Original Research Article

Genetic variability, character association and path coefficient analysis foragro-morphological traits in kodo millet (*Paspalum scrobiculatum* L)

ABSTRACT

Sixty-four genotypes of kodomilletwere evaluated for their genetic variability, heritability, genetic advance as per cent of mean, character associations and path coefficients using 11 agro-morphological traits during kharif 2022 in an Alpha Lattice Design with two replications.The analysisof variance revealed the presence of significant variations among the genotypes for all 11 traits. Slightly higher phenotypic coefficient of variation (PCV) than genotypic coefficient of variation (GCV) for all 11 traits indicatedthat the traits were influenced by environmental factors to some degree.Highest PCV and GCV was observed for the traits*viz*., fodder yield, panicle length and seed yield indicating the presence of greater variability to this trait. High heritability combined with high genetic advance as per cent of mean (GAM)was observed for plant height, peduncle length,panicle length, and fodder yield, indicating the predominance of additive gene action and selection based on these traits would be more reliable. Seed yield exhibited significant and positive correlation with days to 50% flowering, number of tillers, panicle length, number of racemes, seed weight and fodder yield. Genotypic path analysis revealed that highest direct positive effect on grain yield was exhibited by days to 50% flowering, number of tillers, panicle length, seed weight and fodder yield.Hence, the above-mentioned traits exhibiting positive significant correlation and positive direct effect on seed yield are considered as important traits to be included in the selection criteria to achieve genetic improvement of grain yield in kodo millet.

Keywords: kodo millet, genetic variability, grain yield, character association, path analysis

1. INTRODUCTION

Kodo millet (*Paspalum scorbiculatum* L.), a tetraploid (2n=4x=40) small millet species belonging to family Poaceae was domesticated in India about 3000 years ago [1]. It is a self-pollinated crop, which is grown for its grain and fodder. It is grown predominantly in India in the states of Madhya Pradesh, Uttar Pradesh, Chhattisgarh, Tamil Nadu, Gujarat, Maharashtra, Karnataka and various other regions.In addition to being a staple food for the marginal and resource poor farmers, kodo millet is gaining importance as a healthy food among the urban consumers due to its high dietary fiber content and antidiabetic [2], antioxidant properties [3] and higher free radical quenching potential [4]. Kodo millet can be cultivated in poor soils and is more suitable for dryland farming due to its low input requirement in terms of fertilizers, irrigation, and crop protection.

Systematic breeding efforts in this crop have so far been neglected. Knowledge on the availability of genetic variability in the breeding population or germplasm accessions is vital for any crop improvement programme. Presence of high variability in the germplasm of this crop offers much scope for its genetic improvement [5]. Hence, assessment of variability, heritability and genetic advance in the breeding material will help in determining the true potential of genotypes for its utility in breeding programmes. Further, a clear knowledge on the association of characters will help in improving the efficiency of selection in any crop improvement programme. Since grain yield is a complex and quantitatively inherited trait, the information on its correlation with its component traits is important due to the influence of several component traits on this trait.In addition to this, the information on direct and indirect effects of various component traits on grain yield through path coefficient analysis will help in deciding effective selection criteria for the genetic improvement of grain yield. The present study was executed to gain knowledge on variability, heritability, genetic advance, character associations as well as direct and indirect effects of various component traits on grain yield in a set of 64 genotypes of kodo millet, which will help in the identification of desirable genotypes and deciding effective selection criteria to achieve grain yield improvement in kodo millet.

2. MATERIALS AND METHODS

A set of 64 genotypes of kodo millet comprising of germplasm accessions and released varieties were grown in the research farm at the ICAR - Indian Institute of Millets Research, Hyderabad, Telangana, India during kharif 2022 in Alpha Lattice design with two replications, while adhering to the recommended package of practices. The observations were recorded on five randomly chosen plants for nine characters, *viz*, plant height, number of tillers per plant, peduncle length, thumb length, number of racemes, panicle length, grain yield, dry fodder yield, and test weight from both replications, except for days to 50% flowering and days to maturity, which were recorded on a plot basis.The data collected was subjected to the following analysis: Analysis of variance as suggested by Fisher and Yates [6], genotypic and phenotypic coefficient of variation as suggested by Burton [7],heritability in broad senseas suggested byLush [8] and genetic advance as suggested by Johnson et al. [9]. The correlation analysis was performed as suggested by Pearson [10] while the path analysis was performed as suggested by Dewey and Lu[11].

