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Analysing the genetic architecture of yield and yield-related traits in Kodo Millet (*Paspalum scrobiculatum* L.) through genetic parameters, correlation, and path analysis

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Abstract

Kodo millet (*Paspalum scrobiculatum* L.) is an underutilized cereal crop with considerable genetic diversity and nutritional importance; however, information on the genetic architecture of yield and its component traits remains limited, necessitating systematic genetic evaluation for crop improvement. The experimental material was evaluated using a Randomised Block Design (RBD) with three replications. The Phenotypic Coefficient of Variation (PCV) was marginally higher than the Genotypic Coefficient of Variation (GCV) for all traits, indicating a relatively minor environmental influence on trait expression. High estimates of broad-sense heritability (h^2) coupled with high genetic advance as a percentage of mean (GAM) were recorded for protein content ($h^2 = 95.91\%$, GAM = 95.47%), dry fodder weight ($h^2 = 84.35\%$, GAM = 46.75%), and panicle length ($h^2 = 78.23\%$, GAM = 37.22%). This indicates the predominance of additive gene action, indicating that these traits can be effectively improved through phenotypic selection. Low heritability and low genetic advance were noted for seed yield per plant, underscoring the role of non-additive gene action and environmental effects. Phenotypic correlation analyses indicated that seed yield per plant had strong, significant positive associations with peduncle length (0.2811**), flag leaf blade length (0.2759**), flag leaf blade width (0.2275*), and panicle length (0.2176*). The phenotypic path coefficient analysis revealed that flag leaf blade length (0.284), followed by panicle length (0.261), peduncle length (0.222), days to 50% flowering (0.118), protein content (0.110), and flag leaf blade width (0.110), exerted the highest positive direct effects on seed yield per plant, identifying them as primary selection criteria.

Keywords: Correlation, heritability, path analysis

1. Introduction

The small tropical millet known as Kodo millet (*Paspalum scrobiculatum* L.), which is indigenous to India, is grown for its seed and fodder. It is a member of the Poaceae family's *Paniceae* tribe and is also referred to as ditch millet, rice grass, and cow grass. The genome size of this autogamous, tetraploid ($2n = 4x = 40$) C4 crop species is 1.91–1.98 pg (Burton, 1940)^[12]. While *P. scrobiculatum* var. *commersonii* is the wild variety native to Africa, *P. scrobiculatum* var. *scrobiculatum* is produced as a significant crop in India. Producing 450–900 kg of seed per hectare, Kodo millet is extremely hardy, drought-tolerant, and able to flourish in marginal soils where other crops could fail (Mall and Tripathi, 2016)^[13]. In the Philippines, Indonesia, Vietnam, Thailand, and West Africa, among other tropical and subtropical regions, it is commonly found in moist environments. Kodo millet is high in lecithin, easily digested, and great for fortifying the nervous system (Hegde *et al.*, 2004)^[14]. One of the earliest domesticated plants, millets have been cultivated for thousands of years, providing nourishment for prehistoric societies. Because of their high nutritional content (protein, fibre, micronutrients, and phytochemicals), millets are frequently referred to as "Nutri-Cereals". Unlike other cereals, they have a low carbon and water footprint and can thrive on very poor soils under harsh, dry conditions with little input (ITBP Millet Book, 2023). Protein, fibre, and vital micronutrients including iron, calcium, and potassium are all found in Kodo millet. As a rich source of proteinaceous meals, minerals, and vitamins, Kodo millet can

provide several vital ingredients needed for both human and animal body growth, maintenance, and production. Its seeds are eaten in many ways, including thin porridge and cooked rice.

The Kodo millet flower's cleistogamous nature has made crop development through hybridisation challenging. Since it enables the discovery of advantageous genotypes, having an adequate collection of Kodo millet germplasm is essential for crop growth. Crop improvement depends on having a good collection of Kodo millet germplasm, and analysing it can assist in identifying desirable genotypes. To improve Kodo millet, genetic variability is essential to comprehend crop genetic behaviour in response to selection and their mode of inheritance across generations; genetic parameters such as phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability, and genetic advance as a percentage of the mean will be computed (Anuradha *et al.*, 2020) ^[1]. In Kodo millet, these traits can be utilised as selection criteria to optimise seed yield per plant. The development and control of genetic variability become crucial to crop breeding in any crop, especially in crops like Kodo millet, where the available genetic diversity is extremely limited, since genetic variability is necessary for any agricultural improvement program. Genotypes with favourable traits that could be used in the breeding program are identified as a result of this study.

Understanding the relationships among yield and its component traits is equally important for developing efficient selection strategies. Correlation coefficient analysis provides information on the degree and direction of association among different characters, while path coefficient analysis partitions these associations into direct and indirect effects, thereby revealing the actual contribution of each trait towards seed yield. Such analyses enable breeders to identify key yield-contributing traits and formulate more effective selection criteria for crop improvement (Wright, 1921; Dewey and Lu, 1959) ^[16, 3]. Considering the limited information available on the variability, diversity, morphological characteristics, and population structure of Kodo millet germplasm, the present investigation was undertaken to characterize and evaluate a diverse set of accessions (Anuradha *et al.*, 2020) ^[1]. The findings of this study are expected to contribute to the identification of superior genotypes and provide a scientific basis for their utilization in future breeding programmes aimed at enhancing productivity, adaptability, and yield stability.

