RESEARCH ARTICLE

SABRAO Journal of Breeding and Genetics
58 (1) 390-399, 2026
http://doi.org/10.54910/sabrao2026.58.1.36
http://sabraojournal.org/
pISSN 1029-7073; eISSN 2224-8978

TRAITS VARIATION ANALYSIS INFLUENCING FEEDSTOCK QUALITY IN INDONESIAN FOXTAIL MILLET (*SETARIA ITALICA*)

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SUMMARY

Foxtail millet (*Setaria italica*) has great potential as food, feed, and feedstock in the biofuel industries. Currently, its applications are still few, but research on foxtail millet as a feedstock is growing. Feedstock with high-cellulose and low-lignin content is desirable for feed digestion and biofuel production. The following study aimed at characterizing phenotypic variations related to feedstock utilization in eight Indonesian foxtail millet genotypes and identifying superior genotypes for feed or biofuel feedstock development. The experiment was in a randomized complete block design arrangement with genotypes as a single factor and three replications. Acid detergent fiber (ADF) percentage, cellulose content, lignin content, leaf number, and plant height emerged as key traits for selecting superior foxtail millet for feedstock. These traits showed high broad-sense heritability and moderate to high genotypic and phenotypic variation, indicating strong genetic control. Cellulose content displayed a significant correlation ($p < 0.001$) with lignin content, plant height, leaf number, tiller number, and heading time. These associations support their use in multi-trait selection. Heatmap clustering and PCA revealed substantial genotypic variability, enabling effective selection based on feedstock quality traits. Hambapraing, Mauliru2, and ICERI7 appeared as promising genotypes for further hybridization programs, contributing desirable traits for feedstock development.

Keywords: Biofuel, cellulose, genotypes, genotypic variability, feed, lignin, selection criteria

Key findings: Among eight Indonesian foxtail millet (*S. italica* L.) genotypes, Hambapraing, Mauliru2, and ICERI7 emerged as promising parental genotypes, offering favorable attributes for incorporating into breeding programs to improve the feedstock quality.

Communicating Editor: Dr. Tabynbaeva Laila

Manuscript received: August 31, 2025; Accepted: October 13, 2025.

Citation: Pahlevi MR, Luthfiani MV, Ahmadifauzan I, Tsugama D, Ardie SW (2026). Traits variation analysis influencing feedstock quality in Indonesian foxtail millet (*Setaria italica*). *SABRAO J. Breed. Genet. 58 (1) 390-399. http://doi.org/10.54910/sabrao2026.58.1.36*.

INTRODUCTION

Intensive research in foxtail millet (*Setaria italica* [L.] Beauv.) has been steadily increasing over the years, driven by its considerable resilience to climate change and its potential to enhance sustainable food and feedstock security (Ardie *et al.,* 2025). Foxtail millet is a recognized ancient staple food among others used worldwide (Pramitha *et al.,* 2023). Its grain has excellent nutritional value for human consumption, particularly for protein content, with a low glycemic index, and is gluten-free (Arora *et al.,* 2023). The remaining plant residues (stalks and straws) can serve as feedstock for biofuel and animal feed (Dhawi *et al.,* 2018; Kishor *et al.,* 2021).

Foxtail millet, a C4 grass, is popular for its efficient utilization of water, nitrogen, and CO_2 and its ability to convert solar energy into biomass through C4 photosynthesis, which minimizes photorespiration. These characteristics contribute to the potential of foxtail millet as a promising lignocellulosic feedstock suitable for biofuel production (Muthamilarasan *et al.,* 2015). Additionally, foxtail millet hay has gained distinction as a high-quality forage in China due to its elevated crude protein content, an essential nutrient for livestock (Ren *et al.,* 2020). Given foxtail millet's dual potential for biofuel production and animal feed, optimizing its plant cell wall composition—particularly cellulose and lignin content—is crucial for enhancing biofuel yield and increasing nutrient absorption in livestock.

Forages containing higher cellulose and lower lignin work as an ideal commodity for biofuel production, as lower lignin enhances enzymatic hydrolysis, increasing cellulose accessibility, improving yield, and reducing processing costs (Li, 2021; Farobie *et al.*, 2025). Similarly, such cellulose-rich forages also occurred to be preferable as feed for ruminant animals, as their lower lignin content facilitates microbial degradation of cellulose in the digestive system, leading to optimized nutrient and energy absorption (Li, 2021). Despite its promising potential as a feedstock, intensive research on foxtail millet currently predominantly focuses on its development as a food crop, with most research being conducted in China and India (Ardie *et al.,* 2025). Meanwhile, Indonesia has local landraces of foxtail millet (Ardie *et al.,* 2017; Ratnawati *et al.,* 2024), for which research on their potential as feedstock remains limited.

