



ISSN (E): 2277- 7695
 ISSN (P): 2349-8242
 NAAS Rating: 5.23
 TPI 2022; 11(4): 670-673
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www.thepharmajournal.com
 Received: 02-01-2022
 Accepted: 06-02-2022

Prashant Vasisth
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

S Rangaiah
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

Mohit Sharma
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

Vidyut Balar
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

Vaibhav Chittora
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

Corresponding Author:
Prashant Vasisth
 University of Agricultural
 Science, GKVK, Bangalore,
 Karnataka, India

Induced genetic variability and association studies in M₄ mutants of finger millet

Prashant Vasisth, S Rangaiah, Mohit Sharma, Vidyut Balar and Vaibhav Chittora

Abstract

The present investigation was undertaken to access the genetic variability and association studies among M₄ mutants of two gamma rays irradiated genotypes; GPU 28 and KMR 204. A total of 58 M₄ mutant lines (31 of GPU 28 and 27 of KMR 204) of finger millet were evaluated in Randomized Complete Block Design with three replications along with two check cultivars (GPU 28 and KMR 204). Data were collected for eight different quantitative traits on each mutant line. Genetic parameters and correlation coefficients were estimated to access the genetic variability. Study revealed the 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. High heritability with high genetic advance were reported in both the population for the traits viz., 1000-seed weight, productive tillers plant⁻¹, ear weight plant⁻¹ (g) and seed yield plant⁻¹ (g). Traits viz., productive tillers plant⁻¹, Fingers ear⁻¹, Finger length, 1000 seed weight and ear weight plant⁻¹ were found significantly correlated with seed yield plant⁻¹ for both the populations. Usefulness of induced mutagenesis for generating variability among M₄ mutants line of finger millet well demonstrated through present study.

Keywords: Induced mutagenesis, genetic variability, correlation coefficients, finger millet

Introduction

Finger millet (*Eleusine coracana* (L.) Gaertn.) belongs to the family Poaceae/Graminae, and generally known as Ragi, Nachani and Nagli. It is a tetraploid (2n = 36) derived from the wild tetraploid progenitor *E. coracana* subsp. *africana*. Finger millet is a widely grown traditional and highly nutritious grain cereal crop. It is cultivated in the semi-arid areas of Eastern and Southern Africa and South Asia, where it is a staple food for millions of poor people. It is believed to be originated in India as its many forms in this region (Sawardekar 2016) [16]. In India, area of finger millet stands sixth after wheat, rice, maize, sorghum and bajra (Chandra *et al.*, 2016) [4]. In India, area under finger millet is 1004.46 thousand-hectare, production is 1755.06 metric tons with productivity 1747 kg per hectare. Karnataka is the leading producer of finger millet accounting to 58% of its global production having area of 641 thousand hectare with production of 1164 metric tons with productivity 1816 kg per hectare. The nutraceutical importance of finger millet lies in its high content of calcium (0.38%), protein (6%–13%), dietary fiber (18%), carbohydrates (65%–75%), minerals (2.5%–3.5%), phytates (0.48%), tannins (0.61%), phenolic compounds (0.3–3%) and trypsin inhibitory factors, and is recognized for its health beneficial effects, such as anti-diabetic, anti tumorigenic, anti-diarrheal, antiulcer, anti-inflammatory, atherosclerogenic effects, antioxidant and antimicrobial properties. Consumption on daily basis of finger millet as a whole grain and its products can protect the body against the risk of heart related diseases, type II diabetes, and gastrointestinal cancers and other health issues (Chandra *et al.*, 2016) [4].

In a plant breeding programme, availability of vast genetic variability in the crop species is the first crucial step to select better performing genotypes from the divergent group. Global food security disintegrated drastically in 1960's when developing countries were short of the food supply. "Green Revolution Technology" aided to avoid the large-scale starvation for around four decades but food security problem has again seen a major problem in the last few years due to high food prices. As we know, population is still expanding while no significant increase in arable lands is foreseen. Therefore, another green revolution is required to overcome the problem of food insecurity. Productivity of the crop can be enhanced by the use of high yielding cultivars with wide adaptability, high responsiveness to fertility and better management. Improvement in the component traits of yield and harvest index can enhance the yield potential of the varieties.

