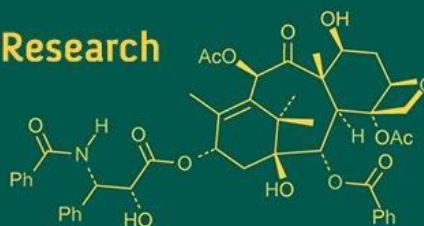


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Assessment of genetic variability, heritability, and genetic advance for yield and yield-attributing traits in kodo millet (*Paspalum scrobiculatum* L.) germplasm

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Abstract

The present investigation assessed genetic variability, heritability, and genetic advance for 12 morpho-agronomic traits in 60 kodo millet (*Paspalum scrobiculatum* L.) germplasm accessions, including four checks, evaluated in an augmented randomized complete block design at IIMR, Hyderabad. Analysis of variance revealed significant differences among genotypes for all traits except thumb length and peduncle length, indicating substantial genetic variability. Genetic parameter estimates showed that phenotypic coefficients of variation (PCV) were consistently higher than genotypic coefficients (GCV), with narrow differences for traits such as days to maturity, flowering, and test weight, suggesting strong genetic control. High heritability coupled with high genetic advance was observed for plant height, early flowering and early maturity, grain yield, fodder yield, and harvest index, highlighting the predominance of additive gene action and the potential effectiveness of direct selection. Mean performance analysis identified GPLM 520 and GPLM 587 as promising dual-purpose types with superior grain and fodder yield, while IPS 69, IPS 699, and KOPKM 3 emerged as early-maturing, stress-resilient accessions. The findings demonstrate the broad scope for improving kodo millet through targeted breeding strategies, potentially enhancing productivity and adaptability under rainfed farming systems.

Keywords: Kodo millet, genetic variability, yield and yield components, heritability, genetic advance, dual-purpose genotypes

Introduction

Kodo millet (*Paspalum scrobiculatum* L.), a tetraploid cereal ($2n = 4x = 40$), belongs to the family Poaceae and is one of the most ancient small millets, domesticated in tropical Africa and later introduced to India, where it has been cultivated for nearly 3,000 years (Burton, 1940; Malleshi and Hadimani, 1993; Upadhyaya *et al.*, 2016) [2, 9, 20]. It is predominantly grown in the states of Madhya Pradesh, Chhattisgarh, Tamil Nadu, Karnataka, and Maharashtra, and is also cultivated in several Asian and African countries (De Wet *et al.*, 1983) [4]. Kodo millet is well adapted to marginal soils and low-input farming conditions, making it an essential cereal for smallholder and rainfed farming systems (Harinarayana, 1989; Padulosi *et al.*, 2009; M'Ribu and Hilu, 1996) [6, 11, 8]. Despite its resilience, the average productivity of kodo millet in India remains low (~312 kg/ha) compared to its potential yield of 2000 kg/ha under improved agronomic practices (Bondale, 1994; Singh, 1994) [1, 17]. Limited genetic improvement and lack of systematic breeding efforts are significant reasons for this wide yield gap. Since genetic variability forms the foundation of crop improvement, the assessment of variability, heritability, and genetic advance in morphological and yield-related traits is crucial for identifying promising genotypes and designing effective breeding strategies (Johnson *et al.*, 1955; Panse and Sukhatme, 1985; Ragini *et al.*, 2015; Thakur *et al.*, 2020) [7, 12, 14, 19]. Previous studies in kodo millet have reported considerable diversity in morphological attributes, including plant height, panicle length, tillering ability, and yield-related characters (Sharma *et al.*, 2017; Patil *et al.*, 2020) [16, 13]. However, systematic information on the nature and magnitude of these genetic parameters is still limited. Therefore, the present investigation was undertaken to study the extent of genetic variability, heritability, and genetic advance in kodo millet for

morphological and yield traits, to identify superior germplasm accessions for future crop improvement programs.

Materials and Methods

The field experiment was conducted during the *Kharif* season of 2024-2025 at the ICAR-Indian Institute of Millets Research (IIMR), Rajendranagar, Hyderabad, India. The primary objective was to evaluate the morpho-agronomic diversity of kodo millet germplasm accessions at the Research Farm of IIMR, Hyderabad, situated at an elevation of 535 m above mean sea level (17.45° N latitude and 78.47° E longitude). The experimental site receives an average annual rainfall of 854.6 mm.

