HAYATI
Journal of Biosciences

Vol. 33 No. 3, May 2026 566-574
DOI:10.4308/hjb.33.3.566-574
ISSN: 1978-3019
EISSN: 2086-4094

Research Article

Panicle Trait Diversity and Its Impact on the Productivity of Indonesian Foxtail Millet (*Setaria italica* L. Beauv.) Genotypes

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ARTICLE INFO

Article history:
Received September 8, 2025
Received in revised form November 3, 2025
Accepted December 8, 2025
Available Online December 19, 2025

KEYWORDS:
correlation,
minor cereals,
primary branch,
principal component,
quantitative traits

ABSTRACT

Foxtail millet is a climate-resilient cereal crop that is growing in importance in food security and sustainable agriculture. This study aimed to identify panicle traits associated with yield, determine functional traits suitable for selecting high-productivity genotypes, and classify superior local Indonesian foxtail millet genotypes. Eight genotypes were evaluated using a randomized complete block design with three replications. Correlation analysis of 31 panicle traits revealed that grain filling rate, panicle weight, grain weight per panicle, grain weight per plant, and grain numbers on the middle and lower primary branches were positively associated with yield. Several of these traits also exhibited high broad-sense heritability and moderate GCV and PCV values, indicating their potential for selection. Principal component and two-way heatmap cluster analyses identified Buru, ICERI-7, Hambapraing, and Mauliru-2 as high-yielding genotypes. The findings provide critical insights for foxtail millet breeding programs in Indonesia focused on improving yield.

1. Introduction

Foxtail millet (*Setaria italica* L. Beauv.) is a minor cereal crop with growing recognition for its resilience to climate stress and its potential as a model species for other cereals (Ardie *et al.* 2025). Its nutritional profile makes it a promising functional staple, with carbohydrate content comparable to rice (75%) and notable levels of protein (11-13.3%), fat (3.36%), and fiber (17%) (Kalsi and Bhasin 2023). Foxtail millet also offers health benefits, including anti-cancer, anti-hypertensive, and anti-diabetic properties (Khan *et al.* 2025). It serves as a gluten-free alternative for individuals with celiac disease (Reaz *et al.* 2023). Its tolerance to drought (Wang *et al.* 2023), salinity (Pan *et al.* 2020), and nutrient-poor soils (Nadeem *et al.* 2020) makes it suitable for cultivation in marginal areas, without competing with major staple crops.

Despite these advantages, foxtail millet remains underutilized (Ardie *et al.* 2025), especially in Indonesia, where no superior varieties have yet been developed. One of the main challenges in foxtail millet breeding is improving yield. Current productivity in the F2 Indonesian population ranges from 0.29 to 2.23 tons ha^{-1} (Sintia *et al.* 2023; Muzzayyanah *et al.* 2024), far below the yield of varieties like 'Jigu37' in China, which can reach 8.91 tons ha^{-1} (Zhang *et al.* 2022). Yield is closely linked to panicle and grain traits (Liu *et al.* 2020; Zhi *et al.* 2021), making their characterization in local genotypes essential.

Studies have shown a wide genetic diversity among Indonesian foxtail millet genotypes (Ardie *et al.* 2017; Ratnawati *et al.* 2024), including variation

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in grain traits (Jannah *et al.* 2024). Selection based on phenotypic traits can improve breeding efficiency (Khadka *et al.* 2020). However, despite several studies on Indonesian foxtail millet diversity, comprehensive characterization of genotypes based specifically on panicle traits remains limited. Identifying panicle traits is crucial for understanding yield potential. Additionally, the potential of individual genotypes to contribute to future breeding efforts aimed at improving yield has not been thoroughly assessed. Analytical methods such as Pearson's correlation, clustering, and principal component analysis are valuable for evaluating trait relationships and genetic diversity (Bhakuni *et al.* 2021; Yang *et al.* 2022; Ramesh *et al*. 2023). Therefore, this study aims to identify panicle traits associated with productivity and to classify promising Indonesian genotypes to support future breeding programs.

