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Studies on genetic variability, character association and path analysis in little millet (*Panicum sumatrense* L.) Genotypes

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Abstract
The present investigation was carried out to study the genetic variability parameters and nature of associations among the traits affecting grain yield in twenty three little millet genotypes at Regional Agricultural Research Station, Chintapalle during *kharif*, 2011. The estimates of genotypic and phenotypic coefficients (GCV and PCV) of variation were moderate for all the traits indicating little influence of the environment on estimates of these parameters. Correlation analysis revealed that, the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the association is largely due to genetic reason. Number of productive tillers exhibited highly significant positive correlation with grain yield both at phenotypic and genotypic level. Path coefficient analysis showed that number of productive tillers had the maximum direct effect on grain yield followed by plant height.

Keywords: genetic variability, heritability, character association, path analysis in little millet

Introduction
The six different small millets grown in India are finger millet, foxtail millet, kodo millet, proso millet, barnyard millet and little millet. The area under these crops during the last 6 decades has significantly decreased from 8 million hectares to around 2.3 million hectares in 2012-13. This is also reflected in diminishing production from 4 million tons to 2.5 million tons in 2011-12. Out of these, little millet commonly known as sama is grown in hill slopes by tribal farmers of High Altitude and Tribal Zone of Andhra Pradesh. The production of this crop is low mainly due to the non availability of improved varieties and non adoption of production strategies.

In the process of development of improved varieties, the breeding strategy mainly depends upon the quantum of genetic variability present in the population. Wider range of genetic variability helps in selecting desired genotypes. In addition to the genetic variability, knowledge on heritability and genetic advance helps the breeder to employ the suitable breeding strategy. Therefore, it is necessary to have knowledge of genetic variability, heritability and genetic advance present in the available genetic material.

Genetic variability together with the heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952 and Swarup and Chaugle, 1962) [3, 16]. Further, the magnitude of heritable variability is the most important aspect, which has close relationship with response to selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance (Johnson *et al.*, 1955) [7].

The correlation studies simply measure the associations between yield and other traits whereas path analysis permits the understanding of cause and effect of related characters. Path co-efficient analysis permits to separate correlation co-efficient into direct and indirect effects of component characters on yield.

Material and Methods
The field experiment was carried out at Regional Agricultural Research Station, Chintapalle during *kharif,* 2011. Twenty three little millet genotypes including 4 checks were raised in Randomized Block Design (RBD) in three replications with spacing of 22.5 × 10 cm. Each genotype was grown in 10 lines of 3 m length.

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Recommended package of practices were followed to raise a healthy crop and observations were recorded for plant height (cm), number of productive tillers, days to 50% flowering, days to maturity and grain yield (q/ ha). The data was subjected to statistical analysis to estimate mean, standard deviation, standard error, skewness and kurtosis by adopting the standard methods (Panse and Sukhatme, 1964) [11]. Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed according to Burton and Devane (1953) [4]. Heritability in broad sense was estimated as per Allard (1960) [1]. Genetic advance was estimated as per the formula proposed by Lush (1940) [9] and genetic advance was expressed as per cent of mean by using the formula suggested by Johnson et al. (1955) [7]. Correlation coefficients were worked out using the formula as suggested by Falconer (1960). The correlation coefficient was partitioned into direct and indirect causes according to Dewey and Lu (1959) [5].

Results and Discussion
The ANOVA revealed highly significant differences among the twenty three genotypes for five characters indicating the existence of sufficient amount of variability among the genotypes (Table.1).

The estimates of genotypic and phenotypic coefficients (GCV and PCV) of variation were moderate for all the traits indicating little influence of the environments on estimates of these parameters. Generally the estimates of phenotypic coefficients of variation were higher than the genotypic coefficients of variation showing that the apparent variation was not only due to genotypes but also due to the influence of environment (Table. 2). Heritability estimates were ranged from 66.39 (no of productive tillers) to 91.19 (days to 50% flowering), high heritability estimates were reported for all the characters. Genetic advance as percent of mean ranged from 23.29 (days to maturity) to 32.80 (days to 50%

flowering), high estimates of genetic advance was reported for all the characters studied. High heritability coupled with high genetic advance was observed for all the traits viz., plant height, no of productive tillers, days to 50% flowering, days to maturity and grain yield (q/ha) suggesting that they can be improved through direct selection due to predominant additive variation. Similar results were also reported by Nirmalakumari et al. (2010) [10], Reddy and Reddy (2012) [13], Selvi et al., (2014) [15], Sasamala et al. (2015) [14] and Patel et al., (2018) [12] in little millet.