Experimental material and design: The study comprised 60 kodo millet germplasm accessions, including four checks (GPUK 3, TNAU 86, JK 41, and JK 36) (Table 1). Each accession was planted in two rows of 2.0 m length, with a spacing of 45 cm between rows and 10 cm between plants within rows. The experiment followed an Augmented Randomized Complete Block Design (Augmented RCBD) with seven blocks, where the check varieties were replicated across all blocks.

Traits recorded: Observations were recorded on a set of morphological and yield traits, including number of tillers per plant, panicle length (cm), thumb length (cm), peduncle length (cm), plant height (cm), days to 50% flowering, days to 100% flowering, days to maturity, 1000-seed weight (g), grain yield per plant (g), fodder yield per plant (g), and harvest index (%).

Statistical analysis: The collected data were subjected to analysis of variance (ANOVA) under the augmented design. Genetic parameters were estimated, including heritability, genetic advance, and genetic advance as a percentage of the mean, phenotypic coefficient of variation (PCV), and genotypic coefficient of variation (GCV). Further, mean performance and variability analyses were conducted using INDOSTAT and R software.

Results and Discussion

Based on the observations of various quantitative and qualitative characteristics studied, the results of this experiment are grouped into

- 1 Analysis of variance (ANOVA)
- 2 Mean performance, descriptive statistics, and variability, and
- 3 Analysis of genetic variability, heritability, and genetic advance

Genetic Variability and Heritability of Yield and Grain Quality Trait

1. Analysis of variance (ANOVA)

The analysis of variance (ANOVA) under an augmented randomized complete block design involving 60 kodo millet genotypes (56 germplasm accessions and four checks) revealed significant variability for all 12 morpho-agronomic traits studied (Table 2). The study highlighted several key findings related to agricultural performance metrics. Significant variation was observed for grain yield and harvest index across blocks, entries, and genotypes, as well as in the interactions between genotypes and checks. For

days to flowering (50% and 100%), differences were likewise detected among blocks, entries, genotypes, and checks. In contrast, the number of tillers and peduncle length differed significantly only when genotypes were compared with checks. Variation was also evident among entries, genotypes, checks, and their interactions for panicle length and plant height. Days to maturity showed significance across blocks, entries, genotypes, and interactions, while test weight differed among blocks, entries, and genotypes. A highly significant response was recorded for fodder yield among entries, genotypes, and checks. In comparison, no meaningful differences were observed for thumb length. These results highlight the presence of wide genetic variability, providing opportunities for identifying superior genotypes through selection, in agreement with earlier reports by Sao *et al.* (2017) ^[15], Nirubana *et al.* (2017a) ^[10], and Suthediya *et al.* (2021) ^[18].

2. Mean performance of genotypes

The mean performance and descriptive statistics of 60 kodo millet germplasm accessions were assessed for 12 yield-related traits using an augmented design with seven blocks. Parameters, including mean, range, standard error, standard deviation, and coefficient of variation (CV%), provided insights into variability and distribution patterns (Tables 3 and 4). There are wide ranges and higher CV% for traits such as fodder yield, grain yield, harvest index, and number of tillers per plant. Conversely, traits with lower CV%, such as early maturity, test weight, days to flowering, thumb length, peduncle length, panicle length, and plant height, showed relative stability across genotypes. These findings offer a valuable baseline for identifying superior genotypes in kodo millet improvement programs.

3. Analysis of genetic variability, heritability, and genetic advance

Genetic parameters (Table 5) indicated that the phenotypic coefficient of variation (PCV) was generally higher than the genotypic coefficient of variation (GCV) for all traits, confirming the influence of environment. However, the differences were narrow for traits such as days to maturity, days to flowering, and test weight, suggesting strong genetic control. High GCV was observed for grain yield per plant, fodder yield per plant, and harvest index. High heritability coupled with high genetic advance was recorded for plant height, days to flowering, days to maturity, grain yield per plant, fodder yield per plant, and harvest index, indicating that these traits are predominantly governed by additive gene action and can be effectively improved through direct selection. Moderate heritability with moderate genetic advance was observed for the number of tillers per plant (with high GAM), panicle length, and peduncle length, implying the involvement of both additive and non-additive gene effects. Overall, traits such as number of tillers, plant height, early flowering, early maturity, grain yield, and fodder yield provide substantial scope for genetic improvement through direct selection. The evaluated kodo millet genotypes thus exhibited significant variability across all morpho-agronomic traits.