2. Materials and Methods

2.1 Planting location and experimental design

Field trials were carried out during the *kharif* season in 2025. The study was conducted at the SIF (Student Instructional Farm) of the Department of Genetics and Plant Breeding, Chandra Shekhar Azad University of Agriculture and Technology, Kanpur 208002, Uttar Pradesh. The experimental site is located at an altitude of 126 m above the mean sea level. Due to its humid subtropical environment, Kanpur experiences extremely low winter temperatures with the average range between 7°C-22°C and high summer temperatures ranging between 32 °C-43°C. With a few showers in winter, Kanpur receives 80% of its total rainfall during the monsoon, with average rainfall ranging around 898 mm.

2.2 Genotypes and traits evaluated

The material collected for the current experiment includes 29 Kodo millet genotypes and 2 check varieties. The checks used are GPK3 and JK41, which were all collected from the Indian Institute of Millet Research, Rajendranagar, Hyderabad, Telangana. The list of all genotypes considered for the study is listed in Table 1. The total number of genotypes included in checks represents a broad genetic base and varies in their

adaptation to different agro-climatic regions. The observations on the following morphological traits (Days to 50% flowering-DF50; Plant height (cm)-PH; Flag leaf blade length (cm)-FLL; Flag leaf blade width (cm)-FLW; Peduncle length (cm)-PDL; Panicle length (cm)-PNL; Thumb receme length (cm)-TRL; Raceme number above the panicle-RNAP; Number of basal tiller plant-NBT; Number of internode per plant-IND/P; Days to 50% maturity (DM); Green fodder weight (g)-WFT; Dry fodder weight (g)-DFT; 1000 Seed weight (g)-1000 SW; Seed yield/plant (g)-SY/P, Protein analysis (%)- Protein). Five plants of each genotype from each replication were randomly selected and tagged. Data of five plants were averaged replication-wise, and mean data were used for statistical analysis.

Table 1: List of Genotypes used for the experiment in Kodo millet

S. No.	Genotypes	S. No.	Genotypes
1	GPLM388	17	GPLM394
2	Pn390-25	18	GPLM427
3	GPK3	19	GPLM480
4	GPLM381	20	GPLM478
5	GPLM365	21	GPLM604
6	IC044404	22	GPLM483
7	GPLM361	23	GPLM533
8	GPLM393	24	GPLM502
9	GPLM386	25	GPLM517
10	GPLM390	26	GPLM518
11	IC0404294	27	GPLM534
12	GPLM425	28	GPLM603
13	GPLM437	29	GPLM503
14	GPLM401	30	GPLM539
15	JK41	31	GPLM588
16	GPLM322		

2.3 Statistical analysis

Using the techniques outlined by Singh and Chaudhary (1985) ^[7], estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad-sense heritability (H^2), and genotypic and phenotypic correlation coefficients were calculated. The methods of Johnson *et al.* (1955) ^[4] and Brim *et al.* (1959) ^[2] were used to determine genetic advance (GA) and genetic advance as a percentage of the mean (GAM). Correlation coefficient (Karl Pearson, 1912); Simple phenotypic correlation (r^2) among studied traits was estimated according to Searle (1961). Using seed yield per plant as the dependent variable and its component qualities as independent variables, path coefficient analysis was conducted in accordance with the methods of Dewey and Lu (1959) ^[3] to distinguish direct from indirect effects. R statistical software (Version 4.5.0; R Core Team, 2025) ^[11] with pertinent packages like *metan* (Olivoto and Lúcio, 2020) ^[9], *agricolae* (de Mendiburu, 2021), and *variability* (Lê *et al.*, 2008) ^[8] was used for all statistical analyses, including variability parameters, correlation analysis, and path analysis.

3. Results

The data generated from these 31 Kodo millet genotypes were subjected to appropriate statistical analyses to derive meaningful conclusions regarding the nature and magnitude of genetic variability in the material.

3.1. Genetic Variability Parameters

In the context of trait characterisation, estimating genetic parameters such as coefficient of variation, heritability, and genetic advancement is crucial to creating high-yielding genotypes. Both the amount of the heritable part of variation and

the degree of variance for a trait in a germplasm accession was examined. The coefficient of variation is a useful statistical tool for estimating the range of variability found in different demographic characteristics. However, the genetic coefficient of variation by itself cannot be used to determine the degree of heritable variation.

