millet were evaluated in Augmented Block Design along with two check cultivars (GPU 28 and KMR 204). Data were collected for eight different quantitative traits on each mutant line. Analysis of genetic parameters, character association, genetic variability and genetic diversity was done. Selection of plants was done on the basis of seed yield and its contributing traits. These selected plants were evaluated in randomized complete block design with three replications along with two checks/parents in two experiments, one for mutants of GPU 28 and other for KMR 204. In general, all treatments showed wider range of variation compared to the parental range. Most treatment populations exhibited reduction in population mean and increase in population variance for all the traits studied. Cluster analysis based on the morphological traits grouped the mutants of GPU 28 into four and KMR 204 into three clusters. Estimates of heritability and genetic advance as per cent of mean showed that selection in M_3 population would be effective to improve the seed yield. Fifty-eight mutants were selected from M_3 generation on the basis of seed yield and its contributing traits. These selected mutants were evaluated in M_4 generation for productivity *per se* traits and compared to the previous generation. Results showed significant improvement for seed yield and its contributing traits in M_4 generation as compared to M_3 generation. Ten high yielding mutant progenies were identified in M_4 generation, were significantly superior over best check. Usefulness of induced mutagenesis for identification of high yielding mutant lines in finger millet was demonstrated through the present study. Identified high yielding mutant lines can be utilized to develop new varieties and also, selection of diverse lines from different clusters will help in exploitation of heterosis.

Keywords: Finger millet, gamma rays, genetic parameters, correlation, mutants

INTRODUCTION

Finger millet is scientifically known as *Eleusine coracana* (L.) Gaertn. sub-species *coracana*, which is a tetraploid ($2n = 36$) and belongs to the family Poaceae/ Graminae.

It is a widely grown traditional and highly nutritious grain cereal crop (Sawardekar, 2016). In India, the area under finger millet stands sixth after wheat, rice, maize, sorghum

and bajra (Chandra *et al.*, 2016). High yielding varieties need to be developed in order to increase the productivity of finger millet. Availability of vast genetic variability is the crucial step to select better performing genotypes but many cases variability does not exist in germplasm for the trait in which breeder is interested and hybridization is very difficult in finger millet due to very small size of florets. So, variability can be created by inducing mutation with mutagens by using best available varieties. The induced mutations have role in enlarging the genetic variability both quantitative as well as qualitative character, thereby creating scope for selection in many traits like seed yield, earliness, plant height, disease resistance and test weight (Muller, 1927; Ganapathy *et al.*, 2021; Vanniarajan and Chandrakala, 2022). Researchers have used physical and chemical mutagens for the creation of variability in finger millet (Wani *et al.*, 2017; Aviya and Mullainathan, 2018). Variability in earlier generation (M_2 - M_3) gives major scope for the selection of useful mutants and these useful mutants can be further evaluated for their yield performance (Muduli and Misra, 2008; Ramya *et al.*, 2013; Surashe *et al.*, 2022). Ambavane *et al.* (2015) isolated early maturing mutants with high yield and yield contributing traits in 500 Gy and 600 Gy doses of gamma irradiation in finger millet. Similarly, Waghmode *et al.* (2020) studied the M_3 generation of thirty-four mutant lines developed from genotype Girge local which was irradiated with 500 Gy dose of gamma rays and identified mutant lines for earliness, high protein content, high yield etc. Keeping above scenario in mind, present investigation has been made to assess the genetic variability for productivity *per se* traits in M_3 - M_4 generations for identification of high yielding desirable mutants for seed yield and its contributing traits.

MATERIALS AND METHODS

The present investigation on induced mutations in finger millet was carried out from summer 2018 to summer 2019 at GKVK, University of Agricultural Sciences; Bangalore. Material used for the present study comprised of M_3 seeds derived from the selfing of selected M_2 plants of two gamma rays irradiated genotypes, 102 progenies of GPU 28 with 3 doses (300, 400, 500 Gy) and 50 progenies of KMR 204 with 2 doses (300, 400 Gy). Plants obtained from un-irradiated seeds of the above varieties were used as checks in the experiments. The mutants of GPU 28 and KMR 204 along with parents (same checks) were grown in an augmented design in M_3 generation. In each progeny of segregating population, competitive plants (excluding male sterile plants) were randomly tagged for the recording of the observations on seed yield and its contributing traits at the time of harvesting along with checks. Mean and variance of the traits in each treatment population were estimated and subjected to statistical analysis using SAS version 9.3. Genetic parameters were estimated to assess the variability among mutants of GPU 28 and KMR 204 and determine genetic and environmental effects on different traits. PCV

and GCV were calculated as per the standard formula (Burton, 1952). Broad sense heritability is estimated to know the extent of variation among mutants (Allard, 1960). Genetic advance was calculated as $GA (\%) = K * \sigma_p * h_{bs} * 100$, where K (selection differential at 5%) = 2.06, σ_p – phenotypic standard deviation and h_{bs} – broad sense heritability. Genetic advance over mean (GAM %) was calculated by taking GA (%) and expressed over mean. Genetic relationship among the different variables estimated by, Pearson correlation coefficients (Snedecor and Cochran, 1994) for every pair of traits using the SPSS version 16.0. Cluster analysis (Ward, 1963) based on the morphological data was performed using Euclidean distances and dendrogram was constructed. Thirty one plants selected from the treated population of GPU 28 and 27 plants selected from the treated population of KMR 204 on the basis of productivity *per se* traits. These selected plants were evaluated in randomized completely block design (Panse and Sukhatme, 1967) with 3 replications along with 2 checks/parents. The statistical analysis in M_4 generation was done, by using WINDOSTAT software version 8.5. High yielding mutant progenies were identified in M_4 generation on the basis of seed yield plant⁻¹.