Phenological and Morphological Traits: The number of tillers per plant ranged from 6.86 to 15.92, with a mean of 11.30. The highest tiller numbers were recorded in GPLM 587 (15.92) and GPLM 596 (15.17). Panicle length varied

between 4.76 cm and 8.32 cm, with a mean of 6.73 cm. The longest panicles were observed in IPS 803 (8.32 cm) and IPS 679 (8.16 cm). Thumb length ranged from 3.16 cm to 6.26 cm, with a mean of 4.73 cm; maximum values were noted in IPS 148 (6.26 cm) and GPLM 598 (5.86 cm). Peduncle length varied between 2.33 cm and 4.02 cm, with a mean of 2.93 cm. The longest peduncle was recorded in IPS 147 (4.02 cm), followed by KOPKM 2 and KOPKM 23 (each 3.71 cm). Plant height ranged widely from 36.17 cm to 84.61 cm, with a mean of 64.20 cm. The tallest plants were IPS 147 (84.61 cm) and GPLM 596 (84.23 cm). Days to 50% flowering ranged from 56.61 to 101.11 days (mean 76.79 days). Early flowering genotypes included IPS 69 (56.61 days) and IPS 699 (58.36 days). Days to 100% flowering varied from 61.96 to 113.96 days, with an average of 85.64 days; IPS 69 (61.96 days) and IPS 699 (62.96 days) were identified as early flowering, and days to maturity extended from 76.32 to 154.82 days, with a mean of 119.54 days. The earliest maturing genotypes were KOPKM 3 (76.32 days), followed by KOPKM 28 and IPS 69 (92.32 days).

Yield and Yield Components: Test weight ranged between 3.66 g and 5.58 g, with a mean of 4.51 g. The heaviest seeds were observed in IPS 148 (5.58 g) and IPS 785 (5.52 g).

Grain yield per plant varied substantially from 1.32 g to 20.42 g, with a mean of 8.65 g. The highest yielding genotypes were GPLM 520 (20.42 g) and JK 41 (17.27 g). Dry fodder yield ranged from 11.44 g to 65.41 g, with a mean of 32.28 g. The top performers were GPLM 587 (65.41 g) and GPLM 520 (58.53 g). Harvest index exhibited wide variation between 5.47% and 41.85%, with a mean of 21.52%. The maximum values were recorded in IPS 181 (41.85%) and IPS 69 (36.30%).

The study highlighted wide diversity among the kodo millet genotypes regarding growth, yield, and maturity traits. GPLM 520 and GPLM 587 emerged as outstanding performers, with GPLM 520 excelling in grain yield and GPLM 587 in fodder yield and tillering ability, making them valuable dual-purpose types for farming communities. IPS 148 and IPS 785 were identified as superior for seed size, while IPS 181 and IPS 69 showed high harvest index values, reflecting efficient biomass partitioning. Early flowering and maturing genotypes such as IPS 69, IPS 699, and KOPKM 3 demonstrated strong adaptability for short-duration environments and stress-prone regions. Tall and vigorous types like IPS 147 and GPLM 596 can contribute to higher biomass yield. Together, these genotypes represent a diverse pool of traits that breeders can exploit to enhance productivity, resilience, and adaptability in kodo millet.

Table 1: List of kodo millet (*Paspalum scrobiculatum* L.) germplasm accessions used in the study

