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**Research Article**

# Trait based selection of superior Kodo millet (*Paspalum scrobiculatum* L.) genotypes

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**Abstract :**
One hundred and eighty eight germ plasm accessions of Kodo millet (*Paspalum scrobiculatum* L.*)* were evaluated in a field study to assess genetic variability, heritability and genetic advance for eight yield component traits. The ANOVA revealed that there were significant differences among the accessions for all the traits studied. High genotypic variance, phenotypic variance, GCV and PCV were observed for dry fodder yield, plant height and grain yield per plant. Broad sense heritability ranged from 97.18 percent for dry fodder yield to 56.63 percent for number of tillers. The highest genetic advance as percentage of mean was recorded by dry fodder yield followed by grain yield per plant and plant height. High heritability coupled with high genetic advance observed in the present study for grain and dry fodder yield per plant indicates that these traits are under the influence of additive gene action. These traits can be considered as favourable attributes for crop improvement through selection.

**Key words:**
kodo,, *Paspalum scrobiculatum,* GCV, PCV, heritability, genetic advance

## Introduction

Kodo millet, *Paspalum scrobiculatum* L., is indigenous cereal of India. It is widely distributed in damp habitats across the tropics and subtropics of the World. It is known to have been grown in southern Rajasthan and Maharashtra for at least 3,000 years (Kajale, 1977, De Wet *et al.*, 1983). It is grown today from Uttar Pradesh to Bangladesh in the north, and Kerala and Tamil Nadu in the south. This cereal is known also as *varagu* , *kodo* , *haraka* and *arakalu*. It forms the main stay of the dietary nutritional requirements of farmers of marginal and dry lands in many parts of India. It occupies an area of 9.08 lakh ha with an annual production of 3.11 lakh tones and average productivity of 342kg/ha . Among the small millets, productivity per unit area is highest in kodomillet (Ahamed and Yadava ,1996). It matures in 3-4 months with yields varying from 250 to 1000 kg/ha (Hulse *et al.*,1980) and a potential yield of 2000kg/ha (Harinarayana, 1989). It has a 1000 kernel weight of 6.7 g.

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.

Estimation of genetic parameters in the context of trait characterization is an essential component of future targeted trait based crop improvement. Hence, an attempt was made to estimate the extent of variation for yield contributing traits in 188 kodo millet germplasm accessions by studying the genetic parameters like Phenotypic coefficient of variation (PCV), Genotypic coefficient of variation ( GCV) , Heritability and genetic advance, which may contribute to formulation of suitable selection indices for crop improvement in this crop.

## Materials and methods

The present study was conducted during summer 2008. A total of 188 accessions of kodo millet in germplasm bank maintained at small millets unit of Department of Millets were raised in Randomised Complete Block Design with three replications in Millet Breeding Station farm of Tamil Nadu Agricultural University, Coimbatore. Observations regarding eight morphological traits *viz.,* plant height, number of productive tillers, length of inflorescence, number of racemes, length of longest raceme, grain yield per plant, test weight and dry fodder yield were recorded in five random plants per entry in each replication. The mean of all the plants for each trait under each replication was subjected to analysis of variance as per the method suggested by Panse and Sukhathme (1967). The estimate of genotypic variance and phenotypic variance were worked out according to the method suggested by

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Johnson *et al*. (1955) using mean square values from the ANOVA table. Phenotypic and genotypic coefficient of variance were calculated based on the method advocated by Burton (1952). Heritability percentage in broad sense was estimated as per the method described by Lush (1940) and traits were classified as having high, moderate and low heritability as per the method of Robinson *et al*. (1949). Genetic advance was estimated according to the method suggested by Johnson *et al*. (1955), and expressed as percentage of mean. Traits were classified as having high, moderate or low genetic advance as per the method suggested by Johnson *et al*. (1955).

## Results and discussion

The area of the world's arable land is decreasing, whilst the human population continues to grow. There is increasing pressure to grow arable and other crops on land with marginal nutrition or water availability. In this scenario, there is considerable scope for increasing the area under kodo millet taking in to consideration the changing climatic scenario and the adaptability of this crop, since it is suited for low and marginal lands and also for harsh weather conditions. Crop improvement is based both on understanding which genes are involved in a phenotype, as well as the degree of environmental variation. Thus the ability to understand the genetic basis and heritability of traits (phenotype) selected in breeding programmes provides the opportunity to deploy novel allelic combinations. The basic objective of any breeding and bio-engineering program is the improvement of crop yield and quality. The measurement and evaluation of variability are essential steps in drawing meaningful conclusions from a given set of phenotypic observations (Mehdi and Khan, 1994; Marwede *et al*., 2004). The genetic variability of a metric trait can be studied through the use of various statistical parameters like mean, range, variance components and coefficients of variation.