RESULTS AND DISCUSSION

Analysis of variance: Significant differences with respect to quantitative traits among the mutant families of GPU 28 and KMR 204 were observed for all the traits studied. Significant mean sum of square for all the traits among mutant families of GPU 28 and KMR 204 indicated that enough variability was present among the mutant families or they were genetically diverse.

Estimation of genetic parameters irrespective of treatments: High values of PCV than GCV for all the traits indicated the effect of the environment (**Table 1**). Moderate values of GCV (10.15%) were recorded for seed yield and moderate value of PCV recorded for productive tillers plant⁻¹ (11.24 %), ear weight plant⁻¹ (14.77 %) and seed yield plant⁻¹ (18.19 %) indicating the presence of variability among mutants of GPU 28. Similarly, moderate value of GCV and PCV recorded for productive tillers plant⁻¹, ear weight plant⁻¹ and seed yield plant⁻¹ indicating the presence of variability among mutants of KMR 204. These results are similar to the findings of John (2006) and Anuradha *et al.* (2017). Both the mutated populations showed high heritability as well as moderate genetic advance over the mean for productive tillers plant⁻¹. This indicated that trait was marginally influenced by the environment and heritability due to the additive gene effect so, effective selection would be applicable for this trait. These findings were in broad conformity with the findings of Reddy *et al.* (2013). Moderate heritability as well as moderate genetic advance over mean was reported for seed yield plant⁻¹ and ear weight plant⁻¹. This indicated that these traits were under moderate effect of environment; effective selection would be applicable for

Table 1. Estimates of descriptive statistics and genetic variability parameters for seed yield and its contributing traits among M₃ mutants of finger millet variety GPU 28 and KMR 204

| Traits* | M ₃ – GPU 28 | | | | | | M ₃ – KMR 204 | | | | | |
|---------|-------------------------|--------------|---------|---------|----------------------------------|---------------------------|--------------------------|-------------|---------|---------|----------------------------------|---------------------------|
| | Mean | Range | GCV (%) | PCV (%) | h ² _{bs} (%) | GAM (as per cent of mean) | Mean | Range | GCV (%) | PCV (%) | h ² _{bs} (%) | GAM (as per cent of mean) |
| DPM | 112.51 | 96 - 121 | 0.96 | 1.83 | 27.14 | 1.03 | 106.22 | 90 – 119 | 1.17 | 2.17 | 28.77 | 1.29 |
| PH (cm) | 80.14 | 55.07 – 102 | 2.86 | 4.07 | 49.25 | 4.13 | 80.74 | 50 – 113 | 3.56 | 4.90 | 52.82 | 5.32 |
| PT | 3.98 | 1.50 – 8 | 8.70 | 11.24 | 60.00 | 13.89 | 4.27 | 1 - 8 | 11.52 | 14.66 | 61.73 | 18.36 |
| FN | 6.97 | 4.60 – 9 | 2.93 | 5.77 | 25.77 | 3.06 | 7.21 | 4.9 – 9 | 3.19 | 6.55 | 23.77 | 3.26 |
| FL (cm) | 7.04 | 3.38 – 9.88 | 4.55 | 8.31 | 29.93 | 5.12 | 6.81 | 4.78 – 8.93 | 3.01 | 7.66 | 15.44 | 2.34 |
| TW (g) | 2.65 | 1.90 – 3.64 | 3.61 | 6.44 | 31.43 | 4.17 | 2.64 | 2.09 – 3.33 | 2.93 | 6.11 | 23.08 | 2.90 |
| EW(g) | 27.14 | 7.63 – 54.93 | 9.30 | 14.77 | 39.66 | 12.07 | 28.16 | 9.2 – 48.18 | 10.68 | 15.03 | 50.51 | 15.63 |
| SY (g) | 14.26 | 2.90 – 31.04 | 10.15 | 18.19 | 31.16 | 11.67 | 14.65 | 3.65 - 30 | 11.42 | 18.13 | 39.72 | 14.83 |

*DPM- Days to panicle maturity, PH- Plant height, PT- Productive tillers plant⁻¹, FN- Fingers ear⁻¹, FL- Finger length, TW- 1000 Seed weight,EW- Ear weight plant⁻¹, SY- Seed yield plant⁻¹

these traits. These results were similar to the findings of Reddy *et al.* (2013), Anuradha *et al.* (2017).

Estimation of genetic parameters with respect to treatments: In general, wide range was reported for all the traits, in all the treated populations compared to the parents indicating the effectiveness of gamma rays in broadening the variability for productive *per se* traits (Table 2a, 2b). Trait mean values increased for days to maturity among the mutants of GPU 28 and KMR 204. Trait mean values decreased for plant height, ear weight plant⁻¹, 1000 seed weight and seed yield plant⁻¹ among the mutants of GPU 28 and KMR 204. Similar results were obtained by Muduli and Misra (2007), Eswari *et al.* (2014) and Aviya and Mullainathan (2018). Trait mean values increased for productive tillers plant⁻¹ and fingers ear⁻¹ among mutants of KMR 204. Shift of mean in both the direction were observed for productive tillers plant⁻¹ and for fingers ear⁻¹ among mutants of GPU 28. Variance increased for all the traits for both the mutated populations of GPU 28 and KMR 204. Among the treatments of KMR 204, K1 (300 Gy) treatment showed high mean value for all the traits as compared to other treatment. Most of the traits showed high mean value from parent mean value in K1 (300 Gy) treatment. This is possibly due to the less drastic effect of K1 (300 Gy) treatment as compared to K2 (400 Gy). In case of treatments of GPU 28, G3 (500 Gy) showed high mean value among the treatment as well as to the parent mean value for days to panicle maturity and fingers ear⁻¹ and G1 (300 Gy) showed high mean value among the treatments for plant height and ear weight plant⁻¹. Most of the traits showed desirable effects in G3 (500 Gy) treatment as compared to other treatments for GPU 28. Waghmode *et al.* (2020) also selected thirty-four mutant lines from M₂ generation of genotype Girge local which was irradiated with 500 Gy dose of gamma rays. Greater numbers of viable and economic mutants

for higher productivity were observed at 500 Gy and 600 Gy, respectively than other mutagenic treatments by Ambavane *et al.* (2015).

