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Estimation of genetic variability in red gram advanced breeding lines

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Abstract

Pigeon pea (*Cajanus cajan* (L.) Millsp) is the major pulse crop in India having 24-25% protein in the grain. To meet the protein requirement of growing population increased production is required. It is very difficult to increase the area under cultivation and hence new varieties are required which can yield better and also early duration varieties are required which fit into the cropping system. Hence, the present research was under taken including early duration variety to study the variability at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *Kharif*, 2018. High variability was recorded for grain yield indicating ample variation which can be further exploited. Grain yield also recorded high heritability coupled with high GAM indicating preponderance of additive gene action. Days to 50% flowering also recorded high heritability and high GAM and these two traits are highly and significantly associated in positive direction. High yielding varieties are more expected in late maturing varieties, however, LRG 274 which is an early duration variety can be utilized in future breeding to develop early maturing high yielding varieties.

Keywords: Genetic variability, heritability, correlation, red gram

Introduction

Pigeon pea (*Cajanus cajan* (L.) Millsp) is grown in more than 50 countries which include tropical and subtropical regions like India, South and Central America and Africa. It is the major pulse crop of India after chickpea, which contributes significantly to the nourishment of Indian population. It ranks fifth in the world. India is the major producer and consumer of pigeonpea in the world and presently occupies an area of about 4.04 million hectare with a production of approximately 2.65 million tonnes. (Anonymous, 2012)^[2].

It belongs to the family 'Fabaceae' and is also known as 'Arhar' or 'Tur'. It is generally used in preparation of dal which is rich in protein (24-25%) and minerals and is the most preferred dish by Indian vegetarians (Sodavadiya *et al.*, 2009)^[16]. Indian vegetarians mostly depend on red gram for protein supplement and is estimated that the per capita availability of protein in the country is only 28 g/day, while WHO recommendation is 80 g/day (Prasad *et al.*, 2013)^[11]. Hence, the burden rests on the breeder to evolve very high yielding varieties suitable for growing under varied weather conditions and also to develop early and high yielding varieties which can address the immediate protein needs of Indian population. Increased grain yields will lead to increased production of red gram which in turn will lead to reduction of its price in the market and thus will be accessible even to the poor.

To develop high yielding varieties of red gram understanding the relative amounts of genetic and non genetic variability of grain yield and related characters is the prerequisite. They can be estimated by various parameters like genetic coefficient of variability (GCV), heritability estimates (H) and genetic advance (GA). Further, knowledge on traits association helps in selection of high yielding genotypes with the help of its associated traits. The present study was conducted to assess genetic variability, heritability and correlation coefficient analysis of yield and its related traits to assess the information that could be useful in pigeonpea improvement programme.

Materials and Methods

The present study constituted of 15 red gram genotypes received from different research stations of Andhra Pradesh. The genotypes were sown in a randomized complete block design (RCBD) in three replications with a spacing of 90 × 20 cm per each entry at Agricultural Research Station, Vizianagaram, Andhra Pradesh during *kharif*, 2018. Each genotype was grown in 6 rows of 3 m length. Fertilizers, 20-50-20 NPK kg/ha and need based plant protection measures were taken to raise a healthy crop. Observations were recorded on plant height (cm), No. of branches, Pod length, No. of pods per plant, No. of grains per pod, days to 50% flowering and yield (q/ha).

Analysis of variance and summary statistics were calculated as per Panse and Sukathme (1967). Phenotypic and genotypic coefficients of variation (PCV and GCV) were computed as per Burton and Devane (1953). Heritability in broad sense was computed as per Allard (1960) [1]. Phenotypic correlations were calculated according to Falconer (1981) [7]. Heritability and genetic advancement were categorized into low, medium and high as per Johnson *et al.*, (1955) [8].

Results and Discussion

The results from analysis of variance (Table No. 1) revealed that all traits exhibited very high significant difference among treatments which indicated existence of ample amount of genetic variability among different genotypes for all traits under study. Similar reports were noticed from Kumara *et al.* (2013) [9], Saroj *et al.* (2013) [14], Pushpavalli *et al.* (2017) [13], Anuradha *et al.* (2017, 2018) [3, 4], Pushpavalli *et al.* (2018) [13], Satyanarayana *et al.* (2018) [15]. It also revealed that few superior cultivars in the present pool can be used for development of new varieties. From Table No. 2, earliest flowering was noticed in LRG 274 (90 days) while all other genotypes were of late type falling in the range of 114 to 143 days which indicates more than 1.2 -1.5 times of early entry. LRG 52 recorded highest yield of 17.2 q/ha followed by BRG 2 (15.8 q/ha) which were almost of 1.5 times more duration than that of LR 274 (4.6 q/ha). Even, the per day productivity of LRG 52 is more compared to all other genotypes including LR 274 which implies that LRG 52 is best genotype among all genotypes. However, early maturing entry, LRG 274 can be managed agronomically through high density planting for obtaining more yield/ha. But prior to releasing and giving it to the farmers as a variety all the economics need to be tested. It can also be used as source for developing high yielding early varieties with high per day productivity.

