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Genetic variability and association studies for seed yield and related trait in pigeonpea [*Cajanus cajan* (L.) Millsp.]

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Abstract
The present investigation was conducted during the *kharif* season 2021-22 at Research cum Instructional Farm IGKV RMD CARS, Ambikapur, Chhattisgarh. The genetic parameters studied namely, genotypic coefficient of variation and phenotypic coefficient of variation, heritability (h^2) and genetic advance. Besides, these parameters, correlation coefficient were also studied for seed yield and its component traits in 16 genotype of pigeonpea. The results indicated that the genotypes showed significant variability for all the traits studied. The components of variance revealed that the phenotypic coefficient of variation (PCV) were higher than genotypic coefficient of variation (GCV) for all the characters studied indicating the role of environmental variance in the total variance. The highest GCV and PCV was recorded for seed yield followed by biological yield. Heritability in broad sense was higher in most of the characters *viz*., number of pods per plant followed by seed yield, number of primary branches per plant, number of seeds per pod, pod length, days to 50% flowering, number of pods per cluster, days to maturity and days to flower initiation. Seed yield, biological yield, number of pods per cluster, pod length and number of primary branches per plant all had highest genetic advance as a percentage of mean. It suggests that these characters are controlled by additive gene activity and that selection will aid in the growth of similar characters. Seed yield was significant positive association with number of pods per cluster followed by number of pods per plant, 100 seed weight, number of primary branches per plant, biological yield, pod length and number of seeds per pod and these are major yield contributing traits to be given selection pressure for improving yield.

Keywords: Pigeonpea, genetic variability, heritability, genetic advance, correlation

Introduction
The pigeonpea [*Cajanus cajan* (L.) Millsp.] Is an often cross pollinated crop with 2n=2x=22 chromosomes that belongs to the fabaceae family. The name of pigeonpea was first used in Barbados where pigeon were fed the seed of *Cajanus cajan* (Plukenet 1692) [12]. It is commonly known as arhar, tur, red gram, Congo pea, and Rahar, is a very old crop of country. Pigeonpea is the 5th most important food legume crop in the world after soybean, groundnut, dry beans, and peas. India is considered as the native of pigeonpea (Vander and Maesan, 1980) [20] because of its natural diversity genetic variability available in the total germplasm and presence of its wild relatives in the country. The major pigeonpea producing areas in the world are India, eastern Africa, Central and South America, the Caribbean and West Indies (Vijyalakshmi *et al.* 2013).

Pigeonpea is India's second most important pulse crop, has various application including food (flour, dry peas or green vegetable peas), feed, fuel, and fodder. It contains 20-21% protein (Sodavadiya *et al.* 2009) [19]. The per capita availability of protein in the country is 48 g/day, while WHO suggests it should be 80 g/day, consequently most serious problem of the malnutrition existing among the poor people, where most of the people have vegetarian diet and avoid the animal protein (Prasad *et al.* 2013) [13].

Pigeonpea is a widely adaptable, deep-rooted, drought-tolerant, leguminous food crop that can be cultivated in areas with annual rainfall of less than 650 mm. Pigeonpea can grow in any warm climate, although it grows best in the tropical and subtropical regions. Pigeonpea can grow in an infertile and relatively dry land (Varshney *et al.* 2012) [21] because of their deep roots (Odeny, 2007) [11]. The deep rooting of this plant does not interfere with the absorption of other plants so pigeon pea can be intercropped (Sheahan, 2012) [18]. According to Cook *et al.* (2005) [3] and Khoiriyah *et al.* (2018) [7], pigeonpea does not need much water and is resistant

to high rainfall intensity. It can survive in arid conditions due to its long rooting system. Pigeonpea can be grown in temperatures ranging from 26 °C to 30 °C during the rainy season (June to October) and 17 °C to 22 °C during the post-rainy season (November to March), with an optimal soil pH of 4.5- 8.4. The area under pigeonpea in India is around 4.54 million hectare with a production is estimated 4.32 million tonnes (Directorate of agriculture and statistics, 2020-21). Pigeonpea is a major pulse crop grown primarily in Karnataka, Chhattisgarh, Odisha, Tamil Nadu, Andhra Pradesh, Bihar, and Maharashtra.

In chhattisgarh, Pigeonpea occupies an area of 95.54 thousand ha, with an average productivity of 643 kg ha^{-1} (Krishi darshikha, 2020) [8].