Genetic correlation and cluster analysis in M₃ generation: Among the mutants of GPU 28, the seed yield plant⁻¹ exhibited highly significant positive correlation with plant height (0.315), productive tillers plant⁻¹ (0.586) and ear weight plant⁻¹ (0.887) (Fig. 1a). Among mutants of KMR 204, the seed yield plant⁻¹ exhibited highly significant positive correlation with productive tillers plant⁻¹ (0.561) and ear weight plant⁻¹ (0.908) (Fig. 1b). High positive significant association of seed yield plant⁻¹ with productive tillers plant⁻¹ was reported by Ganapathy *et al.* (2011) in finger millet, Nandini *et al.* (2016) in little millet, Suman *et al.* (2018) in finger millet, with ear weight plant⁻¹ by Negi *et al.* (2017) in finger millet.

Significant positive association found for productive tiller plant⁻¹ and 1000 seed weight, productive tiller plant⁻¹ and ear weight plant⁻¹, fingers ear⁻¹ and finger length while negative significant association was found for productive tiller plant⁻¹ and finger length in mutated populations of GPU 28, similar significant negative association were also observed by the John (2006) and Jyothsna *et al.* (2016) in finger millet but not significant. In treated population of KMR 204, significant positive association found for productive tillers plant⁻¹ and ear weight plant⁻¹, similar findings were observed by the Muduli and Misra (2007) in both the mutated population of VR 708 and GPU 26 in finger millet. Genetic correlation among morphological traits allows breeder for indirect selection of those traits which are significantly correlated with seed yield plant⁻¹.

Cluster analysis based on the morphological traits grouped the mutants of GPU 28 into four and KMR 204 into three clusters (Fig. 2a, 2b). The cluster analysis was

Table 2a. Descriptive statistics for Productive tillers plant⁻¹, Fingers ear⁻¹, Finger length and seed yield plant⁻¹ among M₃ mutants of variety GPU 28 and KMR 204

| Treatment | Tr. Code | Range | Mean | Variance | Range | Mean | Variance |
|-----------------------|----------|-----------|------|--|-------------|--------------------------------------|----------|
| | | | | Productive tillers plant⁻¹ | | Fingers ear⁻¹ | |
| Tr. of GPU 28 | | | | | | | |
| 300 Gy | G1 | 2.5-6.14 | 4.26 | 1.02 | 5-8.6 | 6.19 | 0.81 |
| 400 Gy | G2 | 1.57-6.89 | 3.88 | 1.48 | 4.6-9 | 6.95 | 0.61 |
| 500 Gy | G3 | 1.5-8 | 3.86 | 2.22 | 5.7-9 | 7.14 | 0.59 |
| Parent(GPU 28) | C1 | 3.35-4.65 | 4.24 | 0.10 | 6.3-7.6 | 6.93 | 0.60 |
| Tr. Of KMR 204 | | | | | | | |
| 300 Gy | K1 | 1-7.33 | 4.45 | 2.72 | 4.9-8.63 | 7.24 | 0.85 |
| 400 Gy | K2 | 1.6-8 | 4.27 | 2.79 | 6.25-9 | 7.44 | 0.53 |
| Parent(KMR 204) | C2 | 3.22-4.50 | 3.83 | 0.14 | 6.5-7.75 | 6.89 | 0.13 |
| | | | | Finger length (cm) | | Seed yield plant⁻¹ | |
| Tr. of GPU 28 | | | | | | | |
| 300 Gy | G1 | 3.7-8 | 6.50 | 1.56 | 6.35-22.62 | 12.94 | 23.58 |
| 400 Gy | G2 | 3.8-9.88 | 7.06 | 1.28 | 2.9-26.27 | 12.42 | 29.10 |
| 500 Gy | G3 | 3.38-9.25 | 7.14 | 1.68 | 5.21-31.04 | 13.46 | 38.92 |
| Parent(GPU 28) | C1 | 6.3-9.2 | 8.55 | 0.60 | 18.64-26.14 | 21.41 | 3.84 |
| Tr. Of KMR 204 | | | | | | | |
| 300 Gy | K1 | 4.78-8.94 | 6.67 | 0.66 | 4.23-30 | 13.93 | 41.47 |
| 400 Gy | K2 | 5.4-7.6 | 6.54 | 0.45 | 3.65-19.22 | 10.05 | 17.86 |
| Parent(KMR 204) | C2 | 4.88-6.8 | 6.11 | 0.41 | 15.1-23.81 | 19.27 | 7.20 |