2. Materials and Methods

2.1. Planting Materials

The experiment was conducted from March to July 2024 in the Leuwikopo Experimental Field (-6.565549260850146, 106.7250459870867), Department of Agronomy and Horticulture, IPB University, West Java. The experiment employed a non-factorial randomized complete block design (RCBD), with genotype as the single factor. Each replication consisted of eight plots measuring 1.5 m × 1.2 m, each containing six rows of 10 plants per row. Three seeds were planted in each plot at a distance of 25 cm between rows and 10 cm between the planting holes. Two sample plants per row were observed in the experimental plots, ensuring that plants were collected from areas without border rows, yielding eight samples per genotype per replication.

The study used eight foxtail millet genotypes: ICERI-5, ICERI-6, and ICERI-7 from the Indonesian Cereal Research Institute; Botok-4(B), Mauliru-2, and Hambapraing from East Nusa Tenggara; Buru from North Maluku; and NTB-1 from West Nusa Tenggara. Field preparation included weed removal, tillage, and plot setup. Manure (2.5 tons ha^{-1}) and dolomite (300 kg ha^{-1}) were applied one week before planting. A protective net was installed to prevent pest damage. Plant maintenance involved regular weeding and fertilization: urea (150 kg ha^{-1}, half dose), SP-36 (150 kg ha^{-1}), and KCl (75 kg ha^{-1}) were applied two weeks after planting, followed by the remaining urea (150 kg ha^{-1}) at six weeks. Pest and disease control was conducted as needed using suitable pesticides and fungicides.

2.2. Data Collection

Data were collected on yield traits, panicle characteristics, and architecture following UPOV (2013) and Zhi *et al.* (2021). Yield traits included heading time (days to 50% flowering), days to maturity (50% panicles matured), and grain filling period (days to maturity minus days to heading). Grain filling rate was calculated as the estimated yield divided by the grain-filling period. Yield estimation used the formula: (number of plants per ha ÷ 8 sample plants) × total grain weight of eight sample plants.

Panicle traits included panicle weight, grain weight per panicle, grain weight per plant, and 1,000-grain weight. Structural traits measured were panicle length (base to tip), diameter (midsection), and panicle exsertion (uppermost node to panicle base). Density was assessed by counting primary branches per panicle length; grain and branch numbers were recorded per panicle. Panicle architecture was analyzed by dividing panicles into upper, middle, and lower zones. In each, three primary branches were measured for length and diameter. The number of primary branches per zone was counted manually, and grains were counted to assess distribution.

2.3. Data Analysis

Foxtail millet data were analyzed using various statistical tools. ANOVA and the least significant difference (LSD) test at the 5% level were used to evaluate yield traits and panicle architecture, with analyses performed in SAS OnDemand for Academics and Microsoft Excel. Broad-sense heritability (h^2bs) was calculated following Allard (1960), using genetic, environmental, and phenotypic variance. Heritability was classified as high ($h^2bs>50\%$), moderate (h^2bs 20–50%), or low ($h^2bs<20\%$) based on Stanfield (1983). Genetic and phenotypic coefficients of variation (GCV and PCV) were computed using formulas from Singh and Chaudhary (1985). Pearson correlation analysis was conducted using the "metan" package. Pearson's correlation coefficient (r), ranging from −1 to 1, quantifies the linear association between two variables: positive values (closer to 1) indicate strong direct relationships, negative values (closer to −1) indicate inverse relationships, and zero indicates no correlation (Lazar *et al.* 2017). Heatmap clustering with "pheatmap" (Hu 2021), and principal component analysis (PCA) using “factoextra” in RStudio (version 4.4.1), following Irnawati *et al.* (2021).