The use of induced mutagenesis is expected to provide a worthy solution to further increase the level of food production by enhancing the grain production and stability of crops. 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 have been made in various crop plants by Muller (1927) [12]. There is sufficient evidence in terms of positive results in many plant species that induced mutation is an efficient way of generating variability in qualitative as well as in quantitative characters. Mutation breeding has great importance as a breeding programme due to presence of many types of mutagens having different modes of action and refinement of techniques for enhanced efficacy. Sawardekar (2016) [16] studied the effect of gamma rays on yield and its component traits, to develop tolerant genotype to blast disease in an established variety of finger millet namely, Dapoli-1 and to analyse quality parameters (Iron, Calcium and Protein) of promising mutant lines. The study was conducted on 23 mutant lines selected from M₅ generation developed by mutagenesis from Dapoli-1 variety of finger millet. Muduli and Misra (2008) [11] estimated the induced genetic divergence in 44 mutant lines of finger millet variety GPU 26, developed by single and combination treatments with gamma rays, EMS and NG using three multivariate analyses. Negi *et al.* (2017) [14] analysed thirty-five diverse genotypes of finger millet along with three checks *viz.*, PRM-1, PRM-2 and VL-149 for variability, heritability and genetics advance. They observed high heritability with high genetic advance for biological yield plant⁻¹, plant height and days to 50 per cent flowering indicated the potential for their improvement through selection. Keeping above scenario in mind, present investigation has been made to assess the genetic variability and association studies for productivity per se traits in M₄ generations.

Material and Methods

The present study on induced mutations in finger millet was carried out at University of Agricultural Sciences; Bangalore. M₄ seeds derived from the selfing of selected M₃ plants on the basis of productivity *per se* traits of two irradiated genotypes, 31 progenies of GPU 28 and 27 progenies KMR 204 were used in present study. Dry seeds of these two varieties were irradiated with gamma radiation at Baba Atomic Research Centre (BARC), Trombay, and Mumbai. M₁, M₂ and M₃ generations were grown in the main field of 'K' block, UAS, GKVK, Bengaluru lying in the Eastern Dry Agro Climatic Zone (Zone V) of Karnataka. Recommended agronomic practices were followed during crop growth period to raise a good crop. These progenies were evaluated in randomized completely block design (Panse and Sukhatme, 1984) with 3 replications along with 2 checks/parents. The replication wise mean values of different entries were considered for analysis of variance as per Panse and Sukhatme (1984). The genotypic and phenotypic co-efficient of variation for all the characters were computed according to formula as suggested by Burton and De vane (1953) [3]. Heritability in broad sense for all the characters was estimated as the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Lush, 1945). The extent of genetic advance for each character that could be expected by selecting certain

proportions of the superior progeny was computed as per the formula suggested by Johnson *et al.* (1955) [7]. The genetic advance as per cent of mean was categorized as suggested by Johanson *et al.* (1955) [7]. Simple correlations were calculated by using the formula as given by Weber and Moorthy (1952) [18].