Table 2b. Descriptive statistics for Plant height, Days to panicle maturity, 1000 seed weight and Ear weight plant⁻¹ among M₃ mutants of variety GPU 28 and KMR 204

| Treatment | Tr. Code | Range | Mean | Variance | Range | Mean | Variance |
|-----------------------|----------|---------------|-------|-----------------------------|---------------|--|----------|
| | | | | Plant height (cm) | | Days to panicle maturity | |
| Tr. of GPU 28 | | | | | | | |
| 300 Gy | G1 | 67.25 - 96.33 | 82.03 | 53.58 | 101 - 120 | 113.52 | 22.51 |
| 400 Gy | G2 | 59 - 92.14 | 75.97 | 64.93 | 105 - 121 | 113.17 | 10.38 |
| 500 Gy | G3 | 55.07 - 88.89 | 74.88 | 83.42 | 96 - 121 | 113.86 | 26.86 |
| Parent(GPU 28) | C1 | 94 - 102 | 99.36 | 5.54 | 110 - 115 | 113.17 | 2.33 |
| Tr. Of KMR 204 | | | | | | | |
| 300 Gy | K1 | 53 - 113 | 78.10 | 155.04 | 99 - 119 | 105.73 | 23.10 |
| 400 Gy | K2 | 47.3 - 87.50 | 73.03 | 121.49 | 99 - 110 | 104.85 | 13.50 |
| Parent(KMR 204) | C2 | 82 - 90 | 85.70 | 5.41 | 100 - 107 | 103.4 | 4.71 |
| | | | | 1000 seed weight (g) | | Ear weight plant⁻¹ (g) | |
| Tr. of GPU 28 | | | | | | | |
| 300 Gy | G1 | 1.9 - 3.31 | 2.56 | 0.15 | 13.71 - 54.93 | 26.27 | 101.24 |
| 400 Gy | G2 | 2.03 - 3.64 | 2.58 | 0.12 | 7.62 - 41.38 | 25.01 | 73.36 |
| 500 Gy | G3 | 1.98 - 3.42 | 2.62 | 0.14 | 14.04 - 49.14 | 25.53 | 105.88 |
| Parent(GPU 28) | C1 | 2.9 - 3.51 | 3.27 | 0.02 | 33 - 42.1 | 37.71 | 8.22 |
| Tr. Of KMR 204 | | | | | | | |
| 300 Gy | K1 | 2.09 - 3.33 | 2.53 | 0.09 | 10.50 - 48.18 | 28.13 | 125.13 |
| 400 Gy | K2 | 2.10 - 3.15 | 2.52 | 0.08 | 9.20 - 34.22 | 22.05 | 58.63 |
| Parent(KMR 204) | C2 | 2.34 - 2.81 | 2.64 | 0.02 | 25.45 - 36.17 | 31.13 | 16.97 |

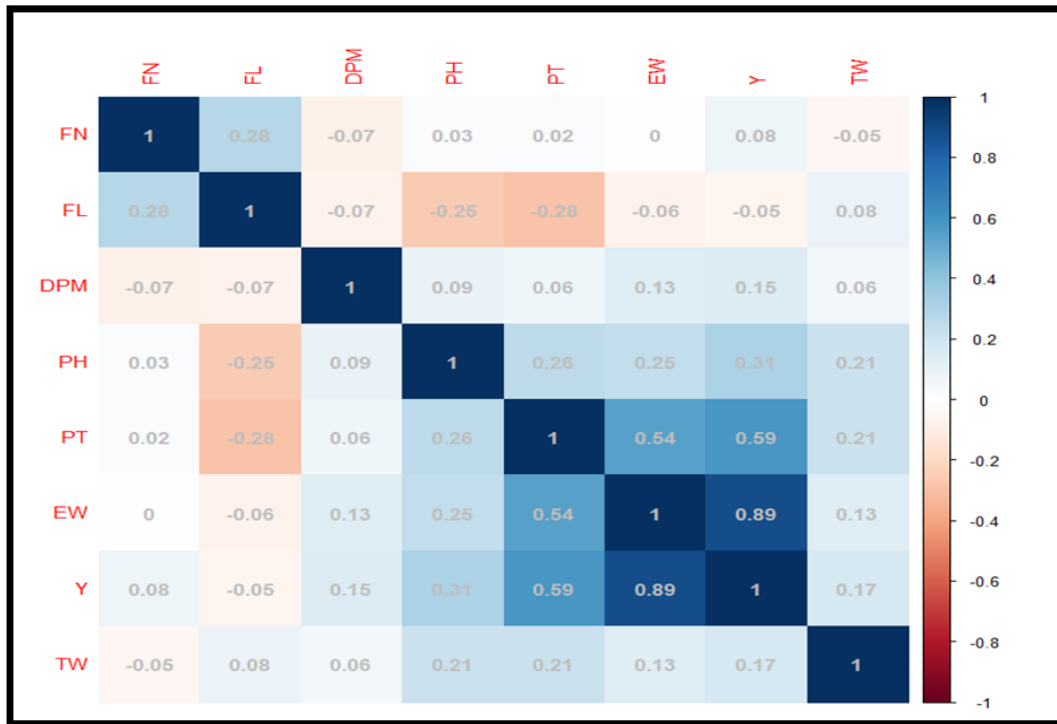


Fig. 1a. Estimates of phenotypic correlation coefficients for seed yield and its contributing traits of GPU 28 in M3 generation

