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# Study of genetic variability, heritability and path analysis for grain micronutrients concentration, yield and component traits in pearl millet (*Pennisetum glaucum* (L.) R. Br.)

**Mithlesh Kumar, Kirti Rani, Ajay BC, MS Patel, KD Mungra and MP Patel**

**Abstract**
Present study was undertaken among 48 diverse pearl millet genotypes in 2 replications in randomized complete block design (RCBD) for genetic variability, heritability, genetic advance as per cent of mean along with path analysis of grain micronutrients concentration, yield and its component traits. The analysis of variance showed highly significant differences among the genotypes for most of the characters studied, indicating the presence of adequate variability. The phenotypic coefficient of variation (PCV) was higher than genotypic coefficient of variation (GCV) signifying influence of environment on the expression of all the characters studied. Moderate to high PCV and GCV were recorded for most of the characters. High to moderate heritability coupled with moderate to high genetic advance as per cent of mean were observed for the plant height, panicle length, panicle girth, panicle weight, grain yield per plant, grain iron (Fe) and zinc (Zn) content revealed the characters are predominantly governed by additive gene action and phenotypic selection for these characters will be effective. Characters like dry fodder yield per plant, panicle weight, plant height and panicle length were shown high positive direct effect on grain yield per plant can be directly used for improvement of pearl millet.

**Keywords:** Variability, heritability, genetic advance, path analysis, PCV, GCV, grain micronutrients, pearl millet

## Introduction
Pearl millet being a dominantly cross pollinated crop due to protogynous flowering exhibits remarkable genetic diversity and wide adaptation under harsh environmental conditions due to its extensive root system (Satyavathi *et al*. 2013 and Singh *et al*. 2013) [32, 34]. It is the important cereal in terms of cultivation area at global level after rice, wheat, maize, barely and sorghum (Khairwal *et al*. 2007) [18]. Globally, it is grown on about 30 m ha with the majority of area in Asia (>10 m ha), Africa (about 18 m ha), and America (>2 m ha) (Gupta *et al*. 2015) [14]. Micronutrient malnutrition resulting from dietary deficiency of one or more micronutrients has been recognized as a massive human health problem afflicting over 2 billion people mostly woman, children and infants worldwide (WHO, 2002) [40]. Mineral deficiencies of iron (Fe), zinc (Zn) and vitamin A are more common among the poor people of Africa and Asia. One third of Indian population contributes to the total global malnourishment (Barthakur *et al*. 2010) [5]. Micronutrient deficiency also termed as 'hidden hunger' (Allen, 2003) leads to serious health problems including poor growth and development and reduced brain development in children, reduced immunity, fatigue and reproductive failure in adults (Stein, 2010) [36].

Biofortification of staple crops designed to increasing the bioavailable micronutrient content of food crops through genetic selection especially for mineral micronutrients is a sustainable and most cost effective approach to tackle malnutrition problem. It has been promise for improving the mineral nutritional status and health of poor population in both rural and urban areas of developing world (Kumar *et al*. 2016) [22]. Biofortified cultivars of staple crops improved for mineral micronutrients are also easily acceptable to consumers as their adoption does not call for change in dietary habits (Kanatti *et al*. 2014) [16]. Fe (iron), Zn (zinc), Cu (copper) and Mn (manganese) are known to play an important role in our body. For instance Fe is an important component of haemoglobin and myoglobin; Zn stimulates the activities of many enzymes in the human body and is closely related to intelligence development in children and adult reproductive function; Cu plays a role in making red blood cells, energy production and

maintaining nerve cells and the immune system and Mn is the vital for the human body and helps in the metabolism of amino acids, cholesterol, glucose and carbohydrates in human body (Ansari *et al*. 2004) [2]. Breeding for high grain Fe and Zn content needs an adequate range of genetic variability in available germplasm and understanding of the genetic control of grain micronutrient density. Large variability for Fe and Zn concentration observed in the breeding lines, improved populations and germplasm (Velu *et al.* 2007, 2008, Anuradha *et al*. 2018, Mahendrakar *et al*. 2019) [38, 39, 3, 25] provides for good avenue to breed improved pearl millet with increased levels of these micronutrients.

The challenge to today's crop improvement is not only to increase the yield potential of the crop but also to enhance micronutrient content in the grain. Any crop improvement initially looks for the amount of genetic variability existing in the population, so that it can be utilized further either by simple selection or though other breeding approaches. Before placing emphasis on breeding for nutritional quality characters the knowledge on the association between yield and yield attributes and also interrelation between yield and nutritional quality traits will enable the breeder for simultaneous improvement of yield with nutritional traits. The correlation coefficient may help to identify characters that have little or no importance in the selection programme. The existence of correlation may be attributed to the presence of linkage or pleiotropic effect of genes or physiological and development relationship or environmental effect or in combination of all. Grain yield and micronutrient contents are complex traits governed by many genes and are influenced by the nearby environment (Owere *et al.* 2015) [26]. Hence, direct selection for these traits is not worthy. Consequently, a sound knowledge on correlation of yield and micronutrients with morphological traits helps in indirect selection of these traits *via* highly heritable traits (Bezaweletaw *et al.* 2006) [6]. The correlation studies alone are often misleading and the actual dependence of grain yield on the correlated yield component characters needs confirmation, which can easily be untangled and unravelled by path coefficient analysis (Bhasker *et al*. 2017) [7]. The path coefficient analysis is simply a standardized partial regression coefficient which measures the direct influence of one variable upon the other and permits the separation of correlation coefficients into components of direct and indirect effects. So, the information on phenotypic correlation and their association with each other generate a preliminary idea for simultaneous improvement of the traits. Therefore, present study aimed to assess the magnitude of genetic variability for grain micronutrients concentrations, yield and its component characters and to study the relationship among them in the diverse breeding lines to genetic improvement for better grain quality in 48 pearl millet genotypes.

