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RESEARCH ARTICLE

Assessment of genetic parameters for selection in advanced finger millet lines

S. Jha, A. Kumar, S. Mishra

Birsa Agricultural University, Kanke, Ranchi 834 006, Jharkhand, India

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shouryajha19@gmail.com

Abstract

An experiment was carried out at Birsa Agriculture University during kharif-2024 to estimate the genetic factors like variability, heritability and genetic advance, among fourty finger millet genotypes. The experiment was conducted in an Alpha lattice design with three replications, four blocks per replication, ten plots per block and data were recorded for 15 quantitative traits. Analysis of variance revealed significant genetic variability across all traits, except number of plants per plot. The ANOVA results indicate the presence of substantial genetic variability for most traits, suggesting good potential for selection and crop improvement. However, the non-significant variation observed for number of plants per plot suggests that this trait is largely influenced by environmental factors and may not be effective for genetic selection. The average grain yield and fodder yield was 24.33 q/ha and 59.29q/ha respectively, Genotype showed maximum yield for grain is CFMV-2 (33.60 q/ha) and for fodder PR-1731(74.8q/ha). The mean performance data showed that genotypes outperformed than the best check are CFMV-2, IIMRFMR-3796 for grain yield and PR-1731, KMR-301, BBM-13, A-404 for fodder yield. In case of grain and fodder yield, Genotypic Coefficient of Variation (GCV) was 19.96 and 13.23, while Phenotypic Coefficient of Variation (PCV) was 22.64 and 16.10 respectively. High heritability coupled with high genetic advance as percent of mean identified for days to fifty percent flowering, finger length, flag leaf area, grain yield per panicle, grain yield, fodder yield per hectare and biological yield per plant. High heritability coupled with high genetic advance (as percent of mean) is one of the most reliable indicators of predominant additive gene action in quantitative traits. Selection of the parents should be based on characters such as earliness, finger length, grain yield per panicle, fodder yield per hectare in finger millet lines to identify the potential for higher grain and fodder production.

Keywords: Alpha lattice design, heritability, GCV, PCV, genetic advance

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Introduction

Finger millet [*Eleusine coracana* (L.) Gaertn.], commonly known as "ragi," is increasingly recognized as a future crop owing to its remarkable adaptability to marginal environments, particularly the semi-arid tropics of Asia and Africa. Its resilience to drought and low-input conditions makes it a sustainable alternative to water-intensive cereals. It is reported that finger millet requires less than one-fourth of the water needed for paddy cultivation (Anuradha *et al.,* 2017), highlighting its significance under conditions of water scarcity and climate change. Cytologically, finger millet is an allotetraploid species with a genomic constitution of AABB and a chromosome number of 2n = 4x = 36, as reported by Goron and Raizada (2015). This polyploid nature contributes to its adaptability and stability across diverse environments. Nutritionally, finger millet is highly valued due to its rich composition, containing approximately 76.32% carbohydrates, 9.2% protein, and about 7% dietary fiber and essential minerals (Gull *et al.,* 2014). Its grains are particularly rich in calcium and iron, making it an important crop for addressing nutritional security. In addition to its role as a staple food, the crop residue serves as an excellent source of fodder for livestock, especially during the summer season, thereby supporting mixed farming systems (Feedipedia, 2025). Despite its potential, the productivity of finger millet in Jharkhand (0.35 lakh hectares area with 914 kg/ha productivity) remains significantly lower than the national average of 10.23 lakh hectares and 1359 kg/ha, respectively (Anonymous, 2025). One of the primary reasons for this yield gap is the lack of high-yielding and well-adapted varieties. Being a predominantly self-pollinated crop, finger millet exhibits limited natural genetic variability within existing populations, which restricts the scope of direct selection. In this context, a comprehensive understanding of the nature and magnitude of genetic variability present in available genotypes becomes essential for effective crop improvement. Estimation of genetic parameters such as variability, heritability, and genetic advance provides valuable insights into the genetic architecture of yield and its component traits. Since grain yield is a complex quantitative trait influenced by multiple genes and environmental factors, direct selection based solely on phenotype may not always be effective. Therefore, indirect selection through yield-attributing component traits is often considered a more reliable approach in plant breeding (Khinchi *et al.,* 2022). The present study was undertaken with the objective of assessing the extent of genetic variability among different finger millet genotypes, along with the estimation of heritability and genetic advance for various traits. Such an analysis facilitates the identification of traits governed by additive gene action, thereby enabling effective selection strategies. Ultimately, this approach aids in the development of superior genotypes with enhanced grain and straw yield, contributing to improved productivity and sustainability of finger millet cultivation.

