Studies of Genetic Parameters for Yield and Yield Attributing Traits of Kodo Millet (*Paspalum scrobiculatum* L.)

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A B S T R A C T

The present study on "Studies of genetic parameters for yield and yield attributing traits of kodo millet (*Paspalum scrobiculatum* L.)" was carried out at Instructional cum Research Farm of S.G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Chhattisgarh. Thirty three kodo millet (*Paspalum scrobiculatum* L.) genotypes were evaluated to measure genetic parameters *i.e.* genetic variability, heritability, genetic advance as percent of mean for nine quantitative traits. The phenotypic coefficient of variance (PCV) slightly higher than genotypic coefficient of variance (GCV) for all traits under studied. Among the trait under studied, tiller per plant showed highest PCV and GCV followed by grain yield per plot (g) and fodder yield (g). Higher broad sense heritability was estimate for days to maturity followed by days to flowering, tillers per plant and panicle length. Results revealed high heritability coupled with high genetic advance as percent of mean was higher for tillers per plant followed by panicle length (cm), plant height (cm), fodder yield (g) and test weight (g), these traits were directly selected because they were under the control of additive gene action. High heritability accompanied with high genetic advance as percent of mean was under the control of additive gene action and therefore simple selection is advantage for these traits.

Introduction

Kodo millet (*Paspalum scrobiculatum* L.) is a small grained cereal belonging to family Poaceae (Gramineae). It is a tetraploid (2n=4x=40) crop species. Kodo millet is grown for its grain and fodder purpose. Kodo millet is also known as varagu, kodo, haraka, arakalu, ditch millet, rice grass, cow grass, native paspalum, or Indian crown grass. It is grown in India, Pakistan, Philippines, Indonesia, Vietnam, Thailand and West Africa (Deshpande *et al.,* 2015). It is widely distributed in damp habitats across the tropics and subtropics of the World. Kodo millet is indigenous to India (De Wet *et al.,* 1983).

In India area of small millet 589.6 (000) ha. With a production of 358.9 (000) metric tons and productivity of 654.9 kg/ha. (Indian Institute of Millet Research 2014). Kodo millet is gaining importance due to dual reasons like nutritional properties and stress tolerance (Kumar *et al.,* 2016). It provides low priced protein, minerals and vitamins in form of sustainable food (Yadava *et al.,* 2006). The

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millet contains a high proportion of complex carbohydrate and dietary fibre which helps in prevention of constipation and slow release of glucose to the blood stream (Kumar *et al.,* 2016).

Kodo contain water soluble fiber and this property may be utilized for maintaining or lowering blood glucose response among diabetic and cardiovascular disease patients, glycemic load (GL) representing both quality and quantity of carbohydrate in a food and allows comparison of the likely glycemic effect of realistic portion of the different foods and low glycemic index foods like kodo, have been shown to improve the glucose tolerance in both healthy and diabetic subjects (Riccardi *et al.,* 2008).

Systematic breeding efforts in this crop have so far been neglected. For starting any crop improvement work, information about the genetic variability available in the population is a prerequisite. Presence of high variability in the germplasm of this crop offers much scope for its improvement (Subramanian *et al.,* 2010).

Estimation of genetic parameters in the context of trait characterization is an essential component in developing high yielding varieties (Reddey *et al.,* 2013). Genetic variability is a basis for any heritable improvement in crop plants. Variability can be observed through biometric parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percent of mean in respect of nine characters.

Materials and Methods

The present study was carried out at Research cum Instructional Farm of S.G. College of Agriculture and Research Station Kumhrawand, Jagdalpur, Chhattisgarh. Jagdalpur is situated in 19°4'0" N and 82°2'0" E. The city is nestled on the Bastar Plateau and is positioned at a height of around 552 meters from the mean sea level. The investigation was conducted during *kharif* 2017-18 in randomized block design. With 80 germplasm of kodo millet in which 33 were selected for genetic analysis presented in table 1. The crop was sown on plot size 2.25m x 3m and the spacing of 22 cm within rows and 10 cm between the plants. The regional crop production practices were followed.

