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VARIABILITY PARAMETERS STUDIES FOR GRAIN YIELD AND YIELD-CONTRIBUTING TRAITS IN PEARL MILLET (*Pennisetum glaucum* L.R. Br.)

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ABSTRACT

The present investigation was undertaken to assess the magnitude of genetic variability, heritability, genetic advance, character association and path coefficients for grain yield and eight yield-contributing traits in twenty-three genotypes of pearl millet evaluated in a randomized block design with three replications at ARSS, Nagaur during [*Kharif* 2025]. Analysis of variance revealed highly significant differences among genotypes for all the traits studied, namely days to 50% flowering (DF), days to maturity (DM), plant height (PH), number of productive tillers per plant (NPT), panicle length (PL), panicle diameter (PD), test (1000-seed) weight (TSW), fodder yield (FY) and grain yield (GY), confirming the presence of substantial exploitable variability. Phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficients of variation for all traits, indicating a comparatively limited role of the environment in trait expression. High heritability coupled with high genetic advance as percentage of mean was recorded for test weight, panicle diameter and days to 50% flowering, suggesting predominance of additive gene action and the scope for effective improvement through direct selection. Genotypic correlation analysis showed that grain yield was significantly and positively associated with number of productive tillers per plant, days to 50% flowering, fodder yield. Path coefficient analysis identified fodder yield as the trait exerting the highest positive direct effect on grain yield, followed by plant height and days to maturity. The results suggest that selection based on these traits would be more rewarding for genetic improvement of grain yield in pearl millet.
***Keywords*:** Pearl millet; genetic variability; correlation coefficient; path coefficient analysis.

Introduction

Pearl millet [*Pennisetum glaucum* (L.) R. Br.] having 2n number 14 and belongs to Poaceace family is one of the most important cereal crops of the semi-arid tropics, valued for its remarkable tolerance to drought, heat and poor soil fertility. It serves as a dual-purpose crop providing both grain for human consumption and fodder for livestock, and is an important source of energy, protein, dietary fibre, iron and zinc for millions of resource-poor farmers in Asia and Africa. Given the increasing pressure of climate variability on cereal production systems, pearl millet continues to gain renewed attention as a climate-resilient crop suited to marginal and rainfed environments. Genetic improvement of any crop is contingent upon the existence and proper understanding of genetic variability in the available germplasm. The total observed phenotypic variability in a population comprises both genotypic and environmental components, and partitioning these components through estimation of genotypic and phenotypic coefficients of variation, heritability and genetic advance provides breeders with reliable information on the heritable proportion of variation and the expected response to selection. Traits governed largely by additive gene action, reflected in high heritability accompanied by high genetic advance, are amenable to improvement through simple mass or pedigree selection, whereas traits with high heritability but low genetic advance point toward non-additive gene action requiring alternative breeding strategies.

Grain yield is a complex quantitative trait resulting from the combined expression and interaction of several component traits. Selection based on yield per se is often inefficient because of its low heritability and the masking effects of trait interrelationships. Correlation studies help identify component traits that move in tandem with yield and can therefore serve as auxiliary selection criteria. However, correlation alone does not distinguish between the direct contribution of a trait to yield and its indirect contribution mediated through other associated traits. Path coefficient analysis overcomes this limitation by partitioning the correlation coefficients into direct and indirect effects, thereby identifying the most reliable and efficient traits for use in selection indices. The present study was therefore undertaken to estimate the extent of genetic variability, heritability and genetic advance, and to work out genotypic correlations and path coefficients among grain yield and its component traits in a set of pearl millet genotypes, with a view to identifying effective selection criteria for yield improvement.

Materials and Methods

The experiment was conducted at Agricultural Research Sub Station, Nagaur, during the *kharif*, 2025. The experimental material comprised twenty-three pearl millet germplasm. The genotypes were evaluated in a Randomized Block Design (RBD) with three replications. Each genotype was sown in plots with a row-to-row spacing of 60 cm and plant-to-plant spacing of 45 cm, following recommended agronomic and plant protection practices for the region. Observations were recorded on five randomly selected, representative plants in each replication for the following nine traits: days to 50% flowering (DF), days to maturity (DM), plant height (PH, cm), number of productive tillers per plant (NPT), panicle length (PL, cm), panicle diameter (PD, cm), 1000-seed/test weight (TSW, g), fodder yield (FY, kg/ha) and grain yield (GY, kg/ha).