3. Results

Heading time, days to maturity, grain-filling period, grain-filling rate, and yield estimation showed variability among eight foxtail millet genotypes (Table 1). The NTB-1 genotype exhibited the longest heading and maturation times, but the lowest yield estimation. In contrast, the Buru genotype displayed the fastest heading and maturation times and achieved the highest yield estimation. The grain filling period of the Buru genotype was similar to that of the NTB-1 genotype. However, the grain-filling rate of the Buru genotype was higher than that of the NTB-1 genotype.

Based on Pearson correlation analysis, six traits were positively correlated with yield estimation (Figure 1). The traits were grain filling rate, panicle weight, grain weight per panicle, grain weight per plant, number of grains on the middle primary branch, and number of grains on the lower main branch. The correlation coefficients (r) ranged from 0.84 to 1.00, indicating a strong relationship. Grain filling rate had a significant positive effect on yield. Still, it was negatively correlated with days to maturity, indicating that faster grain filling both increased yield and shortened time to maturity. Among the genotypes, Buru had the highest grain-filling rate and the shortest harvest time, making it a promising candidate for breeding early-maturing, high-yielding foxtail millet varieties.

The main panicle was divided into upper, middle, and lower zones, each with distinct primary branch architecture (Figure 2). Five traits—panicle weight, grain weight per panicle, grain weight per plant, and grain counts on middle and lower zone branches—showed significant positive correlations with yield estimation (Table 2). The Buru, ICERI-7, and Mauliru-2 genotypes had the highest number of grains per primary branch in the middle and lower zones of the panicle.

Broad-sense heritability, genetic coefficient of variance, and phenotypic coefficient of variance for traits correlated with yield estimation are presented in Table 3. Yield estimation and its six positively correlated traits exhibited high heritability, suggesting strong potential for use in selection. Grain weight per panicle, grain weight per plant, number of grains on the middle primary branch, and number of grains on the lower primary branch had the highest heritability with moderate GCV and PCV values. Although the difference was small, PCV values were consistently higher than GCV values. Grain filling rate and panicle weight showed lower variation, indicating more environmental influence on these traits.

Principal component analysis (PCA) (Figure 3) identified several genotypes with strong yield-related traits. ICERI-7 showed potential in grain development and panicle structure, while Buru excelled in grain weight and overall productivity. Hambapraing demonstrated uniform grain distribution across panicle zones, and Mauliru-2 had structural advantages in primary branch number. ICERI-6 performed well in branch diameter and length, ICERI-5 had the highest 1,000-grain weight, and Botok-4(B) showed the longest panicle exsertion. NTB-1 was characterized by a longer heading time and grain filling duration, indicating late maturity. Genotypes clustered

Table 1. Mean of heading time, days to maturity, grain filling period, grain filling rate, and yield estimation of eight local foxtail millet genotypes

Genotype	HeT (DAP)	DM (DAP)	GFP (DAP)	GFR (kg ha^{-1} DAP^{-1})	Ye (ton ha^{-1})
ICERI-5	66.60^{c}	87.81^{d}	87.81^{d}	137.05^{abc}	2.142^{d}
ICERI-6	69.33^{bc}	89.33^{cd}	89.33^{cd}	110.45^{bcd}	2.198^{cd}
ICERI-7	73.67^{b}	93.00^{bc}	93.00^{bc}	188.37^{a}	3.622^{ab}
Botok-4(B)	71.00^{bc}	97.67^{b}	97.67^{b}	79.91^{cd}	2.128^{d}
Buru	49.33^{d}	73.67^{e}	73.67^{e}	168.45^{ab}	4.105^{a}
Hambapraing	71.33^{b}	92.67^{bcd}	92.67^{bcd}	142.33^{ab}	3.016^{bc}
Mauliru-2	73.67^{b}	97.00^{b}	97.00^{b}	139.20^{ab}	3.178^{b}
NTB-1	87.33^{a}	114.33^{a}	114.33^{a}	73.63^{d}	1.975^{d}
F test	**	**	**	**	**
CV(%)	3.63	3.18	9.32	5.42	7.29