Result and Discussion

Study revealed the 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 (Table 1). In case of mutated population of GPU 28, phenotypic coefficient of variation (PCV) ranged from 6.19 to 22.34 per cent. Highest PCV was recorded for Seed yield plant⁻¹ (g) (22.34) and lowest PCV was recorded for days to panicle maturity (6.19). Coefficient of variation at phenotypic level (PCV) was recorded high for seed yield plant⁻¹. Moderate PCV and GCV were reported for the traits *viz.* productive tillers plant⁻¹, 1000 seed weight (g) and ear weight plant⁻¹ (g). Low PCV and GCV were reported for the traits *viz.*, days to panicle maturity and plant height (Table 2). In case of mutated population of KMR 204, phenotypic coefficient of variation (PCV) ranged from 5.27 to 22.88 per cent. Highest PCV was recorded for Seed yield plant⁻¹ (g) (22.88) and lowest PCV was recorded for days to panicle maturity (5.27). Coefficient of variation at phenotypic level (PCV) and genotypic level were observed high for seed yield plant⁻¹. Moderate PCV and GCV were reported for the traits *viz.* finger length (cm), 1000 seed weight (g) and ear weight plant⁻¹ (g). Low PCV and GCV were reported for the traits *viz.*, days to panicle maturity and fingers ear⁻¹ (Table 3). Low genetic advance over mean for days to panicle maturity were in close association with John (2006) [6], Anuradha *et al.* (2017) [11] and Negi *et al.* (2017) [14]. Similar results of high genetic advance over mean for seed yield plant⁻¹ also reported by Sawardekar (2016) [16]. Among the mutants from the treated population of GPU 28, high heritability with high genetic advance reported for the traits *viz.*, 1000-seed weight, productive tillers plant⁻¹ ear weight plant⁻¹ (g) and seed yield plant⁻¹ (g) indicated that these traits were less influenced by the environment; heritability is due to the additive genes effect so selection is effective. Moderate heritability with moderate genetic advance over mean was reported for finger length indicated that moderate influence of environment and selection may be effective for the trait (Table 2). Among the mutants from the treated population of KMR 204, high heritability with high genetic advance reported for the traits *viz.*, 1000-seed weight, finger length, productive tillers plant⁻¹, ear weight plant⁻¹ (g) and seed yield plant⁻¹ (g) indicated that these traits were less influenced by the environment; heritability is due to the additive genes effect so selection is effective. Moderate heritability with moderate genetic advance over mean was reported for fingers ear⁻¹ indicated that moderate influence of environment and selection may be effective for the trait (Table 3). High heritability with high genetic advance over mean was reported for 1000 seed weight in both the mutated population. The results were in close association with the findings of John (2006) [6], Sonnad *et al.* (2007) [17], Lule *et al.* (2012) [8], Auti *et al.* (2017) [2], and for both the mutated populations.

Table 1: Analysis of variance for seed yield and its attributing traits among M₄ mutants of finger millet variety GPU 28 and KMR 204

| GPU-28 in M ₄ generation | | | | | | | | | |
|--------------------------------------|-------------------|--------------------------|-------------------|--|---------------------------|--------------------|----------------------|------------------------------------|------------------------------------|
| Source of variation | Degree of freedom | Days to panicle maturity | Plant height (cm) | Productive tillers plant ⁻¹ | Fingers ear ⁻¹ | Finger length (cm) | 1000 seed weight (g) | Ear weight plant ⁻¹ (g) | Seed yield plant ⁻¹ (g) |
| Replication | 2 | 3.16 | 63.07 | 0.46 | 0.06 | 6.29 | 0.03 | 84.55 | 3.07 |
| Treatments | 32 | 128.66* | 226.26* | 1.30* | 1.61* | 2.22* | 0.51* | 193.51* | 108.24* |
| Error | 64 | 3.13 | 15.047 | 0.176 | 0.167 | 0.501 | 0.014 | 28.094 | 12.282 |
| KMR-204 in M ₄ generation | | | | | | | | | |
| Source of variation | Degree of freedom | Days to panicle maturity | Plant height (cm) | Productive tillers plant ⁻¹ | Fingers ear ⁻¹ | Finger length (cm) | 1000 seed weight (g) | Ear weight plant ⁻¹ (g) | Seed yield plant ⁻¹ (g) |
| Replication | 2 | 2.49 | 27.455 | 0.0335 | 0.0585 | 0.119 | 0.001 | 11.267 | 28.990 |
| Treatments | 28 | 85.34* | 241.50* | 2.83* | 1.21* | 3.79* | 0.55* | 239.64* | 129.84* |
| Error | 56 | 2.89 | 26.177 | 0.279 | 0.250 | 0.131 | 0.004 | 20.956 | 10.245 |

