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Genetic variability, Correlation and path analysis for seed yield and its components in Redgram [*Cajanus cajan* (L.) Millsp.]

N. Hari Satyanarayana*, G. Sreenivas, J. Jagannadham, P. Amarajyothi, Y. Rajasekhar, B. Swathi
Agricultural Research Station, Amadalavalasa, Srikakulam Ditrict, A. P. 532 185, India
*Contact author: haribckv@gmail.com

ABSTRACT

Sixteen varieties of Redgram (Cajanus cajan L.) have been evaluated to study the genetic variability, correlation and path analysis during Kharif, 2017 in North Coastal Zone of Andhra Pradesh at Agricultural Research Station, Amadalavalasa, Srikakulam district for seed yield and its contributing traits. High variability was observed for all characters under study. Phenotypic as well as genotypic coefficients of variability were high for the important productivity characters like primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, 100 seed weight and seed yield; medium for days to 50% flowering, plant height, pod length, pod width and seeds pod^{-1}. High heritability coupled with high expected genetic advance was observed for all the characters under study. Days to 50% flowering, plant height, primary branches plant^{-1}, secondary branches plant^{-1} and pods plant^{-1} were found to be highly significant and positively correlated with the dependent variable, seed yield. Partitioning of correlation coefficients of various components upon seed yield into direct and indirect contributions revealed that days to 50% flowering, 100 seed weight, secondary branches plant^{-1} and plant height has maximum direct effect on seed yield.

Key words: *Character Association, Genetic Variability, Path Analysis, Redgram, Seed yield*

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INTRODUCTION

Redgram [*Cajanus cajan* (L.) Millsp.] is the fifth most important food legume crop in the world after soybean, groundnut, dry beans and peas. This crop occupies an essential place in our daily diet as very high-quality source of protein. It is mainly cultivated for its dry seeds and green pods in dry areas of the tropics and subtropics (Vijayalakshmi *et al.,* 2013). It belongs to member of family *Fabaceae* and it is invariably cultivated as annual crop. Redgram is an often cross pollinated (20-70%) crop with $2n = 2x = 22$ diploid chromosome number (Kumara et al., 2014). Redgram is a hardy, widely adapted and drought tolerant crop. It has a wide range of maturity which helps in its adaption in a wide range of environments and cropping systems. India ranked first in area and production in the world with 74% and 63% of world area and production, respectively. In productivity, Philippines ranked first with 1669 kg/ha followed by Burundi and Grenada. Redgram is the second most important pulse crop after chickpea in India. The country's total area coverage and production of redgram were 38.35 lakh hectares and 29.92 lakh tonnes, respectively (Tiwari & Shivhare, 2016). The state-wise trend shows that Maharashtra ranked first both in respect of area and production (29.19 % and 29.68 %) followed by Karnataka (19.23 % and 15.96 %) and Madhya Pradesh (13.17% and 13.30 %). The highest yield recorded by Bihar (1739 kg/ha) followed by Haryana (1111 kg/ha) and Gujrat (1105 kg/ha), whereas, lowest yield observed in the state of Andhra Pradesh (521 kg/ha). Therefore, it is necessary to increase the productivity of redgram in India in general and in Andhra Pradesh in particular to meet the demand.

To overcome such situation, genetically stable genotypes having high yield potential are urgently needed. It is therefore, necessary to estimate relative amounts of genetic and non-genetic variability exhibited by different characters using suitable parameters like genetic coefficient of variability, heritability estimates and genetic advance. A complete understanding of the correlation between yield and yield components is a must for a plant breeder towards the improvement of any crop. A study on genetic variability and correlation alone are not enough to give an exact figure of relative importance of direct and indirect influence of each component trait on grain yield. In such case, path coefficient analysis is an important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. It is therefore, genetic variability as well as correlation and path coefficient may be important tools for the breeder to enhancing the production and productivity of any crop. The present study was conducted to assess genetic variability, correlation and path coefficient analysis for seed yield and its component characters to provide necessary information that could be useful in redgram improvement programmes aimed at improving seed yield.

MATERIALS AND METHODS

Sixteen varieties of redgram [*Cajanus cajan* (L.) Millsp.] were studied during *kharif*, 2017 at Agricultural Research Station, Amadalavalasa, Srikakulam district, Andhra Pradesh (altitude 29m above MSL, latitude 18° 41' N and longitude 83° 90'E) The experimental trial was laid out in randomized complete block design with two replications under rainfed conditions. Sowing was done in two rows of 4m length with a spacing of 120 x 25cm and recommended package of practices were followed to raise a good crop. Data on the basis of five randomly selected competitive plants were recorded on days to 50% flowering, plant height (cm), primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, pod length (cm), pod width (mm), seeds pod^{-1}, 100 seed weight (g) and seed yield (q/ha). Genotypic and Phenotypic coefficients of variation were calculated using the formula suggested by Burton and De Vane (1953). Heritability and genetic advance were estimated according to the formulae given by Allard (1960). Genotypic and phenotypic correlations were calculated as suggested by Johnson *et al.* (1955). The phenotypic correlations were used to find out the direct and indirect effects of the component characters on seed yield, according to Dewey and Lu (1959).