## Materials and Methods

### Genetic materials and Field experiments

Forty eight diverse pearl millet lines (24 maintainer and 24 restorer lines) were used during *kharif*, 2016 at Centre for Crop Improvement (CCI), S. D. Agricultural University, S.K. Nagar, Gujarat (Table 1). The genotypes were planted in randomized complete block design (RCBD) with 2 replications. Each genotype represented by 2 rows of 3 m length with 45 cm between rows and 15 cm between plants. Thinning was performed after 15 days of germination to ensure single plant per hill. From sowing to till the harvesting, all the recommended agronomic package of practices was followed to raise the good crops. Five plants were randomly selected and tagged for taking observations. The observations were recorded for days to 50% flower, plant height, panicle length, panicle girth, panicle weight and dry fodder yield. During harvest main panicles of five random plants from each entry were harvested and stored separately in a cloth bag for grain micronutrients (Fe, Zn, Cu and Mn content) analysis.

### Micronutrient analysis

The cleaned grains from each entry were oven dried at 60 ºC for 48 hours and grinded in fine powder using mortar and pestle. Grinded samples were properly labeled and stored in butter paper cover for further analysis. The grain micronutrients were estimated from the acid extract prepared by wet digestion procedure of Singh *et al.* (2005) [35] using diacid mixture at Centre for Bioresearch Laboratory, S. D. Agricultural University, S. K. Nagar, Gujarat. One gram of grinded sample was pre-digested by adding 10 mL concentrated nitric acid ($HNO_3$) and kept for overnight. Further, prepared diacid mixture ($HNO_3$ and $HClO_4$) of approximately 10 mL was added to predigested sample. Then the samples were kept on hot plate for about 200ºC temperatures until the fume that comes out becomes colourless. After that heating was stopped and the digested sample was cooled for 20 minutes. Then about 50-60 mL distilled water was added in conical flask. The volume of digest was filtered with Whatman filter paper and final volume of 100 mL was made by adding double distilled water in conical flask. Care was taken at each step to avoid any contamination of samples with foreign dust particles. The samples were analyzed for iron and zinc content by Atomic Absorption Spectrophotometer (AAS), ELICO SL 194.

### Data analysis

### Variability studied

The experimental data were subjected to the analysis of variance as suggested by Panse and Sukhatme (1967) [27]. Genotypic and phenotypic coefficients of variation were computed based on method given by Burton (1952) [8] as follow:

$$\text{Phenotypic coefficient of variation (PCV\%)} = \frac{\sqrt{\text{Phenotypic variance}}}{\text{Grand mean}} \text{ x } 100$$

$$\text{Genotypic coefficient of variation (GCV\%)} = \frac{\sqrt{\text{Genotypic variance}}}{\text{Grand mean}} \text{ x } 100$$

The genotypic and phenotypic coefficient variance value were categorized as low (0-10%), moderate (10-20%) and high (20% and above) given by Sivasubramanian and Madhavamenon (1973) [33].

Broad-sense heritability was estimated using the following formula derived by Falconer (1989) [12].

$$H2 = \sigma^2 g / (\sigma^2 g + \sigma^2 e/r)$$

where, $H^2$ is broad sense heritability, $\sigma^2 g$ = is genotypic variance; $\sigma^2 e$ = is residual variance and r is the number of replications.

The Heritability was categorized by Robinson *et al*. (1949) [31] as followings: Low = 0-30%, moderate = 30-60% and high = 60% and above.

Genetic advance was expressed as percentage of mean by using formula suggested by Johnson *et al*., (1955) [15].

$$G.A. = H^2 k \sigma p$$

where, $H^2$ = Heritability in broad sense, k = Selection differential which is equal to 2.06 at 5% selection intensity and σp = Phenotypic standard deviation

Genetic advance as per cent of the mean was estimated by the formula suggested by Johnson *et al.* (1955) [15].

$$G.A.(\%\ of\ mean) = \frac{G.A.}{X} \times 100$$

According to Falconer (1989) [12] that the value of genetic advance as per cent of the mean is categorized as: Low = (< 10%), moderate = (10 - 20%) and high = (> 20%)

**Path Coefficient Analysis**

Path coefficient analysis were performed using the phenotypic and genotypic correlation coefficients to know the direct and indirect effect of yield components on grain yield using the general formula of Dewey and Lu (1959) [10] by considering grain yield per plant as dependent variable. The path coefficients were obtained by solving the following simultaneous equations, which express the basic relationship between correlation and path coefficient.

$$rij = pij + \sum rik.pkj$$

Where, $r_{ij}$ = mutual association between the independent character (i) and dependent character (j) as measured by the genotypic correlation coefficient. $p_{ij}$ components of direct effects of the independent character (i) on the dependent variable (j) as measured by the genotypic path coefficient; and $\sum r_{ik}.p_{kj}$ = summation of components of indirect effects of a given independent character (i) on a given dependent character (j) via all other independent character (k).