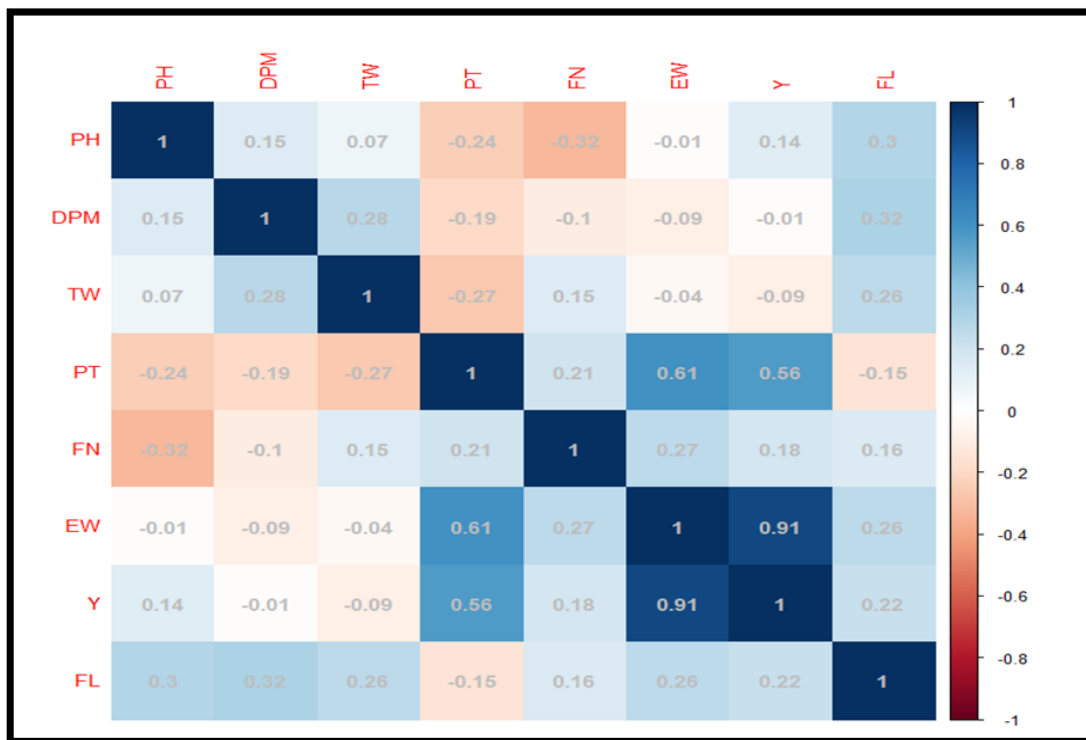


Fig. 1b. Estimates of phenotypic correlation coefficients for seed yield and its contributing traits of KMR 204 in M3 generation

done on the basis of Euclidean distance and dendrograms were constructed for both the mutated populations. Classifying the genotypes based on the morphological traits helps the breeder to select diverse genotypes based on inter-cluster distance. It is desirable for the breeder to select representative genotypes from each cluster which are having high inter-cluster distance. Similarly, a set of germplasm lines of finger millet were grouped in to clusters representing accessions from Africa and India (Upadhyaya *et al.*, 2011).

Identification of desirable mutants: Assessment of genetic variability in M_3 generation strongly indicated the presence of variability for seed yield and its contributing traits. Association studies also showed the correlation between seed yield and its attributing traits. So, thirty-one mutants were selected from the treated population of GPU 28 and twenty-seven mutants were selected from the treated population of KMR 204 from M_3 generation (Fig 3a, 3b). These mutants were selected on the basis of selection criteria which were made in comparison

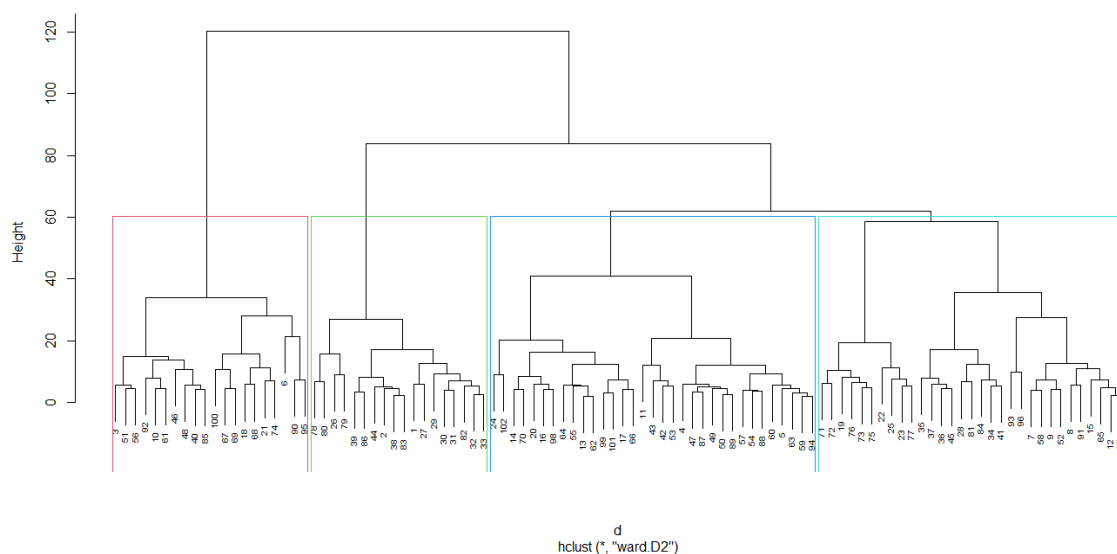


Fig. 2a. Dendrogram depicting clustering of 102 M_3 mutant lines of finger millet var. GPU 28