Numbers followed by the same letter on the same column indicate no significant difference based on the LSD test at $\alpha < 5\%$; HeT: heading time, DM: days to maturity, GFP: grain filling period, GFR: grain filling rate, Ye: yield estimation

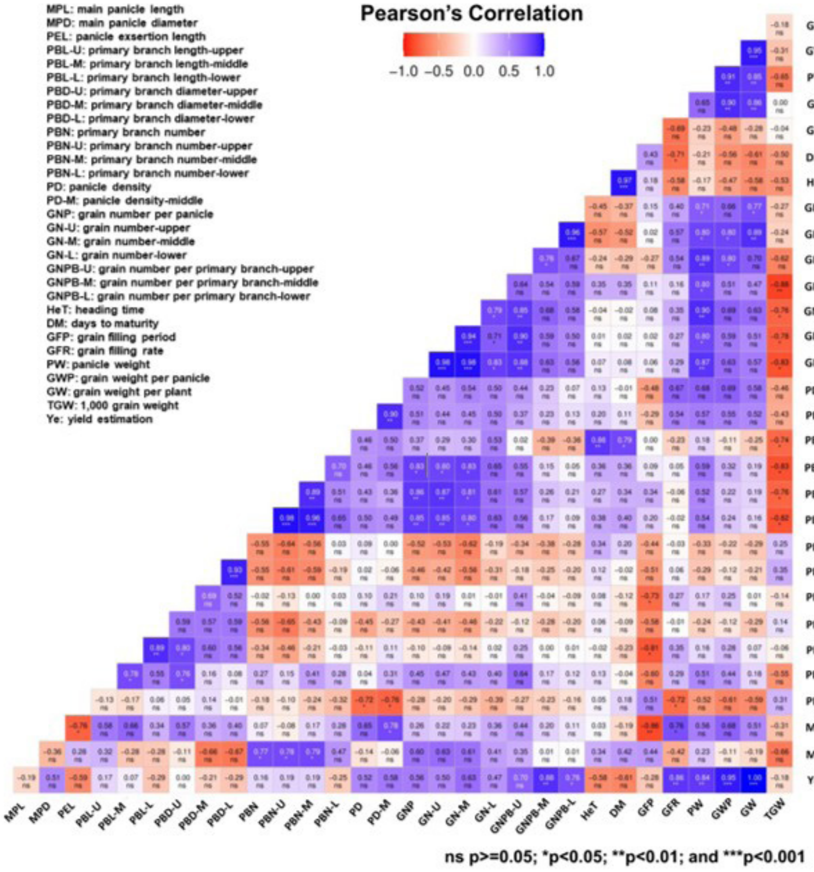

Figure 1. Correlation coefficients between panicle architecture and yield characteristics of eight local foxtail millet genotypes

by quadrant showed similar traits: ICERI-7 and Buru (I), Hambapraing and Mauliru-2 (II), Botok-4(B) and NTB-1 (III), and ICERI-5 and ICERI-6 (IV).

Two-way heatmap clustering (Figure 4) grouped yield-related traits into four clusters and genotypes into two. NTB-1, ICERI-5, ICERI-6, and Botok-4(B) showed consistently low values across most traits. In contrast, Buru and ICERI-7 had high values for grain filling rate, grain weight (per panicle and per plant), grain number per primary branch (middle and lower zones), and yield estimation. Hambapraing and Mauliru-2 excelled in grain number per panicle and zone, grain number per primary branch (upper), and panicle weight. These four genotypes—Buru, ICERI-7, Hambapraing, and Mauliru-2—were identified as having panicle traits strongly associated with high yield.