Observations were recorded on randomly chosen five plants from each entry for 7 quantitative traits *viz.* plant height, number of tillers per plant, number of panicles per plant, panicle length, grain yield, fodder yield and test weight from both replication, except flowering and maturity, they were recorded on plot basis. Broad sense was categorized as the method suggested by Robinson (1966) low (<50 %), moderate (50-70 %) and high (>70 %). The magnitude of genetic advance as percentage of mean easily categorized as high (>20%), moderate (20-10%) and low (<10%) as suggested by Johnson *et al.,* (1955) using mean square values from the ANOVA table.

Observations were recorded on competitive and randomly chosen five plants from each genotype and from both replication, except flowering and maturity, they were recorded on plot basis. Average of the data from the sampled plants in respect of different quantitative characters was used for various statistical analyses.

Estimation of genetic parameters

The mean data of all characters was subjected to ANOVA and ANCOVA analyses to get the estimates of mean sum of squares and mean sum of products and these were utilized for calculation of following parameters.

Genotypic and phenotypic coefficient of variation

Variance

The genotypic and phenotypic variances were calculated as per the formulae proposed by Burton (1952)

$$\text{Genotypic variance } \sigma g^2 = \frac{\text{Number of replications}}{\text{MSS due to genotypes - MSS due to error}}$$

Phenotypic variance $\sigma p^2 = \sigma g^2 + \sigma e^2$

σg^2 = Genotypic variance

σe^2 = Error variance

The genotypic (GCV) and phenotypic (PCV) coefficient of variation was calculated by the formulae given by Burton (1952).

$$\text{GCV (\%)} = \frac{\sigma g}{X} \times 100$$

$$\text{PCV (\%)} = \frac{\sigma p}{X} \times 100$$

Where,

σg, σp and $\overline{x}$ were genotypic standard deviation, phenotypic standard deviation and general mean of the character, respectively.

Categorization of the range of variation was done as proposed by Sivasubramanian and Madhavamenon (1973)

Less than 10% - Low

10 – 20% - Moderate

More than 20% - High

Broad sense heritability

Heritability in broad sense refers to the proportion of genotypic variance to the total variance of the population. Heritability in broad sense [h2 (b)] was calculated by the formula given by Hanson *et al.,* (1956).

$$\text{Broad sense heritability} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance
$\sigma^2 p$ = Phenotypic variance

As suggested by Johnson *et al.,* (1955), heritability estimates were categorized as

Less than 30% - Low
30 – 60 % - Moderate
More than 60% - High

Genetic advance

Genetic advance refers to the expected genetic gain in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates, the genetic advance was estimated by the following formula given by Johnson *et al.,* (1955).

$$\text{GA} = k \, \sigma p \, H$$

Where,

GA = Genetic advance

σp = Phenotypic standard deviation

H = Heritability (broad sense)

K = Selection differential at 5% selection intensity

Genetic advance as percent of mean (GA as percent mean)

Genetic advance as percent of mean was calculated as per the formula.

$$\text{GA as percent of mean} = \frac{\text{GA}}{\overline{\text{X}}} \times 100$$

Where,

GA = Genetic advance
X = Grand mean of the character

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.,* (1955).

Less than 10% - Low
10 – 20 % - Moderate
More than 20% - High

Results and Discussion

Genetic variability represents the genetic differences within or between populations. Several possible factors, including gene flow due to population migration, homologous recombination or crossing over during meiosis, polyploidy and mutations, might contribute to the genetic variability in the population. The recording of means, range, co-efficient of variation, heritability and genetic advance as percent of mean are presented in Table 2.

Genetic variability is a basis for any heritable improvement in crop plants. Additive genetic variation is heritable portion of the total variation in response to selection and helps in arriving at precise conclusion about the true breeding value of the genotype (John 2017).Variability can be observed through biometric parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (broad sense) and genetic advance as percent of mean in respect of nine characters. The trait studied in this investigation showed low, moderate and high GCV and PCV values. The estimation of phenotypic coefficient of variation (PCV) were higher than the genotypic coefficient of variation (GCV) for all the characters this founding is confirmed by Sumathi *et al.,* (2010) in pearl millet, Shinde *et al.,* (2014) and John (2017) in finger millet. The genotypic coefficient of variance was smaller than phenotypic coefficient of variance; it showed that environment did exert masking influence on the expression of genetic variability (Sao *et al.,* 2017b).

