RESEARCH PAPER

Genetic variability, heritability, genetic advance and character association studies in F_3 generation of cross JK8 x Peddasame (purple late) in little millet (*Panicum miliare* L.)

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Genetic variability, correlation and path analysis was carried out for yield and yield components in 542 F_3 progeny lines developed by crossing JK8 x Peddasame (purple late) in little millet during *Kharif* 2015. Seven biometrical characters were studied for estimating genotypic co-efficient of variation (GCV), phenotypic co-efficient of variation (PCV), genetic advance, heritability (broad sense), genetic advance as per cent of mean, correlation co-efficient and path co-efficient among themselves. High GCV and PCV were observed for number of productive tillers per plant and per plant yield. High heritability was observed for plant height and 1000 seed weight. Number of productive tillers per plant showed maximum genetic advance as per cent of mean followed by grain yield per plant, panicle length and plant height. High heritability coupled with moderate genetic advance as per cent of mean were observed for plant height and 1000 seed weight. Grain yield per plant possessed significant positive correlation with plant height, panicle length, number of productive tillers per plant and 1000 seed weight. Number of productive tillers per plant imparted maximum direct effect on grain yield followed by panicle length, 1000 seed weight and plant height.

Key words : Correlation, Genetic advance, Genotypic co-efficient of variability, Heritability, Path analysis, Phenotypic co-efficient of variability

INTRODUCTION

Among rainfed crops, millets as a group figure prominently and often referred to coarse cereal, little millet is one of the coarse cereals consumed in the form of rice. It is a hardy crop which can withstand drought better than most of the other cereal crops and also water logging to a certain degree. It is a good source of protein, very rich in carbohydrate, fat, minerals and vitamins and it is considered as essential food for nutritional security (Nirmalakumari *et al*., 2010). Because of their nutritional superiority they are also referred as 'nutrious grains or

nutri millets.' It is normally cultivated in marginal and poor soil under rainfed situation. The tribal's consume its grains in place of paddy. In urban areas, grains are used during fast-day after removing the seed coat.

Improvement in little millet yield depends on the nature and extent of genetic variability, heritability and genetic advance in the population under improvement. The appropriate knowledge of interrelationships between seed yield and its contributing components can significantly improve the efficiently of breeding programme through the use of appropriate selection indices (Mohammadia *et al*., 2003 and Rafiq *et al.,*

2010). The nature of association between seed yield and its components determine the appropriate traits to be used in indirect selection for improvement in seed yield (Ashoka *et al.*, 2001). The correlation studies simply measure the associations between yield and other traits. Path co-efficient analysis permits to separate correlation co-efficient into direct and indirect effects (Effects exerted through other variables).

Hence, an attempt was made to estimate the extent of variation for yield contributing traits and association analysis to determine the direction of selection and number of characters to be considered in improving grain yield (Idris *et al.,* 2012) in 542 F_3 little millet lines by studying the genetic parameters like phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV), heritability, genetic advance, correlation and path analysis which may contribute to formulation of suitable selection indices for improvement in this crop.

RESEARCH METHODOLOGY

The experiment was conducted in *Kharif* 2015 at Project Co-ordinating Unit (Small Millets), University of Agricultural Sciences, GKVK, Bangalore. The experimental materials comprised of 542 F_3 lines developed from cross JK 8 x Peddasame (purple late). JK 8 an early (65-70 days), dwarf and high tillering, non-lodging and Peddasame (purple late) 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). These two parents were crossed by adapting modified crossing methods during summer 2014. Identified true F_1 s was forwarded to develop F_2 and F_3 generation.

The seeds obtained from F_2 were bulked and raised F_3 generation. F_2 bulked seeds were grown on the field

with spacing of 22.5 cm row to row and 10 cm between plants. Observations were recorded from randomly selected 542 plants of F_3 population. Observations were recorded on seven characters *viz.*, days to 50 per cent flowering, days to maturity, plant height at harvest, number of productive tillers, panicle length, 1000 seed weight and seed yield per plant.

Statistical analysis :

Phenotypic and genotypic variances were estimated according to the formula given by Lush (1940). Phenotypic and genotypic co-efficients of variability were computed according to the method suggested by Burton (1952). Heritability in broad sense was calculated as per the formula given by Allard (1960). Range of heritability was categorized as suggested by Johnson *et al*. (1955). Genetic advance was expressed as per cent of mean by using the formula suggested by Johnson *et al.* (1955). Traits were classified as having high, moderate or low genetic advance as per the method suggested by Johnson *et al.* (1955). Phenotypic correlations between yield and yield related traits were estimated using the method described by Miller *et al*. (1958). Path co-efficients analysis was done following the method suggested by Dewey and Lu (1959).