3.RESULTS AND DISCUSSION

3.1 Genetic variability parameters

Availability of substantial genetic variability in the breeding population is an important pre-requisite for any crop improvement programme. Analysis of variance revealed highly significant differences among the genotypes for the grain yield and its contributing traits, highlighting the presence of substantial variation among the genotypes thereby offering an excellent opportunity for effective selection.The estimates of genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2) and genetic advance as per cent of mean (GAM) for grain yield and its component traitsare presented in Table 1.Estimates of PCV for all the 11 traits were slightly higher than the estimates of GCV, indicating some degree of environmental influence on these traits. PCV estimates ranged from 17.80% to 3.31% while GCV estimates ranged from 16.93% to 3.24%.Among the traits studied, panicle length, seed yield and fodder yield exhibited high PCV and GCV, highlighting the presence of greater variability for these traits.The observation similar to this was reported for seed yield [12], seed yield and panicle length [13] and fodder yield [5; 14] for fodder yield. However, low PCV and GCV estimates were exhibited by days to maturity and days to 50%flowering, indicating the presence of lesser variability.

Comment [ak1]: Add ANOVA TABLE

High heritability was observed for all the characters studied, indicating the effectiveness of selection for these traits. These findings are in accordance with the reports by Nirubana et al., [12] for plant height, days to 50% flowering and seed weight, Suthediya et al., [13] for panicle length, plant height and days to maturity and Sreeja et al., [15] for days to 50% flowering. Estimates of GAM were high for plant height, number of tillers, panicle length, peduncle length, thumb length, grain yield per plant and fodder yield per plant. Similarly, high GAM was reported for panicle length and plant height [13], plant height and seed yield [12] and seed yield and fodder yield [5]. High heritability coupled with high GAM was observed forplant height, number of tillers, panicle length, peduncle length, thumb length, grain yield per plant and fodder yield per plant, which suggested the predominance of additive gene action.Hence, a direct phenotypic selection will be rewarding for the genetic improvement of these traits. In a similar study, Nirubana et al. [12] reported high heritability coupled with high genetic advance as per cent of mean for plant height, number of basal tillers, number of productive tillers, flag leaf width, inflorescence length, thumb length, and grain yield per plant.

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3.2Character association

Grain yield is a complex trait, which is influenced by several independent component traits. Hence, knowledge of the association between grain yield and its components is vital for plant breeders indetermining effective selection criteria.The genotypic and phenotypic correlations among yield and its component traits are presented in Table 2. The genotypic correlation coefficients were higher than their phenotypic correlation coefficients for majority of the traits studied, indicating the presence of strong genetic association between thesetraits and limited role of the environment in modifying their phenotypic expression. However, phenotypic correlation coefficients were same as their corresponding genotypic correlation coefficients in few cases,indicating that genotypic as well as environmental correlation act in the same direction to maximize their expression at phenotypiclevel. At the phenotypic and genotypic levels, seed yield exhibited significant and positive association with days to 50% flowering (0.339**; 0.340**), seed weight (0.235*; 0.260*), number of tillers (0.352**; 0.430**), panicle length (0.445**; 0.501**) and fodder yield (0.419**; 0.479**).Conversely, a significant negative association between grain yield and number of racemes, non-significant positive association for grain yield with days to maturity, plant height and non-significant negative association with peduncle length and thumb length were observed both phenotypic and genotypic levels.The traits *viz*., days to 50% flowering, seed weight, number of tillers, panicle length, and fodder yieldcan be utilized in the genetic improvement of grainyield due to the significant and positive correlation with grain yield.Similar results obtained in this study, significant and positive correlations of grain yield with its component traits such as days to 50% flowering, plant height, number of productive tillers, peduncle length, panicle length, thumb length, test weight and days to maturity were reported [15; 16].

3.3Path analysis

Path coefficient analysis provides the real indication of the direct and indirect influence of each trait associated with the other traits.Phenotypic and genotypic path coefficient analysis showing direct and indirect effects of grain yield and its component traits are presented in Table 3. In phenotypic path analysis,the highest direct positive effect on grain yield was exhibited by fodder yield (0.333) followed by panicle length (0.328) anddays to 50% flowering (0.217).In contrast, number of racemes, thumb length, days to maturity, peduncle length and plant height exhibited a high negative direct effect on seed yield. In genotypic path analysis, the highest direct positive effect on grain yield was exhibited by fodder yield (0.374) followed by panicle length (0.368) and number of tillers (0.176).Similar observations were made by Nirubana et al., [16] for plant height, inflorescence length and number of productive tillers.These resultssuggested that selection for these traits may directly contribute to the genetic improvement of yield in kodo millet.On the contrary, thumb length, number of racemes, days to maturity and peduncle length exhibited a high negative direct effect on seed yield.The indirect effects of plant height, number of tillers, thumb length and test weight influenced the grain yield through panicle length both at phenotypic and genotypic level. The residual values in the present study were 0.492 and 0.352 at phenotypic and genotypic levels, respectively. The result of this study indicated that the traits *viz*., plant height, number of tillers, panicle length, thumb length, test weight and fodder yield played a crucial role in grain improvement of kodo millet.