S. No	Genotypes	Type of material	S. No	Genotypes	Type of material
1	KOPKM 2	Germplasm accession	31	IPS 706	Germplasm accession
2	KOPKM 3	Germplasm accession	32	IPS 741	Germplasm accession
3	KOPKM 4	Germplasm accession	33	IPS 744	Germplasm accession
4	KOPKM 6	Germplasm accession	34	IPS 764	Germplasm accession
5	KOPKM 7	Germplasm accession	35	IPS 777	Germplasm accession
6	KOPKM 14	Germplasm accession	36	IPS 782	Germplasm accession
7	KOPKM 15	Germplasm accession	37	IPS 785	Germplasm accession
8	KOPKM 23	Germplasm accession	38	IPS 803	Germplasm accession
9	KOPKM 28	Germplasm accession	39	IPS 814	Germplasm accession
10	IPS 69	Germplasm accession	40	IPS 828	Germplasm accession
11	IPS 79	Germplasm accession	41	IPS919	Germplasm accession
12	IPS 147	Germplasm accession	42	IPS 928	Germplasm accession
13	IPS 148	Germplasm accession	43	GPLM 358	Germplasm accession
14	IPS 149	Germplasm accession	44	GPLM 505	Germplasm accession
15	IPS 155	Germplasm accession	45	GPLM 514	Germplasm accession
16	IPS 176	Germplasm accession	46	GPLM 520	Germplasm accession
17	IPS 181	Germplasm accession	47	GPLM 522	Germplasm accession
18	IPS 207	Germplasm accession	48	GPLM 568	Germplasm accession
19	IPS 208	Germplasm accession	49	GPLM 570	Germplasm accession
20	IPS 415	Germplasm accession	50	GPLM 578	Germplasm accession
21	IPS 429	Germplasm accession	51	GPLM 580	Germplasm accession
22	IPS 622	Germplasm accession	52	GPLM 587	Germplasm accession
23	IPS 627	Germplasm accession	53	GPLM 589	Germplasm accession
24	IPS 645	Germplasm accession	54	GPLM 596	Germplasm accession
25	IPS 648	Germplasm accession	55	GPLM 598	Germplasm accession
26	IPS 653	Germplasm accession	56	GPLM 614	Germplasm accession
27	IPS 670	Germplasm accession	57	GPK 3 (check)	Released variety
28	IPS 679	Germplasm accession	58	TNAU 86 (check)	Released variety
29	IPS 694	Germplasm accession	59	JK 41 (check)	Released variety
30	IPS 699	Germplasm accession	60	JK 36 (check)	Released variety

Table 2: Analysis of variance and mean sum of squares for yield attributing and grain quality traits

S. No.	Traits	Blocks (d.f=6)	Entries (d.f=59)	Genotypes (d.f=55)	Checks (d.f=3)	Genotype vs checks (d.f=1)	Error (d.f=18)
1	NT	0.97	3.22	4.29*	4.15	21.07**	1.98
2	PL	0.67	1.05**	0.86*	0.78**	1.89*	0.35
3	ThL	0.23	0.27	0.24	0.14	0.315	0.15
4	PDL	0.01	0.10	0.13	0.14	0.32*	0.06
5	PH	62.10	150.6**	130.10**	403.1**	1895.1**	42.00
6	DFF	166.07**	104.6**	129.66**	43.14*	24.38	85.90
7	D100F	203.79**	135.7**	154.58**	79.14**	24.38	14.31
8	DTM	377.4**	242.1**	272.8**	24.40	1136.70**	10.80
9	TSW	0.12**	0.11**	0.11**	0.04	0.050	0.02
10	GYP	4.02*	20.33**	13.76**	108.56**	185.16**	1.46
11	FYP	20.92	110.7**	162.31**	127.29**	61.94	19.23
12	HI	25.70*	63.89**	69.80**	120.40**	684.20**	7.90

*, ** Significant at 5%, 1% level respectively.

NT-No. of tillers per plant, PL-Panicle length (cm), ThL-Thumb length (cm), PDL-Peduncle length (cm), PH-Plant height (cm), DFF-Days to 50% flowering, D100F-Days to 100% flowering, DTM-Days to maturity, TSW-1000 Seed weight (g), GYP-Grain yield/plant (g/plant), FYP-Fodder yield/plant (g/plant), HI-Harvest index (%).

Table 3: Mean performance of kodo millet (*Paspalum scrobiculatum* L.) genotypes for morpho-agronomic traits