Data were subjected to analysis of variance (ANOVA) was evaluated to partition the total variation into components attributable to genotypes, environments, and their interactions, following the model explained by (Panse & Sukhatme, 1985). Genetic parameters, including genotypic and phenotypic coefficients of variation (GCV, PCV), were measured according to (Burton & De Vane, 1953). Broad-sense heritability (h^2_{bs}) and genetic advance (GA) as a percentage of the mean (at 5% selection intensity) were calculated following (Johnson *et al*., 1955). The phenotypic, genotypic and environmental coefficients of correlation were calculated as per (Al-jibouri *et al.*, 1958). Path coefficient analysis, partitioning the genotypic correlation coefficients of each component trait with grain yield into direct and indirect effects, was carried out following Dewey and Lu (1959), with grain yield treated as the dependent variable. All analyses were performed using the *agricolae* and *variability* packages in R software (version 4.5.1; R Core Team, 2024).

Results and Discussion

Analysis of Variance

The mean sum of squares due to genotypes was highly significant ($P \leq 0.001$) for all nine traits studied – DF, DM, PH, NPT, PL, PD, TSW, FY and GY (Table 1) this confirms that the experimental material has substantial and genuine genetic variability for all the characters evaluated. Highly significant genotypic mean squares for yield and yield-contributing traits have similarly been reported in earlier variability studies on pearl millet (Govindaraj *et al*., 2010; Chauhan *et al*., 2020), confirming that adequate exploitable variability for these traits is a recurrent feature of pearl millet germplasm evaluated under diverse environments.

Table 1 : Analysis of Variance (Mean Sum of Squares) for Different Traits

Source of Variation	df	DF	DM	PH	NPT	PL	PD	TSW	FY	GY
Replication	2	20.13	19.84	30.54	1.00	25.23	0.38	0.04	1369024	15463
Genotypes	22	79.28***	34.13***	347.40***	0.97***	21.81***	0.56***	3.15***	908157***	115627***
Error	44	6.93	6.45	14.75	0.19	4.02	0.09	0.05	198625	38378

*Significant at 5% probability level; **significant at 1% probability level; ***significant at 0.1% probability level. GY: Grain yield per plant in g, DM: Days to maturity, DF: Days to 50% flowering, PH: Plant height in cm PL: Panicle length in cm, PD: Panicle diameter in cm, TSW: Thousand seed weight in g, FY: Fodder yield, NPT: Number of Productive tillers,

Genetic Variability, Heritability and Genetic Advance

Mean performance and the genetic parameters estimated for the nine traits are presented in Table 2. For all the traits, the PCV was marginally higher than the GCV, and the difference between the two was narrow throughout indicating that environmental influence on the expression of these traits was comparatively limited and that observed phenotypic variation closely reflected the underlying genotypic variation. This pattern of PCV exceeding GCV by only a narrow margin is consistent with that reported for grain yield components and quality traits in pearl millet accessions by Govindaraj *et al*. (2011), who likewise attributed the small GCV–PCV gap to a comparatively limited role of environmental factors in trait expression. Among the traits, TSW (16.68%), PD (15.08%) and NPT (13.97%) recorded relatively high GCV, whereas DM (3.88%) and PH (5.92%) showed low GCV, reflecting a narrower genetic base for these two traits in the material studied.

Broad-sense heritability was high for TSW (95.56%), PH (88.26%), PD (63.37%) and DF (77.67%), moderate for PL (59.60%), DM (58.88%), NPT (58.46%), GY (40.15%) and FY (54.35%). When heritability is considered jointly with genetic advance as percentage of mean (GAM), following the criteria of Johnson *et al*. (1955), TSW (h^2 = 95.56%, GAM = 33.59%), PD (h^2 = 63.37%, GAM = 24.72%) and DF (h^2 = 77.67%, GAM = 18.54%) combined high heritability with high-to-moderate genetic advance, indicating that additive gene effects predominate in the inheritance of these traits and that direct phenotypic selection should be effective for their improvement. A similar combination of high heritability with high genetic advance, taken as evidence of predominantly additive gene action, has been reported for several yield-related and quality traits in pearl millet by Govindaraj *et al.* (2011) and Bhasker *et al.* (2017). In contrast, PH showed high heritability (88.26%) but only moderate GAM (11.46%), suggesting a greater relative contribution of non-additive gene action and/or genotype × environment interaction, in which case selection based on plant height alone may be less rewarding despite its high heritability. Grain yield itself recorded the moderate heritability (40.15%) among all traits along with moderate GAM (11.30%), reaffirming that yield improvement should rely on associated component traits with more favourable genetic parameters; comparable conclusions on the limited reliability of direct selection for grain yield in pearl millet have been drawn by Bikash *et al*. (2013) and Borkhataria *et al*. (2005), who emphasized component-trait-based selection on the basis of their own variability and correlation studies. Overall, these genetic parameter estimates are broadly in line with earlier reports of genetic variability, heritability and genetic advance for yield and yield-related traits in pearl millet (Sharma *et al*., 2018; Chauhan *et al*., 2020).