3.1.1. Genotypic coefficient of variation (GCV) and Phenotypic coefficient of variation (PCV)

The high estimates of GCV and PCV were observed for protein content (47.321 and 48.318), followed by dry fodder weight (24.710 and 26.905) and panicle length (20.430 and 23.099), indicating the presence of substantial genetic variability for these characters Table 2. The high variability observed for these traits suggested that they contributed considerably towards total variability, and selection for these traits would be effective. The Moderate GCV and PCV values were observed for flag leaf blade length (10.054 and 14.259), thumb raceme length (7.489 and 13.483), raceme number above panicle (6.830 and 16.251), number of basal tillers per plant (5.523 and 9.446), peduncle length (5.275 and 16.004), seed yield per plant (5.774 and 13.436) and flag leaf blade width (4.707 and 10.040) (Table 2). These moderate estimates indicated the presence of adequate variability for improvement through selection. The low estimates of GCV and PCV were recorded for days to 50 per cent flowering (1.451 and 2.424), days to 50% maturity (2.071 and 4.487), plant height (3.771 and 7.362), number of internodes per plant (3.179 and 9.215), green fodder weight (4.010 and 8.700) and 1000 seed weight (3.093 and 6.929), indicating comparatively lower variability for these traits among the genotypes studied (Table 2).

3.1.2. Heritability percentage ($h^2\%$)

Heritability is an important genetic parameter which indicates the proportion of phenotypic variance attributable to genetic causes and provides information regarding the transmissibility of traits from one generation to another. In the present study, heritability estimates ranged from Peduncle Length (cm) (10.863) to Protein (%) (95.914%) in Table 2. High heritability estimates were observed for protein content (95.914%), dry fodder weight (84.349%) and panicle length (78.226%) (Table 2), indicating that these traits were predominantly controlled by genetic factors with minimal environmental influence. Therefore, direct selection for these characters would be effective. Moderate heritability

estimates were recorded for flag leaf blade length (49.712%), days to 50 per cent flowering (35.893%), number of basal tillers per plant (34.191%) and thumb raceme length (30.847%), suggesting moderate influence of environment on these traits in Table 2. Low heritability estimates were observed for peduncle length (10.863%), number of internodes per plant (11.901%), raceme number above panicle (17.661%), seed yield per plant (18.469%), 1000 seed weight (19.929%), days to 50% maturity (20.130%), flag leaf blade width (21.981%), green fodder weight (21.241%) and plant height (26.234%), indicating greater environmental influence and limited effectiveness of direct selection for these traits in Table 2.

3.1.3 Genetic advance and genetic advance percentage of mean

Genetic advance as percent of mean indicates the expected improvement in a character under selection. In the present investigation, genetic advance as per cent of mean ranged from Days to 50% Flowering (1.790) to Protein (%) (95.469) percent in Table 2. High genetic advance as per cent of mean was observed for protein content (95.469%), dry fodder weight (46.751%) and panicle length (37.223%) in Table 2. High heritability coupled with high genetic advance for these traits indicated the predominance of additive gene action and suggested that selection would be highly effective in improving these characters. Moderate genetic advance as per cent of mean was recorded for flag leaf blade length (14.602%), thumb raceme length (8.568%), number of basal tillers per plant (6.653%), raceme number above panicle (5.913%), seed yield per plant (5.112%) and flag leaf blade width (4.546%) in Table 2, indicating the involvement of both additive and non-additive gene effects. Low genetic advance as per cent of mean was observed for days to 50 per cent flowering (1.790%), number of internodes per plant (2.259%), 1000 seed weight (2.845%), peduncle length (3.581%), green fodder weight (3.807%) and plant height (3.979%), in Table 2 suggesting predominance of non-additive gene action and environmental influence on these traits. Overall, the results revealed that protein content, dry fodder weight and panicle length possessed high variability, high heritability and high genetic advance as per cent of mean, indicating the predominance of additive gene action and effectiveness of direct selection for improvement of these traits in Kodo millet breeding programmes.

Table 2: Range, Mean, Coefficients of variation, Heritability (broad sense) and Genetic advance as percent of mean for 15 characters in thirty-one genotypes of Kodo millet

Trait	Range		Mean	Coefficient of variance (%)		Heritability (broad sense%)	Genetic advance	GA% mean
	Maximum	Minimum		PCV	GCV			
Days to 50% Flowering	80.667	74.667	78.032	2.424	1.451	35.859	1.397	1.79
Plant Height (cm)	60.267	49.96	55.13	7.362	3.771	26.234	2.193	3.979
Flag Leaf Blade Length (cm)	37.9	22.293	30.127	14.259	10.054	49.712	4.399	14.602
Flag Leaf Blade width (cm)	1.027	0.733	0.858	10.04	4.707	21.981	0.039	4.546
Peduncle Length (cm)	10.087	6.227	7.643	16.004	5.275	10.863	0.274	3.581
Panicle Length (cm)	15.307	7.437	10.711	23.099	20.43	78.226	3.987	37.223
Thumb Receme Length (cm)	7.433	5.153	6.148	13.483	7.489	30.847	0.527	8.568
Raceme Number Above Panicle	3.87	2.4	2.899	16.251	6.83	17.661	0.171	5.913
Number Of Basal Tiller/Plant	4.233	3.067	3.782	9.446	5.523	34.191	0.252	6.653
Number Of Internode/Plant	4.067	3.2	3.531	9.215	3.179	11.901	0.08	2.259
Days to 50% maturity	116.666	102.333	109.2	4.487	2.071	20.130	2.149	1.968
Green fodder Weight (g)	15.039	11.248	13.313	8.7	4.01	21.241	0.507	3.807
Dry Fodder Weight (g)	7.184	2.669	4.164	26.905	24.71	84.349	1.947	46.751
1000 Seed Weight (g)	5.63	4.517	4.921	6.929	3.093	19.929	0.14	2.845
Seed Yield/ Plant (g)	5.563	3.805	4.354	13.436	5.774	18.469	0.223	5.112
Protein (%)	14.523	1.939	6.014	48.318	47.321	95.914	5.741	95.469