The local landraces of Indonesian foxtail millet are vital plant genetic resources for developing superior cultivars in Indonesia, including those intended for both food and feedstock applications. The Indonesian foxtail millet germplasms exhibited varied morpho-agronomic performances in previous studies (Ardie *et al.,* 2017; Ratnawati *et al.,* 2024), but the lignocellulose content information of the foxtail millet genotypes was not yet available. Therefore, this study aimed to establish the selection criteria and identify the potential genotypes from eight Indonesian foxtail millet genotypes to develop superior cultivars for further improvement in feedstock.

MATERIALS AND METHODS

Experimental site

The field experiment on Indonesian foxtail millet genotypes commenced from September 2024 to January 2025 at the Leuwikopo Experimental Field, IPB University, Bogor, Indonesia (Latitude: 6°33’55.98” S, Longitude: 106°43’30.17” E). Postharvest and biochemical analyses took place at the Post-Harvest Laboratory, Department of Agronomy and Horticulture, Faculty of Agriculture, and the Feed Science and Technology Laboratory, Department of Feed Science and Technology, Faculty of Animal Science, IPB University, Bogor, Indonesia.

Experimental design

This experiment had a randomized complete block design arrangement, with foxtail millet genotype as a single factor and three replications. The eight Indonesian foxtail millet genotypes used comprised ICERI5, ICERI6, and ICERI7 obtained from the Indonesian Cereals Research Institute (ICERI); Botok4, Botok10, Mauliru2, and Hambapraing, procured from East Nusa Tenggara; and Buru, collected from North Maluku, Indonesia.

Crop husbandry

All the foxtail millet genotype seeds involved sowing in a planting tray with soil, goat manure, and rice husk charcoal (ratio 1:1:1, v/v), with three seeds per planting hole inside the shade house (approximately 50% shading) for ±1 month. The preparation of the experimental field occurred two weeks before planting. The preparation included weed removal, land tilling, and planting bed setup. Manure (at 2.5 t ha^{-1}) and dolomite (at 300 kg ha^{-1}) succeeded in equal applications to each bed, leaving the bed to rest for a week. Each replication consisted of eight planting beds, measuring 1.5 m × 1.5 m, with five rows containing 10 planting holes per row (10 plants in a row, for a total of 50 plants per planting bed).

Foxtail millet genotype seedlings proceeded to transplanting in the prepared bed with a distance of 25 cm between rows and 10 cm between planting holes. A net (white color, mesh 40) installation in the field helped protect the plants from pests and storms, providing an approximate shading of 35%. Plant maintenance ensued by applying fertilizer at 14 and 42 days after transplanting, consisting of 300 kg ha^{-1} urea, 150 kg ha^{-1} SP-36, and 75 kg ha^{-1} KCl—split equally between the two applications. Pests and diseases control applied a 0.1 mL L^{-1} insecticide (with active ingredients chlorantraniliprole 100 g L^{-1} + thiamethoxam 200 g L^{-1}) and 1 mL L^{-1} fungicide (with active ingredients propiconazole 125 g L^{-1} + tricyclazole 400 g L^{-1}) at 14 days after planting (DAP). Weeds entailed periodical removal manually.

Plant indicators and measuring method

Ten sample plants per genotype in each replication attained random selection and evaluation. Observations of parameters, when recording, used the methodology of the International Union for the Protection of New Varieties of Plants (UPOV, 2013) and ICRISAT (International Crops Research Institute for the Semi-Arid Tropics) descriptors for foxtail millet (Elangovan *et al.,* 2023). The observed parameters include 1) time of heading/flowering (day): recorded when 50% of the plant emerged from the inflorescence; 2) plant height (cm): measured from ground level to tip of inflorescence at physiological maturity stage; 3) Stem diameter (mm): measured between the third and fourth nodes from the base at the heading stage; 4) number of leaves: the total number of leaves in each plant cluster; 5) number of tillers: recorded at ground level or from basal nodes of primary tillers at the physiological maturity stage; 6) flag leaf length (cm): measured from the ligule to the tip of the flag leaf on primary tillers at the heading stage; 7) flag leaf width (cm): measured at the broadest part of the leaf blade on primary tillers at the heading stage; and 8) flag leaf area (cm^2): measured as Yoshida (1976) described using the following formula:

$$\text{Leaf area} = \text{length} \times \text{width} \times 0.75.$$

The sampling of foxtail millet genotype plants continued at the ripening stage, with their panicles removed before conducting biochemical trait analysis on the remaining forage biomass. The definition of the ripening stage was according to the BBCH scale for cereals with code 85 (soft dough). Each genotype's harvest transpired at different times: 70 DAP (Buru, ICERI6, and ICERI7); 74 DAP (ICERI5); and 104 DAP (Botok4, Botok10, Hambapraing, and Mauliru2). The plant samples were air-dried under sunlight for three days, followed by drying in an oven at 80 °C for two additional days. The forage biomass of each foxtail millet genotype was then chopped and ground into fine powder. The ground samples were sent to the Feed Science and Technology Laboratory to undergo biochemical trait analysis, including acid detergent fiber (ADF), cellulose, and lignin content.