Table 2 : Estimates of Genetic Variability Parameters

Trait	Mean	Range (Min–Max)	GCV (%)	PCV (%)	h^2(bs) (%)	GA	GAM (%)
DF	48.09	39.00–60.00	10.21	11.59	77.67	8.92	18.54
DM	78.23	69.00–87.00	3.88	5.06	58.88	4.80	6.14
PH	177.75	153.00–203.00	5.92	6.31	88.26	20.38	11.46
NPT	3.66	2.00–5.00	13.97	18.26	58.46	0.81	22.00
PL	23.54	17.00–31.00	10.35	13.40	59.60	3.87	16.45
PD	2.63	1.60–3.80	15.08	18.94	63.37	0.65	24.72
TSW	6.10	4.25–8.48	16.68	17.06	95.56	2.05	33.59
FY	4466.49	3194.00–5750.00	10.89	14.77	54.35	738.59	16.54
GY	1854.28	1190.00–2290.00	8.65	13.66	40.15	209.47	11.30

GCV = genotypic coefficient of variation; PCV = phenotypic coefficient of variation; h^2(bs) = heritability in broad sense; GA = genetic advance; GAM = genetic advance as percentage of mean. GY: Grain yield per plant in g, DM: Days to maturity, DF: Days to 50% flowering, PH: Plant height in cm PL: Panicle length in cm, PD: Panicle diameter in cm, TSW: Thousand seed weight in g, FY: Fodder yield, NPT: Number of Productive tillers,

Correlation Studies

Genotypic correlation coefficients among the nine traits are presented in Table 3. Grain yield exhibited a highly significant and very strong positive genotypic correlation with fodder yield (rg = 1.07), and significant positive correlations with number of productive tillers per plant (rg = 0.65) and days to 50% flowering (rg = 0.55). Strong positive genotypic correlation of grain yield with biomass/fodder-related traits and tiller number has been similarly reported in pearl millet by Abuali *et al*. (2012) and Dadarwal *et al.* (2020). Grain yield was significantly and negatively correlated with panicle length (rg = -0.51), implying that genotypes with longer panicles did not necessarily translate this into higher grain yield, possibly on account of unfavourable associations with other yield-determining traits; a negative influence of panicle length on grain yield, mediated through its direct effect in path analysis, was likewise reported by Abuali *et al.* (2012).

Among the other trait pairs, days to maturity was significantly and positively correlated with number of productive tillers (rg = 0.55), panicle diameter was significantly positively correlated with test weight (rg = 0.52), test weight was significantly positively correlated with fodder yield (rg = 0.45). These associations suggest that selection for one trait is likely to influence several other traits simultaneously, underscoring the need for path analysis to disentangle direct and indirect contributions to grain yield, a rationale also emphasized in earlier character-association studies in pearl millet (Bikash *et al*., 2013; Borkhataria *et al*., 2005).

Table 3 : Genotypic Correlation Coefficients Among Traits

Trait	DF	DM	PH	NPT	PL	PD	TSW	FY	GY
DF	1.00	0.37	-0.04	0.21	-0.61**	-0.21	-0.14	0.28	0.55**
DM	–	1.00	-0.09	0.55**	-0.10	-0.15	-0.21	0.02	0.27
PH	–	–	1.00	0.25	-0.01	-0.26	-0.13	-0.10	0.28
NPT	–	–	–	1.00	-0.28	0.12	-0.07	0.23	0.65**
PL	–	–	–	–	1.00	-0.21	0.19	-0.03	-0.51*
PD	–	–	–	–	–	1.00	0.52*	0.19	0.08
TSW	–	–	–	–	–	–	1.00	0.45*	0.01
FY	–	–	–	–	–	–	–	1.00	1.07**
GY	–	–	–	–	–	–	–	–	1.00