Association of characters with yield and among themselves provides guideline to the plant breeder for making improvement through selection and provides a clear cut understanding about the contribution in respect of establishing the association by genetic and non genetic factors. Correlation analysis revealed that the genotypic correlation coefficients in most cases were higher than their phenotypic correlation coefficients indicating the association is largely due to genetic reason. Number of productive tillers exhibited highly significant positive correlation with grain yield at phenotypic and genotypic level (Table.3). Similar findings were reported by Jyothsna et al., (2016) [8] and Anuradha et al., (2017) [2] in little millet. Hence, selection for number of productive tillers per plant will lead to higher grain yield.

Path coefficient analysis showed that number of productive tillers had the maximum direct effect on grain yield (q/ha) followed by plant height (Table. 4). Similar findings in little millet were reported by Jyothsna et al., (2016) [8]. Days to 50% flowering showed negative correlation with yield along with direct negative effect. Days to maturity showed positive effect on grain yield but its correlation with yield is negative. Considering the nature and magnitude of character association and their direct and indirect effects, it can be inferred that improvement of grain yield is possible through simultaneous manifestation of number of productive tillers per plant.

Table 1: Analysis of variance for five characters in 23 little millet genotypes

Source of variation	Df	Mean squares				
		Plant height (cm)	No of productive tillers	Days to 50% flowering	Days to maturity	Grain yield (q/ha)
Replication	2	1.37	0.05	0.02	0.83	0.52
Treatments	22	1286.41**	1.70**	355.77**	365.53**	1.07**
Error	44	117.91	0.24	11.10	19.59	0.13

Table 2: Estimates of genetic variability parameters for grain yield and its attributes in 23 little millet genotypes

Character	Range		Mean	Coefficient of variation			Heritability h^2 (b)	Genetic advance	Genetic advance as percent of mean
	Min	Max		GCV	PCV	ECV			
Plant height (cm)	97.73	160.47	135.40	14.58	16.63	8.01	76.76	35.60	26.31
No. of productive tillers	3.36	6.26	4.62	15.10	18.52	10.73	66.39	1.17	25.33
Days to 50% flowering	57.33	92.00	64.27	16.68	17.47	5.18	91.19	21.08	32.80
Days to maturity	81.00	116.33	87.78	12.23	13.23	5.04	85.47	20.45	23.29
Grain yield (q/ha)	2.12	4.47	3.40	16.37	19.72	10.99	68.90	0.95	27.99

Table 3: Estimates of phenotypic (above diagonal) and genotypic (below diagonal) correlation coefficients for 5 characters in little millet genotypes

	Plant height (cm)	Number of productive tillers	Days to 50% flowering	Days to maturity	Grain yield (q/ha)
Plant height (cm)	1.00	-0.121	0.329**	0.331**	0.162
No. of productive tillers	-0.162	1.00	-0.402**	-0.431**	0.537**
Days to 50% flowering	0.441**	-0.537**	1.00	0.95**	-0.467**
Days to Maturity	0.414**	-0.488**	1.021**	1.00	-0.449**
Grain yield (q/ha)	0.184	0.752**	-0.579**	-0.61**	1.00

Table 4: Path coefficient analysis showing direct and indirect effects.

	Plant height (cm)	Number of productive tillers	Days to 50% flowering	Days to maturity	Grain yield (q/ha)
Plant height (cm)	0.5305	-0.0819	-0.5581	0.2935	0.1841
Number of productive tillers	-0.0861	0.5044	0.6802	-0.3462	0.7523
Days to 50% flowering	0.2339	-0.2710	-1.2657	0.7239	-0.5788
Days to maturity	0.2196	-0.2462	-1.2922	0.7091	-0.6096

Residual effect 0.22

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