Materials and methods

The field experiment was conducted at the Birsa Agricultural University, Ranchi, during the kharif season 2024-25 of July month utilizing the alpha lattice design with three replications. Each replication was partitioned into four blocks of 10 plots each, yielding a total of 40 plots per replication. Each genotype was sown in five rows of 3m length per plot per replication. The Net Plot Size per genotype was kept as 1.25m x 3m (3.75 m^2). The spacing between rows and plant were 25cm and 10cm respectively. The experimental material consisted of 40 breeding lines of finger millet obtained from diverse sources this include 3 checks i.e. National Check (N.C.), Zonal check (Z.C.), Local check (L.C.) as presented in Table 1. The local check BM-3 (Birsa Mardua-3) performed as a stable and high yielding comparison to the traditional varieties in particularly Jharkhand region (BAU, 2021). Similarly in the research of Sood *et al.*, 2016 showed genotype VL-376 performed as early maturing and suitable for several Indian states. Observations were recorded on five randomly selected plants from each plot for the traits such as plant height (m), panicle length (m), number of fingers per panicle, number of tillers per plant, finger length (m), flag leaf area (m^2), test weight (g), grain yield per panicle (g), fodder yield per hectare (q/ha), grain yield (q/ha), number of plants per plot, biological yield per plant (g) and harvest index. However, observations on days to fifty percent flowering and days to maturity were taken on a plot-by-plot basis from each replication. The collected data were subjected to analysis using Rstudio software for ANOVA (Analysis of Variance) test for significant differences among the genotypes. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953) and classified as high, moderate and low suggested by Shivasubramanian and Menon (1973). Heritability in broad sense was calculated as per Allard (1960). Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955). Genotypic and phenotypic correlations were calculated according to Miller *et al.*, (1958) and their classifications give by Searle, 1965. The formulae for the calculation of variance and genetic advance were presented in Gudmewad *et al.*, 2018.

Table 1: List of genotypes with their mean performance for grain and fodder yield

S. No.	Genotype	FYPH (q/ha)	S. No.	Genotype	FYPH (q/ha)
1	A-404	70.6	21	VL-402	57.6
2	IIMRFMR-21-8011	55.4	22	BR-9	60.3
3	PR-1938	57.2	23	KMR-301	72.4
4	IIMRFM-3999	59.6	24	GPU-107	58.6
5	VL-406	54.7	25	PRR-1216	52.9
6	KMR-708	61.8	26	VL-410	35.3
7	VL-352	29.6	27	BFM-5-E	47.2
8	VR-1192	52.7	28	VL-1163	63.4
9	IIMRFM-4715	61.2	29	BR-14-5	64.8
10	BWM-1	42.8	30	PR-1734	65.7
11	TNEC-1345	53.5	31	GE-4449	59.2
12	IIMRFM-3796	67.8	32	CFMV-2	52.8
13	VL-396	59.2	33	BAU-22-2	62.4
14	GPU-67	64.8	34	BBM-13	71.5
15	VL-347	50.6	35	VR-1188	54.6
16	OEB-605	56.5	36	PR-1731	74.8
17	BAU-22-3	63.7	37	IIMRFMR-21-8006	57.8
18	KMR-716	56.5	38	VL-376 (NC)	62.5
19	CFMV-1	53.2	39	PR-202 (ZC)	59.8
20	WN-1585	53.6	40	BM-3 (LC)	69.3

