International Journal of Agriculture and Food Science 2025; 7(10): 516-519

ISSN Print: 2664-844X
ISSN Online: 2664-8458
NAAS Rating (2025): 4.97
IJAFS 2025; 7(10): 516-519
www.agriculturaljournals.com
Received: 09-08-2025
Accepted: 11-09-2025

VS Patil
PG Scholar, Department of Genetics and Plant Breeding, RCSM College of Agriculture, Kolhapur, Maharashtra, India

MS Kamble
Assistant Professor of Agricultural Botany, RCSM College of Agriculture, Kolhapur, Maharashtra, India

SR Karad
Professor of Agricultural Botany, RCSM College of Agriculture, Kolhapur, Maharashtra, India

PN Gajbhiye
Assistant Professor of Soil Science and Agricultural Chemistry, Zonal Agricultural Research Station, Kolhapur, Maharashtra, India

RH Gound
PG Scholar, Department of Genetics and Plant Breeding, RCSM College of Agriculture, Kolhapur, Maharashtra, India

AR Patil
PG Scholar, Department of Genetics and Plant Breeding, RCSM College of Agriculture, Kolhapur, Maharashtra, India

Corresponding Author:
VS Patil
PG Scholar, Department of Genetics and Plant Breeding, RCSM College of Agriculture, Kolhapur, Maharashtra, India

Correlation and Path Coefficient Analysis of Yield and Yield-Attributing Traits in Proso Millet (*Panicum miliaceum* L.)

VS Patil, MS Kamble, SR Karad, PN Gajbhiye, RH Gound and AR Patil

DOI: https://www.doi.org/10.33545/2664844X.2025.v7.i10h.914

Abstract
Proso millet (*Panicum miliaceum* L.) is an important Summer annual crop grown across various Indian states and globally, with diverse common names reflecting its widespread cultivation. The crop's genetic classification comprises five races based on panicle morphology: *miliaceum*, *patentissimum*, *contractum*, *compactum* and *ovatum*. Characterizing germplasm for morpho-agronomic traits is essential for broadening the genetic base and effective breeding. This study evaluated 35 proso millet genotypes at Kolhapur in *S*ummer 2024 through a randomized block design experiment to estimate genotypic correlations and path coefficients among yield and yield-contributing traits. Correlation analysis revealed that grain yield per plant is highly significant and positively correlated with fodder yield, basal tiller number, panicle length, days to physiological maturity, flowering time, plant height and thousand grain weight, while protein content exhibited a highly significant and negative correlation with grain yield per plant. Path coefficient analysis showed that fodder yield per plant exerted the highest positive direct effect on grain yield per plant, followed by panicle length, days to physiological maturity, days to 50 per cent flowering, basal tiller number and thousand grain weight. Traits such as peduncle length, protein content and flag leaf dimensions showed negative direct effects on grain yield. The results emphasize fodder yield and specific agronomic traits as key selection criteria in improving grain productivity. Furthermore, the inverse relationship between protein content and grain yield suggests a trade-off influencing nutritional quality in breeding programs. These insights provide a foundation for marker-assisted selection and accelerated genetic improvement of proso millet, targeting enhanced yield and adaptation. The study highlights the importance of integrating correlation and path coefficient analysis to dissect trait relationships, guiding efficient selection strategies in proso millet breeding.

Keywords: Proso millet, *Panicum miliaceum* L., Correlation analysis, Path coefficient analysis

Introduction
Proso millet (PM) is popularly known as Broomcorn millet (China), Common millet (USA), Barri (India), Broomtail millet, Kashfi Millet, Red Millet, White Millet, Brown Millet, Chinese Millet, Kibi, Mijo (Spain), Panic Millet (France) and Gijang (Korea). It is a Summer annual grass commonly grown as a late-seeded Summer crop, capable of completing its life cycle in 60-100 days (Baltensperger, 2002) [1]. It is classified into five races *viz.*, *miliaceum*, *patentissimum*, *contractum*, *compactum* and *ovatum*, based on differences in panicle morphology and shape. (Vetriventhan *et al.*, 2019).