The Crop improvement depends on the magnitude of genetic variability present in the base population. The nature and degree of the heritable portion of total variation determines the expected improvement in yield components. Selection based on a single character may not always be effective. On the other hand, it is a time-consuming process for a breeder to evaluate a high number of component traits at the same times during the selection method. The presence of genetic variation is important for any breeding effort, and as a result, plant breeders have prioritized the evaluation of germplasm for crop production improvement as well as utilization in breeding program. The evaluation of plant genetic resources is a requirement for future breeding activity.

Genetic parameters such like genotypic and phenotypic coefficients of variation, heritability (bs) and genetic advance are extremely effective in breeding materials. The information on the association of yield with yield attributes will help breeders identify traits that contribute to yield in order to make significant genetic gains. The estimating phenotypic, genotypic and environmental correlation for yield and attribution traits is a basic and important effort in determining plant selection strategies. The range and direction of correlation suggest a future characteristic to also be considered.

Materials and Method

16 pigeonpea genotypes were grown in 4 rows of 3 meter length in Randomized Block Design (RBD) with 2 replications during *kharif* season 2021-22. Row to row and plant to plant spacing were maintained at 60 and 20 cm, respectively. Before sowing, a recommended fertilizer dose of NPK 20:50:20 kg per hectare was put in the rows. To raise a normal crop, a recommended package of practices was used. Observations were recorded for 12 traits including on days to flower initiation, days to 50% flowering, plant height (cm), number of primary branches per plant, number of pods per plant, number of pods per cluster, pod length (cm), number of seeds per pod, days to maturity, 100 seed weight (g), biological yield (q/ha) and seed yield (q/ha). The data were collected on five randomly selected plants from each replication.

Result and Discussion

Variability studies

The Analysis of variance was based on the mean value of 12 quantitative characters in 16 genotypes. The result of ANOVA revealed highly significant differences among the genotypes in respect of all the characters under study (Table 1). These results indicate that there is significant inherent genetic variability among the genotypes which provide ample of scope for identifying genotypes with desirable character to improve yield, provided the material be subjected to sensible selection pressure. Genetic parameters of yield and their components are given in (Table 2).

In the present study, the phenotypic coefficients of variation were slightly greater than the genotypic coefficients of variation indicated that environment had an impact on the expression of the character under study. Seed yield had the highest magnitude of GCV and PCV followed by biological yield. The moderate GCV and PCV were observed for number of pods per cluster, pod length and number of primary branches per plant. Number of seeds per pod, 100 seed weight, Number of pods per plant, plant height, Days to maturity, days to flower initiation and days to 50% flowering were all found to have low GCV and PCV. In this study, the phenotypic variance was high as compared to genotypic variance for all the traits studied which was also observed earlier Chetukuri *et al.* (2013) [2], Kumar *et al.* (2014) [9], Sharma *et al.* (2017) [17] Alaka *et al.* 2020 [1] and Rao *et al.* (2020) [15].

Heritability and genetic advance

The high magnitude of heritability was recorded for the number of pods per plant followed by number of primary branches per plant, number of seed per pod, pod length, days to 50% flowering, number of pods per cluster, seed yield, days to maturity and days to flower initiation. 100 seed weight, plant height and biological yield all had modest estimates of heritability. The seed yield had the highest genetic advance as a percentage of the mean followed by biological yield, number of pods per cluster, pod length and number of primary branches per plant. The number of seeds per pod showed moderate genetic advance as a percentage of mean, followed by the number of pods per plant and 100 seed weight. Days to maturity, days to flower initiation, days to 50% flowering and Plant height showed low genetic advance as a percentage of mean.

High Heritability in broad sense coupled with high genetic advance as percentage of mean was found for number of primary branches per plant, pod length and seed yield which indicated that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose similar findings were reported by Rathnaswamy *et al.* (1973) [16] Jaggal *et al.* (2012) [5] Kesha Ram *et al.* (2016) [6] and Ranjani *et al.* (2018) [14].

Correlation coefficient analysis

The genotypic correlation coefficient of seed yield and its components traits are sown in table 1.3. Correlation analysis in pigeonpea revealed that seed yield positively and significantly correlated with number of pods per cluster, followed by number of pods per plant, 100 seed weight, number of primary branches per plant, biological yield, pod length and number of seeds per pod but negative significant correlation coefficient with days to maturity followed by days to flower initiation, days to 50% flowering whereas negative correlation with plant height at genotypic level. Hence, number of pods per cluster, number of pods per plant, 100 seed weight, number of primary branches per plant, biological yield, pod length and number of seeds per pod may be advantageous for selecting the high yielding genotypes in pigeonpea from the available genotypes.

