RESEARCH PAPER

Estimation of gene actions and character association in F_3 and F_4 generations of little millet cross JK 8 x Peddasame purple early (*Panicum miliare*)

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Abstract : An investigation was carried out in F_3 and F_4 segregating generations of little millet to study gene interactions and correlation for yield and its component traits during *Kharif* 2015 and summer 2016 at UAS, GKVK, Bengaluru. Most of the characters studied were positively skewed and were being governed by several genes indicating quantitative inheritance. Characters seed yield per plant, number of productive tillers per plant and days to maturity were positively skewed indicating complementary gene action hence, to maximize the genetic gain in these characters require intense selection from the existing variability. Panicle length showed negatively skewed distribution indicating duplicate gene action hence, genetic gain will be rapid under mild selection. Seed yield and associated characters showed leptokurtic distribution indicated the involvement of few genes in inheritance of these traits. Seed yield per plant had significant positive association with days to 50 per cent flowering, plant height, number of productive tillers per plant, panicle length and days to maturity. This indicates that selection could be practiced for these component characters to increase seed yield. Variance for majority of the characters has decreased in F_4 over F_3 generation indicated over the generation variability in population has decreased due to increase in homozygosity.

Key Words : Correlation, Skewness, Kurtosis, Gene interaction, Little millet

INTRODUCTION

Little millet is one of the small millet crop have gained attention owing to its inherent quality of early maturity, capacity to yield in fertile soil under low rainfall and management. It has a very high resistance to soil, moisture and weather variations. Therefore, it had become indispensible in Indian agriculture. Besides it is nutritionally rich having high fibre with protein, minerals and essential amino acids. Consumption of this grain has demonstrated positive health benefits among diabetic. Hence, it is immensely sought after food among urbanites and eventually the attention of processing industries.

Progress in breeding programme depends on amount of variability created during hybridization. Simple measures of variability *viz.*, range, variance and standard

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error were commonly used to assess the variability for yield. Breeding for high yield is the main objective of any crop improvement programme. Since yield is polygenically controlled and highly influenced by environment, selection based on yield alone is not effective. Therefore, improvement in yield could be brought about by effecting indirect selection through component characters, which are highly heritable and show strong correlation with yield. The present study was aimed at studying the genetics of different traits, association of yield and its component traits using third and fourth degree statistics in segregating generations of little millet.

MATERIAL AND METHODS

In this study we used F_3 and F_4 generation lines derived from cross JK8 x Peddasame purple early. JK 8 an early (65-70 days), dwarf and high tillering, non-lodging and Peddasame a tall variety with long duration (120 days) high yielding, lengthy and dense panicle (susceptible to lodging) variety of Andhra Pradesh local (collected from Dr. A Seetharam, Ex. Co-ordinator, small millets).280 lines were evaluated in both the generation during *Kharif* 2015 and summer 2016 at All India Co-ordinated Research Project on Small Millets (AICRP on Small Millets), University of Agricultural sciences, Bengaluru, India. Observations were recorded on six characters *viz.*, days to 50 per cent flowering, days to maturity, plant height at harvest, number of productive tillers, panicle length and seed yield per plant.

Statistical analysis :

The association between yield and its associated characters was worked out as a simple phenotypic correlation co-efficient following the method suggested by Goulden(1939). Skewness (K_3), the third degree statistics and Kurtosis (K_4), the fourth degree statistics

were estimated (Snedecor and Cochron, 1967) using PAST statistical software (Hammer *et al*., 2001) to understand the nature of distribution of different traits.

$$K_4 = \frac{n}{(n-1)(n-2)(N-3)}$$

$$\left\{ (n+1)\sum_{j=1}^{n}(Yj-Y)4 - \left(\frac{3(n-1)}{n}\right) \left[\sum_{j=1}^{n}(Yj-Y)^2\right] \right\}$$

where, n-sample size, Yj- observational value of jth sample, Y-sample means.