Data analysis

The analysis of variance (ANOVA) and Duncan's multiple range test (DMRT), as performed, used SAS OnDemand for

Academics to examine the foxtail millet genotypes with various traits (heading time, plant height, stem diameter, number of leaves, number of tillers, and flag leaf length, width, and area) and biochemical traits (ADF, cellulose content, and lignin content). Genetic variance (σ^2_g), environmental variance (σ^2_e), and phenotypic variance (σ^2_p) were calculated to estimate the broad-sense heritability (h^2_{bs}). The broad-sense heritability value received categories as high (>50%), moderate (20% to 50%), and low (<20%) (Mustakim *et al.*, 2019). The computation of genotypic (GCV) and phenotypic (PCV) coefficients of variation also succeeded. Both GCV and PCV value ranges reached classifications as low (0%–10%), moderate (10%–20%), and high (>20%) (Bekele *et al.,* 2013). Analysis of the correlation matrix (based on the Pearson coefficient), upon performing, used the 'GGally' RStudio (R 4.4.1) packages (Schloerke *et al.,* 2024). Additionally, a two-way clustering heatmap and principal component analysis (PCA) proceeded using R packages 'pheatmap' (Kolde and Kolde, 2015) and 'factoextra' (Kassambara and Mundt, 2020).

RESULTS AND DISCUSSION

The analysis of variance of the biochemical and agronomic traits in eight Indonesian foxtail millet genotypes appears in Table 1. The genotypes significantly affected the agronomic and biochemical characteristics, except for stem diameter and flag leaf area. The summary of the genetic variability and broad-sense heritability for the biochemical and agronomic traits occurs in Table 2. The results revealed that all traits exhibited high broad-sense heritability. The higher level of broad-sense heritability suggested that genetic variations predominantly determine the observed phenotypic variance and indicate the stable genotypic responses. With high broad-sense heritability values, the feasible selection can also continue based on the desired traits.

Higher GCV and PCV values achieved estimation for the traits cellulose content, plant height, number of leaves, and number of tillers. Meanwhile, the rest of the traits showed moderate GCV and PCV, except for the flag leaf length and flag leaf area, which had low GCV values. The results further revealed that the estimated PCV values for most characters were only slightly higher than the GCV, demonstrating that the genetic makeup has a considerable effect in determining these traits, while the environmental effect was minimal. Singh *et al*. (2023) reported that a small difference between PCV and GCV reflects a strong genetic control over trait expression. In their study on foxtail millet, plant height showed high PCV and GCV values with minimal difference, indicating it largely has control of genetic factors. Similarly, Kumari *et al.* (2024) observed high GCV and PCV values for plant height and the number of tillers in foxtail millet, indicating that genetic factors also significantly contribute to the expression of these traits. The earlier study explained that traits with high GCV values can serve as selection criteria in breeding programs for further improvement in desired traits (Roka *et al.,* 2024). Hence, to support foxtail millet breeding for feedstock production, the traits plant height, number of leaves, number of tillers, ADF percentage, lignin, and cellulose content could be the main choices as potential selection criteria. This is because of their high broad-sense heritability, moderate to high GCV and PCV values, and a minimum difference between PCV and GCV.

The Indonesian foxtail millet genotypes' performances for agronomic and biochemical traits are available in Tables 3 and 4, respectively. The foxtail millet genotypes Botok4 and Botok10 exhibited the maximum plant height, followed by Hambapraing and Mauliru2 with moderate plant height, while the other genotypes were considerably short with the minimum plant height. These findings contrast slightly with a previous study conducted by Ratnawati *et al*. (2024), who found Botok10 was the tallest genotype, with Botok4, Mauliru2, and Hambapraing exhibiting similar, shorter heights. The genotypes Hambapraing and Mauliru2 had the most leaves and tillers and were nonsignificantly different from the two other genotypes, ICERI5

Table 1. Analysis of variance of the biochemical and agronomic traits of eight Indonesian foxtail millet genotypes.

Traits	Mean squares		CV (%)
	Replications	Genotypes	
ADF percentage	0.39^{ns}	54.25^{**}	2.71
Cellulose content	0.67^{ns}	99.37^{**}	2.88
Lignin content	0.24^{ns}	10.57^{**}	7.07
Plant height	51.75^{ns}	$6,166.98^{**}$	6.11
Number of leaves	19.83^{ns}	534.78^{**}	21.60
Stem diameter	1.15^{ns}	2.55^{ns}	19.81
Number of tillers	0.14^{ns}	2.61^{**}	27.26
Flag leaf length	8.99^{ns}	54.97^{**}	7.26
Flag leaf width	0.02^{ns}	0.30^{**}	7.18
Flag leaf area	45.31^{ns}	224.24^{ns}	12.92
Heading time	9.29^{ns}	540.55^{**}	5.13

Note: *: significant at α = 5%, **: significant at α =1%, ns = not significant (p > 0.05), and CV = coefficient of variation.

Table 2. Genetic variability and heritability of the biochemical and agronomic traits in eight Indonesian foxtail millet genotypes.