Analysis revealed a sufficient amount of variability present at both genotypic (σ^2p) and phenotypic variance (σ^2p) level for several traits, including plant height (σ^2p = 106.1 and σ ^{2}g = 47.3), days to maturity (σ ^{2}p = 99.0 and σ^2p = 94.8), days to fifty percent flowering (σ^2p = 86.0 and σ^2p = 85.4), fodder yield per hectare (σ^2p = 91.23 and σ^2p = 61.5), and grain yield (σ^2p = 30.23 and σ 2g = 23.61). In contrast, traits such as the number of tillers per plant (σ^2p = 0.06 and σ^2p = 0.03), number of fingers per panicle (σ^2p = 1.18 and σ^2p = 0.54), finger length (σ^2p = 1.32 and σ^2p = 0.8), and test weight (σ^2p = 0.1 and σ^2p = 0.08) showed comparatively low variability. These findings align with similar reports by Sindhuja *et al.*, (2019) and Devaliya *et al.*, (2018), as they also observed high variability for plant height, days to maturity, and days to fifty percent flowering, and low variability for traits like the number of tillers and fingers. The result showed that PCV was consistently greater than GCV for all traits, which is typically, confirms the influence of environmental influence. Based on the classification given by Burton and DeVane (1953) for coefficients of variation, high variability found for grain yield per panicle (PCV 24.5%, GCV 21.9%) and grain yield (PCV 22.6%, GCV 19.9%). These high values indicate that these traits having good amount of genetic variability, making them excellent candidates for direct selection to improve yield (Table 3). In case of moderate variability reported in flag leaf area (PCV 20.1%, GCV 16.0%), panicle length (PCV 18.6%, GCV 12.3%), number of tillers per plant (PCV 18.4%, GCV 13.8%), biological yield per plant (PCV 16.9%, GCV 13.9%), finger length (PCV 16.1%, GCV 13.15%), number of fingers per panicle (PCV 15.5%, GCV 10.7%), days to fifty percent flowering (PCV 14.1%, GCV 14.0%), test weight (PCV 13.5%, GCV 9.4%). These findings are consistent with previous studies by Devaliya *et al.*, (2018), Mahalle *et al.*, (2024), and Charitha *et al.*, (2023), who also reported similar levels of variability for many of these traits in finger millet. According to the classification of Robinson *et al.*, (1966), traits with high heritability was observed for days to fifty percent flowering (99.2%), days to maturity (95.9%), grain yield per panicle (79.9%), grain yield (77.7%), finger length (66.5%), and biological yield per plant (65.8%), flag leaf area (63.5%) indicating that these traits are largely governed by genetic factors and can be effectively improved through selection. Moderate heritability was recorded for plant height (43.6%), panicle length (44.15%), number of fingers per panicle (47.31%), test weight (48.57%), harvest index (58.8%) and number of tillers per plant (55.8%) suggesting a considerable influence of environmental factors on these traits, though selection may still be moderately effective. This trend was also shown by Charitha *et al.*, (2023) for days to 50% flowering, followed by days to maturity, flag leaf area, plant height, finger length, fodder yield, biological yield and grain yield; Mahalle *et al.*, (2024) also recorded similar findings for most of the traits. Madhavilatha *et al.*, (2021) found moderate heritability for plant height and number of effective tillers per plant. GAM classified according to Johnson et al. (1955), traits having moderate genetic gain observed in table 3 for days to maturity (19.7%), panicle length (16.9%), number of fingers per panicle (15.1%), test weight (13.5%) and harvest index (11.6%), and traits with GAM greater than 20% considered high and reported for days to fifty percent flowering (28.8s3%), finger length (22.1%), number of tillers per plant (21.25%), flag leaf area (26.43%), grain yield per panicle (40.47%), grain yield (36.24%) and biological yield per plant (23.18%). Also found by Devaliya *et al.*, (2018) for grain yield per plant, number of productive tiller had high genetic gain while moderate for number of fingers and test weight; Charitha *et al.,* (2023) reported high genetic gain for finger length, biological yield per plant and days to flowering while moderate genetic gain for days to maturity, number of fingers and harvest index. Patil *et al.,* (2023) reported same result for plant height. In the present study considerable variability was observed among the selected genotypes, indicating the presence of sufficient variability within the experimental material. The value of fodder yield per hectare (PCV 16.1%, GCV 13.2%), suggested moderate variability present among the genotypes and genetic improvement through selection is possible. Also the high heritability (67.6%) coupled with high genetic advance (22.4%) indicate direct selection would be effective in improving the fodder production in further generation (Raulwar *et al.*, 2025).