For a normal distribution, skewness is equal to zero in absence of gene interaction; it is greater and smaller than zero in presence of average complementary and duplicate interactions, respectively. Also, gene interactions can be detected by studying fourth degree statistics, kurtosis which is always negative or near to zero in absence of gene interaction and positive only in presence of gene interaction.

The standard error for co-efficient of skewness and kurtosis were estimated as per Fisher (1950) as follows:

$$SEK3 = \sqrt{\frac{6n(n-1)}{(n-2)(n+1)(n+3)}}$$

$$SEK4 = \sqrt{\frac{24(n-1)^2}{(n-3)(n+2)(n+S)(n+3)}}$$

Frequency distribution for each trait significantly deviated from zero (P≤ 0.05) probability level if that value was greater than twice of its standard error.

RESULTS AND DISCUSSION

The results obtained from the present investigation as well as relevant discussion have been summarized under following heads :

Genetics of traits :

The study of distribution using skewness and kurtosis provides information about nature of gene action (Fisher

Table 1: Variability, mean, skewness and kurtosis for yield and its component traits in F_3 and F_4 generations of a cross JK8 x Peddasame purple early in little millet

Sr. No.	Characters	Mean		Variance		Skewness		Kurtosis	
		F_3	F_4	F_3	F_4	F_3	F_4	F_3	F_4
1.	Days to 50% flowering	39.204	41.139	3.295	6.672	0.646	-0.235	-0.763	-0.354
2.	Plant height (cm)	138.268	137.164	304.182	87.672	-0.394	0.046	0.097	-0.259
3.	No. of productive tillers per plant	6.093	10.115	7.303	6.903	0.611	0.671	-0.403	0.557
4.	Panicle length (cm)	31.159	28.412	31.406	11.919	-0.009	-0.410	-0.337	2.759
5.	Days to maturity	79.375	78.461	6.099	10.350	0.670	0.294	-0.562	0.085
6.	Yield per plant (g)	14.052	11.731	38.006	7.901	1.092	0.133	2.979	0.224

et al., 1932) and nature of genes controlling the traits (Robson, 1956), respectively. Positive skewness is associated with complementary gene interactions while negative skewness is associated with duplicate (additive x additive) gene interactions. The genes controlling the traits with skewed distribution tend to be predominantly dominant irrespective of whether they have increasing or decreasing effect on the trait. The trits with leptokurtic and platykurtic distribution are controlled by fewer and large number of genes, respectively. Kurtosis is negative or close to zero in the absence of gene interaction and is positive in the presence of gene interactions (Pooni *et al.*, 1977; Choo and Reinbergs, 1982 and Kotch *et al.*, 1992). Studies on the amount of gene interaction are undoubtedly needed so as to increase the efficiency of our selection and breeding programmes. Selection intensity could be higher under complementary than under duplicate relationship. Probably, progress in improving population performance may be greater under complementary interaction than under duplicate gene interaction (Choo and Reinbergs, 1982). The skewness and kurtosis co-efficients are given in Table 1.