Among the trait under studied, tiller per plant showed highest PCV (31.31) and GCV (29.18). These finding are in conformity with those of Salini *et al.,* (2010) for high GCV, Ganapathy *et al.,* (2011) and Yogesesh *et al.,* (2015) for high GCV and PCV. The lowest PCV and GCV were seen for days to 50% flowering *i.e.* 9.03 and 8.89 respectively indicated less variation among genotypes under studied. This founding is conformity with Nirmalakumari (2010) for low GCV and PCV and Salini *et al.,* (2010) for low GCV. The difference between genotypic coefficient of variation and phenotypic coefficient of variation was low, showing less variation between genotypes or less influence of environment in the expression of this character. The genotypic coefficient of variation and phenotypic coefficient of variation for plant height was moderate *i.e.* 13.74% and 15.47% respectively. This finding is conformity with those of John (2007) and Dhamdhere *et al.,* (2011) for moderate PCV in finger millet. The character showed moderate genotypic coefficient of variation indicating good scope for selection (Kumari and Singh, 2015). Days to maturity showed lowest PCV and GCV (9.0%, 9.1%). This finding is conformity with Chaurasiya (2014) and

Reddey *et al.,* (2013). The phenotypic coefficient of variation estimates in panicle per plant was moderate *i.e.* 15.11% and the genotypic coefficient of variation for this trait was low *i.e.* 9.91%, indicating less variation. Genotypic and phenotypic coefficient of variation for panicle length was moderate *i.e.* 14.26% and 15.61%. This founding is conformity with Ganapathy *et al.,* (2011). The genotypic and phenotypic coefficient of variation estimates in days to maturity was low *i.e.* 9.03% and 9.10% respectively. For grain yield genotypic and phenotypic coefficient of variation was high *i.e.* 19.08% and 25.79% respectively. This finding is conformity with Salini *et al.,* (2010), Anuradha *et al.,* (2017) and Sao *et al.,* (2017 b) in kodo millet. Higher difference in values of GCV and PCV revealed that variation is not only due to genotypes but also due to influence of environment and therefore selection can be misleading (Das, 2013).

Fodder yield exhibited genotypic and phenotypic coefficient of variation was high (20.50% and 22.94%). Similar result was reported by Sabiel *et al.,* (2014) for high GCV and Sao *et al.,* (2017 b) for high GCV and PCV. Test weight exhibited moderate value for GCV and PCV 11.16% and 12.42% respectively. The moderate value for these parameters indicated lesser amount of variation, therefore minimum scope for improvement under direct selection for these characters. The result for panicle length and test weight showed that the traits are less influenced by the environment due to less difference between the genotypic and phenotypic coefficient of variation for these traits. On the contrary, the magnitude of phenotypic coefficient of variation was high as compared to genotypic coefficient of variation for the plant height, tillers per plant, grain yield per plot, fodder yield per plot indicating the role of environmental variance in expression of characters. The magnitude of

genetic variability is the possibility of crop improvement. The genotypic components being the heritable part of total variability, its magnitude for yield and its components characters influence the selection strategies to be adopted by the breeder (John, 2017).