Traits	$σ^2_e$	$σ^2_g$	$σ^2_p$	h^2_{bs}	Means	GCV (%)	PCV (%)
ADF percentage	0.97	17.76	18.08	98.21	36.30	11.61	11.72
Cellulose content	0.52	32.95	33.12	99.48	25.06	22.90	22.96
Lignin content	0.51	3.35	3.52	95.18	10.15	18.05	18.50
Plant height	97.38	2,023.20	2,055.66	98.42	161.51	27.85	28.07
Number of leaves	37.96	165.61	178.26	92.90	28.52	45.11	46.81
Stem diameter	1.13	0.47	0.85	55.69	5.38	12.79	17.14
Number of tillers	0.36	0.75	0.87	86.21	2.21	39.14	42.16
Flag leaf length	8.33	15.55	18.32	84.85	39.76	9.92	10.77
Flag leaf width	0.03	0.09	0.10	90.00	2.55	11.76	12.40
Flag leaf area	95.68	42.85	74.75	57.33	75.74	8.64	11.41
Heading time	12.39	176.05	180.18	97.71	68.58	19.35	19.57

Note: $σ^2_e$ = environmental variance, $σ^2_g$ = genotypic variance, $σ^2_p$ = phenotypic variance, h^2_{bs} = broad-sense heritability, GCV = genetic coefficient of variation, and PCV = phenotypic coefficient of variation.

Table 3. Agronomic traits' metrics observed in eight Indonesian foxtail millet genotypes.

Geno	PH (cm)	NL	SD (mm)	NT	FLL (cm)	FLW (cm)	FLA (cm^2)	HeT (DAP)
B4	214.79±11.8	33.9±3.4	5.60±0.2	2.3±0.4	48.11±2.4	2.57±0.3	92.88±11.4	79.0±3.0
B10	229.52±0.2	30.5±7.0	6.33±0.3	1.4±0.7	43.22±1.6	2.08±0.1	67.97±7.1	85.7±4.0
BU	126.88±15.2	17.1±3.4	4.67±0.4	1.7±0.5	36.00±3.5	2.93±0.2	80.42±13.5	55.0±3.0
HBP	176.80±6.5	50.6±9.2	5.48±0.1	3.5±0.7	40.51±4.1	2.24±0.1	65.70±2.5	79.0±5.2
I5	116.95±3.4	20.2±2.2	4.21±0.3	2.6±0.5	37.62±3.7	2.67±0.1	75.38±9.5	57.3±3.5
I6	115.92±7.5	19.1±1.4	4.29±0.3	2.8±0.7	36.64±3.4	2.66±0.2	73.72±12.3	54.0±2.0
I7	129.53±9.3	13.6±3.2	6.71±2.9	0.6±0.4	35.62±1.5	2.95±0.2	79.45±7.7	58.7±2.5
MAU2	181.68±12.9	43.1±10.6	5.72±0.4	2.8±0.7	40.39±1.8	2.31±0.1	70.40±6.6	80.0±3.5

Geno = Genotypes, B4 = Botok4, B10 = Botok10, BU = Buru, HBP = Hambapraing, I5 = ICERI5, I6 = ICERI6, I7 = ICERI7, MAU2 = Mauliru2, PH = plant height, NL = number of leaves, SD = stem diameter, NT = number of tillers, FLL = flag leaf length, FLW = flag leaf width, FLA = flag leaf area, and HeT = heading time.

Table 4. Biochemical traits' metrics observed in eight Indonesian foxtail millet genotypes.

Genotypes	ADF (%)	Cellulose (%)	Lignin (%)
Botok4	40.70±1.0	28.71±0.7	11.53±0.6
Botok10	37.60±1.0	26.68±1.4	10.63±0.4
Buru	35.03±0.1	19.64±0.9	13.28±0.8
Hambapraing	40.55±1.2	31.47±0.8	8.56±0.5
ICERI5	31.45±1.0	19.47±0.6	10.29±0.5
ICERI6	33.33±1.1	20.40±0.2	10.80±1.1
ICERI7	30.70±0.8	20.57±0.6	8.69±0.9
Mauliru2	41.02±1.1	33.57±0.5	7.39±0.4

ADF = acid detergent fiber.

and ICERI6. The foxtail millet genotypes Botok4, Hambapraing, and Mauliru2 had the maximum acid detergent fiber (ADF) levels.