Table 2: Genetic variability parameters for seed yield and its component traits of finger millet variety GPU 28 in M₄ population

| Sl. No. | Traits | GCV (%) | PCV (%) | Broad sense heritability h ² (%) | GAM (as per cent of mean) |
|---------|--|---------|---------|---|---------------------------|
| 1 | Days to panicle maturity | 5.97 | 6.19 | 93.04 | 11.86 |
| 2 | Plant height (cm) | 8.79 | 9.68 | 82.39 | 16.43 |
| 3 | Productive tillers plant ⁻¹ | 14.37 | 17.41 | 68.10 | 24.42 |
| 4 | Fingers ear ⁻¹ | 8.97 | 10.41 | 74.23 | 15.92 |
| 5 | Finger length (cm) | 9.82 | 13.46 | 53.31 | 14.78 |
| 6 | 1000 seed weight (g) | 13.93 | 14.50 | 92.33 | 27.57 |
| 7 | Ear weight plant ⁻¹ (g) | 15.27 | 18.77 | 66.25 | 25.61 |
| 8 | Seed yield plant ⁻¹ (g) | 18.99 | 22.34 | 72.25 | 33.25 |

Table 3: Genetic variability parameters for seed yield and its component traits of finger millet variety KMR 204 in M₄ population

| Sl. No. | Traits | GCV (%) | PCV (%) | Broad sense heritability h ² (%) | GAM (as per cent of mean) |
|---------|--|---------|---------|---|---------------------------|
| 1 | Days to panicle maturity | 5.01 | 5.27 | 90.49 | 9.82 |
| 2 | Plant height (cm) | 9.52 | 11.12 | 73.28 | 16.79 |
| 3 | Productive tillers plant ⁻¹ | 19.45 | 22.41 | 75.33 | 34.78 |
| 4 | Fingers ear ⁻¹ | 7.25 | 9.67 | 56.17 | 11.19 |
| 5 | Finger length (cm) | 15.82 | 16.66 | 90.27 | 30.97 |
| 6 | 1000 seed weight (g) | 14.55 | 14.72 | 97.63 | 29.61 |
| 7 | Ear weight plant ⁻¹ (g) | 17.21 | 19.53 | 77.67 | 31.25 |
| 8 | Seed yield plant ⁻¹ (g) | 20.41 | 22.88 | 79.55 | 37.49 |

Correlation analysis among M₄ mutants of GPU 28 and KMR 204

The seed yield is a complex trait and govern by many genes. Selection on the basis of seed yield may be misleading. Seed yield is a super character which results from interactions of several other characters named as yield contributing traits. To develop high yielding variety by effective selection, association of important yield components with seed yield and among themselves has important role. The correlation coefficient provides the degree of association between two variables which help us in understanding the nature and magnitude of association among seed yield and its component traits. In present study, among the mutants of GPU 28, the seed yield plant⁻¹ exhibited highly significant positive

correlation with productive tillers plant⁻¹ (0.844), Fingers ear⁻¹ (0.810), Finger length (0.842), 1000 seed weight (0.796) and ear weight plant⁻¹ (0.939) while, other traits did not exhibit significant correlation with seed yield plant⁻¹ (Table 4). In mutated population of KMR 204, the seed yield plant⁻¹ exhibited highly significant positive correlation productive tillers plant⁻¹ (0.809), Fingers ear⁻¹ (0.848), Finger length (0.793), 1000 seed weight (0.610) and ear weight plant⁻¹ (0.950) (Table 5). High positive significant association of seed yield with productive tillers plant⁻¹ were also reported by Ganapathy *et al.* (2011)^[5] in ragi, Nandini *et al.* (2016)^[13] in little millet, Anuradha *et al.* (2017)^[1] in ragi, Suman *et al.* (2018) in ragi, with ear weight plant⁻¹ by Muduli and Misra (2007)^[10].