The residual effect, which determines how best the causal factors account for the variability of the dependent factor, was calculated using the following formula.

$$1 = p2r + \sum piy.riy$$

Where, $p^2r$ is the residual factor, $p^{iy}$ is the direct effect of yield by $i^{th}$ trait, and $r^{iy}$ is the correlation of yield with the $i^{th}$ trait.

The data were analysed using indostat and R statistical software, version 3.4.1 (R Development Core Team, 2017) [30].

**Results and Discussion**

**Genetic variability and heritability studies**

Analysis of variance for the eleven characters studied are presented in Table 2 which revealed highly significant differences ($p<0.01$) between the genotypes for all the characters studied. The mean values and range for each trait are given in the Table 3 along with value of genotypic and phenotypic variance, phenotypic and genotypic coefficients of variability, heritability in broad sense and genotypic advance as percentage of mean. The wide range of variability observed for the most of the traits studied. Variability is the key for success in plant breeding (Kumar *et al*. 2012) [19]. Among them grain yield ranged from 0.01 to 0.22 kg, fodder yield from 0.33 to 2.93 kg, plant height and yield contributing trait *viz*., panicle length 13.00 cm to 28.84 cm, panicle girth from 18.55 to 29.88 mm and panicle weight ranged from 0.02 to 0.44 kg per plant. Similarly for grain micronutrients content Fe ranged from 14.00 to 122.00 ppm (parts per million), Zn from 11.50 to 56.00 ppm, Cu from 4.50 to 10.50 ppm and Mn 4.50 to 14.50 ppm (Table 3). The analysis of variance revealed that the significant differences which indicated presence of variability among the genotypes being evaluated and ample scope of improvement by selection. The similar results were also reported by previous worker in pearl millet (Dapke *et al.* 2014, Anuradha *et al*. 2018, Mahendrakar *et al*. 2019 and Kumar *et al*. 2020) [9, 3, 25, 20].

The comparative values of genotypic and phenotypic coefficient of variation provide information on the magnitude of variation. The phenotypic coefficient of variation per cent was maximum for grain yield (83.15) followed by panicle weight (76.22), dry fodder yield (75.69), grain iron content (45.95), manganese content (41.27), zinc content (40.34), copper content (27.21) and panicle length (20.82). Moderate phenotypic coefficients of variation observed for the panicle girth (16.34). Low phenotypic variation was obtained for the days to 50% flower (7.37) (Table 3). Genotypic coefficient of variation per cent was highest for grain yield (67.45), panicle weight (61.14), grain Fe content (44.81), grain Zn content (36.98) and dry fodder yield (21.20). Moderate genotypic variation was obtained for the plant height (17.80) followed by grain Mn content (16.04), panicle length (15.36) and Cu content (14.10). Low genotypic coefficient of variation were observed for panicle girth (10.21) followed by days to 50% flower (4.51) (Table 3). The magnitude of phenotypic coefficient of variation was significantly higher than genotypic coefficient of variation for almost all the characters; this implies that more influence of environment for the expression of all the traits studied. High PCV and GCV for most of the traits indicating variation for these traits contributed markedly to the total variability and scope for genetic improvement through selection (Lakshmana *et al*. 2010, Choudhary *et al*. 2012, Dapke *et al*. 2014, Talawar *et al*. 2017) [24, 4, 9, 37]. In the present study, moderate to high PCV and GCV reported in grain yield per plant, panicle weight, dry fodder yield per plant, panicle length, grain Fe, Zn, Cu and Mn content and low to moderate for panicle girth and days to 50% flowering. Earlier Lakshmana *et al*. 2010 [24], Choudhary *et al*. 2012 [4], Dapke *et al*. 2014 [9], Kumar *et al*. 2014 [23], Talawar *et al*. 2017 [37] also reported similar variation for these characters in pearl millet.