Seed yield per plant, days to maturity and number of productive tillers per plant showed positively skewed leptokurtic distribution in both the generations except plant and number of productive tillers per plant showed platykurtic distribution in F$_3$ generation. This positively skewed and leptokurtic distribution suggested the involvement of relatively fewer number of segregating genes with majority of them having decreasing effect in the inheritance of these traits. These results are in agreement with the earlier studies (Zhang and Zhou *et al.*, 2006 and Samak *et al.*, 2011). For maximizing the genetic gain in respect of these with positively skewed distribution requires intense selection from the existing variability (Roy, 2000). Distribution curve for plant height and panicle length are depicted in Fig1a, 1b, 1c and 1d.
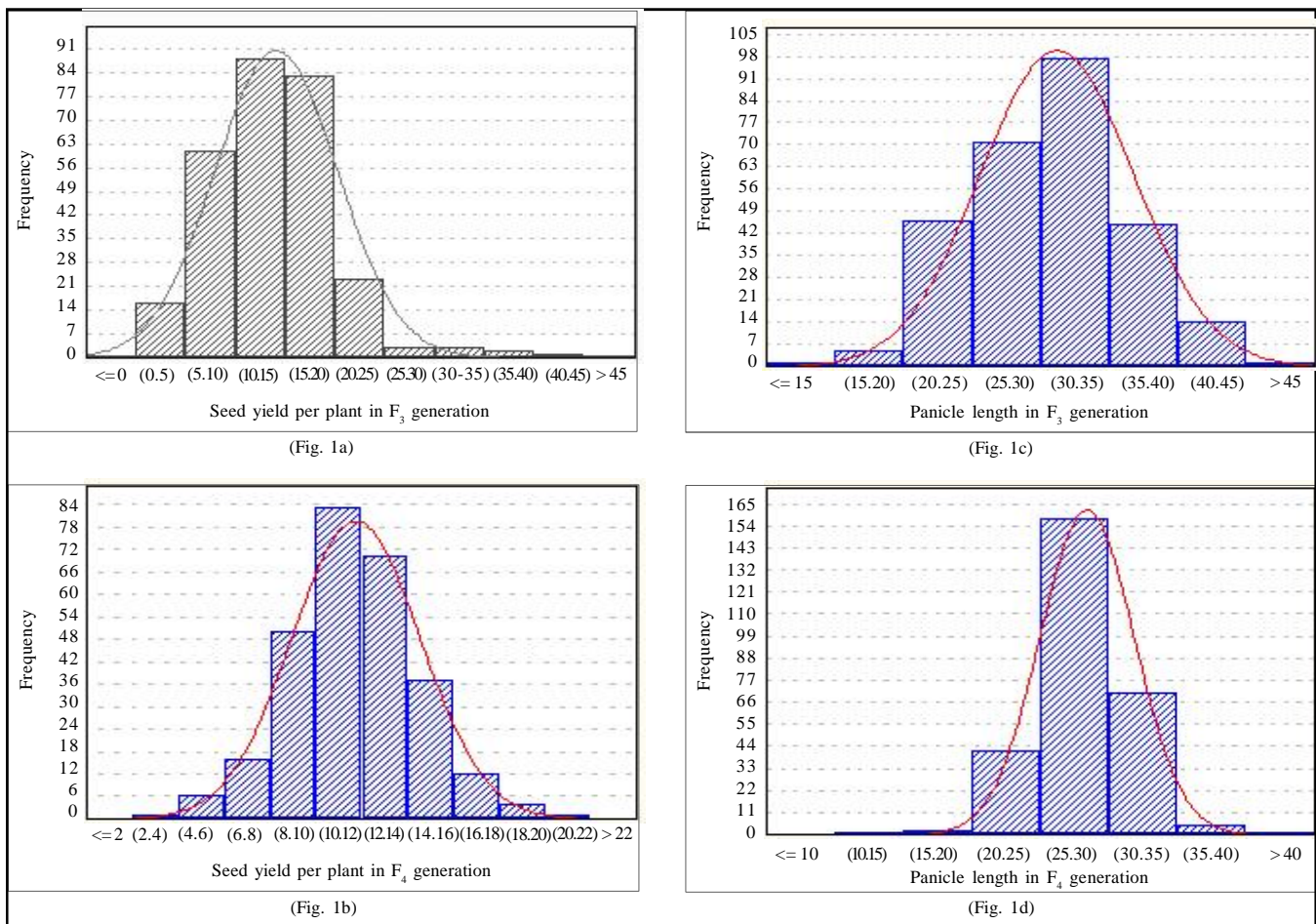
Trait panicle length showed negatively skewed

(Fig. 1a)

(Fig. 1c)

(Fig. 1b)

(Fig. 1d)

