Original Research Article

Influenceof genetic variability parameters, character association and path analysisfor grain yield and its attributing traits in kodo millet improvement

ABSTRACT

A set of 64 genotypes of kodomilletcomprising of germplasm accessions and released varieties were 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 the traits evaluated. High PCV and GCV were observed for the traits viz., plant height, number of tillers, panicle length, peduncle length, thumb length, grain yield, and fodder yield. It indicated the presence of substantial variability and a low environmental influence on these traits.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, which indicated the predominance of additive gene action and selection based on these traits would be more reliable.Grain yieldexhibited significant and positive correlation with days to 50% flowering, number of tillers, panicle length, number of racemes, test 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, test weight and fodder yield.Hence, the above-mentioned traits exhibiting positive significant correlation and positive direct effect on grain yieldcould be 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 (*Paspalumscorbiculatum* 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 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 breeding programme. Identification of attributed traits of grain yield is important for crop improvement since it is a complex trait, which is influenced by several traits.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. A healthy crop was raised by following the recommended package of practices. The observations were recorded on five randomly chosen plants for eight characters, *viz*, plant height, number of tillers per plant, peduncle length, thumb length, number of racemes, panicle length, dry fodder yield, and test weight from both replications, except for days to 50% flowering, days to maturity and grain yield, 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 (Table 1)revealed highly significant differences among the genotypes for 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 2.The results revealed that PCVwas slightly greater than GCV for all the 11 traits,which indicated alesser influence of environmenton these traits. PCV estimates ranged from 3.31% to 17.80% while GCV estimates ranged from 3.24% to 16.93%. Among the traits studied, panicle length,grain yield and fodder yield exhibited high PCV and GCV, highlighting the presence of greater variability for these traits.Similar observation was reported for grain yield and its components [5; 12; 13; 14; 15] in kodo millet.However, low PCV and GCV estimates were exhibited by days to maturity and days to 50%flowering,which indicatedthe presence of lesser variability.

High heritability observed for all the traits studied indicated the predominance of genetic variation and less influence of environment, which will help the crop breeder in the effective selection of genotypes. 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., [16] for days to 50% flowering. Estimates of GAM were high for plant height, number of tillers, panicle length, peduncle length, thumb length, grain yield and fodder yield. 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]in kodo millet. High heritability coupled with high GAM was observed forplant height, number of tillers, panicle length, peduncle length, thumb length, grain yield and fodder yield, 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 GAM for plant height, number of basal tillers, number of productive tillers, flag leaf width, inflorescence length, thumb length, and grain yield per plant”.

3.2Character association

Grain yield is a complex trait, which is influenced by several independent component traits. Hence, knowledge on the association between grain yield and its component traits is vital for crop breeders.The genotypic and phenotypic correlations among grain yield and its component traits are presented in Table 3. The genotypic correlation coefficients were higher than their phenotypic correlation coefficients for majority of the traits studied, which highlighted the presence of strong genetic association between thesetraits and a 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, grain yield exhibited significant and positive association with days to 50% flowering (0.339**; 0.340**, respectively), test weight (0.235*; 0.260*, respectively), number of tillers (0.352**; 0.430**, respectively), panicle length (0.445**; 0.501**, respectively) and fodder yield (0.419**; 0.479**, respectively).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 at phenotypic and genotypic levels.The traits *viz*., days to 50% flowering, test weight, number of tillers, panicle length, and fodder yieldcould be utilized in the genetic improvement of grainyield due to their significant and positive correlation with grain yield.Similar to the 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 earlierin this crop [15; 17; 18].

3.3Path analysis

Path coefficient analysis provides the real indication of the direct and indirect influence of each trait associated with other traits.Phenotypic and genotypic path coefficient analysis showing direct and indirect effects of grain yield and its component traits are presented in Table 4. 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 grain 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., [19] 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 grain 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 grain 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 levels. The residual values in the present study were 0.492 and 0.352 at phenotypic and genotypic levels, respectively. These values indicate the unexplained error between the predicted value of a response variable derived from a model and the actual observed value. 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 yieldimprovement of kodo millet.

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 slightly 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 and fodder yield, highlighted the predominance of additive gene action, indicating the effectiveness of direct phenotypic selection aiding the genetic improvement of 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 Analysis of variance for yield and its component traits

Source of Variation	Degrees of freedom	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	Fodder yield
Replication	1	2.53	59.13***	13.952***	8.596***	0.057	0.200*	0.006	0.026	0.018*	30.79	4.39
Genotypes	63	49.72***	35.76***	20.122***	3.853***	1.621***	0.709***	0.301***	0.060***	0.340***	178.02***	89.84***
Blocks	14	1.63	1.42**	0.854	0.634*	0.038	0.018	0.081	0.008	0.002	11.54	6.96
Residuals	19	1.81	0.54	0.504	0.234	0.034	0.029	0.049	0.0068	0.002	19.43	4.11

, **, * significant at 5%, 1%, and 0.1%, respectively*

Table 2 Genetic components of variance for yield and its component traits

Traits	Mean	Range	CV	GCV (%)	PCV (%)	Heritability (%)	Genetic Advance as % mean
Days to 50% flowering	78.39	89.00 - 66.50	6.44	6.24	6.47	92.91	12.39
Days to maturity	129.28	134.50 - 101.50	3.33	3.24	3.31	95.87	6.53
Plant height	20.42	27.45 - 12.70	15.77	15.30	15.75	94.38	30.62
Number of tillers	9.40	12.65 - 6.90	15.55	14.27	15.19	88.23	27.60
Panicle length	5.40	8.40 - 4.10	17.21	16.45	16.76	96.34	33.19
Peduncle length	3.80	7.52 - 2.80	15.91	15.34	15.93	92.70	30.43
Thumb length	2.76	4.30 - 1.99	15.91	12.65	15.31	68.36	21.55
Number of racemes	2.14	3.00 - 2.10	15.25	6.78	7.63	78.82	12.46
Test weight	4.33	5.86 - 3.40	9.52	9.48	9.55	98.49	19.38
Grain yield	55.78	92.50 - 47.50	17.60	15.96	17.80	80.40	29.49
Fodder yield	38.66	65.60 - 30.17	17.72	16.93	17.72	91.24	33.29

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

Table3 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	Fodder yield
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	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	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*

Table4 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	Grain yield
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	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**

Residual value P: 0.492 and G: 0.352

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