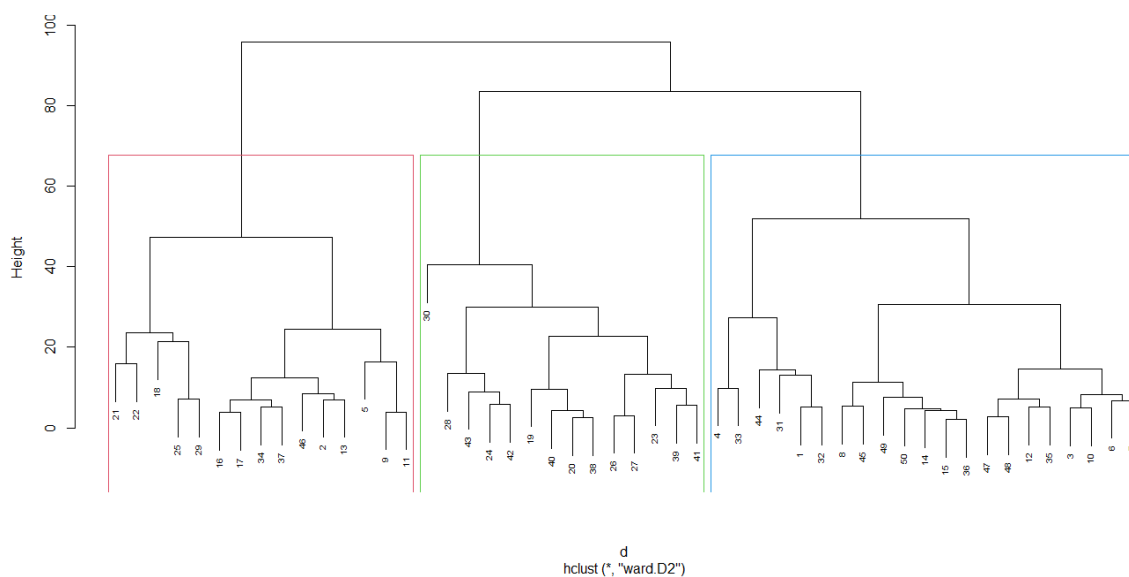


Fig. 2b. Dendrogram depicting clustering of 50 M_3 mutant lines of finger millet var. KMR 204



Fig. 3(a) Desirable M_3 mutant of GPU 28 along with parent GPU28 (b) Desirable M_3 mutant of KMR 204 along with parent KMR 204 (Parents are those which are closer to the scale)

Table 3. Selected mutants from M_3 population of GPU 28 and KMR 204

| Traits* | M_3 – GPU 28 | | | M_3 – KMR 204 | | |
|---------|------------------|----------|----------------------------|-------------------|----------|----------------------------|
| | Control (GPU 28) | Criteria | Number of mutants selected | Control (KMR 204) | Criteria | Number of mutants selected |
| FN | 6.94 | >8 | 8 | 6.90 | >8 | 2 |
| FL (cm) | 8.67 | >9 | 5 | - | - | - |
| PT | 4.24 | >7 | 6 | 3.83 | >6 | 12 |
| SY (g) | 21.41 | > 25 | 12 | 19.27 | > 22 | 13 |
| Total | | | 31 | | | 27 |

*PT- Productive tillers plant⁻¹, FN- Fingers ear⁻¹, FL- Finger length, SY- Seed yield plant⁻¹

with their respective parents (Table 3). Traits such as productive tillers plant⁻¹, fingers ear⁻¹, finger length (cm) and seed yield plant⁻¹ have been taken up for the selection, in comparison with the parents. These 58 selected mutants were advanced to next generation and evaluated in randomized complete block design with three replications with two checks and data recorded on same set of observations as in M_3 generation.

Progeny testing is crucial for the selection of the plants. "Genetic worth of plants as assessed based on the testing of their progeny performance is defined as breeding value" (Falconer and Mackay, 1996). The M_3 selected plants whose M_4 progenies had high trait mean were considered as having high breeding value for that trait. A comparison has been done between the mean and range of the base population (M_3 generation) to the mean of the progenies of selected mutants from base population

(Table 4). Mean seed yield plant⁻¹ of the progenies of selected mutants found to be much higher than the mean seed yield plant⁻¹ of the base population for both of the mutated genotypes. Similarly, comparison of the range between the two showed the shifting of range in positive direction. This trend indicated the efficacy of the selection which led to the improvement in the seed yield plant⁻¹. From M_4 generation, superior mutant progenies (5 each from both M_4 populations) were identified on the basis of significant superiority of seed yield over both the parents (Table 5).

In present study, selection of high yielding mutants from M_3 population indicated that there was vast variability present in the population which leads to the selection of mutants for productivity per se traits. Progeny evaluation of selected mutants showed the significant improvement in productivity per se traits over previous generation.

Table 4. Comparison of descriptive statistics for seed yield and its contributing traits among M₃ and M₄ generations of GPU 28 and KMR 204

| Traits* | Mutants of GPU 28 | | | | Mutants of KMR 204 | | | |
|---------|------------------------|------------------------|-------------------------|-------------------------|------------------------|------------------------|-------------------------|-------------------------|
| | Mean (M ₃) | Mean (M ₄) | Range (M ₃) | Range (M ₄) | Mean (M ₃) | Mean (M ₄) | Range (M ₃) | Range (M ₄) |
| DPM | 112.51 | 108.40 | 96 - 121 | 99 - 119 | 106.22 | 104.63 | 90 - 119 | 99.33 - 116 |
| PH (cm) | 80.14 | 95.49 | 55.07 - 102 | 77.33 - 118.81 | 80.74 | 88.96 | 50 - 113 | 72 - 112.1 |
| PT | 3.98 | 4.27 | 1.50 - 8 | 2.90 - 5.53 | 4.27 | 4.74 | 1 - 8 | 2.90 - 6.50 |
| FN | 6.97 | 7.73 | 4.60 - 9 | 6.30 - 9.28 | 7.21 | 7.81 | 4.9 - 9 | 6.60 - 9.03 |
| FL (cm) | 7.04 | 7.70 | 3.38 - 9.88 | 5.20 - 9.56 | 6.81 | 6.98 | 4.78 - 8.93 | 4.70 - 8.60 |
| TW (g) | 2.65 | 2.91 | 1.90 - 3.64 | 2.16 - 3.69 | 2.64 | 2.92 | 2.09 - 3.33 | 2.16 - 3.68 |
| EW(g) | 27.14 | 48.61 | 7.63 - 54.93 | 30.63 - 63.89 | 28.16 | 49.61 | 9.2 - 48.18 | 31.14 - 71.51 |
| SY (g) | 14.26 | 29.78 | 2.90 - 31.04 | 18.24 - 39.02 | 14.65 | 30.94 | 3.65 - 30 | 18.29 - 46.69 |