Furthermore, the correlation analysis, heatmap clustering, and principal component analysis (PCA), as also performed, investigated the relationship among the phenotypic traits and eight foxtail millet genotypes. It identified key traits suitable for multi-trait selection in breeding programs targeting feedstock production. The correlation matrix showed the correlation between phenotypic traits (Figure 1). Cellulose content emerged to be significantly positively correlated with ADF percentage, plant height, the number of leaves and tillers, and heading times ($p < 0.05$ to $p < 0.001$). However, the cellulose content expressed a significantly negative correlation with lignin content ($p < 0.01$) and flag leaf width ($p < 0.001$). These results aligned with a previous study that reported cellulose content as significantly positively correlated with ADF and negatively associated with lignin content (Li *et al.*, 2025). The heatmap cluster analysis depicted the clustering based on phenotypic traits and foxtail millet genotypes, and the hue in the plot indicated the value of each trait (Figure 2a). The genotype-based clustering method revealed two major groups within the dataset. The first group comprised the genotypes Botok4, Botok10, Hambapraing, and Mauliru2, with moderate heading time and superior plant height, flag leaf length, number of leaves, cellulose content, ADF percentage, and stem diameter. In contrast, the second group included the foxtail millet genotypes ICERI5, ICERI6, ICERI7, and Buru, with fewer superior traits, such as flag leaf width and length and lignin content, with an early heading time. The clustering analysis results were greatly analogous to past findings, which reported genotypes Botok4, Botok10, Mauliru2, and Hambapraing forming a closely related group. Meanwhile, foxtail millet genotypes ICERI5 and ICERI6 clustered together based on agromorphological traits (Ratnawati *et al.*, 2024).

The PCA biplot illustrated the contribution of each trait to the principal components and their interrelationship, represented by axes, along with the distances among the foxtail millet genotypes (Figure 2b). The Dim1 (horizontal axis) (PC1) explained 57.3% of the total variance, whereas Dim2 (vertical axis) (PC2) accounted for 18.9%, cumulatively capturing 76.2% of the total variability in the obtained data. Vectors (arrows) represent phenotypic traits, and their length and proximity to the PC axis indicate the contribution of the variable to the variance explained. Cellulose content and number of leaves significantly contributed to PC1, whereas flag leaf length was more influential in PC2. The PCA biplot also highlighted the individual observations of the eight foxtail millet genotypes represented by dots. The foxtail millet genotypes with closely positioned dots, such as ICERI7-Buru (Quadrant I), Botok4-Botok10 (Quadrant II), ICERI5-ICERI6 (Quadrant III), and Mauliru2-Hambapraing (Quadrant IV), revealed the genetic similarity. However, the distinct phenotypic traits characterize each quadrant. The arrow length, direction, and proximity between the vector

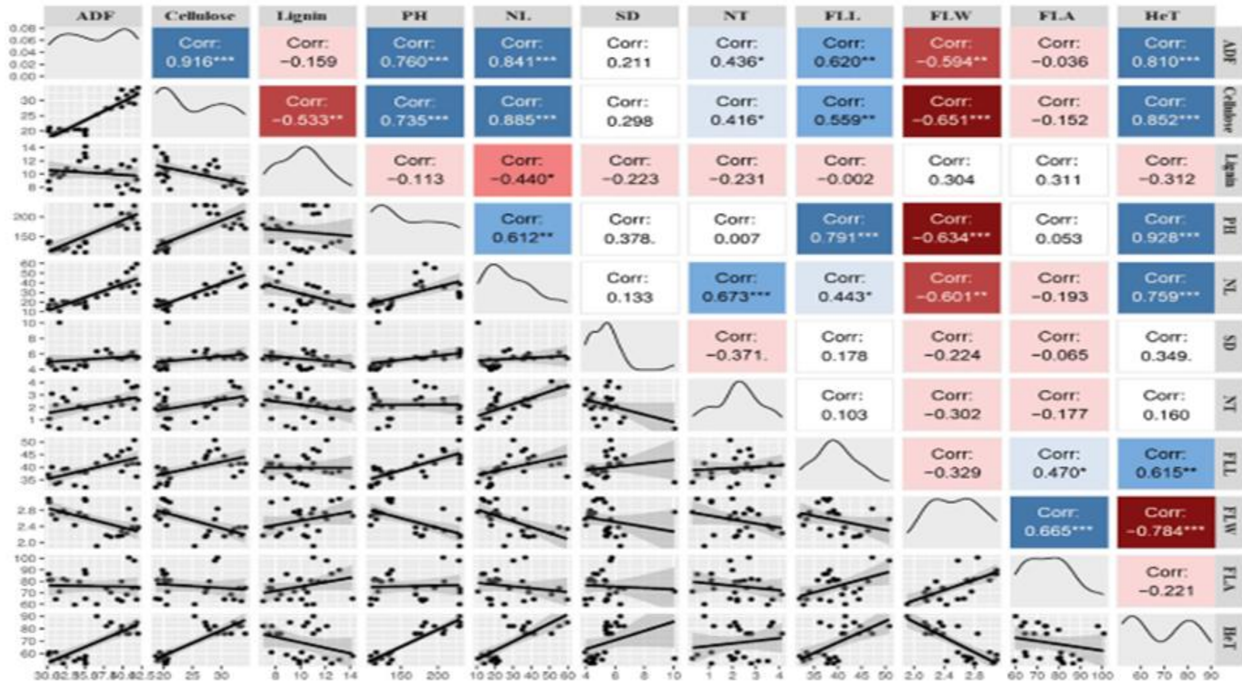

Figure 1. Correlation matrix (Pearson's coefficient) between phenotypic traits and eight foxtail millet genotypes. PH = plant height, NL = number of leaves, SD = stem diameter, NT = number of tillers, FLL = flag leaf length, FLW = flag leaf width, FLA = flag leaf area, HeT = heading time, and ADF = acid detergent fiber. *: significant at p < 0.05, **: significant at p < 0.01, ***: significant at p < 0.001, and ns = not significant (p > 0.05).