The variation between PCV values GCV values were smaller indicating that most of the variability is due to genetic cause

rather than environmental effect (Table No. 3). Higher GCV and PCV values were scored by grain yield indicating more variability for this trait compared to other traits in the present population. Similar results were obtained by Saroj *et al.* (2013) [14], Pushpavalli *et al.* (2018) [13], Satyanarayana *et al.* (2018) [15], Anuradha and Patro (2019) [3].

Broad sense Heritability values ranged from moderate (No. of grains/pod) to very high (days to 50% flowering). Genetic Advance as percent Mean ranged from low (No. of grain/pod, plant height) to high (grain yield). No. of grains/pod recorded moderate heritability with low GAM indicating less additive gene action. Days to 50% flowering and grain yield recorded high heritability with high GAM indicate presence of additive gene action which respond to simple selection.

However, trait correlations are important to gain knowledge on selection of high yielding genotypes with good agronomic traits. Plant height is significantly associated with No. of branches and No. of pods/plant indicating that increased plant height will put up more branches and with increase in branches the pod clusters will also increase and hence to have more pods/plant increased plant height was one indicator in this population. Days to 50% flowering was significantly associated with all the traits studied. Hence, while breeding for early maturing cultivars care should be taken to avoid linkage drag between days to 50% flowering and other traits. The positive significant association of grain yield with pod length and No. of pods/plant is advantageous for simultaneous selection, but its positive significant association with days to 50% flowering may not be advantageous when selection is oriented for early maturing variety with high yield. One can go for further utilization of early duration variety in developing high yielding variety with a compromise at one point. These results are in accordance with Saroj *et al.* (2013) [14], Pushpavalli *et al.* (2018) [13], Satyanarayana *et al.* (2018) [15], Anuradha and Patro (2019) [3].

Table 1: ANOVA of 15 red gram genotypes

Source of Variations	df	Mean Squares						
		Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)
Treatments	14	629.47	1528.49	103.83	0.98	1398.03	0.24	29.30
Replications	2	0.80	473.32	11.05	0.30	74.34	0.11	0.56
Error	28	6.40	333.32	18.92	0.11	295.49	0.08	2.83
P value for treatments		5.3E-20	3.0E-04	6.6E-05	6.0E-07	2.3E-04	8.0E-03	1.2E-07
P value for replications		0.88	0.26	0.56	0.08	0.78	0.26	0.82

Table 2: Mean values of 15 red green gram entries for yield and its component traits

S. No	Entry Name	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)
1	LRG 52	138.7	241.7	48.1	5.7	212.1	3.7	17.2
2	LRG 229	125.0	248.7	36.9	6.2	174.9	4.2	13.8
3	LRG 231	121.0	235.8	42.9	5.2	176.9	3.7	14.6
4	TRG 108	119.0	246.7	32.3	5.2	153.5	3.7	14.5
5	Maruthi	121.0	246.8	37.4	5.2	173.7	3.6	12.6
6	TRG 111	114.0	266.5	48.7	5.0	184.3	3.7	10.8
7	LRG 224	116.7	228.5	46.3	5.2	156.9	3.5	10.2
8	LRG 211	139.0	260.2	44.0	5.0	168.9	3.9	10.5
9	LRG 274	90.0	181.1	27.6	4.3	121.3	3.2	4.6
10	LRG 275	113.7	261.1	45.5	5.3	172.5	3.7	9.7
11	LRG 267	114.7	271.1	39.3	5.3	177.9	3.6	11.0
12	BRG 2	142.7	263.3	42.1	6.9	207.8	4.3	15.8
13	TRG 113	139.0	248.9	43.5	5.4	179.9	3.4	14.2
14	LRG 208	141.3	271.2	45.3	5.4	170.8	3.5	15.0
15	LRG 41	116.7	259.5	40.3	5.3	157.5	3.5	12.3
	Mean	123.53	248.74	41.35	5.37	172.59	3.69	12.46

	CD (0.05)	4.23	30.53	7.27	0.55	28.75	0.48	2.81
	CD (0.01)	5.7	41.19	9.81	0.75	38.78	0.64	3.79
	CV (%)	2.05	7.34	10.52	6.17	9.96	7.72	13.49