RESULTS AND DISCUSSION

The analysis of variance revealed significant difference among the genotypes for all the ten characters studied. The characters primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1}, 100 seed weight and seed yield showed high genotypic and phenotypic coefficient of variation (Table-1) suggesting that these characters are under the influence of genetic control. Moderate values of genotypic and phenotypic coefficient of variation were found for the characters days to 50% flowering, plant height, pod length, pod width and seeds pod^{-1}. Further, the estimates of PCV were generally higher than their corresponding GCV for all the characters studied suggesting thereby the important role of environment in the expression of these traits. Hence, phenotypic selection may not hold good for genetic improvement in these traits.

Table 1: Genetic variability parameters in Redgram [*Cajanus cajan* (L.) Millsp.] for seed yield and its contributing characters

Character	Mean	Range	GCV (%)	PCV (%)	Heritability	GAM
Days to 50% flowering	110.75	55.67 to 117.00	13.36	13.41	99.17	27.40
Plant height (cm)	192.19	68.33 to 214.33	17.65	18.59	90.15	34.53
No. of primary branches plant^{-1}	15.03	8.00 to 20.93	22.27	27.91	63.71	36.62
No. of secondary branches plant^{-1}	40.84	9.93 to 66.60	41.34	44.08	87.95	79.86
No. of pods plant^{-1}	313.98	22.33 to 493.33	39.85	43.14	85.30	75.81
Pod length (cm)	4.97	4.63 to 6.11	17.34	17.54	97.67	35.30
Pod width (mm)	5.21	3.97 to 7.77	17.94	19.04	88.82	34.84
No. of seeds pod^{-1}	4.06	3.97 to 4.83	12.24	12.87	90.49	23.99
100 seed weight (g)	10.71	7.56 to 19.43	24.78	25.83	92.10	48.99
Seed yield (q/ha)	20.40	2.17 to 26.76	31.54	36.63	74.14	55.95

Practically, heritability estimates are of greater value to the breeder, since, they indicate the degree of dependence of genotypic value on phenotypic value. All the characters studied in this experiment have showed high estimates of heritability. High heritability indicates the scope of genetic improvement of these characters through selection. The estimates of heritability, however, indicate only the effectiveness with which the selection of genotypes can be made based on their phenotypic performance, but fail to indicate the amount of progress expected from selection. For an effective selection, the knowledge alone on the estimates of heritability is not sufficient and genetic advance (%) of mean if studied alongwith heritability is more useful. High heritability coupled with high genetic advance of mean was observed for all the characters indicate that these traits are simply inherited and most likely the heritability is due to additive gene effects and selection may be effective in early generation for these traits. These findings are in agreement with Saroj *et al.* (2013), Kumara *et al.* (2014) and Kesha Ram *et al.* (2016).

The correlation coefficients for different pairs of characters (Table-2) indicated that seed yield was found to be highly significant and positively correlated with the traits, secondary branches plant^{-1} (0.708) followed by plant height (0.699), pods plant^{-1} (0.691), days to 50% flowering (0.651) and primary branches plant^{-1} (0.550) suggesting that selection for these traits will improve the seed yield. The traits pod length and seeds pod^{-1} showed significant negative correlation with seed yield. However, the traits pod width and 100 seed weight recorded non significant association with seed yield. These findings are in agreement with Padi (2003), Sarsamkar *et al.* (2007), Hamid *et al.* (2011), Saroj *et al.* (2013), Vijayalakshmi *et al.* (2013), Chandana *et al.* (2014), Kumara *et al.* (2014), Kesha Ram *et al.* (2016), Singh and Singh (2016) and Laxmi Narayanan *et al.* (2018).

Table 2: Correlation coefficients between seed yield and its component characters in Redgram [*Cajanus cajan* (L.) Millsp.]

Character	**Days to 50% flowering**	**Plant height (cm)**	**No. of primary branches plant^{-1}**	**No. of secondary branches plant^{-1}**	**No. of pods plant^{-1}**	**Pod length (cm)**	**Pod width (mm)**	**No. of seeds pod^{-1}**	**100 seed weight (g)**	**Seed yield (q/ha)**
Days to 50% flowering	1.000	0.919**	0.463**	0.504**	0.612**	0.247	0.108	0.258	0.013	0.651**
Plant height (cm)		1.000	0.500**	0.521**	0.622**	0.102	0.102	0.122	0.002	0.699**
No. of primary branches plant^{-1}			1.000	0.676**	0.705**	-0.419**	-0.348*	-0.350*	-0.320*	0.550**
No. of secondary branches plant^{-1}				1.000	0.796**	-0.460**	-0.574**	-0.360*	-0.490**	0.708**
No. of pods plant^{-1}					1.000	-0.456**	-0.510**	-0.395**	-0.529**	0.691**
Pod length (cm)						1.000	0.747**	0.930**	0.679**	-0.306*
Pod width (mm)							1.000	0.613**	0.865**	-0.204
No. of seeds pod^{-1}								1.000	0.588**	-0.307*
100 seed weight (g)									1.000	-0.121
Seed yield (q/ha)										1.000

