

ISSN Print: 2617-4693 ISSN Online: 2617-4707 NAAS Rating (2025): 5.29 IJABR 2025; SP-9(8): 1844-1846 www.biochemjournal.com Received: 09-06-2025 Accepted: 13-07-2025

SN Jaybhaye

M.Sc. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Badnapur, Maharashtra, India

AB Bagade

Associate Professor, Department of Genetics and Plant Breeding, National Agriculture Research Project, Chhatrapati Sambhajinagar, Maharashtra, India

SB Kadam

Assistant Professor (Agronomy), National Agriculture Research project. Chhatrapati Sambhajinagar, Maharashtra, India

Mahesh D Patil

Ph.D Scholar, Department of Genetics and Plant Breeding, Punjab Agricultural University, Ludhiana, Punjab, India

Corresponding Author: SN Jaybhaye

M.Sc. Scholar, Department of Genetics and Plant Breeding, College of Agriculture, Badnapur, Maharashtra, India

Correlation analysis of yield and yield-contributing traits in pearl millet (*Pennisetum glaucum* L.) germplasm

SN Jaybhaye, AB Bagade, SB Kadam and Mahesh D Patil

DOI: https://www.doi.org/10.33545/26174693.2025.v9.i8Sy.5452

Abstract

An experiment entitled "Genetic diversity studies in pearl millet [Pennisetum glaucum (L.) R. Br.]". was carried out during Kharif 2024 at the Research Farm of National Agriculture Research Project, Chhatrapati Sambhajinagar. The experiment was laid out in Randomized Block Design (RBD) with 42 genotypes and two replications to estimate the extent of genetic variability, heritability, genetic advance, correlation coefficient and path coefficient analysis among all the genotypes.

The characters, including the number of productive tillers per plant, panicle girth, 1000 Grain Wt. (g), and Fodder yield per plot, demonstrated a positive and significant correlation with grain yield per plant. In contrast, traits such as panicle length, days of maturity, Harvest Index, plant height showed a positive yet non-significant effect. This indicates the substantial role and importance of these characters in the development of superior genotypes with high yield potential.

Keywords: Pearl millet, genetic divergence, correlation and path analysis

Introduction

Pearl millet (*Pennisetum glaucum* L. R. Br.) is an annual, diploid (2n = 14), highly cross-pollinated cereal crop belonging to the family Poaceae, subfamily Panicoideae. Believed to have originated in West Africa (Vavilov, 1950), it is now extensively cultivated in arid and semi-arid regions owing to its exceptional drought tolerance, short growth cycle, and high photosynthetic efficiency. In India, it is primarily grown during the kharif season, with Rajasthan, Maharashtra, Uttar Pradesh, Gujarat, and Haryana accounting for the majority of production.

The crop thrives under 400-600 mm of annual rainfall and temperatures between 15 °C and 40 °C, with optimum growth occurring at 30-35 °C. It performs well in sandy loam to clay loam soils, tolerates marginal conditions, and is well adapted to low-input farming systems. Nutritionally, pearl millet surpasses many staple cereals, providing high protein, dietary fiber, essential minerals such as iron and zinc, and health-promoting polyunsaturated fatty acids (Singh *et al.*, 2021) ^[8]. Its low glycemic index and high resistant starch content make it particularly beneficial for managing lifestyle-related disorders (Anuradha *et al.*, 2021).

Genetic improvement in pearl millet relies on understanding variability, heritability, and genetic advance for key traits, alongside correlation and path coefficient analyses to identify traits exerting the greatest influence on yield. Assessing genetic diversity within germplasm helps identify superior and genetically divergent parents for hybridization, thereby accelerating the development of high-yielding, climate-resilient, and nutrient-dense cultivars (Singh *et al.*, 2021) [8].

Materials and Methods

The present study, entitled "Genetic Diversity Studies in Pearl Millet Germplasm [Pennisetum glaucum (L.) R. Br.]", was conducted during Kharif 2024-2025. The experimental material, selected from the germplasm maintained at the National Agricultural Research Project, Chhatrapati Sambhajinagar, was evaluated in a Randomized Block Design (RBD) with two replications.

A total of 42 genotypes, comprising 40 inbred lines and two checks (ABPC 4-3 and AIMP 92901), were used.