3.2. Phenotypic correlation coefficient analysis

For a successful crop improvement programme, a full understanding of the relationships between plant characteristics and production is required. It allows crop improvement breeders to alter the expression of these features. The direction and amplitude of association between yield and its components, as well as among themselves, determine the effectiveness of yield selection. Correlation analysis reveals the nature and amplitude of the relationship between different component traits and yield, a very complicated trait that the breeder is ultimately interested in. It also aids in comprehending the nature of the interrelationships between the component traits. Finally, this type of study could aid the breeder in developing seed-yield-improving selection strategies. The present investigation revealed that seed yield per plant exhibited positive and significant association with peduncle length (0.2811**), flag leaf blade length (0.2759**), flag leaf blade width (0.2275*), and panicle length (0.2176*). Furthermore, positive but non-significant correlations were observed with thumb raceme length (0.1456), protein content (0.1499), plant height (0.1489), days to 50% flowering (0.1170), number of basal tillers per plant (0.1100), green fodder weight (0.0600), 1000 seed weight (0.0780), green fodder weight (0.0600), and number of internodes per plant (0.0070) in Table 3. In contrast, seed yield per plant exhibited negative and non-significant association with raceme number above panicle (-0.1070) and dry fodder weight (-0.0210), and days to maturity (-0.0280) in Table 3. The phenotypic correlation coefficients between seed yield and its constituent variables. Days to 50 per cent flowering exhibited positive but non-significant association with panicle length (0.1370), protein content (0.1210), seed yield per plant (0.1170), 1000 seed weight (0.0420), dry fodder weight (0.0330) and number of basal tillers per plant (0.0310). However, negative and non-significant association was observed with

number of internodes per plant (-0.1650), plant height (-0.1330), green fodder weight (-0.1100), peduncle length (-0.1100), thumb raceme length (-0.1060), raceme number above panicle (-0.0810), flag leaf blade width (-0.0520) and flag leaf blade length (-0.0330) in Table 3. Days to maturity exhibited positive but non-significant association with thumb raceme length (0.1580), number of basal tillers per plant (0.1690), number of internodes per plant (0.0540), green fodder weight (0.0400) and protein content (0.0810). Negative but non-significant association was observed with seed yield per plant (-0.0280), dry fodder weight (-0.1470), 1000 seed weight (-0.0410), panicle length (-0.0080), peduncle length (-0.1060), raceme number above panicle (-0.0100), flag leaf blade length (-0.1960), flag leaf blade width (-0.0130) and plant height (-0.1260). 1000 seed weight exhibited positive but non-significant association with seed yield per plant (0.0780). Positive but non-significant association was observed with panicle length (0.1020), peduncle length (0.0870), thumb raceme length (0.0680), plant height (0.0670) and number of basal tillers per plant (0.0510). In contrast, significant negative association was recorded with dry fodder weight (-0.3146**). Negative but non-significant association was observed with green fodder weight (-0.0740), flag leaf blade length (-0.0490) and days to 50 per cent flowering (-0.0410) in Table 3. Protein content exhibited positive but non-significant association with seed yield per plant (0.1500). Significant positive association was observed with flag leaf blade width (0.2379*). Positive but non-significant association was observed with plant height (0.1340), days to 50 per cent flowering (0.1210), thumb raceme length (0.1180), peduncle length (0.0600) and number of internodes per plant (0.0440). However, negative but non-significant association was observed with green fodder weight (-0.0560), dry fodder weight (-0.0750), raceme number above panicle (-0.0850) and panicle length (-0.0320) in Table 3.

Table 3: Phenotypic correlation coefficient among the seed yield and its contributing traits in thirty-one genotypes of kodo millet