4. Discussion

The development of early-maturing genotypes with high productivity is a target for foxtail millet breeding. However, research on the F2 generation of foxtail millet from a cross between ICERI-5 and Botok-10 (including reciprocal crosses) revealed a positive correlation between heading and maturation times and productivity, indicating that early-maturing genotypes generally exhibit low productivity (Sintia *et al.* 2023; Muzzayyanah *et al.* 2024). Interestingly, the NTB-1 and Buru genotypes in the present study showed contrasting results. This suggests that breeding early-maturing, high-productivity foxtail millet is achievable, particularly by focusing on grain-filling rate as a key selection trait.

Selecting traits strongly correlated with productivity is a critical step in breeding programs. Enhancing such traits can significantly improve foxtail millet yield. Han *et al.* (2024) reported that higher grain filling rates lead to greater yields, with grain weight also increasing accordingly (Wu *et al.* 2018). In maize and rice, grain weight per panicle and per plant are key indicators of yield (Mushtaq *et al.* 2021; Garko *et al.* 2023). More primary branches contribute to higher grain and panicle weight (Agalya *et al.* 2023), and grain number per primary branch has been linked to increased total grain number in rice (Hastini *et al.* 2019). These findings highlight

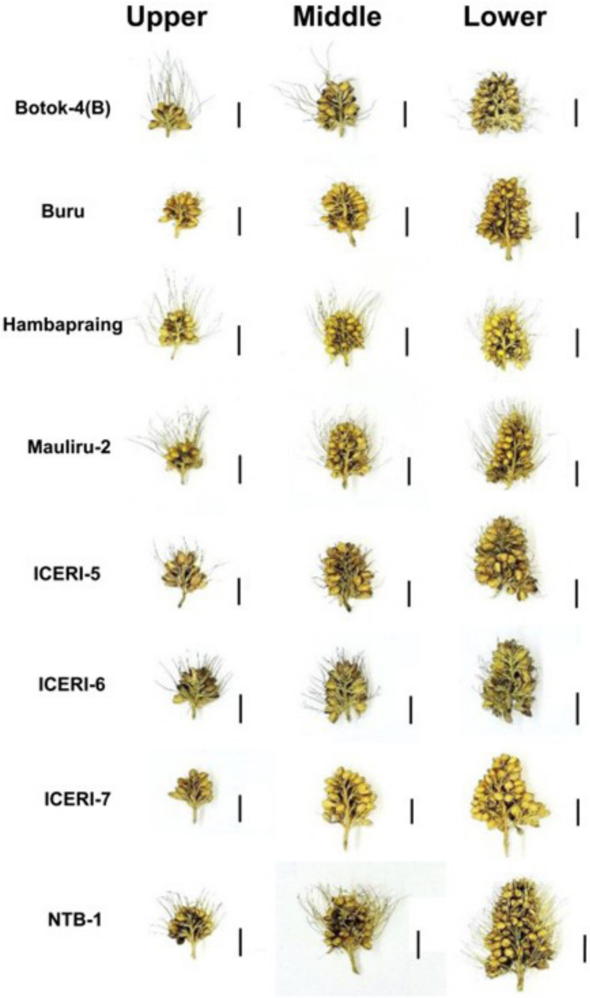

Figure 2. Primary branch diversity at each zone in eight foxtail millet genotypes; Scale bar: 0.5 cm

Table 2. Mean of panicle weight, grain weight per panicle, grain weight per plant, grain number per primary branch in the middle and lower zones of eight local foxtail millet genotypes

Genotype	PW (g)	GWP (g)	GW(g)	GNPB-M	GNPB-L
ICERI-5	3.81^{c}	3.50^{d}	5.35^{d}	16.1^{c}	21.1^{c}
ICERI-6	4.90^{abc}	3.92^{bcd}	5.50^{cd}	23.7^{bc}	37.7^{b}
ICERI-7	7.03^{a}	5.92^{a}	9.05^{ab}	29.0^{ab}	42.7^{ab}
Botok-4(B)	4.44^{bc}	3.26^{d}	5.32^{d}	24.1^{bc}	36.5^{b}
Buru	6.92^{ab}	5.86^{ab}	10.26^{a}	40.3^{a}	59.6^{a}
Hambapraing	7.33^{a}	5.48^{ab}	7.54^{bc}	27.3^{b}	37.4^{b}
Mauliru-2	7.15^{a}	5.20^{abc}	7.95^{b}	29.9^{ab}	41.8^{b}
NTB-1	5.17^{abc}	3.10^{d}	4.94^{d}	21.1^{bc}	37.0^{b}
F test	*	**	**	*	**
CV(%)	11.70	10.63	8.07	11.82	11.74