S. No.	Genotypes	NT	PL	ThL	PDL	PH	DFF	D100F	DTM	TSW	GYP	FYP	HI
1	KOPKM 2	8.48	6.06	4.9518	3.71	51.23	79.36	95.96	122.32	4.3125	6.82	18.14	30.65
2	KOPKM 3	11.73	6.06	4.9518	2.83	45.73	68.36	71.96	76.32	5.1925	4.12	25.84	15.62
3	KOPKM 4	10.73	6.18	4.8268	2.33	44.98	68.36	72.96	102.32	4.3225	5.87	20.79	24.87
4	KOPKM 6	9.23	7.18	4.3268	2.33	41.98	79.36	84.96	107.32	4.9025	5.47	28.59	17.23
5	KOPKM 7	11.98	6.43	4.8268	2.83	49.48	64.36	72.96	107.32	4.9525	6.72	31.49	18.21
6	KOPKM 14	10.23	6.93	4.9518	2.96	46.98	64.36	69.96	107.32	4.6525	6.87	31.29	18.63
7	KOPKM 15	11.73	5.93	5.4518	2.46	41.23	92.36	99.96	136.32	4.6125	10.32	29.09	26.76
8	KOPKM 23	13.23	6.06	4.3268	3.71	56.98	79.36	89.96	128.32	4.1425	10.92	24.89	31.6
9	KOPKM 28	12.04	5.28	4.758	3.07	56.61	62.61	65.96	92.32	4.435	9.53	25.56	28.21
10	IPS 69	12.29	5.2	5.258	3.57	74.86	56.61	61.96	92.32	4.475	11.78	21.98	36.3
11	IPS 79	11.04	6.78	5.133	3.32	71.61	90.61	95.96	126.32	4.985	10.71	24.98	31.06
12	IPS 147	11.79	5.63	4.383	4.02	84.61	90.61	95.96	134.32	4.255	5.43	27.08	17.79
13	IPS 148	10.54	6.9	6.258	3.27	60.36	66.61	76.96	92.32	5.575	8.98	29.48	23.95
14	IPS 149	11.79	6.53	4.508	3.4	69.11	86.61	95.96	126.32	4.715	5.78	24.48	20.56
15	IPS 155	12.79	7.03	4.133	3.65	76.61	86.61	95.96	126.32	4.755	10.78	23.23	32.99
16	IPS 176	10.29	7.03	4.258	3.02	50.61	71.61	76.96	120.32	4.435	3.38	21.23	16.04
17	IPS 181	9.61	7.2	4.4518	3.13	55.92	75.61	87.71	113.82	4.6525	10.13	12.54	41.85
18	IPS 207	8.86	6.83	5.08	3.01	67.42	68.61	74.71	98.82	5.02	9.33	38.29	19.71
19	IPS 208	9.11	7.20	4.70	2.88	46.17	60.61	63.71	98.82	4.28	6.23	17.79	24.16
20	IPS 415	8.86	6.95	5.20	2.88	43.67	64.61	74.71	98.82	4.43	1.48	13.74	7.06
21	IPS 429	8.36	6.70	4.70	2.63	51.17	61.61	70.71	98.82	4.88	1.93	14.04	9.47
22	IPS 622	9.61	7.33	3.95	3.01	58.67	75.61	82.71	98.82	4.41	6.18	30.99	16.36
23	IPS 627	11.36	6.95	5.33	2.88	36.17	75.61	83.71	126.82	4.62	3.98	31.44	11.02
24	IPS 645	8.36	8.08	4.45	3.13	74.17	88.61	93.71	126.82	4.71	8.93	33.39	20.97
25	IPS 648	6.86	7.16	3.64	2.82	58.42	68.36	76.96	103.82	4.40	1.97	11.44	13.49
26	IPS 653	9.36	7.78	4.26	2.82	54.67	79.36	90.96	103.82	4.21	9.02	39.94	18.59
27	IPS 670	9.36	6.91	4.26	3.07	62.17	64.36	66.96	103.82	3.74	6.62	24.24	21.27
28	IPS 679	9.86	8.16	4.26	2.82	67.17	88.36	95.96	137.82	4.55	11.97	40.54	22.97
29	IPS 694	11.86	7.66	4.39	2.82	56.42	73.36	76.96	124.82	5.04	8.77	22.12	28.14
30	IPS 699	9.36	7.53	3.99	3.07	49.67	58.36	62.96	103.82	4.12	7.37	32.19	18.66
31	IPS 706	10.86	7.28	4.64	2.69	59.67	88.36	99.96	137.82	4.15	9.52	49.19	16.48
32	IPS 741	7.86	7.16	3.39	2.44	59.67	88.36	106.96	137.82	4.15	8.17	24.89	24.56
33	IPS 744	13.23	7.82	4.48	2.91	70.79	77.86	86.71	128.57	4.75	5.88	36.96	13.97
34	IPS 764	8.73	7.82	5.11	2.78	74.54	86.86	94.71	128.57	5.09	13.38	27.71	32.16
35	IPS 777	8.73	7.69	4.61	2.66	75.04	86.86	95.71	128.57	4.86	6.78	14.26	29.71
36	IPS 782	12.48	7.82	3.16	2.78	65.79	86.86	94.71	128.57	4.83	9.43	27.51	25.11
37	IPS 785	14.23	6.69	4.78	2.91	83.29	86.86	96.71	128.57	5.52	15.88	53.16	23.72
38	IPS 803	12.73	8.32	3.61	3.03	77.79	62.86	67.71	95.57	4.48	12.13	36.51	25.09
39	IPS 814	8.23	7.19	4.81	2.41	50.79	70.86	77.71	101.57	4.61	5.98	19.36	22.23
40	IPS 828	12.23	5.84	3.98	3.01	64.04	73.86	81.71	96.57	4.77	9.58	37.51	20.56
41	IPS 919	14.11	5.25	4.90	2.59	69.54	67.11	83.96	122.82	4.25	12.12	55.73	17.33
42	IPS 928	12.86	5.63	5.15	3.04	76.79	67.11	83.96	122.82	4.33	8.67	50.83	13.73
43	GPLM 358	12.61	5.28	4.78	2.64	71.79	77.11	84.96	122.82	4.42	9.97	53.73	14.94
44	GPLM 505	12.11	5.63	4.78	2.87	75.54	71.11	79.96	122.82	4.48	5.82	44.48	10.32
45	GPLM 514	11.11	6.40	5.28	2.62	48.79	75.11	83.96	127.82	4.05	8.77	37.28	18.35
46	GPLM 520	9.11	7.15	3.90	2.87	82.54	101.11	113.96	154.82	3.66	20.42	58.53	25.82