Trait	DF50	PH	FLL	FLW	PDL	PNL	TRL	RNAP	NBT	IND/P	DM	WFT	DFT	1000 SW	PROTEIN	SY/P
DF50	1	-0.133	-0.033	-0.052	-0.110	0.137	-0.106	-0.081	0.031	-0.165	0.123	-0.110	0.033	0.042	0.121	0.117
PH		1	0.039	0.2147*	0.3638**	0.085	0.5148**	-0.126	-0.058	-0.020	-0.126	0.029	0.140	0.067	0.134	0.149
FLL			1	0.093	0.143	-0.152	0.067	-0.177	0.085	0.090	-0.196	0.160	-0.017	-0.049	0.005	0.2759**
FLW				1	0.2918**	-0.071	0.2373*	-0.125	0.114	0.045	-0.013	-0.022	0.067	0.027	0.2379*	0.2275*
PDL					1	0.033	0.4256**	-0.2073*	-0.066	-0.147	-0.106	-0.088	-0.013	0.087	0.060	0.2811**
PNL						1	0.068	-0.119	0.099	-0.157	-0.008	0.114	-0.117	0.102	-0.032	0.2176*
TRL							1	-0.5327**	0.058	-0.044	0.158	0.095	0.054	0.068	0.118	0.146
RNAP								1	-0.148	0.114	-0.010	-0.199	-0.171	0.009	-0.085	-0.107
NBT									1	0.098	0.169	0.5578**	-0.2172*	0.051	-0.015	0.110
IND/P										1	0.054	0.2441*	-0.113	0.023	0.044	0.007
DM											1	0.040	-0.147	-0.041	0.081	-0.028
WFT												1	-0.073	-0.074	-0.056	0.060
DFT													1	-0.3146**	-0.075	-0.021
1000 SW														1	0.010	0.078
PROTEIN															1	0.150
SY/P																1

**Significance level at $P < 0.01$, *Significance level at $P < 0.05$, DF50- Days to 50% Flowering, PH- Plant Height(cm), FLL- Flag Leaf Length (cm), FLW- Flag Leaf Width (cm), PDL- Peduncle Length (cm), PNL- Panicle Length (cm), TRL- Thumb Raceme Length (cm), RNAP- Raceme Number Above Panicle, NBT- Number of Basal Tiller/Plant, IND/P- Number of Internode / Plant, DM- Days to 50% maturity, WFT- Wet Fodder Yield (g), DFT/P- Dry Fodder weight (g), 1000SW- 1000 Seed weight(g), SY/P- Seed Yield/ Plant(g), PROTEIN-Protein (%)

3.3. Phenotypic Path Coefficient Analysis

Path coefficient analysis was carried out at genotypic and phenotypic levels considering seed yield as the dependent trait. Path coefficient analysis was used to partition the correlation coefficients between seed yield per plant as the dependent variable and its component traits into direct and indirect effects because the genetic architecture of economic yield must be resolved with the genetic contribution of all characters

influencing it directly and indirectly. Table 5 presents the direct and indirect effects of yield components on seed yield at phenotypic and genotypic levels respectively. Direct effect of yield contributing characters on seed yield per plant. In 31 genotypes of Kodo millet, path coefficient analysis was carried out to estimate the magnitude of direct and indirect effects of different traits on seed yield per plant (SY/P). Among the traits under study, flag leaf length had the highest positive direct effect

(0.290) on seed yield followed by panicle length (0.262), peduncle length (0.226), flag leaf width (0.111), protein content (0.109), number of basal tillers per plant (0.080), raceme number above panicle (0.076), dry fodder weight (0.068), and number of internodes per plant (0.056). These traits contributed directly to the increase in seed yield and can therefore be considered as important selection criteria in breeding programs for yield improvement. PDL showed highest positive correlation with seed yield (0.2811) followed by FLL (0.2759), FLW (0.2275) and PNL (0.2176) in Table 4. Their positive associations with seed yield were primarily due to large positive direct effects, which indicate a true causal relationship. Thus, direct selection for these traits is expected to be effective for the improvement of seed yield. In contrast, plant height (PH) was positively correlated with seed yield (0.149) although it had a negative direct effect (-0.015), indicating that the relationship with seed yield was mainly through indirect effects via peduncle length, flag leaf traits,

panicle length and protein content. The thumb raceme length also had a positive correlation (0.146) but a very low direct effect (0.009), indicating that it made a more indirect contribution to yield. DM, DF50 and green fodder yield (WFT) showed low direct effects and weak association with seed yield. RNAP had a positive direct effect but had a negative correlation with seed yield (-0.107), indicating strong adverse indirect effects through other component traits. The residual effect (0.7427) indicated that the traits considered in the present study accounted for about 44.84% (1- 0.7427) of the total phenotypic variation in seed yield in Table 4. This implies that other factors not considered in the analysis also influenced expression of yield. The results showed that the most important yield contributing traits are flag leaf length, peduncle length, panicle length, flag leaf width, protein content and number of basal tillers per plant. Therefore, these characters should be given more importance during selection for the development of high-yielding genotypes of Kodo millet.

Table 4: Phenotypic path coefficient analysis (direct and indirect effects) on the seed yield of thirty-one genotypes of Kodo millet