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4. CONCLUSION

Evaluation of 64 genotypes of kodo millet comprising of germplasm accessions and released varieties for 11 grain yield and its component traits revealed that the estimates of PCV was higher than the estimates of GCV for all traits, suggesting that the variability is not solely due to genetic differences but also influenced by environmental factors. High heritability coupled with high GAM exhibited by plant height, number of tillers, panicle length, peduncle length, thumb length, grain yield per plant and fodder yield per plant, highlighted the predominance of additive gene action, suggesting the effectiveness of direct phenotypic selection aiding the genetic improvement grain yield. Further, character association and path co-efficient analysis revealed the importance of plant height, number of tillers, panicle length, thumb length, test weight and fodder yield as the selection criteria for achieving effective grain yield improvement in kodo millet.

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Table 1 Genetic components of variance for yield and its component traits

Traits	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance as % mean
Days to 50% flowering	6.24	6.47	92.91	12.39
Days to maturity	3.24	3.31	95.87	6.53
Plant height	15.30	15.75	94.38	30.62
Number of tillers	14.27	15.19	88.23	27.60
Panicle length	16.45	16.76	96.34	33.19
Peduncle length	15.34	15.93	92.70	30.43
Thumb length	12.65	15.31	68.36	21.55
Number of racemes	6.78	7.63	78.82	12.46
Test weight	9.48	9.55	98.49	19.38
Grain yield per plant	15.96	17.80	80.40	29.49
Fodder yield per plant	16.93	17.72	91.24	33.29

GCV: genotypic coefficient of variation *PCV: phenotypic coefficient of variation*

Comment [ak4]: Add ANOVA table

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Table2 Character association among genotypes for yield and its component traits

Traits		Days to 50% flowering	Days to maturity	Plant height	Number of tillers	Panicle length	Peduncle length	Thumb length	Number of racemes	Test weight	Grain yield per plant	Fodder yield per plant
Days to 50% flowering	P	1.000**	0.287**	0.496**	0.294**	0.595**	0.294**	0.215*	0.023	0.282**	0.339**	0.076
	G	1.000**	0.287*	0.532**	0.307*	0.632**	0.324**	0.309*	0.013	0294*	0.340**	0.095
Days to maturity	P	0.287**	1.000**	0.272**	0.058	0.016	0.197*	-0.179*	-0.346**	0.193*	0.078	0.083
	G	0.287*	1.000**	0.291**	0.078	0.020	0.207	-0.238	-0.374**	0.202	0.075	0.088
Plant height	P	0.496**	0.272**	1.000**	0.106	0.496**	0.449**	0.512**	0.032	0.199*	0.064	0.108
	G	0.532**	0.291*	1.000**	0.136	0.513**	0.466**	0.637**	0.051	0.212	0.092	0.128
Number of tillers	P	0.294**	0.058	0.106	1.000**	0.330**	0.001	0.166	-0.050	0.058	0.352**	0.233**
	G	0.307*	0.078	0.136	1.000**	0.364**	0.011	0.201	-0.130	0.055	0.430**	0.275*
Panicle length	P	0.595**	0.016	0.496**	0.330**	1.000**	0.306**	0.411**	0.073	0.325**	0.445**	0.287**
	G	0.632**	0.02	0.513**	0.364**	1.000**	0.310*	0.467**	0.100	0.330**	0.501**	0.321**
Peduncle length	P	0.294**	0.197*	0.449**	0.001	0.306**	1.000**	0.378**	0.029	0.106	-0.021	0.154
	G	0.324**	0.207	0.466**	0.011	0.310*	1.000**	0.421**	0.003	0.113	-0.019	0.161
Thumb length	P	0.215*	-0.179*	0.512**	0.166	0.411**	0.378**	1.000**	0.146	0.236**	-0.004	0.200*
	G	0.309*	-0.238	0.637**	0.201	0.467**	0.421**	1.000**	0.272*	0.281*	0.016	0.236
Number of racemes	P	0.023	-0.346**	0.032	-0.050	0.073	0.029	0.146	1.000**	0.053	-0.252**	0.008
	G	0.013	-0.374**	0.051	-0.130	0.100	0.003	0.272*	1.000**	0.057	-0.276*	0.022
Test weight	P	0.282**	0.193*	0.199*	0.058	0.325**	0.106	0.236**	0.053	1.000**	0.235**	0.330**
	G	0294*	0.202	0.212	0.055	0.330**	0.113	0.281*	0.057	1.000**	0.260*	0.348**
Grain yield per plant	P	0.339**	0.078	0.064	0.352**	0.445**	-0.021	-0.004	-0.252**	0.235**	1.000**	0.419**
	G	0.340**	0.075	0.092	0.430**	0.501**	-0.019	0.016	-0.276*	0.260*	1.000**	0.479**
Fodder yield per plant	P	0.076	0.083	0.108	0.233**	0.287**	0.154	0.200*	0.008	0.330**	0.419**	1.000**
	G	0.095	0.088	0.128	0.275*	0.321**	0.161	0.236	0.022	0.348**	0.479**	1.000**