Numbers followed by the same letter on the same column indicate no significant difference based on the LSD test at $\alpha < 5\%$; PW: panicle weight, GWP: grain weight per panicle, GW: grain weight per plant, GNPB-M: grain number per primary branch of the middle zone, GNPB-L: grain number per primary branch of the lower zone

Table 3. Broad-sense heritability values, genetic coefficients of variance, and phenotypic coefficients of variance for yield-related traits in Indonesian local foxtail millet genotypes

Traits	Mean square		σ^2e	σ^2g	σ^2p	h^2bs	Mean	GCV (%)	PCV (%)
	Block	Genotype							
Ye	0.14	0.14^{**}	0.02	0.04	0.05	85.71	1.80	11.11	12.00
GFR	0.05	0.06^{**}	0.01	0.02	0.02	83.33	1.08	6.21	6.80
PW	0.23	0.24^{*}	0.09	0.05	0.08	62.50	2.50	8.94	11.31
GWP	0.40	0.23^{**}	0.06	0.06	0.08	73.91	2.21	10.77	12.53
GW	0.39	0.39^{**}	0.05	0.11	0.13	87.18	2.70	12.47	13.35
GNPB-M	1.33	1.43^{*}	0.37	0.35	0.48	74.13	5.12	11.61	13.48
GNPB-L	3.42	2.23^{**}	0.53	0.57	0.74	76.23	6.21	12.12	13.88

Ye: yield estimation, GFR: grain filling rate, PW: panicle weight, GWP: grain weight per panicle, GW: grain weight per plant, GNPB-M: grain number per primary branch of middle zone, GNPB-L: grain number per primary branch of lower zone, σ^2e: environmental variance, σ^2g: genetic variance, σ^2p: phenotypic variance, h^2bs: broad-sense heritability, GCV: genetic coefficient of variation, PCV: phenotypic coefficient of variation

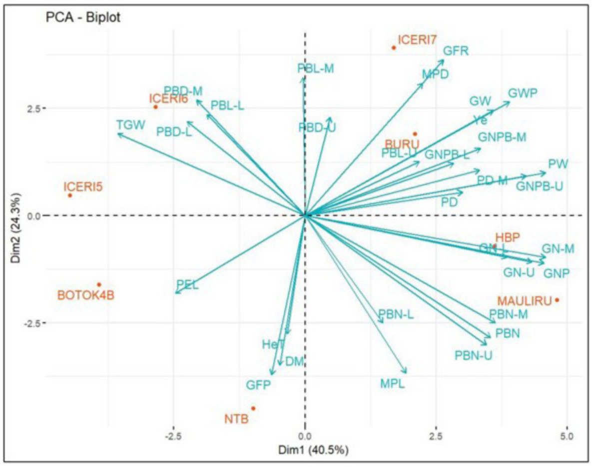

Figure 3. PCA biplot between PC 1 and PC 2 of panicle architecture and yield-related traits among eight Indonesian foxtail millet genotypes