47	GPLM 522	10.36	6.78	5.53	2.87	73.29	101.11	113.96	154.82	3.78	11.07	31.08	26.22
48	GPLM 568	11.61	8.03	4.78	2.74	78.79	96.11	103.96	154.82	4.52	11.27	43.03	20.30
49	GPLM 570	14.42	5.21	5.31	3.22	70.48	80.11	93.71	129.32	4.26	1.32	27.56	5.47
50	GPLM 578	14.92	4.76	5.24	3.22	76.23	80.11	93.71	129.32	4.29	6.87	36.21	16.71
51	GPLM 580	13.42	4.94	5.69	2.55	74.23	80.11	93.71	129.32	4.19	13.67	51.16	22.20
52	GPLM 587	15.92	5.79	5.56	2.47	79.98	73.11	83.71	129.32	4.16	10.52	65.41	15.38
53	GPLM 589	14.17	7.21	5.56	2.55	72.23	73.11	83.71	128.32	3.95	16.22	45.31	27.20
54	GPLM 596	15.17	5.56	5.51	2.55	84.23	73.11	83.71	129.32	4.24	2.82	37.66	8.14
55	GPLM 598	14.42	7.34	5.86	2.92	73.48	80.11	87.71	128.32	4.74	8.27	48.60	15.76
56	GPLM 614	12.67	7.46	4.94	2.80	63.48	80.11	93.71	128.32	4.55	10.97	30.06	26.80
57	GPUK 3	11.82	7.84	4.41	3.14	72.61	78.14	88.00	128.29	4.51	10.58	31.54	25.27
58	TNAU 86	12.86	5.41	4.63	3.04	76.36	76.86	87.43	126.00	4.51	10.35	31.43	25.02
59	JK 41	13.04	7.61	4.63	3.18	81.75	81.14	89.57	128.43	4.48	17.27	34.74	33.39
60	JK 36	11.46	7.25	4.75	2.86	63.71	75.29	81.86	124.57	4.36	8.16	24.61	24.99
	Mean	11.30	6.73	4.73	2.93	64.20	76.79	85.64	119.54	4.51	8.65	32.28	21.52
	CV (%)	12.14	8.67	8.19	8.37	9.69	4.30	4.40	2.70	3.14	12.73	13.79	12.14

NT-No. of tillers per plant, PL-Panicle length (cm), ThL-Thumb length (cm), PDL-Peduncle length (cm), PH-Plant height (cm), DFF-Days to 50% flowering, D100F-Days to 100% flowering, DTM-Days to maturity, TSW-1000 Seed weight (g), GYP-Grain yield/plant (g/plant), FYP-Fodder yield/plant (g/plant), and HI-Harvest index (%).