High heritability estimates was observed for grain Fe (95.12%), grain Zn (84.04%), grain yield (65.80%), panicle weight (64.30%), plant height (61.90%) and moderate for panicle length (54.40%), panicle girth (39.10) and days to 50% flower (37.40%) (Table 3 and figure 1). The expected genetic advance was high for grain yield (112.72%), panicle weight (101.03%), grain Fe (90.04%), grain Zn (69.84%), plant height (28.85%), panicle length (23.33%) intermediate for panicle girth (13.16%) and dry fodder yield (12.23%) and remaining traits shown lower genetic advance (Table 3 and figure 2). High to moderate heritability coupled with moderate to high genetic advance as per cent of mean were observed for the plant height, panicle length, panicle girth, panicle weight, grain yield per plant, grain Fe and Zn content revealed the characters are predominantly governed by additive gene action and phenotypic selection for these characters will be effective for genetic improvement. High heritability coupled with high genetic advance values for yield and related traits were reported in pearl millet by Govindaraj *et al*. 2011 [13], Singh *et al*. 2013 [34], Dapke *et al*. 2014 [9], Kumar *et al*. 2014 [23], Talawar *et al*. 2017 [37]. High heritability and high genetic advance for grain iron and zinc content were reported by Anuradha *et al*. 2018 [3] and

Mahendrakar *et al*. 2019 [25] which revealed scope for selection in pearl millet.

**Path analysis**

Path coefficient analysis was worked out to determine the direct and indirect contributions of different traits towards grain yield per plant. Positive direct effect on grain yield per plant was observed by the dry fodder yield per plant followed by panicle weight, plant height and panicle length (Table 4). The direct selection for these traits might be highly effective for the improvement of grain yield per plant in pearl millet. Days to 50% flower, grain Zn content, grain Fe content, panicle girth and grain Mn content had negative direct effect which showed that selection should be done in negative direction for these traits (Table 4). It is recommended that these traits can be considered as key components for selection in a breeding programme for higher grain yield in pearl millet. Indirect effects of independent traits indicated that panicle length, panicle girth, days to 50% flower, plant height, dry fodder yield, grain Fe, Zn, Cu and Mn content contributed indirectly to grain yield per plant *via* other characters (Table 4). The present investigation were close corresponds with the previous findings of Dapke *et al.* (2014) [9], Kumar *et al.* (2014) [23], Rakesh *et al.* (2015) [29], Yahava *et al.* (2015) [41], Eric *et al.* (2016) [11], Bhasker *et al.* (2017) [7], Kumar *et al.* (2017) [21] and Kaushik *et al.* (2018) [17] in pearl millet. The minimum value of residual effect (0.1509) indicates that most of the characters contributing towards grain yield per plant are reliable and realistic.

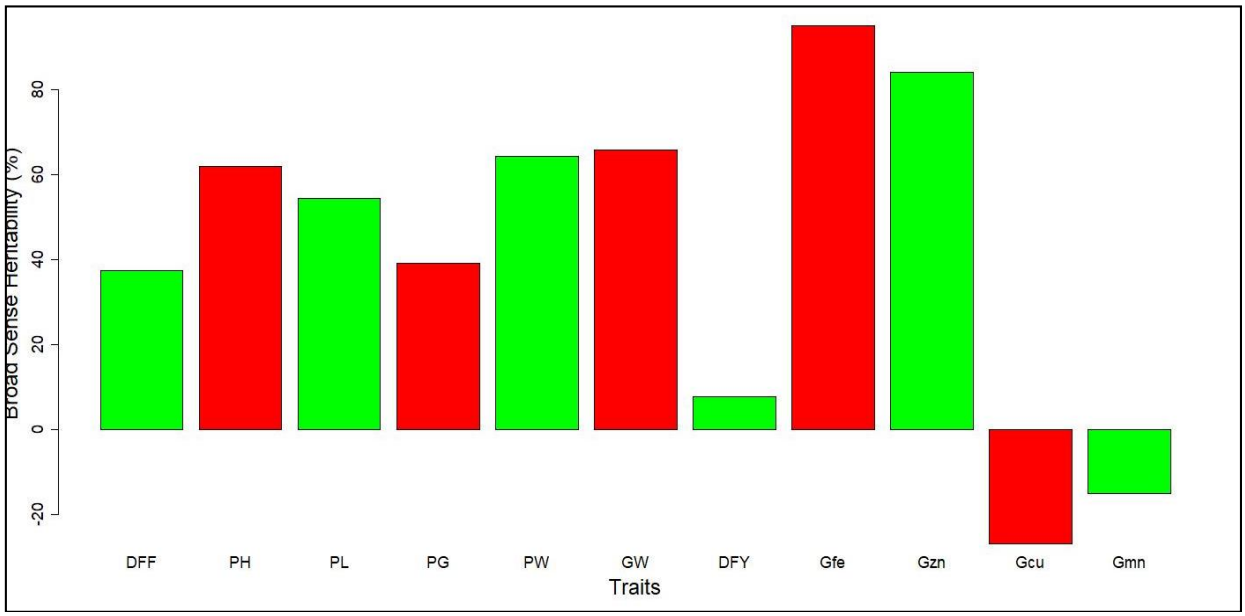


**Fig 1:** Heritability of 11 quantitative traits in pearl millet, DFF= Days to 50% flowering, PH= Plant height, PL= Panicle length, PG= Panicle girth, PW= Panicle weight, GW traits= Grain yield per plant, DFY= Dry fodder yield per plant, Gfe= Grain Fe content, Gzn= Grain zinc content, Gcu= Grain copper content, Gmn= Grain manganese content