Table 4: Estimates of Genotypic correlation coefficients for seed yield and its component traits of GPU 28 in M₄ generation

| | Days to panicle maturity | Plant height (cm) | Productive tillers plant ⁻¹ | Fingers ear ⁻¹ | Finger length (cm) | 1000 seed weight (g) | Ear weight plant ⁻¹ (g) | Seed yield plant ⁻¹ (g) |
|--|--------------------------|-------------------|--|---------------------------|--------------------|----------------------|------------------------------------|------------------------------------|
| Days to panicle maturity | 1 | 0.748** | -0.03 | 0.175 | 0.249 | 0.097 | 0.124 | 0.02 |
| Plant height (cm) | | 1 | -0.167 | 0.11 | 0.129 | -0.045 | 0.017 | -0.086 |
| Productive tillers plant ⁻¹ | | | 1 | 0.634** | 0.793** | 0.641** | 0.823** | 0.844** |
| Fingers ear ⁻¹ | | | | 1 | 0.652** | 0.677** | 0.783** | 0.810** |
| Finger length (cm) | | | | | 1 | 0.769** | 0.852** | 0.842** |
| 1000 seed weight (g) | | | | | | 1 | 0.715** | 0.796** |
| Ear weight plant ⁻¹ (g) | | | | | | | 1 | 0.939** |
| Seed yield plant ⁻¹ (g) | | | | | | | | 1 |

** Correlation is significant at the 0.01 level (2-tailed)

* Correlation is significant at the 0.05 level (2-tailed)

Table 5: Estimates of Genotypic correlation coefficients for seed yield and its component traits of KMR 204 in M4 generation

| | Days to panicle maturity | Plant height (cm) | Productive tillers plant ⁻¹ | Fingers ear ⁻¹ | Finger length (cm) | 1000 seed weight (g) | Ear weight plant ⁻¹ (g) | Seed yield plant ⁻¹ (g) |
|--|--------------------------|-------------------|--|---------------------------|--------------------|----------------------|------------------------------------|------------------------------------|
| Days to panicle maturity | 1 | 0.636** | -0.226 | -0.264 | 0.012 | 0.046 | -0.163 | -0.278 |
| Plant height (cm) | | 1 | -0.024 | -0.063 | 0.188 | 0.222 | 0.072 | -0.066 |
| Productive tillers plant ⁻¹ | | | 1 | 0.652** | 0.593** | 0.561** | 0.783** | 0.809** |
| Fingers ear ⁻¹ | | | | 1 | 0.643** | 0.494** | 0.785** | 0.848** |
| Finger length (cm) | | | | | 1 | 0.447* | 0.753** | 0.793** |
| 1000 seed weight (g) | | | | | | 1 | 0.572** | 0.610** |
| Ear weight plant ⁻¹ (g) | | | | | | | 1 | 0.950** |
| Seed yield plant ⁻¹ (g) | | | | | | | | 1 |

** . Correlation is significant at the 0.01 level (2-tailed)

* . Correlation is significant at the 0.05 level (2-tailed)

Conclusion

Analyses of variation showed that mean sum of squares of both the population were significant indicating the presence of enough variability among M₄ mutants of both the genotypes. High heritability with high genetic advance were reported in both the population for the traits viz., 1000-seed weight, productive tillers plant⁻¹, ear weight plant⁻¹ (g) and seed yield plant⁻¹ (g) indicated that these traits were less influenced by the environment; heritability is due to the additive genes effect so selection is effective. Traits viz., productive tillers plant⁻¹, Fingers ear⁻¹, Finger length, 1000 seed weight and ear weight plant⁻¹ were found significantly correlated with seed yield plant⁻¹ for both the population which will be helpful in selection of high yielding lines.

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