Trait	DF50	PH	FLL	FLW	PDL	PNL	TRL	RNAP	NBT	IND/P	DM	WFT	DFT	1000 SW	PROTEIN	SY/P
PH	-0.015	0.014	0.011	0.022	0.082	0.022	0.004	-0.010	-0.005	-0.001	-0.004	0.000	0.010	0.003	0.015	0.149
FLL	-0.004	0.001	0.290	0.009	0.032	-0.040	0.001	-0.014	0.007	0.005	-0.006	-0.002	-0.001	-0.002	0.000	0.2759**
FLW	-0.006	0.003	0.027	0.111	0.066	-0.019	0.002	-0.009	0.010	0.002	0.000	0.000	0.004	0.002	0.026	0.2275*
PDL	-0.012	0.005	0.042	0.030	0.226	0.009	0.004	-0.016	-0.005	-0.008	-0.003	0.001	-0.001	0.004	0.007	0.2811**
PNL	0.016	0.001	-0.044	-0.007	0.007	0.262	0.001	-0.009	0.008	-0.009	0.000	-0.002	-0.008	0.005	-0.003	0.2176*
TRL	-0.012	0.007	0.019	0.024	0.096	0.018	0.009	-0.041	0.005	-0.003	0.005	-0.001	0.004	0.003	0.013	0.146
RNAP	-0.009	-0.002	-0.051	-0.013	-0.047	-0.031	-0.005	0.076	-0.012	0.006	0.000	0.003	-0.012	0.000	-0.009	-0.107
NBT	0.004	-0.001	0.025	0.013	-0.014	0.026	0.001	-0.011	0.080	0.005	0.005	-0.008	-0.015	0.002	-0.002	0.110
IND/P	-0.019	0.000	0.026	0.004	-0.033	-0.041	0.000	0.008	0.008	0.056	0.002	-0.003	-0.008	0.001	0.005	0.007
DM	0.014	-0.002	-0.057	-0.001	-0.024	-0.002	0.001	-0.001	0.013	0.003	0.031	-0.001	-0.010	-0.002	0.009	-0.028
WFT	-0.013	0.000	0.046	-0.002	-0.020	0.030	0.001	-0.015	0.044	0.014	0.001	-0.014	-0.005	-0.004	-0.006	0.060
DFT	0.004	0.002	-0.005	0.006	-0.003	-0.031	0.000	-0.013	-0.017	-0.006	-0.005	0.001	0.068	-0.015	-0.008	-0.021
1000 SW	0.005	0.001	-0.014	0.003	0.019	0.027	0.001	0.000	0.004	0.001	-0.001	0.001	-0.021	0.048	0.001	0.078
PROTEIN	0.014	0.002	0.001	0.024	0.014	-0.008	0.001	-0.007	-0.001	0.003	0.002	0.001	-0.005	0.000	0.109	0.150
Residual	=0.7427															

DF50- Days to 50% Flowering, PH- Plant Height(cm), FLL- Flag Leaf Length (cm), FLW- Flag Leaf Width (cm), PDL- Peduncle Length (cm), PNL- Panicle Length (cm), TRL- Thumb Raceme Length (cm), RNAP- Raceme Number Above Panicle, NBT- Number of Basal Tiller/Plant, IND/P- Number of Internode / Plant, WFT- Wet Fodder Yield (g), DFT/P- Dry Fodder weight (g), 1000SW- 1000 Seed weight(g), SY/P- Seed Yield/ Plant(g), PROTEIN- Protein (%)

4. Discussion

One of our own special superfoods is millet, and the health advantages of millet are also demonstrated by the reduced rates of illness and longer lifespans of our ancestors who, a few generations ago, ate millet. Millets present a strong argument for boosting biodiversity and diversifying the food seed supply since they are adaptable to a wide range of climates and cropping patterns. Because millets can adapt to climate change and guarantee sustainable seed production with few inputs, they are the most dependable food crops for humanity in the event of climate change, particularly for resource-poor dryland farmers worldwide. Kodo millet is one of the most important crops that can survive drought because of its high nutritional value, dietary fibre, and antioxidant properties. It has a significant production potential in marginal and low-fertility soils with a variety of environmental conditions. Even under typical storage conditions, Kodo millet seeds have good storage properties and can be stored for several years without experiencing pest infestations. As a result, Kodo millet is known as the "famine seed" in some parts of the country.

The success of any crop improvement programme depends largely on the extent of genetic variability present in the breeding material. Although the range provides a preliminary indication of variability, the magnitude of variation is more accurately assessed through phenotypic coefficient of variation (PCV) and genotypic

coefficient of variation (GCV). In the present investigation, PCV estimates were higher than the corresponding GCV estimates for all the characters studied, indicating the influence of environmental factors on trait expression. However, the differences between PCV and GCV were relatively narrow for traits such as protein content, dry fodder weight and panicle length, suggesting that these traits were less affected by environmental fluctuations and that the observed variability was predominantly genetic in nature. Among the sixteen characters studied, the highest PCV and GCV values were recorded for protein content (48.318 and 47.321, respectively), followed by dry fodder weight (26.905 and 24.710) and panicle length (23.099 and 20.430). High estimates of both PCV and GCV indicate the presence of substantial genetic variability and provide greater scope for improvement through direct selection. The high variability observed for these traits may be attributed to the diverse genetic constitution of the genotypes included in the study. Similar findings were reported by Subramanian *et al.* (2010) [30] in Kodo millet, Anuradha *et al.* (2017) [17] in little millet, Sharma *et al.* (2018) [18] in pearl millet, Singamsetti *et al.* (2018) [23] in finger millet, and Vikram *et al.* (2020) [29] in barnyard millet. Moderately high PCV and GCV values were observed for flag leaf blade length (14.259 and 10.054), thumb raceme length (13.483 and 7.489), seed yield per plant (13.436 and 5.774), raceme number above panicle (16.251 and 6.830), and number of