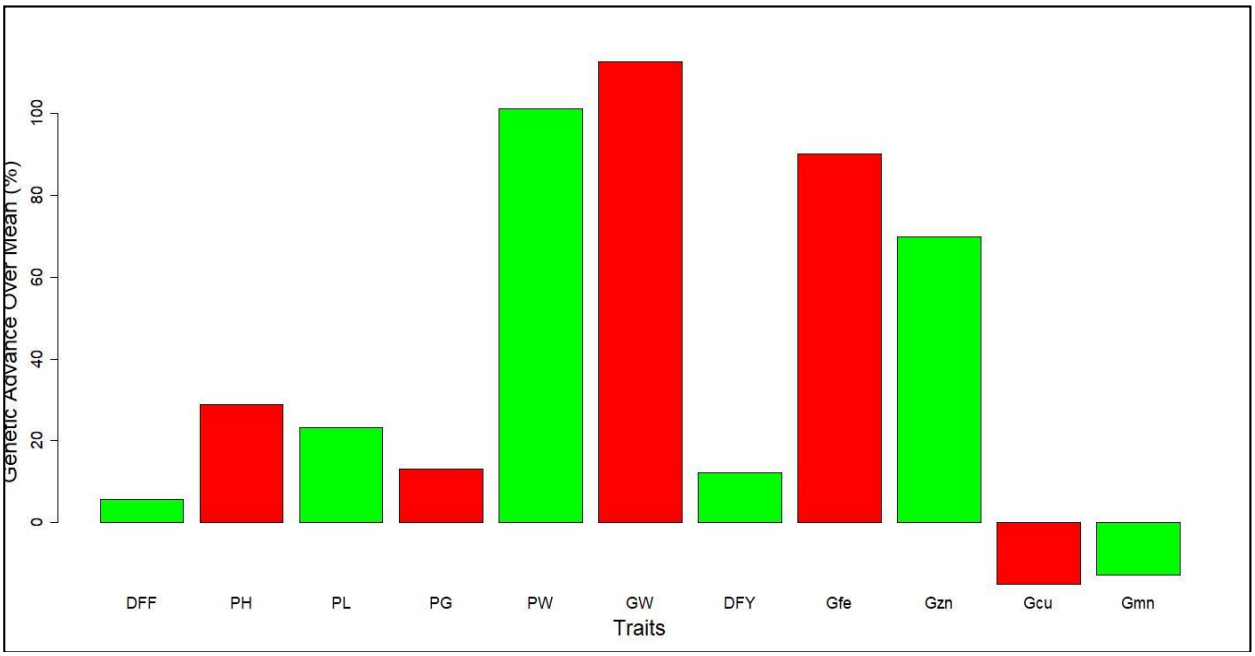


**Fig 2:** Genetic advance over mean(%) of 11 quantitative traits in pearl millet, DFF= Days to 50% flowering, PH= Plant height, PL= Panicle length, PG= Panicle girth, PW= Panicle weight, GW traits= Grain yield per plant, DFY= Dry fodder yield per plant, Gfe= Grain Fe content, Gzn= Grain zinc content, Gcu= Grain copper content, Gmn= Grain manganese content