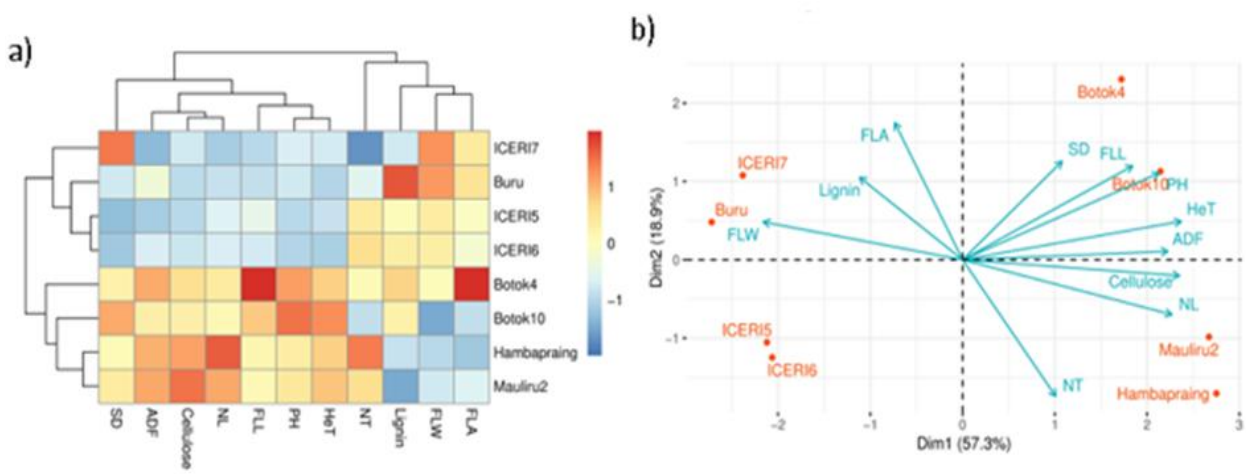

Figure 2 a) Heatmap cluster, b) PCA–Biplot between phenotypical traits and eight foxtail millet genotypes. PH = plant height, NL = number of leaves, SD = stem diameter, NT = number of tillers, FLL = flag leaf length, FLW = flag leaf width, FLA = flag leaf area, HeT = heading time, and ADF = acid detergent fiber.

point and the genotype dot determine the trait levels for each genotype cluster. These results confirmed that PCA can identify the primary traits mainly contributing to the population's variability (Venujayakanth *et al.,* 2017).

The analysis of variance, correlation, cluster heatmap, and PCA analyses allowed us to identify the potential key traits for selection and potential foxtail millet genotypes for hybridization for improving feedstock production. The primary traits identified are cellulose content, the number of leaves, and plant height. These important traits possessed high broad-sense heritability values, GCV, and PCV values, and also revealed considerable positive correlation with each other, making them suitable for multi-trait selection. Additionally, lignin content emerged as a critical trait despite its moderate GCV and PCV values. Its high broad-sense heritability, minimal difference between PCV and GCV, and negative correlation with cellulose content underscore its genetic stability and relevance to feedstock quality. Lower lignin levels enhance digestibility in livestock and enhance enzymatic hydrolysis efficiency during biofuel production (Li, 2021; Farobie *et al.*, 2025). Bhat *et al.* (2020) reported that lignin content proved to be one of the crucial selection criteria to increase forage quality in sorghum genotypes. Therefore, lignin should be a priority alongside other key traits in multi-trait selection strategies to optimize breeding programs for dual-purpose foxtail millet cultivars.

The foxtail millet genotypes Hambapraing and Mauliru2 most likely appeared to be suitable for feedstock despite their high ADF percentage. The ADF comprises cellulose, lignin, and ash. Even though a lower ADF forage is generally desirable for easier digestibility, only the lignin is indigestible. Nevertheless, the high cellulose content in the genotypes Hambapraing and Mauliru2 supports their continued viability as feedstock candidate landraces. Cellulose serves as a fermentable sugar substrate for biofuel production (Fatriasari *et al.,* 2023). Past research also stated that cellulose contributes to gut health maintenance in animal nutrition (Kim *et al.,* 2020). In contrast, the foxtail millet genotype ICERI7 exhibited consistently low levels across all biochemical parameters, indicating its potential utility as a parental line in breeding programs aimed at optimizing the feedstock traits.