Table 4: Descriptive statistics and coefficient of variation for yield attributing and grain quality traits

S. No.	Traits	Count	Mean	SE	SD	Minimum	Maximum	CV
1	NT	60	11.30	0.73	1.93	6.86	15.92	12.14
2	PL	60	6.73	0.37	0.98	4.76	8.32	8.67
3	ThL	60	4.73	0.15	0.39	3.16	6.26	8.19
4	PDL	60	2.93	0.12	0.33	2.33	4.02	8.37
5	PH	60	64.20	4.43	11.71	36.17	84.61	9.69
6	DFF	60	76.79	3.82	10.11	56.61	101.11	4.30
7	D100F	60	85.64	4.20	11.11	61.96	113.96	4.40
8	DTM	60	119.54	5.67	14.20	76.32	154.82	2.70
9	TSW	60	4.51	0.05	0.14	3.66	5.58	3.14
10	GYP	60	8.65	1.51	3.99	1.32	20.42	12.73
11	FYP	60	32.28	4.12	10.89	11.44	65.41	13.79
12	HI	60	21.52	2.99	7.90	5.47	41.85	12.14

NT-No. of tillers per plant, PL-Panicle length (cm), ThL-Thumb length (cm), PDL-Peduncle length (cm), PH-Plant height (cm), DFF-Days to 50% flowering, D100F-Days to 100% flowering, DTM-Days to maturity, TSW-1000 Seed weight (g), GYP-Grain yield/plant (g/plant), FYP-Fodder yield/plant (g/plant), HI-Harvest index (%), SE-Standard error, SD-Standard deviation and CV-Coefficient of variation.

Table 5: Genetic variability parameters for morpho-agronomic traits

S. No	Traits	Phenotypic Variance	Genotypic Variance	Environmental variance	PCV (%)	GCV (%)	ECV (%)	Heritability in the broad sense%	Genetic advancement	Genetic advance as % mean
1	NT	4.29	2.31	1.98	18.32	13.44	12.44	53.86	2.30	20.35
2	PL	0.77	0.43	0.35	13.08	9.70	8.78	54.95	0.10	14.83
3	ThL	0.21	0.07	0.15	9.76	5.51	8.06	31.87	0.30	6.40
4	PDL	0.13	0.06	0.06	12.08	8.62	8.47	50.84	0.37	12.68
5	PH	130.09	88.05	42.04	17.76	14.62	10.10	67.68	15.93	24.80
6	DFF	129.66	118.69	10.98	14.83	14.19	4.31	91.53	21.50	28.00
7	D100F	154.58	140.27	14.31	14.52	13.83	4.42	90.74	23.27	27.17
8	DTM	272.78	261.98	10.81	13.82	13.54	2.75	96.04	32.72	27.37
9	TSW	0.09	0.06	0.02	6.56	5.57	3.46	72.15	0.44	9.74
10	GYP	13.76	12.30	1.46	42.88	40.54	13.97	89.39	6.84	79.07
11	FYP	162.31	143.07	19.23	39.47	37.05	13.59	88.15	23.17	71.77
12	HI	69.83	61.95	7.88	38.83	36.58	13.05	88.71	15.29	71.07

NT-No. of tillers per plant, PL-Panicle length (cm), ThL-Thumb length (cm), PDL-Peduncle length (cm), PH-Plant height (cm), DFF-Days to 50% flowering, D100F-Days to 100% flowering, DTM-Days to maturity, TSW-1000 Seed weight (g), GYP-Grain yield/plant (g/plant), FYP-Fodder yield/plant (g/plant), HI-Harvest index (%), GCV-Genotypic coefficient of variation, PCV-Phenotypic coefficient of variation, and ECV-Environmental coefficient of variation.

Conclusion

This study demonstrated that kodo millet possesses a broad genetic diversity across agronomic traits, underscoring its potential for yield improvement. The observed variation in flowering behavior and yield components suggests that different genotypes can be strategically utilized depending on production environments and breeding goals. The moderate to high heritability estimates coupled with

substantial genetic advance for key traits indicate that meaningful progress can be achieved through selection. Overall, the findings reaffirm the value of kodo millet as a resilient, climate-smart crop with scope for dual-purpose use. Future breeding efforts should focus on combining early maturity and high yield to deliver varieties that meet both farmer and consumer needs, thereby strengthening the role of kodo millet in food and nutritional security.