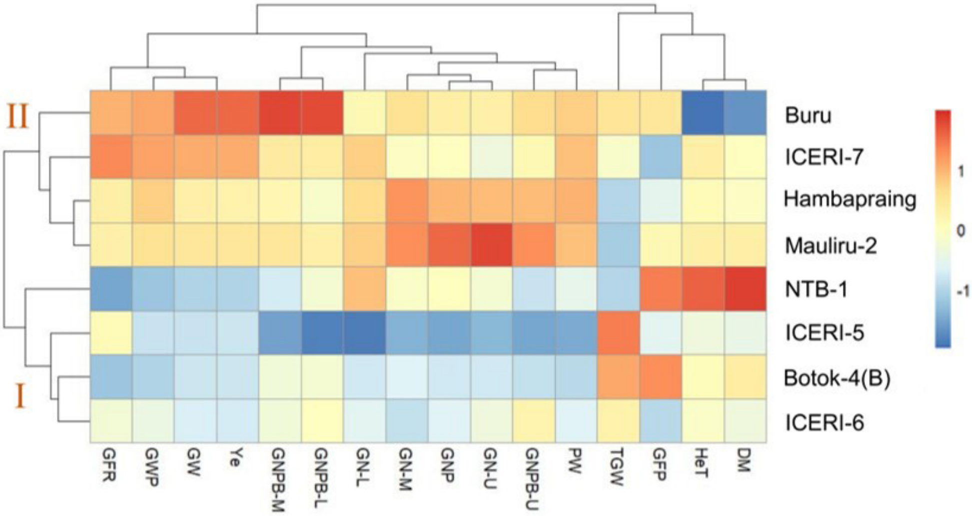

Figure 4. Two-way heatmap clustering analysis of local foxtail millet genotypes that was based on yield-related traits; Color scale represents correlation strength, with 1 indicating a strong positive association and -1 indicating a strong negative association

the importance of selecting traits that influence grain productivity. Consistent with these studies, our results confirm that several panicle traits are strongly associated with productivity in Indonesian foxtail millet genotypes. These findings highlight the importance of selecting traits that influence grain productivity.

In addition to evaluating trait-productivity correlations, it is important to consider heritability, genetic coefficient of variation (GCV), and phenotypic coefficient of variation (PCV) for the traits studied. Heritability helps guide selection decisions by indicating how much of a trait is genetically controlled (Anuradha and Patro 2020). According to Nyquist and Baker (1991), traits with high broad-sense heritability are more efficient to select. In this study, PCV values were slightly higher than GCV values for several traits, but the differences were small, suggesting limited environmental influence and stable trait expression (Patel *et al.* 2021). Mounika *et al.* (2024) also found that grain weight per plant in rice had moderate GCV and PCV but high heritability. Cooper *et al.* (2020) emphasized that both GCV and heritability are essential for effective trait improvement in breeding programs. Based on these findings, traits such as grain weight per panicle, grain weight per plant, and grain number per primary branch in the middle and lower zones are promising selection criteria for identifying high-yielding genotypes.

To further validate trait associations and genotype performance, PCA and heatmap clustering were used. PCA identified key traits influencing yield and helped highlight superior genotypes for breeding (Kumari *et al.* 2021). It has been widely applied to classify genotypes of rice and wheat based on panicle traits (Adilova *et al.* 2020; Banjare *et al.* 2024). Supporting this, Singh *et al.* (2023) found panicle weight positively correlated with grain yield, while Herlina *et al.* (2016) and Zhao *et al.* (2016) reported that longer panicle exsertion may reduce the rice yield. Grain weight per panicle and per plant was confirmed as a key yield trait (Behera *et al.* 2020; Mushtaq *et al.* 2021; Garko *et al.* 2023). Heatmap clustering complemented PCA by grouping genotypes and traits into two clear clusters (Sakinah *et al.* 2021). Aligned with previous findings, our study clustered genotypes into two groups. Genotypes such as Buru, Hambapraing, Mauliru-2, and ICERI-7 demonstrated strong performance in yield-related traits, making them promising candidates for future breeding. These findings provide valuable insights for the targeted selection and development of high-yielding foxtail millet genotypes.

Acknowledgements

The authors are grateful to the manager and technicians of the Leuwikopo Experimental Field and to the Department of Agronomy and Horticulture, Faculty of Agriculture, IPB University, for their support with research facilities.

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