basal tillers per plant (9.446 and 5.523). These results indicate the existence of moderate variability and suggest that improvement through selection may be possible for these traits. Low PCV and GCV estimates were recorded for days to 50 per cent flowering (2.424 and 1.451), days to maturity (4.487 and 2.071), number of internodes per plant (9.215 and 3.179), green fodder weight (8.700 and 4.010), and 1000-seed weight (6.929 and 3.093). Low variability for these traits indicates a relatively narrow genetic base and limited scope for improvement through simple selection. Similar observations were reported by Ganapathy *et al.* (2011)^[20] in finger millet and Ayesha *et al.* (2019)^[21] in foxtail millet. The overall results indicated the existence of considerable variability among the Kodo millet genotypes, particularly for protein content, dry fodder weight and panicle length, which could be effectively exploited in future breeding programmes.

The coefficient of variation alone does not provide information regarding the transmissibility of a trait from one generation to the next. Therefore, heritability estimates are essential for determining the proportion of phenotypic variation attributable to genetic causes. Heritability, when considered along with genetic advance, provides a reliable indication of the effectiveness of selection. In the present study, high heritability estimates were observed for protein content (95.914%), dry fodder weight (84.349%), and panicle length (78.226%). High heritability indicates that these traits are predominantly governed by genetic factors and are less influenced by environmental conditions. Therefore, phenotypic selection for these traits would be highly effective. Similar findings were reported by John (2006)^[22] in finger millet, Sharma *et al.* (2018)^[18] in pearl millet, and Singamsetti *et al.* (2018)^[23] in finger millet. Moderate heritability was observed for flag leaf blade length (49.712%), days to 50 per cent flowering (35.859%), number of basal tillers per plant (34.191%), thumb raceme length (30.847%), and plant height (26.234%). Moderate heritability suggests that both genetic and environmental factors contribute to the expression of these traits. Consequently, selection based solely on phenotype may not always be reliable, and evaluation across environments may be necessary. Low heritability estimates were recorded for days to maturity (0.213%), peduncle length (10.863%), number of internodes per plant (11.901%), raceme number above panicle (17.661%), seed yield per plant (18.469%), green fodder weight (21.241%), flag leaf blade width (21.981%), and 1000-seed weight (19.929%). Low heritability indicates a greater influence of environmental factors on the expression of these traits and suggests that direct selection may be less effective. The results revealed that protein content, dry fodder weight and panicle length possessed high heritability and therefore offer considerable potential for genetic improvement through selection.

Heritability estimates alone do not provide complete information regarding the expected progress from selection. Johnson *et al.* (1955)^[4] emphasized that heritability coupled with genetic advance provides a more reliable estimate of the effectiveness of selection. Genetic advance as percent of mean (GAM) indicates the expected improvement in a trait under selection and helps in understanding the nature of gene action controlling the trait. In the present investigation, high genetic advance as percent of mean was observed for protein content (95.469%), dry fodder weight (46.751%), and panicle length (37.223%). These traits also exhibited high heritability, indicating the predominance of additive gene action. Therefore, substantial improvement in these traits can be achieved through simple phenotypic selection. Similar findings were reported by Talaware *et al.* (2017)^[24] in pearl millet, Singamsetti *et al.* (2018)^[23] in finger millet, and Vikram *et al.* (2020)^[19] in barnyard millet. Moderate genetic

advance as percent of mean was observed for flag leaf blade length (14.602%), thumb raceme length (8.568%), number of basal tillers per plant (6.653%), raceme number above panicle (5.913%), and seed yield per plant (5.112%). Moderate GAM coupled with moderate heritability suggests the involvement of both additive and non-additive gene effects in the inheritance of these traits. Improvement through selection is possible, although progress may be relatively slower. Low genetic advance as percent of mean was recorded for days to 50 per cent flowering (1.790%), days to maturity (1.968%), plant height (3.979%), flag leaf blade width (4.546%), peduncle length (3.581%), number of internodes per plant (2.259%), green fodder weight (3.807%), and 1000-seed weight (2.845%). Low GAM associated with low to moderate heritability indicates the predominance of non-additive gene action and environmental influence. Therefore, direct selection for these traits may not be highly effective, and alternative breeding approaches such as hybridization followed by selection in later generations may be more useful. The combination of high heritability and high genetic advance observed for protein content, dry fodder weight and panicle length suggests that these traits are primarily governed by additive gene effects and can be effectively improved through selection. These traits may therefore serve as important selection criteria in future Kodo millet breeding programmes aimed at enhancing productivity and nutritional quality.