Fig. 1 : Normality distribution of seed yield and panicle length in F$_3$ and F$_4$ generations of a cross JK8 x Peddasame purple early in little millet

distribution in both generations and leptokurtic and platykurtic distribution in F_4 and F_3 generations, respectively. Negatively skewed and leptokurtic distribution was an evidence for involvement of fewer number of dominant genes with increasing effect and also co-efficient of skewness significantly deviates from zero indicating presence of duplicate gene interaction in the inheritance of this trait. Genetic gain in respect of above mentioned trait showing negatively skewed distribution will be rapid under mild selection from the existing variability (Roy, 2000). Days to fifty per cent flowering showed positively skewed distribution in F_3 generation and negatively skewed distribution in F_4 generation. This negatively skewed platykurtic distribution indicates the involvement of large of genes with increasing effects. Genetic gain in respect of above mentioned trait will be rapid under mild selection from the existing variability. Trait plant height showed negatively skewed leptokurtic and positively skewed platykurtic distribution in F_3 and F_4 generations, respectively. Selection will be carried out in F_4 generation in future hence, in F_4 generation negatively skewed platykurtic distribution indicating duplicate gene action with many genes. Hence, genetic gain will be rapid under mild selection from the existing variability. These results are in agreement with the earlier studies. (Sulistyowati *et al,*. 2015 and Ajay *et al*., 2016). The variation recorded seed yield per plant, panicle length, number of productive tillers per plant and plant height has decreased in F_4 over F_3 generation. It indicates that over the generation variability in population has decreased due to increase in homozygosity. Similar results were observed by Ajay *et al*. (2016) in pigeonpea segregating generations.

Character association :

Seed yield per plant had significantly positive correlation with days to fifty per cent flowering, plant height, number of productive tillers per plant, panicle length and days to maturity in F_4 generation (Table 2). Similar association of these characters with seed yield per plant has been reported previously by several workers in their study in finger millet crop (Sharathbabu *et al.,* 2008 and Nandini *et al.,* 2010). Hence, selection could be practiced for these component characters to increase seed yield.

Similarly days to maturity has significant positive association with days to 50 per cent flowering, plant height and panicle length in both generation and with number of productive tillers per plant it had significant negative association only in F_4 generation. Panicle length had significant positive association with plant height and number of productive tillers per plant. Similarly plant height had significant positive association with days to fifty per cent flowering in F_4 generation. Number of productive tillers per plant had significant positive association in F_3 generation and significant negative association in F_4 generation.

This kind of shifts in correlation co-efficients between generations was attributed to difference in gene complementation of linkage blocks and an indication of unstable nature of breeding population (Preetha and Raveendran, 2008). It is concluded that yield contributing

Table 2: Correlation co-efficient matrix among yield related characters in F_3 and F_4 generations of a cross JK8 x Peddasame purple early in little millet

Characters	Generation	Days to 50% flowering	Plant height (cm)	No. of productive tillers per plant	Panicle length (cm)	Days to maturity	Seed yield per plant (g)
Days to 50% flowering	F_3	1.000	0.061	0.028	0.095	0.905**	0.327**
	F_4	1.000	0.293**	-0.319**	0.173**	0.765**	0.004
Plant height (cm)	F_3		1.000	0.188**	0.625**	0.087	0.328**
	F_4		1.000	-0.241**	0.638**	0.148**	-0.034
No. of productive tillers per plant	F_3			1.000	0.203**	0.043	0.440**
	F_4			1.000	-0.223**	-0.232**	-0.037
Panicle length (cm)	F_3				1.000	0.120*	0.410**
	F_4				1.000	0.119*	0.037
Days to maturity	F_3					1.000	0.325**
	F_4					1.000	-0.088
Seed yield per plant (g)	F_3						1.000
	F_4						1.000

* and ** indicate significance of values at P=0.05 and 0.01, respectively

traits such as number of productive tillers per plant, panicle length and plant height are inter correlated among themselves. Selection in any one of these traits will result in the improvement of other trait and hence, expected to result in increased yield.

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