P: phenotypic *G: genotypic*
, **, * significant at 5%, 1%, and 0.1%, respectively*

Table3 Genotypic path coefficient analysis showing direct and indirect effects of different component traits on grain yield

Traits		Days to 50% flowering	Days to maturity	Plant height	Number of tillers	Panicle length	Peduncle length	Thumb length	Number of racemes	Test weight	Fodder yield per plant	Grain yield per plant
Days to 50% flowering	P	**0.217**	-0.037	-0.040	0.038	0.195	-0.029	-0.040	-0.006	0.016	0.025	0.339**
	G	**0.156**	-0.069	0.038	0.054	0.233	-0.032	-0.104	-0.004	0.032	0.035	0.340**
Days to maturity	P	0.062	**-0.129**	-0.022	0.007	0.005	-0.019	0.033	0.100	0.011	0.027	0.078
	G	0.045	**-0.242**	0.021	0.013	0.007	-0.020	0.080	0.115	0.022	0.033	0.075
Plant height	P	0.108	-0.035	**-0.081**	0.014	0.136	-0.045	-0.096	-0.009	0.012	0.036	0.064
	G	0.083	-0.070	**0.072**	0.024	0.189	-0.046	-0.215	-0.015	0.023	0.047	0.092
Number of tillers	P	0.064	-0.007	-0.008	**0.111**	0.108	-0.0002	-0.031	0.015	0.003	0.078	0.352**
	G	0.048	-0.019	0.009	**0.176**	0.134	-0.001	-0.068	0.040	0.006	0.103	0.430**
Panicle length	P	0.129	-0.002	-0.040	0.043	**0.328**	-0.031	-0.077	-0.020	0.019	0.095	0.445**
	G	0.099	-0.004	0.037	0.064	**0.368**	-0.031	-0.157	-0.030	0.036	0.120	0.501**
Peduncle length	P	0.064	-0.025	-0.036	0.0003	0.101	**-0.100**	-0.071	-0.010	0.006	0.051	-0.021
	G	0.050	-0.050	0.033	0.001	0.114	**-0.099**	-0.142	-0.001	0.012	0.060	-0.019
Thumb length	P	0.046	0.023	-0.041	0.021	0.134	-0.038	**-0.188**	-0.044	0.014	0.066	-0.004
	G	0.048	0.057	0.046	0.035	0.172	-0.042	**-0.337**	-0.084	0.030	0.088	0.016
Number of racemes	P	0.004	0.044	-0.002	-0.006	0.023	-0.003	-0.028	**-0.289**	0.003	0.002	-0.252**
	G	0.002	0.090	0.003	-0.023	0.036	-0.0003	-0.092	**-0.308**	0.006	0.008	-0.276*
Test weight	P	0.061	-0.024	-0.016	0.007	0.107	-0.010	-0.045	-0.015	**0.060**	0.110	0.235**
	G	0.046	-0.049	0.015	0.009	0.121	-0.011	-0.095	-0.017	**0.109**	0.130	0.260*
Fodder yield per plant	P	0.016	-0.010	-0.008	0.030	0.094	-0.015	-0.037	-0.002	0.019	**0.333**	0.419**
	G	0.014	-0.021	0.009	0.048	0.118	-0.016	-0.079	-0.006	0.038	**0.374**	0.479**

P: phenotypic *G: genotypic*
, **, * significant at 5%, 1%, and 0.1%, respectively*