**Table 1:** List of genotypes, pedigree, source / origin and their category

| Sr. No. | Genotype Name | Pedigree | Source / Origin | B line |
|---|---|---|---|---|
| 1 | ICMB 99222 | (BSECBPT/91-40 x SPF3/S91-94)-3-1-1-2 | ICRISAT, Patancheru | B line |
| 2 | ICMB 05888 | (SRC II C3 S1-1-1-2 x HHVBC)-5-1-1-2 | ICRISAT, Patancheru | B line |
| 3 | ICMB 92777 | [843 B x (ICMPES-500-4-4-3 x ICMPES-800-3-1-2(3-4)]-7-1-3 | ICRISAT, Patancheru | B line |
| 4 | ICMB 06777 | (ICMB 96333 x HHVBC-2-D2-HS-259-2)-4-B | ICRISAT, Patancheru | B line |
| 5 | ICMB 95222 | {[843B x (GNS x SS-48-40-4)-29-7-4-B] x (843B x ICMPES-29)-23-2-3}-16 | ICRISAT, Patancheru | B line |
| 6 | 213-SU-14B | [ICMB 96111 x 4017-2-1-B)-7-2-3 x (SRC II C3 S1-19-3-2 x HHVBC)-17-3}-1-3-19-2-2-2-B-2-4 | PMRS, JAU, Jamnagar | B line |
| 7 | 230-SU-14B | {[78-7088/3/SER3 AD//B282/(3/4)EB x PBLN/S95-359]-7-4-B-B-2-B-B x HHVDBC HS-10-1-2-1-1-1-4-1-1}-10-3-3-B | PMRS, JAU, Jamnagar | B line |
| 8 | ICMB 05333 | (MC 94 S1-30-2-B x HHVBC)-16-3-1-1 | ICRISAT, Patancheru | B line |
| 9 | ICMB 89111 | [843B x (CNS x SS-48-40-4)-1-9-8] | ICRISAT, Patancheru | B line |
| 10 | ICMB 96222 | 126B x (81B x SLR 50-1)-1-1-2 x 852B)-69-1-1 | ICRISAT, Patancheru | B line |
| 11 | 225-SU-14B | {(MC 94 S1-34-1-B x HHVBC)-16-2-1-1-1-1-B-B-5 x (MC 94 S1-34-1-B x HHVBC)-10-4-1-2-1-B-B-1-30-2-4-3-6-4-3 | PMRS, JAU, Jamnagar | B line |
| 12 | ICMB 04999 | (EBC-Gen-S1-40-2-2-1 x B-line bulk)-25-B-B | ICRISAT, Patancheru | B line |
| 13 | 218-SU-14B | [(SRC II C3 S1-1-1-2 x HHVBC)-2-2-1-1-1-B-B x (81B x 4017-5-4-B)-12-3-1-3]-6-2-3-3-2 | PMRS, JAU, Jamnagar | B line |
| 14 | 227-SU-14B | [(MC 94 S1-34-1-B x HHVBC)-16-1-3-1-2-2-B-B-2-B-B x ICMB 99222]-13-2-1-2 | PMRS, JAU, Jamnagar | B line |
| 15 | 212-SU-14B | (ICMB 04777 x ICMB 04111)-2-2-2-2-1 | PMRS, JAU, Jamnagar | B line |
| 16 | 211-SU-14B | [ICMB 96111 x 4017-2-1-B)-7-2-3 x ((SRC II C3 S1-19-3-2 x HHVBC)-17-3]-1-3-19-2-2-2-B-2-2 | PMRS, JAU, Jamnagar | B line |
| 17 | 215-SU-14B | {[(843B x ICTP 8202-161-5)-20-3-B-B-3 x B-bulk]-2-B-1-2-2-B-B-B-11-1 x B-bulk (3981-4011/S06 G1)}-3-2-4- | PMRS, JAU, Jamnagar | B line |
| 18 | ICMB 05222 | (ICMR-312S1-8-3-3-B x HHVBC)-9-4-1-1 | ICRISAT, Patancheru | B line |
| 19 | 224-SU-14B | [EEDBC S1-425-2-1-2-3-B-1-B-7-1 x B-bulk (3981-4011/S06 G1)]-2-2-1-B | PMRS, JAU, Jamnagar | B line |
| 20 | ICMB 08444 | HHVBC II D2 HS-410-1-2-4-1-3-B-2-2-3-2 | ICRISAT, Patancheru | B line |
| 21 | 226-SU-14B | (ICMB 99555 x ICMB 00555)-11-1-3-B-2-B-2 | PMRS, JAU, Jamnagar | B line |
| 22 | ICMB 98222 | ARD-288-1-10-1-2(RM)-5 | ICRISAT, Patancheru | B line |
| 23 | ICMB 841 | DM.RESI.SELE.FROM SEED LOT NO.8015 OF 5141B | ICRISAT, Patancheru | B line |
| 24 | 261-SU-14B | 09888B x [(HHVDBC HS-246-1-2-1-2 x ICMB 01222)-4-2-1-1]-2-1 | PMRS, JAU, Jamnagar | B line |

| Sr. No. | Genotype Name | Pedigree | Source / Origin | R line |
|---|---|---|---|---|
| 25 | 121-SM-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-17-4-3-2 | PMRS, JAU, Jamnagar | R line |
| 26 | J-2510 | JBV 3-S1-231 | PMRS, JAU, Jamnagar | R line |
| 27 | J-2500 | AIB-1-2-B | PMRS, JAU, Jamnagar | R line |
| 28 | J-2480 | AS-14 (B-Senegal-2-5 x 700651)-2-1-4 (IPC-655) | PMRS, JAU, Jamnagar | R line |
| 29 | 123-SB-14 | (J-2340 x J-2454)-15-10-8-3-1-1-1 | PMRS, JAU, Jamnagar | R line |
| 30 | 106-SB-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-34-4-1 | PMRS, JAU, Jamnagar | R line |
| 31 | 131-SM-14 | (MRC HS-86-1-1-5-B-B-B-B-B x MRC S1-54-2-3-B-B-1-B-B)-19 | PMRS, JAU, Jamnagar | R line |
| 32 | J-2523 | MRC HS 130-2-2-1-B-B-1-B-B | PMRS, JAU, Jamnagar | R line |
| 33 | 113-SB-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-34-4-1 | PMRS, JAU, Jamnagar | R line |
| 34 | 124-SB-14 | (J-2405 x J-2480)-13-10-2-1-1-1-1 | PMRS, JAU, Jamnagar | R line |
| 35 | J-2549 | (IPC 107 × SDMV 90031-S1-84-1-1-1-1)-1-2-1-3-B | PMRS, JAU, Jamnagar | R line |
| 36 | 237-SM-13 | ICTP 8203 | PMRS, JAU, Jamnagar | R line |
| 37 | 94-SB-13 | (EERC-HS-8)-20-1-5 | PMRS, JAU, Jamnagar | R line |
| 38 | 128-SM-14 | (EERC-HS-32)-B-8-1-1-B | PMRS, JAU, Jamnagar | R line |
| 39 | 199-SM-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-22-2-1 | PMRS, JAU, Jamnagar | R line |
| 40 | 109-SB-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-34-4-1 | PMRS, JAU, Jamnagar | R line |
| 41 | 123-SM-14 | (J-2340 x J-2454)-15-10-8-3-1-1-1 | PMRS, JAU, Jamnagar | R line |
| 42 | 99-SM-13 | (SRC II C3 S1-19-3-2 x HHVBC)-3-5-1P2 x ((ICMV IS 94206 S1-15-2) x {(SRC II C3 S1-19-3-2 x HHVBC)-5-3-1})-B-1-2-1-1)-B-2-2-2-1 | PMRS, JAU, Jamnagar | R line |
| 43 | 93-SM-13 | CGP S1-14-1 | PMRS, JAU, Jamnagar | R line |
| 44 | 95-SM-13 | (ICMB 04888 x ICMB 02333)-3-1-3-1 | PMRS, JAU, Jamnagar | R line |
| 45 | 110-SB-13 | (MC 94 C2-S1-3-2-2-2-1-3-B-B x ICMR 312 S1-3-2-3-2-1-1-B-B)-B-17-4-3-2-B-B | PMRS, JAU, Jamnagar | R line |
| 46 | 108-SB-13 | (J 834 x 700516)-1-4-4-2-4-B-2-2-B-B-B-1 | PMRS, JAU, Jamnagar | R line |
| 47 | 73-SB-13 | ICMR 312 S1-8-1-1-1-1-B-B-B-1-B | PMRS, JAU, Jamnagar | R line |
| 48 | J-2512 | (PPMI-362 x IP-5738-1) x RIB-3135-18-5-3-8-B | PMRS, JAU, Jamnagar | R line |