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Competing Interests

Authors have declared that no competing interests exist.

References

- Bondale KV. Status of small millets in India. In: National Seminar on Ragi and Small Millets; 1994 Jan; Bangalore, India. p. 6-7.
- Burton GW, De Vane DE. Estimating heritability in tall fescue (*Festuca arundinacea*) from replicated clonal material. *Agron J*. 1953;45:478-481.
- Glenn WB. A cytological study of some species in the genus *Paspalum*. *J Agric Res*. 1940;60:193-218.
- de Wet JM, Brink DE, Rao KP, Mengesha MH. Diversity in kodo millet (*Paspalum scrobiculatum*). *Econ Bot*. 1983;37(2):159-163.
- Falconer DS. Introduction to quantitative genetics. 4th ed. Harlow: Pearson Education; 1996.
- Harinarayana G. Breeding and varietal improvement of small millets in India. In: Riley KW, Gupta SC, Seetharam A, Mushonga JN, editors. Small millets in global agriculture. New Delhi: Oxford & IBH; 1989. p.59-70.
- Johnson HW, Robinson HF, Comstock RE. Estimates of genetic and environmental variability in soybeans. *Agron J*. 1955;47:314-318.
- M'Ribu HK, Hilu KW. Application of random amplified polymorphic DNA to study genetic diversity in *Paspalum scrobiculatum* L. (kodo millet, Poaceae). *Genet Resour Crop Evol*. 1996;43(3):203-210.
- Malleshi NG, Hadimani NA. Nutritional and technological characteristics of small millets and preparation of value added products from them. In: Riley KW, Gupta SC, Seetharam A, Mushonga JN, editors. Advances in small millets. New Delhi: Oxford & IBH; 1993. p. 270-287.
- Nirubana V, Ganesamurthy K, Ravikesavan R, Chitdeshwari T. Genetic variability studies for yield and yield components in kodo millet (*Paspalum scrobiculatum* L.). [Incomplete citation — need journal, year, volume, pages].
- Padulosi S, Mal B, Ravi SB, Gowda J, Gowda KT, Shanthakumar G, *et al*. Food security and climate change: role of plant genetic resources of minor millets. *Indian J Plant Genet Resour*. 2009;22(1):1-6.
- Panse VG, Sukhatme PV. Statistical methods for agricultural workers. 2nd ed. New Delhi: ICAR; 1967. [Edition/year may need confirmation]
- Patil RB, Vijayalakshmi KG, Vijayalakshmi D. Physical, functional, nutritional, phytochemical and antioxidant properties of kodo millet (*Paspalum scrobiculatum*). *J Pharmacogn Phytochem*. 2020;9(5):2390-2393.
- Ragini S, Subramanian A, Nirmalakumari A, Bapu JK. Genetic diversity in kodo millet (*Paspalum scrobiculatum*) relative to culm strength and yield. *J Crop Improv*. 2015;29(4):420-431.
- Sao A, Singh P, Kumar P, Pradhan A. Estimates of genetic parameters for yield and contributing traits in kodo millet (*Paspalum scrobiculatum* L.). *Res J Agric Sci*. 2017;8(1):120-122.
- Sharma S, Sharma N, Handa S, Pathania S. Evaluation of health potential of nutritionally enriched finger millet (*Eleusine coracana*) grown in Himachal Pradesh, India. *Food Chem*. 2017;214:162-168.
- Singh SV. Seed improvements in small millets and role of minikit programme in their development. In: National Seminar on Ragi and Small Millets; 1994 Jan; Bangalore, India. p.6-7.
- Suthediya VR, Desai SS, Pethe UB, Naik KV, Mahadik SG, Pendyala S. Genetic diversity studies in kodo millet (*Paspalum scrobiculatum* L.). [Incomplete citation — need journal, year, volume, pages].
- Thakur J, Kumar V, Kanwar RR. Genetic divergence studies in kodo millet (*Paspalum scrobiculatum* L.). *J Pharmacogn Phytochem*. 2020;9(6):1373-1377.
- Upadhyaya HD, Vetriventhan M, Dwivedi SL, Pattanashetti SK, Singh SK. Proso, barnyard, little, and kodo millets. In: Singh M, Upadhyaya HD, Kumar J, Bisht IS, editors. Genetic and genomic resources for grain cereals improvement. London: Academic Press; 2016. p. 321-343.