Table 1: Analysis of variance for seed yield and its components in pigeonpea

S. No.	Source of variance	Mean sum of square		
	Characters	Replication (1)	Treatment (15)	Error (15)
1	Days to flower initiation	1.13	16.43**	1.59
2	Days to 50% flowering	0.28	16.65**	1.21
3	Plant height (cm)	62.16	88.4**	18.12
4	Number of primary branches per plant	0.01	1.12**	0.05
5	Number of pods per plant	1.37	130.72**	1.90
6	Number of pods per cluster	0.12	0.64**	0.05
7	Pod length (cm)	0.07	1.15**	0.01
8	Number of seeds per pod	0.08	0.36**	0.02
9	Days to maturity	0.12	44.1**	4.12
10	100 seed weight (g)	0.70	1.36**	0.26
11	Biological yield (q/ha)	2837.43	11355**	2406.76
12	Seed yield (q/ha)	0.01	13.13**	1.14

** Significant at 1% level of probability, * Significant at 5% level of probability

Table 2: Genetic variability parameters for seed yield and its components in pigeonpea

S. No.	Characters	MEAN	RANGE		GCV (%)	PCV (%)	h^2 (bs) (%)	Genetic Advance 5%	GA as % of mean
			Max.	Min.					
1	Days to flower initiation	115.62	119.50	109.50	2.36	2.60	82.33	5.09	4.40
2	Days to 50% flowering	134.84	139.00	128.50	2.06	2.21	86.40	5.31	3.94
3	Plant height (cm)	264.7	278.55	257.05	2.23	2.75	65.97	9.91	3.74
4	Number of primary branches per plant	6.48	7.46	5.03	11.26	11.82	90	1.43	22.09
5	Number of pods per plant	138.93	150.82	128.35	5.77	5.86	97	16.29	11.72
6	Number of pods per cluster	3.20	4.09	2.22	16.88	18.25	85.55	0.03	32.16
7	Pod length (cm)	5.10	6.15	4.00	13.67	14.55	88.24	1.34	26.45
8	Number of seeds per pod	4.41	4.85	3.25	9.37	9.95	88.78	0.80	18.20
9	Days to maturity	186.37	197.00	179.50	2.39	2.63	82.89	8.38	4.49
10	100 seed weight (g)	11.23	12.80	10.20	6.61	8.02	67.99	1.26	11.24
11	Biological yield (q/ha)	138.01	542.31	243.04	19.78	24.54	65.02	111.11	32.87
12	Seed yield (q/ha)	10.29	16.76	6.78	23.77	25.94	83.95	4.62	44.86

Table 3: Genotypic correlation coefficient between seed yield and other characters

Genotype	Days to flower initiation	Days to 50% flowering	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of pods per cluster	Pod length (cm)	Number of seeds per pod	Days to maturity	100 seed weight (g)	Biological yield (q/ha)	Seed yield (q/ha)
Days to flower initiation	1.000											
Days to 50% flowering	0.805**	1.000										
Plant height (cm)	-0.120	-0.195**	1.000									
Number of primary branches per plant	-0.542**	-0.507**	-0.314	1.000								
Number of pods per plant	-0.608**	-0.520**	-0.415*	0.793**	1.000							
Number of pods per cluster	-0.607**	-0.577**	-0.363*	0.859**	0.870**	1.000						
Pod length (cm)	-0.551**	-0.530**	-0.391*	0.867**	0.871**	0.946**	1.000					
Number of seeds per pod	-0.473**	-0.519**	-0.364*	0.852**	0.677**	0.794**	0.784**	1.000				
Days to maturity	0.608**	0.517**	0.292	-0.677**	-0.587**	0.738**	0.611**	-0.730**	1.000			
100 seed weight (g)	-0.631**	-0.493**	-0.217	0.765**	0.859**	0.897**	0.891**	0.684**	-0.691**	1.000		
Biological yield (q/ha)	-0.564**	-0.479**	-0.320	0.693**	0.693**	0.767**	0.707**	0.621**	-0.630**	0.733**	1.000	
Seed yield (q/ha)	-0.644**	-0.471**	-0.304	0.811**	0.838**	0.841**	0.787**	0.729**	-0.743**	0.823**	0.795**	1.000

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