**Table 2:** ANOVA (Analysis of Variance) of 11 quantitative traits in pearl millet

| Source of Variation | Degree of Freedom | Days to 50% Flower | Plant Height (cm) | Panicle Length (cm) | Panicle Girth (mm) | Panicle Weight (kg) | Grain Yield (kg) | Dry Fodder Yield (kg) | Grain Fe Content (ppm) | Grain Zn Content (ppm) | Grain Cu Content (ppm) | Grain Mn Content (ppm) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Replication | 1 | 110.51** | 0.01 | 35.97* | 0.02 | 0.001 | 0.01* | 0.04 | 10.01 | 11.35 | 2.35 | 5.51 |
| Genotypes | 47 | 25.38** | 1028.73** | 25.55** | 21.24** | 0.03** | 0.01** | 0.63 | 1518.07** | 223.29** | 3.11 | 16.81 |
| Error | 47 | 11.55 | 241.90 | 7.54 | 9.30 | 0.01 | 0.00 | 0.54 | 38.50 | 23.79 | 5.39 | 22.79 |
| SEm.± | | 2.38 | 10.89 | 1.93 | 2.14 | 0.05 | 0.03 | 0.52 | 4.35 | 3.42 | 1.63 | 3.35 |
| C.D. at 5% | | 6.84 | 31.29 | 5.53 | 6.14 | 0.15 | 0.07 | NS | 12.49 | 9.82 | NS | NS |

**Table 3:** Mean, range, coefficient of variability (genotypic, phenotypic and environment), heritability and genetic advance as per cent of mean of pearl millet

| Characters | Mean | Range | | | | | | | Heritability (Broad sense) | Expected GA | GA as % of mean |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | PV | GV | EV | PCV | GCV | ECV | | | |
| Days to 50% Flower | 58.30 | 50.00-65.00 | 18.47 | 6.91 | 11.55 | 7.37 | 4.51 | 5.83 | 37.40 | 3.31 | 5.68 |
| Plant Height(cm) | 111.45 | 61.67-153.80 | 635.32 | 393.41 | 241.90 | 22.62 | 17.80 | 13.96 | 61.90 | 32.15 | 28.85 |
| Panicle Length(cm) | 19.54 | 13.00-28.84 | 16.55 | 9.00 | 7.54 | 20.82 | 15.36 | 14.06 | 54.40 | 4.56 | 23.33 |
| PanicleGirth(mm) | 23.93 | 18.55-29.88 | 15.27 | 5.97 | 9.30 | 16.34 | 10.21 | 12.75 | 39.10 | 3.15 | 13.16 |
| Panicle Weight(kg) | 0.17 | 0.02-0.44 | 0.02 | 0.01 | 0.01 | 76.22 | 61.14 | 45.51 | 64.30 | 0.17 | 101.03 |
| Grain Yield(kg) | 0.071 | 0.01-0.22 | 0.00 | 0.00 | 0.00 | 83.15 | 67.45 | 48.63 | 65.80 | 0.08 | 112.72 |
| Dry Fodder Yield(kg) | 1.01 | 0.33-2.93 | 0.59 | 0.05 | 0.54 | 75.69 | 21.20 | 72.66 | 7.80 | 0.12 | 12.23 |
| Grain Fe Content(ppm) | 60.44 | 14.00-122.00 | 771.24 | 733.59 | 37.65 | 45.95 | 44.81 | 10.63 | 95.12 | 54.63 | 90.04 |
| Grain Zn Content(ppm) | 29.54 | 11.50-56.00 | 141.95 | 119.29 | 22.66 | 40.34 | 36.98 | 17.11 | 84.04 | 18.49 | 69.84 |
| Grain Cu Content(ppm) | 7.58 | 4.50-10.50 | 4.25 | -1.14 | 5.39 | 27.21 | 14.10 | 30.65 | -26.85 | -1.14 | -15.05 |
| Grain Mn Content(ppm) | 10.79 | 4.50-17.50 | 19.80 | -2.99 | 22.79 | 41.27 | 16.04 | 44.28 | -15.10 | -1.38 | -12.84 |