Table 2: Analysis of variance (ANOVA) for studied traits in finger millet genotype

Source of variation	Replication	Genotype	Block	Error	CD at (5%)	CV (%)
Degree of Freedom	2	39	9	69	-	-
Days to fifty percent flowering	1.0	257.0**	0.6	0.6	1.3	1.2
Plant height (cm)	13.0	200.**	94.7	58.7	12.4	8.0
Panicle length (cm)	0.3	4.2**	1.7	1.1	1.7	13.
No. of fingers per ear	0.3	2.2**	0.4	0.6	11.5	9.5
Finger length (cm)	0.2	3.0**	0.2	0.4	1.1	9.5
No. of tillers per plant	0.0	0.1**	0.0	0.0	0.2	12.
Days to maturity	5.6	288.7**	2.6	4.2	3.3	2.1
Flag leaf area (cm^2)	6.9	71.7**	15.6	10.9	5.3	11.9
Number of plants per plot	20.3	74.1	54.6	10.9	-	5.2
Test weight (g)	0.0	0.3**	0.0	0.0	0.4	9.8
Grain yield per panicle (g)	0.3	6.5**	0.4	0.5	1.1	11.1
Grain yield (q/ha)	8.9	77.4**	7.7	6.6	4.1	10.6
Fodder yield per ha(q/ha)	32.3	214.2**	28.0	29.7	8.8	9.3
Biological yield per plant (g)	4.5	56.8**	13.4	7.7	4.5	9.8
Harvest Index (%)	0.65	16.77**	2.15	3.28	2.95	5.80

** = significant at 1% level

Table 3: Overall statistical parameters use to access variability in finger millet

Variables	Range (Min)	Range (Max)	Overall mean	σ^2_g	σ^2_p	h^2 (Broad sense) %	GAM	PCV (%)	GCV (%)
Days to 50% flowering (cm)	45	79	66	85.4	86.0	99.2	28.8	14.1	14.0
Plant height (cm)	83.2	113.3	97.6	47.3	106.1	43.6	9.5	10.6	7.0
Panicle length (cm)	5.8	10.3	8.0	1.0	2.1	44.1	16.9	18.6	12.3
Number of finger per panicle	5	9	7	0.5	1.1	47.3	15.1	15.5	10.7
Finger length (cm)	4.5	9.3	7.1	0.8	1.3	66.5	22.1	16.1	13.1
Number of tillers per plant	1	1.7	1.3	0.0	0.0	55.8	21.2	18.4	13.8
Days to maturity	78	112	99	94.8	99.0	95.9	19.7	10.0	9.7
Number of plants per plot	123	146	133	10.4	57.9	15.1	1.7	5.6	2.2
Flag leaf Area (cm)	18.4	35.5	27.8	20.2	31.2	63.5	26.4	20.1	16.0
Test weight (g)	2.4	3.6	3.01	0.0	0.1	48.5	13.5	13.5	9.4
Grain yield per panicle (g)	2.4	9.7	6.4	2.01	2.5	79.9	40.4	24.5	21.9
Grain Yield (q/ha)	10.8	33.6	24.3	23.6	30.2	77.7	36.2	22.6	19.9
Fodder yield per hectare (q/ha)	29.6	74.8	59.2	61.5	91.2	67.6	22.4	16.1	13.2
Biological yield per plant (g)	18	36.5	28.9	16.3	24.0	65.8	23.1	16.9	13.9
Harvest index (%)	22.1	33.2	28.9	4.4	7.7	58.	11.	9.6	7.3

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