Table 3: Summary statistics and genetic parameters of 15 red gram genotypes

S. No	Parameter	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod	Grain Yield (q/ha)
1	Mean	123.5	248.7	41.4	5.37	172.6	3.7	12.5
2	Minimum	90.0	181.1	27.6	4.3	121.3	3.2	4.6
3	Maximum	142.7	271.2	48.7	6.9	212.1	4.3	17.2
4	GCV	11.67	8.02	12.87	10.02	11.11	6.14	23.85
5	PCV	11.84	10.87	16.62	11.77	14.92	9.87	27.40
6	ECV	2.05	7.34	10.52	6.17	9.96	7.72	13.50
7	H ² (Broad Sense)	97.01	54.45	59.93	72.53	55.43	38.77	75.75
8	Genetic Advance	29.24	30.34	8.48	0.94	29.40	0.29	5.32
9	GAM	23.67	12.20	20.52	17.58	17.04	7.88	42.76

Table 4: Phenotypic correlation of yield and other characters in 15 red gram genotypes

S. No.	Traits	Days to 50% flowering	Plant height (cm)	No. of Branches/pl	Pod length (cm)	No. of pods/pl	No. of grain/pod
1	Plant height (cm)	0.58*					
2	No. of Branches/pl	0.54*	0.56*				
3	Pod length (cm)	0.64*	0.47	0.25			
4	No. of pods/pl	0.72**	0.60*	0.66**	0.72**		
5	No. of grain/pod	0.49	0.45	0.17	0.81**	0.60*	
6	Grain Yield (q/ha)	0.79**	0.50	0.38	0.70**	0.75**	0.47

References

- Allard RW. Principles of Plant Breeding. John Wiley and Sons Inc., New York. 1960, 485.
- Anonymous, In: All India Co-ordinated Research Project on Pigeonpea. Project Coordinator's Report. Annual group meet at UAS, Bangalore, 2012, 13-15.
- Anuradha N, Patro TSSK. Genetic variability, heritability and correlation in advanced red gram genotypes. International Journal of Chemical Studies, 2019; 7(3):2964-2966.
- Anuradha N, Patro TSSK, Divya M, Sandhya Rani Y, Triveni U. Genetic Variability, Heritability and Association in Advanced Breeding Lines of Finger Millet [*Eluesine coracana* (L.) Gaertn.]. International Journal of Chemical Studies, 2018; 5(5):1042-1044.
- Anuradha N, Satyavathi CT, Meena MC, Sankar SM, Bharadwaj C, Bhat J *et al.* Evaluation of pearl millet [*Pennisetum glaucum* (L.) R. Br.] for grain iron and zinc content in different agro climatic zones of India. Indian Journal of Genetics and Plant Breeding (The), 2017; 77(1):65-73.
- Burton GW, Devane EW. Estimating heritability in tall fescue (*Festuca arundinaceae*) from replicated clonal material. Agronomy Journal. 1953; 45:478-481.
- Falconer DS. Introduction to Quantitative Genetics. 2nd ed. Longman, London, 1981.
- Johnson HW, Robinson HF, Comstock RE. Estimate of genetic and environmental variability in Soybeans. Agronomy Journal 1955; 47:314-318.
- Kumara BN, Santoshagowda GB, Nishanth GK, Dharmaraj PS. Genetic diversity, variability and correlation studies in advanced genotypes of Pigeon pea [*Cajanus cajan* (L.) Millsp.]. Acta biologica indica, 2013; 2(2):406-411.
- Panse VG, Sukathme PV. Statistical Method for Agricultural Workers. ICAR, New Delhi. 1967, 381.
- Prasad Y, Kumar K, Mishra SB. Studies on genetic parameters and inter-relationships among yield and yield contributing traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]. The bioscan. 2013; 8(1):207-211.
- Pushpavalli SNCVL, Sudhakar C, Rani CS, Rajeswari R, Rani CJ. Genetic divergence, correlation and path coefficient analysis for the yield components of pigeonpea genotypes. Legume Res, 2017; 40(3):439-443.
- Pushpavalli SNCVL, Yamini KN, Anuradha Rajani, Kumar G, Rani CS, Sudhakar C *et al.* Genetic variability and correlation in pigeonpea genotypes. Electronic Journal of Plant Breeding, 2018; 9:343-349. 10.5958/0975-928X.2018.00038.8.
- Saroj SK, Singh MN, Kumar R, Singh T, Singh MK. Genetic variability, correlation and path analysis for yield attributes in pigeonpea. The bioscan, 2013; 8(3):941-944.
- Satyanarayana N, Sreenivas G, Jagannadham J, Amarajyothi P, Rajasekhar Y, Swathi B. Genetic variability, Correlation and path analysis for seed yield and its components in Redgram [*Cajanus cajan* (L.) Millsp.]. Bulletin of Environment, Pharmacology and Life Sciences. 2018; 7[SPL1]:53-57.
- Sodavadiya MS, Pithia JJ, Savaliya AG, Pansuriya, Korat VK. Studies on characters association and path analysis for seed yield and its components in pigeonpea (*Cajanus cajan* (L.) Millsp.). Legume Res. 2009; 32(3):203-205.