RESEARCH FINDINGS AND ANALYSIS

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

Estimates of phenotypic and genotypic co-efficient of variability :

Presence of variability was also confirmed through the range of variation for various characters in F_3 generation. Genotypic co-efficient of variation (GCV)

Table 1 : Genetic variability parameters for different quantitative traits in F_3 population of a cross JK 8 x Peddasame (purple late) in little millet							
Characters	Range	Mean ± S.E.	PCV (%)	GCV (%)	Heritability (%)	Genetic advance	Genetic advance as % mean
Days to 50% flowering	36-46	39.29±0.10	5.97	4.35	53.12	2.57	6.53
Days to maturity	73-88	79.09±0.13	3.87	2.86	54.75	3.45	4.36
Plant height (cm)	99-226	147.26±0.78	11.76	9.29	62.28	22.26	15.12
No. of productive tillers	1.0-15	4.86±0.11	51.57	39.79	59.52	3.07	63.23
Panicle length (cm)	17-46	30.19±0.22	17.31	11.83	46.70	5.03	16.66
Yield per plant (g)	2-39.80	10.92±0.20	30.18	21.39	50.23	3.41	31.23
1000 seed weight (g)	2.027-2.99	2.53±0.01	5.96	5.72	91.86	0.29	11.29

was ranged from 2.86 (days to maturity) to 39.79 (number of productive tillers). Phenotypic co-efficient of variation (PCV) was ranged from 3.87 (days to maturity) to 51.57 (number of productive tillers). PCV and GCV were high for number of productive tillers (51.57, 39.79) and seed yield per plant (30.18, 21.39). PCV and GCV was moderate for panicle length (17.31, 11.83) and low for characters namely days to flowering (5.97, 4.35), days to maturity (3.87, 2.86) and 1000 seed weight (5.96, 5.72). The result pertaining to this has been presented in Table 1.

The high values of GCV and PCV suggested that there is a possibility of improvement through direct selection for the traits. The PCV and GCV estimates were relatively high for per plant yield and number of productive tillers per plant suggests that presence of considerable variation. Hence, individual plant selection can be practiced for the above mentioned characters to get higher yields. Similar findings of higher estimates of GCV and PCV were obtained by Gowda *et al*. (1996); John *et al*. (2007) and Parameshwarappa and Girish (2007) in groundnut and Vetriventhan and Nermalakumari (2007) in pearl millet. Moderate estimates of PCV and GCV were observed for characters like panicle length and plant height indicating presence of variability for these characters. Whereas low estimates of PCV and GCV was observed for characters days to flowering, days to maturity and 1000 seed weight. On the whole co-efficient of variation values indicated considerable amount of variability for most of the characters hence this population can be further used to select some good genotypes with early, dwarf and high yielding.

The close correspondence between GCV and PCV for traits like days to flowering, days to maturity, plant height and 1000 seed weight indicated less environmental influence in their expression; hence these can be used for further selection.

According to Panse (1957) where high genetic advance is associated with high heritability, heritability could be attributed to additive gene effects. High heritability coupled with moderate genetic as per cent of mean was reported for characters like plant height and 1000 seed weight. This shows that these characters are under the control of additive gene action hence, there is lot of scope for improvement of these characters in further breeding programme. Similarly moderate heritability coupled with high genetic advance as per cent of mean was observed for characters number of productive tillers per plant and per plant yield. Moderate heritability along with moderate genetic advance was reported by Bharadwaj *et al.* (2007) in rice F₂ generation. Which indicates that the trait was highly controlled by additive gene effect which can be further improved through mass selection. Moderate heritability coupled with low genetic advance as per cent of mean was observed for days to flowering and maturity indicate the presence of non-additive gene action. This suggests that narrow scope for selection for these traits.

Heritability in broad sense :

The heritability estimates provide information on transmission of trait (s) from parents to offspring. Such estimates facilitate the evaluation of genetic and environmental effects, aiding in selection. Estimates of heritability can also be used to predict genetic advance under selection, so that the plant breeder can anticipate improvement from different types and intensities of selection. Genetic (Vg) and environmental (Ve) variances were computed from the mean squares in the analysis of variance of each trait. Heritability estimates were

Table 2 : Phenotypic correlation co-efficient values for different traits in F₃ population of a cross JK 8 x Peddasame (purple late) in little millet

Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers	1000 seed weight (g)	Days to maturity	Yield per plant (g)
Days to 50% flowering	1.000	0.295**	0.111*	0.089*	-0.040	0.901**	0.026
Plant height (cm)		1.000	0.434**	0.086	0.050	0.267**	0.099*
Panicle length (cm)			1.000	0.123**	-0.002	0.113*	0.163**
No. of productive tillers				1.000	-0.019	0.071	0.384**
1000 seed weight (g)					1.000	-0.054	0.095*
Days to maturity						1.000	0.030
Yield per plant (g)							1.000

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

calculated by the formulate used by Khan *et al.* (1992). According to Stansfield (1986), heritability estimate were grouped into high (>50%), moderate (20-50%) and low (>20%).