Analysis of variance for characters under study in the present experiment showed significant differences among the accessions for all the characters studied (Table 1). The extent of variability in respect of range, mean, phenotypic and genotypic coefficients of variation, heritability and genetic advance as percentage of mean are presented in Table 2. Presence of wide variation indicated the scope for improving the population . High genotypic variance, phenotypic variance, GCV and PCV were observed for dry fodder yield, plant height and grain yield per plant. More consistency was observed in test weight and number of productive tillers per plant and this was indicated by minimum level of GCV observed for this character. Dry fodder yield exhibited maximum PCV ( 50.62), followed by seed yield per plant (44.19). It was least in the case of test weight. Magnitude of PCV was grater than GCV for all the traits studied, which indicated the environmental influence in their expression. However, the difference between PCV and GCV was low, which indicated little influence of environment over the phenotype of the traits and hence selection based on phenotype for the above traits could be rewarding in the present set of genetic material.

Broad sense heritability ranged from 97.18 percent for dry fodder yield to 56.63 percent for number of tillers. The maximum genetic advance as percentage of mean was recorded by dry fodder yield followed by grain yield per plant and plant height. Similar results were reported for the two traits by Anantharaju (2001), John (2005) and Satish *et al*., (2004) in Ragi. The traits were classified based on heritability and genetic advance as per the method suggested by Robinson *et al*. (1949) and Johnson *et al*. (1955) respectively. Except for the character number of productive tillers, all the other traits fell under the category high for both heritability and genetic advance. High heritability coupled with high genetic advance observed in the present study for these traits indicates that these traits are under the influence of additive gene action. These traits can be considered as favourable attributes for crop improvement through selection. Li and Song (1991), Jha and Ghosh (1998) and Singh and Dash (2000) reported similar finding in maize for yield per plant. In the present study, the accessions GPU 72/2 and RK 31 registered highest mean grain yield per plant, while for dry fodder yield per plant TNAU 82 and Aamo 184 recorded the maximum yield. Hence these genotypes could be exploited for future breeding programs in this crop.

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**Table – 1 Analysis of variance for different traits in Kodo millet**

| Source | Df | Plant Height | No. tillers | Length of inflorescence | No. racemes | Length of longest raceme | Per plant yield | Test weight | Dry fodder yield |
|---|---|---|---|---|---|---|---|---|---|
| Replication | 2 | 0.27 | 3.80 | 0.31 | 0.02 | 0.72 | 1.45 | 0.02 | 18.61 |
| Genotypes | 187 | 358.25 | 6.06 | 14.48 | 1.07 | 2.68 | 153.62 | 0.81 | 393.49 |
| Error | 374 | 5.09 | 1.23 | 1.53 | 0.11 | 0.34 | 5.65 | 0.01 | 3.77 |

**Table 2 Estimates of different parameters in kodo millet**

| Trait | Mean | Range | Vg | Ve | Vp | GCV | PCV | Heritability ($H^2$) % | | GA as % of mean | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | Value | Category | Value | Category |
| Plant Height | 49.7cm | 25.3 – 87.0 cm | 117.7 | 8.1 | 122.8 | 21.8 | 22.3 | 95.9 | High | 44.0 | High |
| No. tillers | 9.8 | 5.3 – 13.3 | 1.6 | 1.2 | 2.8 | 12.9 | 17.2 | 56.6 | Low | 20.0 | Low |
| Length of inflorescence | 12.5 cm | 8.7 – 23.3 cm | 4.3 | 1.5 | 5.8 | 16.7 | 19.4 | 73.9 | High | 29.5 | High |
| No. racemes | 3.1 | 2.0 – 6.7 | 0.3 | 0.1 | 0.4 | 18.3 | 21.2 | 73.9 | High | 32.3 | High |
| Length of longest raceme | 6.3 cm | 4.3 – 9.5 cm | 0.80 | 0.4 | 1.1 | 14.0 | 16.8 | 69.2 | High | 24.1 | High |
| Seed yield per plant | 16.8g | 3.1 – 52.1g | 49.3 | 5.7 | 55.0 | 41.9 | 44.2 | 89.7 | High | 81.7 | High |
| Test weight | 4.3 g | 2.7 – 7.1 g | 0.3 | 0.1 | 0.3 | 12.0 | 12.2 | 97.0 | High | 24.4 | High |
| Dry fodder yield | 22.8 g | 10.0– 33.3 g | 129.9 | 3.8 | 133.7 | 49.9 | 50.6 | 97.2 | High | 101.3 | High |