In India, proso millet is grown across several states, including Tamil Nadu, Maharashtra, Karnataka, Andhra Pradesh, Bihar, Madhya Pradesh and Uttar Pradesh, covering about 0.41 lakh hectares with a production of 0.22 lakh tonnes of grain (Elangovan *et al.*, 2023) [3]. Characterization of available germplasm for morpho-agronomic traits is essential to assess genetic diversity, broaden the genetic base and facilitate effective genetic improvement (Pucher *et al.*, 2015) [9]. In proso millet breeding, correlation and path coefficient analyses are crucial for dissecting the relationships among yield and its component traits. Correlation analysis reveals the strength and direction of trait associations, while path analysis distinguishes direct and indirect effects, providing insight into causal relationships influencing grain yield. These tools aid breeders in identifying key traits with significant direct effects on yield, such as productive tillers, grain weight and flowering time, allowing for precise selection and effective genetic improvement. (Rajput *et al.*, 2024) and (Mishra *et al.*, 2022) [10, 7] Hence, a study was undertaken to estimate the correlation and path coefficient among yield contributing traits in proso millet genotypes, providing valuable information for optimizing trait selection in plant breeding programs.

Materials and Methods

The study was carried out at RSJRS, Kolhapur, Maharashtra State during Summer 2024. Thirty-five genotypes of proso millet were obtained from AICRP on Small Millets, Zonal Agricultural Research Station, Shenda Park, Kolhapur, Maharashtra State. The experiment was laid out in randomized block design (RBD). The field was divided into three homogeneous replication blocks. Thirty-five genotypes were planted randomly in three replications. Each entry is represented by a single row of 4 m length spaced at 22.5 cm between the rows and 10 cm between the plants. Five random plants from each treatment in each replication were selected for recording observations. The association among the characters was assessed by estimating genotypic correlation coefficient using the procedure outlined by Singh and Chaudhary (1981) [13]. Path coefficient analysis was done according to the procedure suggested by Dewey and Lu (1959) [2].

Results and Discussion

Correlation of grain yield per plant with its components

Correlation analysis reveals the interrelationships between quantitative traits, aiding in the selection of appropriate breeding strategies for crop enhancement. Genotypic correlation coefficients, estimated for all trait combinations represented in Table 1, reveal the direction and strength of genetic relationships. These insights help identify key traits for selection, thereby enhancing the efficiency and precision of crop improvement programs. Grain yield per plant had highly significant and positive correlation with fodder yield per plant (0.942), basal tiller number (0.869), panicle length (0.762), days to physiological maturity (0.740), days to 50 per cent flowering (0.725), plant height (0.648), flag leaf blade length (0.490) thousand grain weight (0.476), flag leaf blade width (0.371) and peduncle length (0.236), indicating that these traits contributed substantially to enhanced grain productivity. While, a highly significant and negative correlation was observed with protein content (-0.253), suggesting a possible inverse relationship between grain yield and grain protein percentage. The findings of the present study are in close agreement with those reported by Mishra *et al.,* (2022) [7], who observed a strong and significant positive correlation of grain yield with days to 50 per cent flowering, days to maturity, plant height and panicle length. Similarly, Santhoshkumar *et al.,* (2023) [12] documented highly significant positive associations between grain yield per plant and traits such as basal tiller number, flag leaf blade dimensions and peduncle length. Furthermore, Hawlader (1991) and Kumar *et al.,* (2022) [4, 6] also reported a significant and positive relationship between grain yield and 1000-grain weight.

Path coefficient analysis

Path coefficient analysis enables the breakdown of correlation coefficients into direct and indirect effects, allowing for the identification of key contributing traits and a clearer understanding of each component's actual influence on yield. This method considers the cause and-effect relationships among variables by dividing the overall association into direct and indirect effects those mediated through other independent traits. The method helps breeders in formulating selection criteria by emphasizing characters with high direct effects on yield. When used alongside correlation analysis, path analysis offers deeper insights into the nature and strength of relationships between any two quantitative characters. The path coefficient analysis at the genotypic level represented in Table 2, revealed that fodder yield per plant exerted the highest positive direct effect (0.5548) on grain yield per plant, indicating its primary role in determining grain yield. It was followed by panicle length (0.2569), days to physiological maturity (0.1638), days to 50 per cent flowering (0.0807), basal tiller number (0.0749) and thousand grain weight (0.0624), all of which showed positive direct effects on grain yield. These traits can be considered as key selection criteria for yield improvement. In contrast, characters like peduncle length (-0.0923), protein content (-0.0691), flag leaf blade width (-0.0628), flag leaf blade length (-0.0072) and plant height (-0.0009) exhibited negative direct effects. The present study revealed that fodder yield per plant exerted the highest positive direct effect on grain yield, identifying it as a key driver of productivity in proso millet. Similar results were reported by Patil *et al.,* (2024) [8], who also highlighted fodder yield as the most influential contributor to grain yield. In addition, traits such as panicle length, basal tiller number, days to physiological maturity and 1000-grain weight also exhibited notable direct effects, suggesting their potential as reliable selection indices. These findings are consistent with those of Santhoshkumar *et al.,* (2023) and Rajput *et al.,* (2024) [12, 10], who found that traits such as number of grains per panicle, basal tiller number and days to maturity exhibited strong positive direct effects on grain yield per plant in proso millet. Salini *et al.,* (2010) [11] reported similar results for 1000 grain weight. On the other hand, protein content showed a negative direct effect, indicating a possible trade-off between yield and nutritional quality, as also reported by Kalinova and Moudry (2006). Traits like basal tiller number, panicle length, days to physiological maturity and days to 50 per cent flowering showed strong indirect effects on grain yield per plant primarily through fodder yield. Similar trends were observed by Santhoshkumar *et al.,* (2023) [12]. Kumar *et al.,* (2022) [6] found that traits like panicle length and flag leaf blade width exhibited significant positive indirect effects *via* thousand-grain weight, plant height and flag leaf sheath length.