*DPM- Days to panicle maturity, PH- Plant height, PT- Productive tillers plant⁻¹, FN- Fingers ear⁻¹, FL- Finger length, TW- 1000 Seed weight, EW- Ear weight plant⁻¹, SY- Seed yield plant⁻¹

Table 5. Performance of selected desirable M₄ mutant families for seed yield and its contributing traits during 2018-19

| Mutants* | DPM** | PT** | FN** | FL (cm)** | TW (g)** | EW (g)** | SY (g)** |
|---|--------|------|------|-----------|----------|----------|----------|
| Promising M₄ mutant families of GPU 28 | | | | | | | |
| G-30 | 102.00 | 5.27 | 9.00 | 9.27 | 3.69 | 63.89 | 39.00 |
| G-19 | 119.00 | 5.53 | 8.51 | 9.55 | 3.60 | 60.13 | 38.56 |
| G-25 | 100.00 | 4.93 | 8.47 | 8.23 | 3.46 | 53.77 | 37.37 |
| G-20 | 111.00 | 5.03 | 7.73 | 8.73 | 3.35 | 56.60 | 37.06 |
| G-6 | 114.00 | 5.00 | 8.70 | 8.69 | 3.22 | 59.55 | 37.05 |
| GPU 28 | 113.00 | 2.90 | 6.91 | 7.16 | 3.41 | 51.10 | 32.46 |
| CD at 5% | 2.89 | 0.69 | 0.67 | 1.16 | 0.19 | 8.67 | 5.73 |
| Promising M₄ mutant families of KMR 204 | | | | | | | |
| K-16 | 100.67 | 6.50 | 9.03 | 8.60 | 3.68 | 71.51 | 46.69 |
| K-14 | 102.33 | 6.16 | 8.63 | 8.33 | 3.50 | 64.28 | 42.69 |
| K-23 | 100.00 | 6.13 | 8.70 | 8.10 | 3.43 | 65.00 | 40.52 |
| K-26 | 100.33 | 5.73 | 8.60 | 7.90 | 3.39 | 58.17 | 38.04 |
| K-21 | 104.33 | 5.93 | 8.50 | 8.23 | 3.10 | 55.09 | 36.73 |
| KMR 204 | 100.00 | 3.64 | 7.62 | 5.20 | 2.43 | 37.21 | 18.30 |
| CD at 5% | 2.79 | 0.87 | 0.82 | 0.60 | 0.11 | 7.51 | 5.25 |

*K denotes KMR 204, G denotes GPU 28, CD denotes critical difference at 5%

**DPM- Days to panicle maturity, PT- Productive tillers plant⁻¹, FN- Fingers ear⁻¹, FL- Finger length, TW- 1000 Seed weight, EW- Ear weight plant⁻¹, SY- Seed yield plant⁻¹

High yielding mutant progenies which were significantly superior from checks were identified. Cluster analysis in the study grouped the M₃ population in different diverse groups which is very helpful in the making of heterotic hybrids. Identified mutants' progenies can be evaluated further for their stability performance in the next generation to ultimately select the top performing mutant lines. Identified high yielding mutant lines can be utilized to develop new varieties and also, selection of diverse lines from different clusters will help in exploitation of heterosis.

ACKNOWLEDGEMENT

The first author is grateful to the Department of Genetics and Plant Breeding, College of Agriculture, UAS, GKVK, Bangalore for providing facilities, support and guidance during experiment.

REFERENCES

Allard, R. W. 1960. *Principals of Plant Breeding*. John Wiley and Sons, Inc., New York, USA.