***Significant at 5% level** ****Significant at 1% level**

Days to 50% flowering exhibited highly significant and positive association with plant height, primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1} and seed yield. Plant height exhibited significant positive association with days to 50% flowering, primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1} and seed yield; whereas primary branches plant^{-1} exhibited positive significant association with days to 50% flowering, plant height, secondary branches plant^{-1}, pods plant^{-1} and seed yield. Secondary branches plant^{-1} exhibited positive significant association with days to 50% flowering, plant height, primary branches plant^{-1}, pods plant^{-1} and seed yield. Pods plant^{-1} exhibited significant positive association with days to 50% flowering, plant height, primary branches plant^{-1}, secondary branches plant^{-1} and seed yield. By this it is evident that selection for the characters days to 50% flowering, plant height, primary branches plant^{-1}, secondary branches plant^{-1}, pods plant^{-1} and seed yield would improve the seed yield of redgram.

Partitioning of correlation coefficients for various component characters with seed yield into direct and indirect contributions (Table-3) revealed that days to 50% flowering has maximum direct effect (0.5650) on seed yield followed by 100 seed weight (0.5622), secondary branches plant^{-1} (0.3446) and plant height (0.1617). These results are in conformity with Padi (2003), Sarsamkar *et al.* (2007), Saroj *et al.* (2013), Vijayalakshmi *et al.* (2013), Chandana *et al.* (2014), Kesha Ram *et al.* (2016) and Laxmi Narayanan *et al.* (2018). The high correlation coefficient of secondary branches plant^{-1} (0.708) with seed yield was majorly due to its own direct effect (0.3446) followed by days to 50% flowering (0.2850) and seeds pod^{-1} (0.1427). Similarly, for plant height (0.699) it was due to the indirect effects of days to 50% flowering (0.5190) followed by secondary branches plant^{-1} (0.1796) and its own direct effect (0.1617). Likewise, the high correlation coefficient of pods plant^{-1} (0.691) with seed yield was due to the indirect effects of days to 50% flowering (0.3459) followed by secondary branches plant^{-1} (0.2743) and seeds pod^{-1}(0.1564) in spite of negative indirect effects of 100 seed weight (-0.2975).

Table 3: Direct and indirect contributions of component characters for seed yield in Redgram [*Cajanus cajan* (L.) Millsp.]

Character	Days to 50% flowering	Plant height (cm)	No. of primary branches plant^{-1}	No. of secondary branches plant^{-1}	No. of pods plant^{-1}	Pod length (cm)	Pod width (mm)	No. of seeds pod^{-1}	100 seed weight (g)	Correlation with seed yield
Days to 50% flowering	**0.5650**	0.1485	-0.0750	0.1738	0.0107	-0.0537	-0.0231	-0.1025	0.0074	0.651**
Plant height (cm)	0.5190	**0.1617**	-0.0810	0.1796	0.0109	-0.0221	-0.0217	-0.0484	0.0014	0.699**
No. of primary branches plant^{-1}	0.2612	0.0809	**-0.1620**	0.2328	0.0124	0.0909	0.0742	0.1386	-0.1798	0.550**
No. of secondary branches plant^{-1}	0.2850	0.0843	-0.1094	**0.3446**	0.0140	0.1000	0.1222	0.1427	-0.2753	0.708**
No. of pods plant^{-1}	0.3459	0.1006	-0.1142	0.2743	**0.0175**	0.0991	0.1086	0.1564	-0.2975	0.691**
Pod length (cm)	0.1398	0.0165	0.0678	-0.1586	-0.0080	**-0.2170**	-0.1590	-0.3688	0.3817	-0.306*
Pod width (mm)	0.0612	0.0165	0.0564	-0.1977	-0.0089	-0.1620	**-0.2130**	-0.2429	0.4864	-0.204
No. of seeds pod^{-1}	0.1460	0.0198	0.0566	-0.1240	-0.0069	-0.2020	-0.1305	**-0.3964**	0.3308	-0.307*
100 seed weight (g)	0.0075	0.0003	0.0518	-0.1687	-0.0093	-0.1474	-0.1843	-0.2332	**0.5622**	-0.121

Bold: Direct effects **Residual effect: 18.88%**

The value of residual effects was 18.88% suggesting that about 81% of the total variations for seed yield in redgram were explained. Finally, the path coefficient analysis revealed importance of days to 50% flowering, 100 seed weight, secondary branches plant^{-1} and plant height for their contribution either directly or indirectly to seed yield and hence, during selection these traits should be given utmost attention for developing of high seed yielding redgram varieties.

CONCLUSION

In conclusion, based on character association and path analysis studies seed yield of redgram may be improved by selection of traits viz., days to 50% flowering, plant height, primary branches plant^{-1}, secondary branches plant^{-1} and pods plant^{-1} which are also having high heritability with genetic advance.

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