Table 1: Genotypic correlation coefficients of twelve characters in 35 genotypes of proso millet.

Trait	DFF	DPM	PH	PanL	PedL	FLBL	FLBW	BTN	TW	FYPP	PC	GYPP
DFF	1.000											
DPM	0.814**	1.000										
PH	0.283*	0.329**	1.000									
PanL	0.369**	0.437**	0.601**	1.000								

PedL	0.048	0.159	0.339**	0.454**	1.000							
FLBL	0.183	0.309**	0.531**	0.664**	0.565**	1.000						
FLBW	0.311**	0.272**	0.080	0.476**	0.057	0.464**	1.000					
BTN	0.724**	0.763**	0.481**	0.619**	0.104	0.445**	0.422**	1.000				
TW	0.568**	0.410**	-0.017	0.290**	0.199*	0.094	0.126	0.343**	1.000			
FYPP	0.641**	0.611**	0.714**	0.730**	0.273**	0.515**	0.385**	0.811**	0.407**	1.000		
PC	0.059	-0.150	-0.389**	-0.165	-0.255**	-0.256**	0.040	-0.284**	-0.013	-0.221*	1.000	
GYPP	0.725**	0.740**	0.648**	0.762**	0.236*	0.490**	0.371**	0.869**	0.476**	0.942**	-0.253**	1.000

, ** significant at 5 and 1 per cent probability respectively.

Where, DFF - Days to 50 per cent flowering	FLBL - Flag leaf blade length	PedL- Peduncle length
DPM - Days to physiological maturity	FLBW - Flag leaf blade width	FYPP - Fodder yield per plant
PH - Plant height	BTN - Basal tiller number	TW - 1000 grain weight
PanL - Panicle length	PC - Protein content	GYPP - Grain yield per plant

Table 2: Direct (diagonal) and indirect (above and below diagonal) effects of different characters towards grain yield per plant at genotypic level in proso millet.

Trait	DFF	DPM	PH	PanL	PedL	FLBL	FLBW	BTN	TW	FYPP	PC
DFF	0.0807	0.0657	0.0229	0.0298	0.0039	0.0148	0.0251	0.0585	0.0458	0.0518	0.0048
DPM	0.1333	0.1638	0.0539	0.0716	0.0260	0.0506	0.0445	0.1249	0.0671	0.1002	-0.0246
PH	-0.0002	-0.0003	-0.0009	-0.0005	-0.0003	-0.0005	-0.0001	-0.0004	0.0000	-0.0006	0.0003
PanL	0.0947	0.1123	0.1545	0.2569	0.1167	0.1706	0.1224	0.1591	0.0746	0.1874	-0.0424
PedL	-0.0044	-0.0146	-0.0313	-0.0419	-0.0923	-0.0521	-0.0053	-0.0096	-0.0183	-0.0252	0.0235
FLBL	-0.0013	-0.0022	-0.0038	-0.0048	-0.0041	-0.0072	-0.0033	-0.0032	-0.0007	-0.0037	0.0018
FLBW	-0.0195	-0.0171	-0.0050	-0.0299	-0.0036	-0.0291	-0.0628	-0.0265	-0.0079	-0.0242	-0.0025
BTN	0.0542	0.0571	0.0360	0.0464	0.0078	0.0333	0.0316	0.0749	0.0257	0.0607	-0.0213
TW	0.0354	0.0256	-0.0010	0.0181	0.0124	0.0058	0.0078	0.0214	0.0624	0.0254	-0.0008
FYPP	0.3559	0.3392	0.3963	0.4048	0.1516	0.2859	0.2135	0.4499	0.2260	0.5548	-0.1226
PC	-0.0041	0.0104	0.0269	0.0114	0.0176	0.0177	-0.0027	0.0196	0.0009	0.0153	-0.0691
GYPP	0.7247	0.7399	0.6484	0.7619	0.2357	0.4899	0.3707	0.8686	0.4756	0.9419	-0.2528