In foxtail millet, developing feedstock with lower lignin could increase the feedstock's digestibility and quality, but the risk is the plant becoming prone to lodging. An inverse relationship exists between lodging resistance and digestibility, where increased digestibility often relies on reducing lodging resistance (lower lignin content) and vice versa (Mengistie and McDonald, 2023). Additionally, Muhammad *et al.* (2020) declared that plants with higher lignin content provide greater strength of the stem in wheat crops. Nevertheless, the foxtail millet genotypes Hambapraing, Mauliru2, and ICERI7 were still suitable for good-quality feedstock due to their low lignin content, while the genotypes Botok4, Botok10, Buru, ICERI5, and ICERI6 emerged to be suitable for improvement in lodging resistance. Therefore, the foxtail millet ideotype to increase feedstock quality consisted of moderate height, with more tillers and leaves, higher cellulose, and lower ADF and lignin content. The genotypes Hambapraing and Mauliru2 had the potential as parental genotypes to achieve moderate height, high cellulose content, low lignin content, and the maximum tillers and leaves. Moreover, the genotype ICERI7 can potentially be effective as a donor parent in breeding programs aimed at reducing ADF percentage due to its low ADF content.

CONCLUSIONS

In foxtail millet genotypes, the key traits, including ADF percentage, cellulose content, lignin content, leaf number, and plant height, exhibited high broad-sense heritability alongside moderate to high GCV and PCV values. These showed their potential as effective selection criteria in the development of superior cultivars for feedstock purposes. Multi-trait selection using these traits is possible based on their considerable association. The heatmap cluster and PCA analyses revealed the genotype variability, allowing selection based on these traits among the foxtail millet genotypes. The genotypes Hambapraing, Mauliru2, and ICERI7 emerged as promising genotypes beneficial in a hybridization program, contributing desirable traits for improvement in feedstock.

ACKNOWLEDGMENTS

The authors extend their sincere appreciation to the managerial and technical staff of the Leuwikopo Experimental Station and the Plant Molecular Biotechnology-2 Laboratory at IPB University for their valuable contributions and assistance throughout the execution of this research.

REFERENCES

Ardie SW, Khumaida N, Fauziah N, Yudiansyah (2017). Biodiversity assessment of foxtail millet (*Setaria italica* L.) genotypes based on RAPD marker. *J. Trop. Crop. Sci*. 4(1): 21–25. https://doi.org/10.29244/jtcs.4.1.21-25.

Ardie SW, Nugroho RB, Dirpan A, Anshori MF (2025). Foxtail millet research in supporting climate change resilience efforts: Bibliometric analysis and focused literature review. *Heliyon* 11: e42348. https://doi.org/10.1016/j.heliyon.2025.e42348.

Arora L, Aggarwal R, Dhaliwal I, Gupta OP, Kaushik P (2023). Assessment of sensory and nutritional attributes of foxtail millet-based food products. *Front. Nutr*. 10: 1146545. https://doi.org/10.3389/fnut.2023.1146545.

Bekele BD, Rakhi S, Naveen GK, Kundura PJ, Shashidhar H (2013). Estimation of genetic variability and correlation studies for grain Zinc concentrations and yield-related traits in selected rice (*Oryza sativa* L.) genotypes. *Asian J. Exp. Biol. Sci.* 4(3): 391–397.

Bhat BV, Venkateswarlu R, Tonapi VA (2020). Breeding sorghum for forage and feed: Status and approaches. In: Sorghum in the 21st century: Food–Fodder–Feed–Fuel for a Rapidly Changing World. Singapore: Springer Singapore. pp. 393–420. https://doi.org/10.1007/978-981-15-8249-3_17.

Dhawi F, Datta R, Ramakrishna W (2018). Metabolomics, biomass and lignocellulosic total sugars analysis in foxtail millet (*Setaria italica*) inoculated with different combinations of plant growth-promoting bacteria and mycorrhiza. *Commun. Plant Sci*. 8: 8. http://doi.org/10.26814/cps2018002.

Elangovan M, Hariprasanna K, Pandey S, Pradheep K, Vetriventhan M, Alercia A, Cerutti AL, Lopez F (2023). Key Descriptors for Foxtail Millet. ICAR-IIMR, ICAR-NBPGR, ICRISAT, FAO, Italy. pp. 1–15. https://doi.org/10.4060/cc7531en.

Farobie O, Ariyanta HA, Fatriasari W, Azelee NI (2025). Valorization of lignin for sustainable biochemicals. In: Handbook of Lignin. Singapore: Springer Nature Singapore. pp. 1–29. https://doi.org/10.1007/978-981-97-2664-6_52-1.

Fatriasari W, Solihat NN, Sari FP, Karimah A, Sohail A (2023). Sugar production from bamboo. In: Multifaceted Bamboo: Engineered Products and Other Applications. Singapore: Springer Nature Singapore. pp. 217–241. https://doi.org/10.1007/978-981-19-9327-5_11.

Kassambara A, Mundt F (2020). Factoextra: Extract and visualize the results of multivariate data analyses. R package version 1.0.7.999, https://github.com/kassambara/factoextra.

Kim Y, Hwang SW, Kim S, Lee YS, Kim TY, Lee SH, Kim SJ, Yoo HJ, Kim EN, Kweon MN (2020). Dietary cellulose prevents gut inflammation by modulating lipid metabolism and gut microbiota. *Gut. Microbe*. 11(4): 944–961.