The genotypes were sown in two rows of 4 m length each, with a spacing of 45 cm between rows and 15 cm between plants. Standard agronomic practices, including timely weeding, irrigation, and other intercultural operations, were carried out as per the crop's growth stage and requirements. Fertilizer was applied at the recommended dose, and all crop management activities were performed according to standard guidelines.

The experimental material was selected to represent wider diversity for various morphological and yield-related traits, ensuring comprehensive assessment of genetic variability.

Table 1: List of Genotypes

| Sr. No | Entry | Sr. No | Entry | | | |
|----------|-------------|-----------|-------------|--|--|--|
| 1 | AUBI-15333R | 21 | AUBI-15280R | | | |
| 2 | AUBI-15452R | 22 | AUBI-15287R | | | |
| 3 | AUBI-15313R | 23 | AUBI-15050R | | | |
| 4 | AUBI-15448R | 24 | AUBI-15309R | | | |
| 5 | AUBI-15352R | 25 | AUBI-15221R | | | |
| 6 | AUBI-15387R | 26 | AUBI-15346R | | | |
| 7 | AUBI-15262R | 27 | AUBI-15286R | | | |
| 8 | AUBI-15260R | 28 | AUBI-15052R | | | |
| 9 | AUBI-15279R | 29 | AUBI-18097R | | | |
| 10 | AUBI-15241R | 30 | AUBI-15022R | | | |
| 11 | AUBI-15348R | 31 | AUBI-15071R | | | |
| 12 | AUBI-15245R | 32 | AUBI-15024R | | | |
| 13 | AUBI-15233R | 33 | AUBI-15415R | | | |
| 14 | AUBI-15265R | 34 | AUBI-16287R | | | |
| 15 | AUBI-15385R | 35 | AUBI-15374R | | | |
| 16 | AUBI-15358R | 36 | AUBI-15184R | | | |
| 17 | AUBI-15453R | 37 | AUBI-15137R | | | |
| 18 | AUBI-15468R | 38 | AUBI-16630R | | | |
| 19 | AUBI-15230R | 39 | AUBI-15043R | | | |
| 20 | AUBI-1549R | 40 | AUBI-18801R | | | |
| Checks I | ABPC 4-3 | Checks II | AIMP-92901 | | | |

Results and Discussion Correlation Studies

Tables 4.8 and 4.9, present the genotypic and phenotypic correlation coefficients for grain yield and its component traits. Only statistically significant positive or negative associations are discussed in detail. In general, phenotypic correlation coefficients were observed to be higher than their corresponding genotypic coefficients.

Association of Grain Yield with Its Components

Grain yield per plant exhibited a significant positive association with days to maturity (P = 0.2054; G = 0.1400), plant height (P = 0.1611; G = 0.2050), number of productive tillers per plant (P = 0.4140; G = 0.5736), panicle girth (P = 0.2285; G = 0.3194), 1000-grain weight (P = 0.2326; G = 0.2854), fodder yield per plot (P = 0.3538; G = 0.5615), and harvest index (P = 0.0672; G = 0.1244) at both phenotypic and genotypic levels.

Days to 50% Flowering with Other Characters

Days to 50% flowering showed a significant positive correlation with days to maturity ($G=0.3319;\ P=0.2631$) at both levels. Non-significant positive correlations were observed with harvest index ($G=0.0669;\ P=0.0593$) and

plant height (G=0.0426; P=0.0375). Significant negative correlations were recorded with number of productive tillers per plant (G=-0.2890; P=-0.2647) and fodder yield per plot (G=-0.4907; P=-0.4141). Non-significant negative associations were observed with panicle girth (G=-0.0414; P=-0.0337) and 1000-grain weight (G=-0.1668; P=-0.1709). Grain yield per plant had a significant negative correlation with days to 50% flowering (G=-0.3627; P=-0.2476).

Days to Maturity with Other Characters

Days to maturity had non-significant negative correlations with number of productive tillers per plant (G=-0.1959; P=-0.1924) and panicle length (G=-0.0760; P=-0.0670). It showed a non-significant positive association with 1000-grain weight (G=0.0980; P=0.0619), panicle girth (G=0.1974; P=0.1895), and harvest index (G=0.1415; P=0.0801). A significant positive correlation was recorded with fodder yield per plot (G=0.4692; P=0.2710). Association with plant height was positive but non-significant at the genotypic level (G=0.0207) and negative non-significant at the phenotypic level (P=-0.0165). Grain yield per plant showed a non-significant positive correlation with days to maturity (G=0.1400; P=0.2054).