Residual Effect = 0.1970

Where, DFF - Days to 50 per cent flowering	FLBL - Flag leaf blade length	PedL- Peduncle length
DPM - Days to physiological maturity	FLBW - Flag leaf blade width	FYPP - Fodder yield per plant
PH - Plant height	BTN - Basal tiller number	TW - 1000 grain weight
PanL - Panicle length	PC - Protein content	GYPP - Grain yield per plant

Conclusions

The present study revealed that traits such as fodder yield per plant, basal tiller number, panicle length, days to 50 per cent flowering, days to physiological maturity, plant height and 1000-grain weight exhibited a highly significant and positive correlation with grain yield per plant. This suggests a direct linear relationship, implying that enhancing these traits could lead to an increase in grain yield. Conversely, protein content showed a highly significant and negative association with grain yield. Path analysis at the genotypic level showed that fodder yield per plant had the highest positive direct effect on grain yield, followed by panicle length, days to maturity, basal tillers, days to 50 per cent flowering and 1000 grain weight. Traits like flag leaf blade width, peduncle length, protein content, flag leaf blade length and plant height showed negative direct effects.

Acknowledgement

The Authors are thankful to AICRP on Small Millet, Zonal Agricultural Research Station, Shenda Park, Kolhapur, Maharashtra State for providing proso millet genotypes to conduct the experiment.

References

1. Baltensperger DD. Progress with proso, pearl and other millets. Trends New Crops New Uses. 2002;100:100-3.
2. Dewey DR, Lu K. A correlation and path-coefficient analysis of components of crested wheatgrass seed production. Agron J. 1959;51(9):515-8.
3. Elangovan M, Singode A, Venkatesh K, Amasiddha B, Karthik AS, Pandey S, *et al*. Agro-morphological characterization of proso millet germplasm for utilization. Int J Plant Soil Sci. 2023;35(16):381-92.
4. Hawlader MSH. Genetic variability and correlation study in proso millet (Panicum miliaceum L.) in Bangladesh. Ann Bangladesh Agric. 1991;1(2).
5. Kalinová J, Moudrý J. Content and quality of protein in proso millet (Panicum miliaceum L.) varieties. Plant Foods Hum Nutr. 2006;61(1):43-7.
6. Kumar GA, Vanniarajan C, Vetriventhan M, Sudhagar R, Saravanan S. Association and variability studies of quantitative traits in proso millet (Panicum miliaceum L.). Biol Forum Int J. 2022;14(3):208-14.
7. Mishra N, Tiwari S, Sapre S, Sahu VK, Tiwari PN. Morphological characterization and correlation assessment of quantitative and qualitative traits of proso millet (Panicum miliaceum L.) germplasm. Front Crop Improv. 2022;10(Special Issue III):1202-6.
8. Patil PB, Karad SR, Gajbhiye PN, Mote MS. Genetic diversity in proso millet (Panicum miliaceum L.). Biol Forum Int J. 2024;16(1):299-302.
9. Pucher A, Sy O, Angarawai II, Gondah J, Zangre R, Ouedraogo M, *et al*. Agro-morphological characterization of West and Central African pearl millet accessions. Crop Sci. 2015;55(2):737-48.
10. Rajput SG, Khound R, Santra DK. Phenotypic diversity for morpho-agronomic traits in the US proso millet

(Panicum miliaceum L.) core collection. Crop Sci. 2024;64(3):2599-611.
11. Salini K, Nirmalakumari A, Muthiah AR, Senthil N. Evaluation of proso millet (Panicum miliaceum L.) germplasm collections. [Unpublished].
12. Santhoshkumar C, Vaithiyalingan M, Murugan E, Renuka R, Hemalatha G. Genetic variability, trait association and diversity study in proso millet (Panicum miliaceum L.). Electron J Plant Breed. 2023;14(3):1127-34.
13. Singh RK, Chaudhary BD. Biometrical methods in quantitative genetic analysis. New Delhi: Kalyani Publishers; 1981.
14. Vetriventhan M, Azevedo VC, Upadhyaya HD, Naresh D. Variability in the global proso millet (Panicum miliaceum L.) germplasm collection conserved at the ICRISAT genebank. Agriculture. 2019;9(5):112.