Heritability is a measure of the extent of phenotypic variation caused by the action of genes. For making effective improvement in the character for which selection is practiced, heritability has been adopted by large number of workers as a reliable indicator (Chaurasiya, 2014). Heritability helps in distinguish the similarities between parents and their offspring while genetic advance provides the knowledge about expect gain for a particular trait after selection. High heritability coupled with high genetic advance is said to be governed by additive gene action indicating direct selection for trait. Yet, high heritability with low genetic advance is the result of non-additive gene action and selection for such trait not be rewarding (John 2007). The coefficient of variation reveals the extent of variability, present for different characters but it does not indicate the heritable portion of the variability, it is essential to know the heritability estimates of different attributes (Jyothsna *et al.,* 2016). Heritability estimations are given in Table 2. An attempt has been made in the present investigation to estimate heritability in broad sense and categorized as low (<50 %), moderate (50-70 %) and high (>70 %) as suggested by Robinson (1966). The magnitude of genetic advance as percentage of mean easily categorized as high (>20%), moderate (20-10%) and low (<10%) as suggested by Johnson *et al.,* (1955). Higher broad sense heritability was estimate for days to maturity (98.40%) followed by days to flowering (96.90%), tillers per plant (86.90%), panicle length (83.40%). The lowest heritability was estimate for panicle per plant (43.10%) followed by grain yield per plot (54.80%).

Table.1 List of selected 33 genotypes of kodo millet for genetic analysis

S.N.	Genotype name	S.N.	Genotype name	S.N.	Genotype name
1	BK-19	12	BK-48	23	BK-6
2	BK-20	13	BK-49	24	BK-7
3	BK-21	14	BK-50	25	BK-8
4	BK-34	15	BK-64	26	BK-9
5	BK-35	16	BK-81	27	BK-10
6	BK-36	17	PCGK-8	28	BK-11
7	BK-38	18	PCGK-12	29	BK-12
8	BK-42	19	BK-1	30	BK-13
9	BK-43	20	BK-2	31	BK-14
10	BK-45	21	BK-3	32	IK-01*
11	BK-46	22	BK-5	33	IK-02*

Table.2 Genetic parameters for seed yield and its attributing traits in kodo millet

Characters		Plant Height (cm)	Tillers/ Plant	Panicles / Plant	Panicle Length (cm)	DAS to 50% Flowering	DAS to Maturity	Grain Yield kg /Plot	Fodder Yield kg /Plot	Test weight (g)
Range	Max	56.00	7.00	4.00	8.50	86.00	124.00	2.00	17.15	10.30
	Min	33.50	2.50	2.00	4.55	60.50	91.00	0.90	8.20	6.30
GCV		13.75	29.19	9.92	14.26	8.89	9.03	19.09	20.51	11.16
PCV		15.48	31.31	15.11	15.61	9.03	9.11	25.79	22.95	12.43
h² bs		0.79	0.87	0.43	0.83	0.97	0.98	0.55	0.80	0.81
GA		11.38	2.10	0.39	1.74	12.74	19.92	0.41	4.47	1.71
GA% of Mean		25.15	56.05	13.41	26.83	18.02	18.45	29.10	37.75	20.64
Mean		45.24	3.74	2.89	6.48	70.70	107.95	1.40	11.83	8.27

The character days to maturity (19.91) exhibited higher genetic advance followed by days to 50% flowering (12.74), plant height (11.37) and the character panicles per plant (0.38) showed lowest genetic advance followed by grain yield per plot (0.46), test weight (1.70) and panicle length (1.73). The genetic advance expressed as percentage of mean was highest for tillers per plant (56.04) followed by fodder yield (37.75), grain yield (29.10), and panicle length (26.83). The character panicles per plant (13.40) showed lowest genetic advance as percent of mean followed by days to 50% flowering (18.02)

and days to maturity (18.45). The observed heritability estimate for tillers per plant was high (86.90%) with high genetic advance as percent of mean (56.04). In accordance to report of John (2006), Ganapathy *et al.,* (2011) and Priyadarshini *et al.,* (2011) in finger millet. High heritability coupled with high genetic advance as percent of mean for this character indicated the predominance of additive gene action and selection may be rewarding in improving this character. The panicle per plant possessed low heritability (43.10%) and moderate genetic advance (13.40). Sabeil *et al.,* (2014) reported low