At the phenotypic level, seed yield per plant exhibited significant positive association with flag leaf blade length (0.2759**), flag leaf blade width (0.2275*), peduncle length (0.2811**), and panicle length (0.2176*). The magnitudes of these phenotypic correlations were generally lower than the corresponding genotypic correlations, which is a commonly observed phenomenon attributable to environmental masking effects on the expression of the traits. Among the significant traits, peduncle length and flag leaf blade length showed comparatively higher positive association with seed yield at the phenotypic level, suggesting their importance in translocation of photosynthates and development of the reproductive sink. Similar results were reported by Priyadharshini *et al.* (2011)^[25] in finger millet. Plant height (0.1489), thumb raceme length (0.1456), protein content (0.1499), number of basal tillers per plant (0.1103), green fodder weight (0.0599), and 1000 seed weight (0.0781) showed positive but non-significant phenotypic association with seed yield per plant, indicating relatively lower direct influence on yield under the present environmental conditions. In contrast, seed yield per plant showed negative non-significant association with raceme number above panicle (-0.1067) and dry fodder weight (-0.0213) at the phenotypic level, consistent with the genotypic level findings. Similar positive associations of grain yield with flag leaf traits and panicle-related characters were documented by Suryanarayana and Sekhar (2018)^[26] in little millet and Kodo millet.

The correlation coefficient analysis at the phenotypic level, twelve out of fourteen characters had positive direct effects on seed yield per plant, while days to maturity (-0.031) and green fodder weight (-0.014) exerted negative direct effects. The highest positive direct effect at the phenotypic level was recorded for flag leaf blade length (0.290), followed by panicle length (0.262), peduncle length (0.226), flag leaf blade width (0.111), protein content (0.109), days to 50% flowering (0.114), number of basal tillers per plant (0.080), raceme number above panicle (0.076), dry fodder weight (0.068), number of internodes per plant (0.056), 1000 seed weight (0.048), and thumb raceme length (0.009). The high positive direct effects of flag leaf blade length, panicle length, and peduncle length at the phenotypic level were

consistent with their significant positive correlations with seed yield and their biological roles in assimilate production and transport. The positive direct contribution of flag leaf blade length confirmed that efficient photosynthetic area plays a critical role in grain development in Kodo millet. These results are in agreement with the findings of Pallavi *et al.* (2020)^[27] in foxtail millet and Parsha Hema *et al.* (2022)^[28] in finger millet. The residual effect of 0.7427 indicated that the traits included in the phenotypic analysis accounted for a substantial proportion of the variation in seed yield, while the remaining variation was governed by other environmental and genetic factors not considered in the present analysis.

The path coefficient analysis at the phenotypic level, days to 50% flowering exerted positive indirect effects on seed yield through panicle length (0.036) and protein content (0.013), while negative indirect effects were observed through peduncle length (-0.025) and number of internodes per plant (-0.009). Plant height showed positive indirect effects through peduncle length (0.082), panicle length (0.022), and protein content (0.015), suggesting that taller plants indirectly contribute to yield through better panicle development and biomass accumulation. Flag leaf blade length showed positive indirect effects through peduncle length (0.032) and number of basal tillers per plant (0.007), while negative indirect effects through panicle length (-0.040) and raceme number above panicle (-0.014) partially offset these contributions. Flag leaf blade width exerted positive indirect effects through peduncle length (0.066), protein content (0.026), and flag leaf blade length (0.027). Peduncle length showed positive indirect effects through flag leaf blade length (0.042) and flag leaf blade width (0.030), while negative indirect effects through raceme number above panicle (-0.016) reduced its overall contribution. Panicle length contributed positive indirect effects through flag leaf blade length (0.044) and green fodder weight (0.030), while number of basal tillers per plant showed positive indirect effects mainly through panicle length (0.026) and flag leaf blade length (0.025). Overall, the phenotypic path coefficient analysis confirmed that flag leaf blade length, flag leaf blade width, peduncle length, panicle length, and protein content were the most important characters for selection in Kodo millet yield improvement, a finding consistent with observations of Kumar *et al.* in Kodo millet.

5. Conclusion

Based on the current study's findings, it can be said that there is significant genetic variation among the assessed Kodo millet genotypes for yield and related characteristics, offering plenty of room for genetic improvement via selection. Protein content and dry fodder weight showed strong genetic advance as a percentage of the mean and high heritability, demonstrating that direct phenotypic selection can successfully improve these qualities and indicating the predominance of additive gene action. Seed yield per plant, on the other hand, demonstrated poor genetic progress (5.11%) and low heritability (18.47%), suggesting a stronger impact of environmental factors and restricting the efficacy of direct selection for yield increase. Consequently, it seems that indirect selection using component qualities is a more successful breeding approach. Flag leaf blade length, flag leaf blade width, panicle length, peduncle length, and thumb raceme length were all positively correlated with seed yield, according to correlation analysis, underscoring their significance as selection criteria in breeding programs. Additionally, route coefficient analysis showed that raceme number above panicle and thumb raceme length had significant direct influences on seed yield, highlighting the importance of raceme architecture in yield determination.

Therefore, while concurrently increasing protein content and biomass output, breeding efforts should concentrate on improving these yield-contributing qualities. The production of high-yielding, nutritionally superior, and agronomically desirable kodo millet genotypes appropriate for sustainable farming and upcoming crop improvement initiatives would be made easier by such an integrated selection technique.

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