- Ambavane, A. R., Sawardekar, S. V., Sawantdesai, S. A. and Gokhale, N. B. 2015. Studies on mutagenic effectiveness and efficiency of gamma rays and its effect on quantitative traits in finger millet (*Eleusine coracana* L. Gaertn). *Journal of Radiation Research Applied Science*, **8**: 120-125. [Cross Ref]
- Anuradha, N., Patro, T. S. S. K., Divya, M., Rani, Y. S. and Triveni, U. 2017. Genetic variability, heritability and association in advanced breeding lines of finger millet [*Eleusine coracana* (L.) Gaertn.]. *International Journal of Chemical Studies*, **5**: 1042-1044.
- Aviya, K. and Mullainathan, L. 2018. Studies on effect of induced mutagenesis on finger millet (*Eleusine coracana* (L.) Gaertn.) Var-Co 13 in M₁ generation. *Horticultural Biotechnology Research*, **4**: 23-25. [Cross Ref]
- Burton, G. W. 1952. Quantitative inheritance in grasses. *Proceeding of 6th International Grassland Congress*, 227-283.
- Chandra, D., Chandra, S. and Sharma, A. K. 2016. Review of finger millet (*Eleusine coracana* (L.) Gaertn): A power house of health benefiting nutrients. *Food Science and Human Wellness*, **5**(3): 149-155. [Cross Ref]
- Eswari, K., Gogulan, G., Hari Prathab, K. A. and Sakila, M. 2014. Development of early maturing mutants in finger millet. *Research Journal of Agriculture and Forestry Science*, **2**: 1-9.
- Falconer, D. S. and Mackay, T. F. C. 1996. Introduction to quantitative genetics. 4th Edn., Pearson education Ltd., UK.
- Ganapathy, K. N., Patro, T. S. S. K., Palanna, K. B., Das, I. K., Elangovan, M., Prashant, B., Venkatesha, S. C., Anuradha, N., Nagaraja, T. E. and Tonapi, V. A. 2021. Development of improved mutants for grain yield and related traits in finger millet (*Eleusine coracana* L. Gaertn.) through gamma mutagenesis. *International Journal of Plant and Soil Science*, **33**: 225-235. [Cross Ref]
- Ganapathy, S., Nirmalakumari, A. and Muthiah, A. R. 2011. Genetic variability and inter relationship analyses for economic traits in finger-millet germplasm. *World Journal of Agricultural Sciences*, **7**: 185-188.
- John, K. 2006. Variability and correlation studies in quantitative traits of finger millet (*Eleusine coracana* Gaertn). *Agricultural Science Digest*, **26**: 166 – 169.
- Jyothisna, S., Patro, T. S. S. K., Ashok, S., Rani, Y. S. and Neeraja, B. 2016. Studies on genetic parameters, character association and path analysis of yield and its components in finger millet (*Eleusine coracana* L. Gaertn). *International Journal of Theoretical and Applied Sciences*, **8**: 25-30.
- Muduli, K. C. and Misra, R. C. 2007. Efficacy of mutagenic treatments in producing useful mutants in finger millet (*Eleusine coracana* L. Gaertn.). *Indian Journal of Genetics*, **67**: 232-237.
- Muduli, K. C. and Misra, R. C. 2008. Induced polygenic variability in M₂ generation and its relationship with production of high-yielding mutants in finger millet. *Indian Journal of Genetics*, **68**: 419-425.
- Muller, H. J. 1927. Artificial transmutation of the gene. *Science*, **66**: 84 -87. [Cross Ref]
- Nandini, C., Sujata, B., Krishnappa, M. and Aruna, Y. R. 2016. Genetic variability, heritability, genetic advance and character association studies in F₃ generation of cross JK8 x Peddasame (purple late) in little millet (*Panicum miliare* L.). *Asian Journal of Bio Science*, **11**: 244-249. [Cross Ref]
- Negi, S., Kumar, V. and Bhatt, A. 2017. Characterization and genetic analysis of finger millet (*Eleusine coracana* (L.) Gaertn) germplasm. *International Journal of Bio-resource Stress Management*, **8**: 469-472.
- Panse, V. G. and Sukhatme, P. V. 1967. Statistical methods for agricultural workers. 2nd Edn., ICAR Publication, New Delhi.
- Ramya, G., Madhusudan, K., Pradeep, P. E., Kalappanavar, I. K. and Sujay, V. 2013. Genetic variability and inter-relationship among M₃ and F₃ M₃ mutant of tetraploid wheat (*Triticum* sp.) for yield and quality parameters. *Mysore Journal of Agricultural Sciences*, **47**: 47-53.
- Reddy, C. V. C. M., Reddy, P. V. R. M., Munirathnam, P. and Gowda, J. 2013. Studies of genetic variability in yield and yield attributing traits of finger millet [*Eleusine coracana* (L.) Gaertn]. *Indian Journal of Agricultural Research*, **47**: 549 – 552.
- Sawardekar, S. 2016. Study of M₅ Generation of finger Millet (*Eleusine coracana* L. Gaertn.) promising mutants with quality parameters. *Journal of Agriculture Research and Technology*, **41**: 324-328.
- Snedecor, G. W. and Cochran, W. G. 1994. Statistical Methods. 8th Edn., Iowa State University Press, Ames, Iowa, USA.
- Suman, A., Surin, S., Ahmad, E., Ekka, S., Tuti, A. and Xaxa, E. 2018. Study of correlation and path analysis of elite finger millet germplasm (*Eleusine coracana* L. Gaertn). *Journal of Pharmacognosy and Phytochemistry*, **1**: 2257-2258.

- Surashe, S. M., Kalpande, H. V., Badignavar, A., More, A. and Ganapathi, T. R. 2022. Mutation induced phenotypic variation for yield traits in sorghum [*Sorghum bicolor* (L.) Moench]. *Electronic Journal of Plant Breeding*, **13**(2): 312-318. [\[Cross Ref\]](#)
- Upadhyaya, H. D., Ramesh, S., Sharma, S., Singh, S. K., Varshney, S. K., Sarma, N. D. R. K., Ravishankar, C. R., Narasimhudu, Y., Reddy, V. G., Sahrawat, K. L., Dhanalakshmi, T. N., Mgonja, M. A., Parzies, H. K., Gowda, C. L. L. and Singh, S. 2011. Genetic diversity for grain nutrients contents in a core collection of finger millet (*Eleusine coracana* (L.) Gaertn.) germplasm. *Field Crops Research*, 121: 42-52. [\[Cross Ref\]](#)
- Vanniarajan, C. and Chandirakala, R. 2022. Genetic variability and diversity analyses in Electron Beam and Gamma Ray induced mutants for yield attributing traits in urdbean [*Vigna mungo* (L.)]. *Electronic Journal of Plant Breeding*, **13**(2): 512-518. [\[Cross Ref\]](#)
- Waghmode, B. D., Sable, P. S., Sonone, N. G. and Burondkar, M. M. 2020. Genetical studies of mutant lines in M₃ generation of finger millet (*Eleusine coracana* (L.) Gaertn). *International Journal of Current Microbiology and Applied Sciences*, **9**:1833-1844. [\[Cross Ref\]](#)
- Wani, M. R., Dar, A. R., Tak, A., Amin, I., Shah, N. H., Rehman, R., Baba, M. Y., Raina, A., Laskar, R., Kozgar, M. I. and Khan, S. 2017. Chemo-induced pod and seed mutants in mungbean (*Vigna radiata* L. Wilczek). *SAARC Journal of Agriculture*, **15**: 57-67. [\[Cross Ref\]](#)
- Ward, J. 1963. Hierarchical grouping to optimize an objective function. *Journal of American Statistical Association*, **38**: 236–244. [\[Cross Ref\]](#)