heritability for this trait while genetic advance was also low in pearl millet. Low heritability coupled with moderate genetic advance as percent of mean indicated the predominance of non-additive gene action in the inheritance of this trait and desired result may not be obtained by direct selection and selection should be practiced at later segregating generation. The heritability estimate for panicle length was high heritability (83.40%) with high genetic advance (26.83). high heritability accompanied with high genetic advance as percent of mean for this trait (Bezaweletaw *et al.,* 2006; Govindrajan *et al.,* 2010). High heritability with high genetic advance indicated the predominance of additive gene action and therefore improving can be anticipated by simple selection. The heritability estimate for days to 50% flowering was high (96.90%) with moderate genetic advance as percent of mean (18.02). Moderate genetic advance as percent of mean for this trait in proso millet and Chaurasiya (2014) found high heritability for this trait while genetic advance percent of mean was low. Days to maturity showed heritability which was high (98.40%) with moderate genetic advance (18.45). Chaurasiya (2014) reported high heritability for this character. High heritability coupled with moderate genetic advance as percent of mean indicated that this trait appear to be under the control of both additive and non-additive gene action and selection might be postponed to latter generation to harness the non-additive gene action (Bezaweletaw *et al.,* 2006). The heritability estimate for plant height was high (78.90%) with high genetic advance (25.14). this founding is conformity with Ganapathy *et al.,* (2011) and Priyadarshini *et al.,* (2011) in finger millet. High heritability coupled with high genetic advance as percent of mean for this trait indicated the predominance of additive gene action hence improvement can be anticipated by simple selection (Shinde *et al.,* 2014, Kumari and Singh 2015).Grain

yield per plot showed moderate heritability (54.80%) with high genetic advance (29.10). Govindrajan *et al.,* (2010) and Nirmalakumari (2010) reported for this parameter high heritability coupled with high genetic advance and Kadam *et al.,* (2010) for high variability and genetic advance. Moderate heritability combine with high genetic advance as percent of mean indicated the predominance of additive and non-additive gene action. The observed heritability estimate for fodder yield per plot was high (79.90%) with high genetic advance (37.75). This founding is conformity with Sao *et al.,* (2017). The heritability estimates for test weight was high (80.60%) coupled with high genetic advance (20.64). Earlier reported by Auti *et al.,* (2011) high variability for this trait in finger millet and Chaurasiya (2014) reported high GCV and PCV for this trait. High heritability accompanied with high genetic advance as percent of mean was under the control of additive gene action and therefore simple selection is advantage for these traits. Conclusively high values of broad sense heritability coupled with high genetic advance as percent of mean was observed for tillers per plant, panicle length, plant height, fodder yield per plot and for test weight. So these traits were predominantly under the control of additive gene action and they were least influenced by environmental modification *i.e.* phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable (Singh, 2017). Low heritability with moderate gene action were observed in panicles per plant, low heritability showed that these trait is more influenced by the environment hence not suitable for direct selection. Moderate heritability with high genetic advance were reported in grain yield per plot and high heritability with moderate gene action were recorded for days to 50% flowering and days to maturity, indicating predominance of both additive and non-additive gene action. It is

suggested that genetic gain should be considered in conjugation with heritability estimates (Johnson *et al.,* 1955) Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton 1952). Studied of coefficient of variation showed that the estimation of phenotypic coefficient of variation for all the traits were slightly higher than genotypic coefficient of variation showing that the characters were less influenced by the environment. Hence on the basis of phenotype, selection will be effective for improvement of these characters. Under selection estimates of heritability coupled with genetic advance are more useful in predicting the gain than alone estimates of heritability.

Estimation of phenotypic coefficient of variation for all the traits were slightly higher than genotypic coefficient of variation showing that the characters were less influenced by the environment. Hence on the basis of phenotype, selection will be effective for improvement of these characters. Among the trait under studied, tiller per plant showed highest PCV and GCV followed by grain yield per plot (g) and fodder yield (g). Higher broad sense heritability was estimate for days to maturity followed by days to flowering, tillers per plant and panicle length. High values of broad sense heritability coupled with high genetic advance as percent of mean was observed for tillers per plant, panicle length (cm), plant height (cm), fodder yield per plot and for test weight (g). So these traits were predominantly under the control of additive gene action and they were least influenced by environmental modification. The traits panicles per plant, days to 50% flowering, days to maturity, grain yield were under the control of both additive and non-additive gene action and therefore direct selection is un rewarding.

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