Plant Height with Other Characters

Plant height showed a significant positive correlation with panicle girth (G=0.8060; P=0.7310) and harvest index (G=0.6440; P=0.6150). Non-significant positive correlations were recorded with number of productive tillers per plant (G=0.1195; P=0.1138), fodder yield per plot (G=0.0462; P=0.0405), and grain yield per plant (G=0.1195; P=0.1138). Non-significant negative associations were observed with panicle length (G=-0.2126; P=-0.1333) and 1000-grain weight (G=-0.0403; P=-0.0434).

Number of Productive Tillers per Plant with Other Characters

Number of productive tillers per plant had a significant positive correlation with 1000-grain weight (G=0.2536; P=0.2343), fodder yield per plot (G=0.3528; P=0.2586), and grain yield per plant (G=0.5736; P=0.4140). Nonsignificant positive associations were observed with panicle length (G=0.1832; P=0.1528), panicle girth (G=0.1152; P=0.1076), and harvest index (G=0.1002; P=0.1071).

Panicle Length with Other Characters

Panicle length had non-significant positive correlations with 1000-grain weight (G=0.2536; P=0.2343), panicle girth (G=0.1152; P=0.1076), fodder yield per plot (G=0.3528; P=0.2586), and harvest index (G=0.1002; P=0.1071). Grain yield per plant showed a non-significant positive association with panicle length at the genotypic level (G=0.0159) and a non-significant negative association at the phenotypic level (P=-0.0011).

Panicle Girth with Other Characters

Panicle girth had significant positive correlations with fodder yield per plot (G=0.3721; P=0.2729), harvest index (G=0.6535; P=0.5950), 1000-grain weight (G=0.4171; P=0.3992), and grain yield per plant (G=0.3194; P=0.2285).

1000-Grain Weight with Other Characters

1000-grain weight exhibited significant positive correlations with fodder yield per plot (G=0.4599; P=0.3387) and grain yield per plant (G=0.2854; P=0.2326). Nonsignificant positive correlations were observed with harvest index (G=0.0064; P=0.0030).

Fodder Yield per Plot with Other Characters

Fodder yield per plot showed a significant positive

correlation with grain yield per plant (G = 0.5615; P = 0.3538). It also had a non-significant positive correlation at the genotypic level (G = 0.0429) and a non-significant negative correlation at the phenotypic level (P = -0.0323).

Harvest Index with Other Characters

Harvest index showed a non-significant positive association with grain yield per plant ($G=0.1244;\ P=0.0672$) at both levels.

| Table 4.8: Estimation of | phenotypic | correlation | coefficient | in E | Baira. |
|---------------------------------|------------|-------------|-------------|------|--------|
| | | | | | |

| Characters | Days to 50% Flowering | Days to Maturity | Plant Height (cm) | No. of Tillers/Plant | Panicle Length (cm) | Panicle Girth (cm) | 1000- Grain Wt.(g) | Fodder Yield/plant (g) | Harvest Index (%) | Grain Yield/plant (g) |
|-----------------------------|-----------------------|---------------------|-------------------------|-------------------------|---------------------------|--------------------------|--------------------------|------------------------------|----------------------|-----------------------------|
| Days to 50% flowering | 1.0000 | 0.2631* | 0.0375 | -0.2647* | -0.0305 | -0.0337 | -0.1709 | -0.4141*** | 0.0593 | -0.2476 |
| Days To Maturity | | 1.0000 | -0.0165 | -0.1924 | -0.0670 | 0.1895 | -0.0689 | 0.2710* | 0.0801 | 0.2054 |
| Plant height (cm) | | | 1.0000 | 0.1138 | -0.1333 | -0.2318* | -0.0434 | 0.0405 | -0.2765* | 0.1611 |
| Number of tillers per plant | | | | 1.0000 | 0.1528 | 0.1076 | 0.2343* | 0.2586* | 0.1071 | 0.4140 |
| Panicle length(cm) | | | | | 1.0000 | 0.0655 | 0.0950 | 0.0365 | 0.1155 | -0.0011 |
| Panicle girth (cm) | | | | | | 1.0000 | 0.3992*** | 0.2729* | 0.5950*** | 0.2285 |
| 1000-Grain Wt.(g) | | | | | | | 1.0000 | 0.3387** | 0.0030 | 0.2326 |
| Fodder Yield/plot(kg) | | | | | | | | 1.0000 | -0.0323 | 0.3538 |
| Harvest Index (%) | | | | | | | | | 1.0000 | 0.0672 |

^{*, **} indicate significance at the 5% and 1% probability levels, respectively.