Kishor PBK, Kumar SA, Naravula J, Kumari PH, Kummari D, Guddimalli R, Edupuganti S, Karumanchi AR, Venkatachalam P, Suravajhala P, Polavarapu R (2021). Improvement of small seed for big nutritional feed. *Physiol. Mol. Biol. Plants* 27: 2433–2446. https://doi.org/10.1007/s12298-021-01071-6.

Kolde R, Kolde MR (2015). Package 'pheatmap'. R package 2; 1(7): 790.

Kumari P, Kharor N, Pahuja SK, Phogat DS (2024). Principal component analysis of foxtail millet accessions under rainfed condition. *Electr. J. Plant. Breed*. 15(2): 296–303. https://doi.org/10.37992/2024.1502.044.

Li W, Xiao Q, Fang Z, Zheng Q, Li H, Li Z (2025). The half-heading stage may represent the optimal harvest time for the first cut of tall wheatgrass. *Agronomy* 15(4): 763. https://doi.org/10.3390/agronomy15040763.

Li X (2021). Plant cell wall chemistry: Implications for ruminant utilization. *J. Appl. Anim. Nutr*. 9(1): 31–56. https://doi.org/10.3920/JAAN2020.0017.

Mengistie E, McDonald AG (2023). Effect of cell wall compositions on lodging resistance of cereal crops. *J. Agric. Sci.* 161(6): 794–807. https://doi.org/10.1017/S0021859624000091.

Muhammad A, Hao H, Xue Y, Alam A, Bai S, Hu W, Sajid M, Hu Z, Samad RA, Li Z, Liu P (2020). Survey of wheat straw stem characteristics for enhanced resistance to lodging. *Cellulose*. 27(5): 2469–2484. https://doi.org/10.1007/s10570-020-02972-7.

Mustakim, Samuddin S, Maemunah (2019). Genetic diversity, heritability and correlation between local cultivars of upland rice. *The Agric. Sci. J.* 6(1): 20–26.

Muthamilarasan M, Khan Y, Jaishankar J, Shweta S, Lata C, Prasad M (2015). Integrative analysis and expression profiling of secondary cell wall genes in C4 biofuel model *Setaria italica* reveals targets for lignocellulose bioengineering. *Front. Plant. Sci.* 6: 965. https://doi.org/10.3389/fpls.2015.00965.

Pramitha L, Choudhary P, Rana S, Singh RK, Das P, Sharma S, Rajasekaran R, Prasad M, Muthamilarasan M (2023). Foxtail millet (*Setaria italica* L.): A model for small millets. Academic Press, In: Neglected and Underutilized Crops. pp. 305–324. https://doi.org/10.1016/B978-0-323-90537-4.00020-X.

Ratnawati S, Jannah RM, Dewi YI, Rizqullah R, Suwarno WB, Ardie SW (2024). The genetic variability of Indonesian local foxtail millet accession based on agro-morphological traits and early salinity tolerance evaluation utilizing *SiDREB2*-based SNAP marker. *HAYATI J. Biosci*. 31(1): 82–93. https://doi.org/10.4308/hjb.31.1.82-93.

Ren XL, Li SG, Cui JH, Liu M, Song SJ, Liu F, Nan CM, Wang XG, Wang J, Xia XY (2020). Evaluation of nutritional components of different foxtail millet (*Setaria italica*) germplasm for hay. *Indian J. Agric. Sci.* 90(4): 713–716. https://doi.org/10.56093/ijas.v90i4.102208.

Roka P, Shrestha S, Adhikari SP, Neupane A, Shreepaili B, Bista MK (2024). A review on genetic parameters estimation, trait association, and multivariate analysis for crop improvement. *Arch. Agric. Environ. Sci*. 9(3): 618–625. https://doi.org/10.26832/24566632.2024.0903029.

Schloerke B, Cook D, Larmarange J, Briatte F, Marbach M, Thoen E, Elberg A, Crowley J (2024). GGally: Extension to 'ggplot2'. *HAL SHS*. https://dx.doi.org/10.5281/zenodo.5009047.

Singh D, Lawrence K, Marker S, Bhattacharjee I, Lawrence R, Choudhary R, Ercisli S, Karunakaran R (2023). Rainfed assessment of foxtail millet (*Setaria italica* L. Beauv) germplasms through genotyping and principal component analysis. *Front. Plant. Sci*. 14: 1017652. https://doi.org/10.3389/fpls.2023.1017652.

UPOV (2013). The International Union for the Protection of New Varieties of Plants (2013). Foxtail millet. TG/SETARIA (PROJ.5). Geneva, Switzerland.

Venujayakanth B, Dudhat AS, Swaminathan B, Anurag ML (2017). Assessing crop genetic diversity using principle component analysis: A review. *Trend. Biosci*. 10(2): 523–528.

Yoshida S, Forno DA, Cock JH (1976). Laboratory manual for physiological studies of rice. IRRI, Los Baños, Philippines.