*Significant at 5% probability level; **significant at 1% probability level. GY: Grain yield per plant in g, DM: Days to maturity, DF: Days to 50% flowering, PH: Plant height in cm PL: Panicle length in cm, PD: Panicle diameter in cm, TSW: Thousand seed weight in g, FY: Fodder yield, NPT: Number of Productive tillers,

Path Coefficient Analysis

The genotypic correlation coefficients of grain yield with its component traits were partitioned into direct and indirect effects through path coefficient analysis (Table 4). Fodder yield recorded the highest positive direct effect on grain yield (1.3830), markedly higher than that of any other trait, followed by plant height (0.3700) and days to maturity (0.2525), both of which also exerted moderate positive direct effects. A single biomass-related trait exerting a markedly larger direct effect on grain yield than any other component, as observed here for fodder yield, parallels the finding of Abuali *et al.* (2012), who reported that number of fertile tillers per plant exerted the highest direct effect on grain yield among the traits they examined in pearl millet. Notably, several traits with negative or negligible direct effects nevertheless showed strong positive genotypic correlations with grain yield because of substantial positive indirect effects channeled mainly through fodder yield. For instance, number of productive tillers per plant, despite a small negative direct effect (-0.0203), recorded a high positive indirect effect via fodder yield (0.3113) and via panicle length (0.1431), which explains its significant overall positive correlation with grain yield (0.65). Similarly, days to 50% flowering, with a negative direct effect (-0.2803), showed large positive indirect effects via fodder yield (0.3871) and panicle length (0.3109), together accounting for its significant positive correlation with yield (0.55). The residual effect was estimated at 0.7498, indicating that a sizeable proportion of the variability in grain yield remains unaccounted for by the eight component traits included in the present study. This suggests that additional yield-contributing traits should be incorporated in future path analyses to achieve a more complete understanding of the yield architecture in pearl millet.

Table 4 : Path Coefficient Analysis for yield and yield related traits

Trait	DF	DM	PH	NPT	PL	PD	TSW	FY
DF	**-0.2803**	0.0943	-0.0164	-0.0042	0.3109	-0.0091	0.0679	0.3871
DM	-0.1046	**0.2525**	-0.0349	-0.0111	0.0531	-0.0064	0.0994	0.0239
PH	0.0124	-0.0238	**0.3700**	-0.0051	0.0047	-0.0114	0.0640	-0.1330
NPT	-0.0581	0.1379	0.0938	**-0.0203**	0.1431	0.0050	0.0326	0.3113
PL	0.1704	-0.0262	-0.0034	0.0057	**-0.5112**	-0.0093	-0.0903	-0.0457
PD	0.0588	-0.0373	-0.0977	-0.0024	0.1099	**0.0433**	-0.2514	0.2615
TSW	0.0394	-0.0520	-0.0491	0.0014	-0.0956	0.0225	**-0.4825**	0.6273
FY	-0.0784	0.0044	-0.0356	-0.0046	0.0169	0.0082	-0.2189	**1.3830**

Residual effect = 0.7498 (genotypic). GY: Grain yield per plant in g, DM: Days to maturity, DF: Days to 50% flowering, PH: Plant height in cm PL: Panicle length in cm, PD: Panicle diameter in cm, TSW: Thousand seed weight in g, FY: Fodder yield, NPT: Number of Productive tillers,

Conclusion

The present study demonstrated the presence of significant and exploitable genetic variability among the twenty-three pearl millet genotypes evaluated for all nine traits studied. High heritability accompanied by high genetic advance for test weight, panicle diameter and days to 50% flowering indicated the predominance of additive gene action for these traits, making them amenable to improvement through direct selection. Correlation and path coefficient analyses jointly identified fodder yield as the principal direct and indirect contributor to grain yield, with number of productive tillers per plant, days to 50% flowering and test weight also exerting substantial favourable indirect effects largely mediated through fodder yield. It is therefore recommended that breeding programmes aimed at enhancing grain yield in pearl millet adopt a multi-trait selection approach that gives weight to fodder yield, number of productive tillers per plant and test weight, alongside grain yield itself, to achieve more efficient and reliable genetic gains.

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