Table 4.9: Estimation of genotypic correlation coefficient in Bajra.

| Characters | Days to 50% Flowering | Days to Maturity | Plant Height (cm) | No. of Tillers/Plant | Panicle Length (cm) | Panicle Girth (cm) | 1000- Grain Wt.(g) | Fodder Yield/plant (g) | Harvest Index (%) | Grain Yield/plant (g) |
|-----------------------------|-----------------------|---------------------|-------------------------|-------------------------|---------------------------|--------------------------|--------------------------|------------------------------|-------------------------|-----------------------------|
| Days to 50% flowering | 1.0000 | 0.3319*** | 0.0426 | -0.2890** | -0.0340 | -0.0414 | -0.1668 | -0.4907*** | 0.0669 | -0.3627 |
| Days to maturity | | 1.0000 | 0.0207 | -0.1959 | -0.0760 | 0.1974 | -0.0894 | 0.4692*** | 0.1415 | 0.1400 |
| Plant height (cm) | | | 1.0000 | 0.1195 | -0.2126 | -0.2494* | -0.0403 | 0.0462 | -0.3613 | 0.2050 |
| Number of tillers per plant | | | | 1.0000 | 0.1832 | 0.1152 | 0.2536* | 0.3528*** | 0.1002 | 0.5736 |
| panicle length(cm) | | | | | 1.0000 | 0.0754 | 0.0917 | 0.0558 | 0.0694 | 0.0159 |
| panicle girth (cm) | | | | | | 1.0000 | 0.4171** | 0.3721*** | 0.6435*** | 0.3194 |
| 1000-Grain Wt.(g) | | | | | | | 1.0000 | 0.4599*** | 0.0064 | 0.2854 |
| Fodder Yield/plot(kg) | | | | | | | | 1.0000 | 0.0429 | 0.5615 |
| Harvest Index (%) | | | | | | | | | 1.0000 | 0.1244 |

^{*, **} indicate significance at the 5% and 1% probability levels, respectively.

References

- 1. Chittem K, *et al.* Genome-wide association mapping of *Fusarium* wilt resistance in *Phaseolus vulgaris*. Plant Genome. 2020;13(2):e20013. doi:10.1002/tpg2.20013
- Doddamani D, et al. Deployment of genomics tools for enhancing resistance to Fusarium wilt in Cicer arietinum. Front Genet. 2019;10:1106. doi:10.3389/fgene.2019.01106
- 3. Gao C, et al. Breeding for Fusarium wilt resistance in Solanum lycopersicum using genomic and molecular tools. Hortic Res. 2022;9:uhac017. doi:10.1093/hr/uhac017
- 4. Jha UC, *et al.* Genomic approaches for improving *Fusarium* wilt resistance in grain legumes. Theor Appl Genet. 2020;133:1585-1602. doi:10.1007/s00122-020-03566-y
- 5. Li W, *et al.* Genetic mapping and molecular breeding for *Fusarium* wilt resistance in crops. Crop J. 2021;9(5):1041-1052. doi:10.1016/j.cj.2021.03.004
- 6. Sarker A, *et al.* Genetic resistance to *Fusarium* wilt in lentil: current status and future prospects. Euphytica. 2019;215:157. doi:10.1007/s10681-019-2485-4
- 7. Sharma M, et al. Molecular breeding for resistance to Fusarium wilt in Cajanus cajan: current status and

- future prospects. Plant Breed. 2020;139(5):807-820. doi:10.1111/pbr.12836
- 8. Singh RP, *et al.* Advances in breeding for *Fusarium* wilt resistance in wheat and other cereals. Euphytica. 2021;217:114. doi:10.1007/s10681-021-02840-y
- 9. Wu L, *et al.* Functional genomics of *Fusarium oxysporum* and host-pathogen interactions. Plant Pathol. 2021;70(1):27-39. doi:10.1111/ppa.13261
- 10. Zhang J, *et al.* Molecular mapping of resistance genes to *Fusarium* wilt in *Gossypium* spp. Theor Appl Genet. 2020;133:1433-1443. doi:10.1007/s00122-020-03549-z