PV= Phenotypic variance, GV= Genotypic variance, EV= Environmental variance, PCV= Phenotypic coefficient of variation, GCV= Genotypic coefficient of variation, ECV= Environmental coefficient of Variation, GA= Genetic advance

**Table 4:** Estimate of direct effect (diagonal) and indirect effects (off diagonal) at genotypic level of 48 B and R lines in pearl millet

| | Panicle Length (cm) | Panicle Girth (mm) | Days to 50% Flower | Plant Height (cm) | Panicle Weight (kg) | Dry Fodder Yield (kg) | Grain Fe Content (ppm) | Grain Zn Content (ppm) | Grain Cu Content (ppm) | Grain Mn Content (ppm) | rg |
|---|---|---|---|---|---|---|---|---|---|---|---|
| PanicleLength (cm) | -0.1346 | 0.0548 | -0.0124 | -0.0599 | -0.0448 | -0.095 | 0.0089 | 0.0553 | -0.0375 | 0.0032 | -0.0373 |
| Panicle Girth (mm) | 0.0687 | -0.1689 | 0.0162 | 0.0468 | 0.0071 | 0.038 | 0.0253 | 0.0355 | 0.0271 | -0.0662 | 0.0207 |
| Days to 50% Flower | 0.0001 | -0.0001 | 0.001 | -0.0002 | -0.0005 | -0.0001 | 0.0002 | 0.0001 | 0.0003 | 0.0001 | -0.0005 |
| Plant Height (cm) | -0.0407 | 0.0253 | 0.0145 | -0.0914 | -0.0451 | -0.1645 | 0.0307 | 0.0306 | -0.0347 | 0.008 | -0.0411 |
| Panicle Weight (kg) | 0.3461 | -0.0437 | -0.5562 | 0.513 | 1.0396 | 1.6549 | -0.1223 | -0.2074 | 0.0633 | 0.0521 | 1.0146** |
| Dry Fodder Yield (kg) | 0.0006 | -0.0002 | -0.0001 | 0.0016 | 0.0014 | 0.0009 | -0.0007 | -0.0006 | -0.0001 | 0.0002 | 0.0013 |
| Grain Fe Content (ppm) | 0.0018 | 0.0041 | -0.0054 | 0.0092 | 0.0032 | 0.0215 | -0.0274 | -0.0083 | 0.0116 | -0.018 | 0.0035 |
| Grain Zn Content (ppm) | 0.0338 | 0.0173 | -0.0047 | 0.0275 | 0.0164 | 0.0618 | -0.025 | -0.0822 | 0.0079 | -0.0011 | 0.0146 |
| Grain Cu Content (ppm) | 0.0004 | -0.0002 | 0.0004 | 0.0005 | 0.0001 | -0.0002 | -0.0006 | -0.0001 | 0.0013 | 0.0009 | 0.00 |
| Grain Mn Content (ppm) | 0.0007 | -0.011 | -0.0036 | 0.0025 | -0.0014 | -0.0057 | -0.0184 | -0.0004 | -0.0184 | -0.028 | 0.0014 |
| Grain Yield(kg) | 0.2769 | -0.1226 | -0.5504 | 0.4496 | 0.9759 | 1.5116 | -0.1293 | -0.1776 | 0.0207 | -0.0489 | -0.0373 |
| Residual effects: 0.1509 | | | | | | | | | | | |

rg= Genetic correlation coefficients between grain yield and other component traits, ** = significance at 0.01 per cent level of probability

## Conclusion

The value of heritability estimates high for all characters; therefore, the genotypic variability prevails over the general phenotypic variability in all studied characters. This indicated that the greatest genotypic variability was observed for these traits and that variability could be utilized in breeding programs. This suggests a definite scope for improvement of these characters through direct selection. It is also suggested that hybridization of genotypes possessing combination of above characters is most useful for obtaining desirable high yielding segregation. Due to high positive direct effect of characters like dry fodder yield per plant, panicle weight, plant height and panicle length on grain yield per plant can be directly used for improvement of pearl millet productivity. Finally, the presence of variability among the lines, heritability and genetic advance of the grain micronutrients concentration, yield and component traits of the genotypes confirmed possibility to increase pearl millet yield.

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