Vp =Vg+Ve

H² (BS) = Vg/Vp

Heritability estimates were relatively high for 1000 seed weight (91.86%) and plant height (62.28%); moderate heritability was observed for characters days to flowering (53.12%), days to maturity (54.75%), number of productive tillers (59.52%), panicle length (46.70%) and yield per plant (50.23%) (Table 1). According to Allard (1960) if a trait has high heritability, it indicates that the influence of the environment on the trait is less. Moreover, as the value of broad sense heritability becomes high it is used as an indicator of the ease of phenotype based selection particularly when it is accompanied by a relatively high variability and genetic advance. Hence, in the present study for all traits high and moderate heritability was observed indicating direct phenotypic selection can be followed in further breeding programme.

Correlation and path analysis :

Knowledge on the association between single plant yield and their biometrical traits and also among the component traits help in improving the efficiency of selection. The idea about the nature of association will be useful to identify the key characters for which selection can be successfully made. In the present study, the simple correlation co-efficients was estimated between single plant yield and contributing characters and intercorrelation among yield components in F_3 generation of cross JK8 x Peddasame (purple late).

In the present study phenotypic correlation values between traits were calculated by regressing phenotypic values of one trait on those of other. The result pertaining to this has been presented in Table 2. It was observed that number of productive tillers (0.384), panicle length (0.163), plant height (0.099) and 1000 seed weight (0.095) were positively and significantly correlated with seed yield per plant. Likewise among the component characters, plant height was significantly and positively correlated with days to flowering (0.295). The association between panicle length and characters like days to flowering and plant height (0.111, 0.434) were significantly and positively correlated. Productive tillers per plant were positively significantly correlated with days to flowering (0.089) and panicle length (0.123). Characters days to flowering (0.901), plant height (0.267) and panicle length (0.113) were significantly and positively correlated with days to maturity.

Phenotypic correlation co-efficients revealed that per plant yield had strong positive correlation with number of productive tillers per plant, panicle length, plant height and 1000 seed weight indicating that improvement in these characters will lead to improvement in yield. Similar results were observed by Sharathbabu *et al.* (2008) and Nandini *et al.* (2010) in finger millet. Association of these characters suggests that individual plant selection can be practiced for plants with higher panicle length, more number of productive tillers and more test weight which ultimately leads to improvement in per plant yield in the later generations.

Path co-efficient analysis:

Yield is a complex resultant character and influenced by several components and environment. Due to adjustments among the components increase in one component result in a decrease in other components (s) and hence, does not affect the resultant like yield. Path analysis is very useful in such complex situation to analyze

Table 3 : Phenotypic path co-efficient analysis showing direct and indirect effects of different characters on plant yield in F_3 population of a cross JK 8 x Peddasame (purple late) in little millet

Characters	Days to 50% flowering	Plant height (cm)	Panicle length (cm)	No. of productive tillers	1000 seed weight (g)	Days to maturity	r
Days to 50% flowering	-0.07178	0.00622	0.01215	0.03303	-0.00412	0.05003	0.026
Plant height (cm)	-0.02117	0.02108	0.04768	0.03204	0.00497	0.01484	0.099*
Panicle length (cm)	-0.00794	0.00915	0.10985	0.0457	-0.00018	0.00628	0.163**
No. of productive tillers	-0.00636	0.00181	0.01347	0.37275	-0.00201	0.00397	0.384**
1000 seed weight(g)	0.00288	0.00102	-0.00019	-0.00733	0.10244	-0.00305	0.095*
Days to maturity	-0.06467	0.00563	0.01242	0.02665	-0.00562	0.05553	0.030

Residual effect- 0.909   * and ** indicate significance of values at P=0.05 and 0.01, respectively

the direct effect of each character and the indirect effect via other characters on yield.

Looking to the data in Table 3 in respect of direct and indirect effect it was observed that the character, number of productive tillers per plant recorded the highest magnitude of direct effect (0.3727) followed by panicle length (0.10985) and 1000 seed weight (0.10244) and their correlation with seed yield was also highly significant and of the same magnitude indicating the perfect association between these characters on seed yield. Hence, one can rely upon these character to select high seed yield types in segregating generations of little millet. However, days to flowering (0.07178) plant height (0.02108) and days to maturity (0.0555) exhibited positive direct effect of low magnitude on seed yield per plant. Similar results were observed by Sharathbabu *et al.* (2008) and Nandini *et al.* (2010) in finger millet. Hence, less importance has to be given for these characters while selecting plants for higher yield. Therefore, due consideration has been given to characters namely, tillers per plant, panicle length and 1000 seed weight while planning a breeding strategy for increased seed yield per plant.

Conclusion :

On the basis of result obtained from this experiment, high and moderate PCV and GCV observed for majority of traits and indicates sufficient variability for these traits. High heritability coupled with moderate genetic advance as per cent of mean was observed for plant height and 1000 seed weight indicating that direct selection for these traits. Characters namely tillers per plant, panicle length and 1000 seed weight showed higher positive direct effect and significant correlation value for per plant yield. Therefore, one can rely upon these traits to select high yield in little millet for further breeding programme.

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