Original Research Article

Genetic Studies ~~for~~ on Yield and its Components in Pigeonpea (*Cajanus cajan* (L.) Mill~~.~~sp.)

ABSTRACT:

Aims: To study the genetic parameters for yield and its components ~~among~~ in pigeonpea genotypes in order to develop a suitable ~~which provides in developing an apt~~ selection index ~~to be included in the~~ that can improve breeding programs

Place and Duration of Study: International Crop Research Institute for the Semi-arid Tropics, Patancheru, Hyderabad during *Kharif,* 2023-24

Methodology: The present study ~~investigation entitled~~ was carried out on 200 pigeonpea genotypes ~~over~~ to evaluate seven ~~characters~~ traits. Data were ~~The data was~~ analyzed to compute analysis of variance (ANOVA), phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), broad sense heritability ~~in broad sense~~ (h^2_{bs}) and estimated genetic advance as percentage of mean ~~per cent mean~~ using R software v 4.3.1.

Results: ~~The a~~Analysis of variation revealed highly significant difference between genotypes in~~for~~ days to 50% flowering, plant height (cm), hundred seed weight and seed yield per plant. ~~among the genotypes.~~ The genotypic coefficient of variance was lower than the ~~genotypic~~ phenotypic coefficient of variance for all ~~the~~ traits under selection. A ~~H~~higher ~~extent of~~ genotypic coefficient of variation was found for the traits~~is manifested by~~ days to 50% flowering, plant height, seeds per pod, hundred seed weight and seed yield per plant. A ~~H~~high heritability coupled with genetic advance as ~~per cent mean~~ percentage of mean was found for ~~observed in~~ seed yield per plant, days to 50% flowering and plant height.

Conclusion: The results obtained suggest ~~concluded~~ that seed yield per plant, days to 50% flowering and plant height are the traits that should be~~to be~~ emphasized for selection index in the pigeonpea breeding programs.

Keywords: *Pigeonpea, Genetic variability, Heritability, Genetic advance as per~~-~~cent~~age of~~ mean*

1. INTRODUCTION:

Pigeonpea is ~~the~~a versatile crop that is cultivated across the arid and semi-arid ~~tracts~~regions of the world. It belongs to the Fabaceae ~~F~~family ~~Fabaceae~~, the ~~G~~genus Cajanus, the species Cajan, the ~~T~~tribe *Phaseoleae*, and the ~~S~~sub-tribe *Cajaninae* [1]. It is an often~~-~~ cross~~-~~pollinated species with 11 pairs of chromosomes (2n = 2x = 22) and a genome size of 833.07 Mbp [2]. It is ~~C~~commonly known

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as Tur or Arhar in India, and it is the second most important pulse crop in the country after gram (chana). It is well regarded valued for its many usesmultiple utility as a food, feed, fodder and fuel. Mainly consumed as split dhal in the Indian subcontinent and a whole seed in the African community, it caters to the food and nutrition needs of the developing and under-developed countries of the world. On the Indian subcontinent, it is mainly consumed in the form of split dhal, while in Africa it is eaten as a whole grain. It meets the food and nutritional needs of the developing and underdeveloped countries of the world. Globally, redgram is grown inon an area of 63.57 lakh hectares with a production of 54.75 lakh tonnes and a productivity of 861.25 kg/ha. In India, the total area under cultivation coverage and production of pigeon pea has been estimated was recorded at 4.23 million hectares and 3.89 million tons, with a productivity of respectively with 919 kg per /ha productivity [3].

Since Yyield isbeing a complex trait, it is influenced together stimulated by multiple component characters, which are polygenically inherited and stronglytremendously influenced by environmental variations. The Ddevelopment of a character in a population is a result of the variability present in the population. In order to divide phenotypic variation into heritable (genetic) and non-heritable (environmental) components, the variability present in it should be essential to analyse the existing variability in the population must be analysed. By iIsolating the genetic variance from the environmental variance, this would improve the genotype's breeding value for accurate evaluationassessment.

Therefore, in the this present study, the variance components of variance such as the phenotypic coefficient of variance (PCV), the genotypic coefficient of variance (GCV), the broad sense heritability in broad sense (h^2_{bs}) and the estimated genetic advance as per cent mean percentage of mean were calculatedcomputed. Thus, the analysis was carried outdone over for six characterstraits in among 200 genotypes to evaluateassess the genetic variability, heritability, genetic advance and diversity in among pigeonpea genotypes.

2. MATERIALS AND METHODS:

The experimental material of present investigation comprised of 200 genotypes laid out in alpha lattice design with two replications at International Crop Research Institute for the Semi-arid Tropics, Patancheru, Hyderabad during *Kharif* 2023-24. The experimental material of the present study comprised 200 genotypes established at International Crop Research Institute for the Semi-arid Tropics, Patancheru, Hyderabad, during Kharif 2023-24 in an alpha lattice design with two replications. Each entry was accommodated in a two rows of 3m each with a spacing of 75 cm X 15 cm. The oObservations were recorded on five randomly selected plants from each line in each replication except for days to 50 per cent flowering, where all plants in the of plot were considered. All cultivationural practices were followed and timely plant protection measures were taken to avoid damage throughfrom pests and diseases. The Oobservations were carried out made on seven characters traits namely days to 50% flowering, plant height (cm), number of primary branches per plant, number of secondary branches per plant, seeds per pod, hundred seed weight (g) and seed yield per plant (g). The data recorded collected for the different characters traits were subjected to various statistical analysizes.

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The analysis of variance for the alpha lattice design was performeddone for each character with the method by using the residual maximum likelihood (REML) procedure using with ASREML-R v4 in the R software v 4.3.1 [4]. From ANOVA table, environmental, genotypic and phenotypic variances were estimated [5]. The Pphenotypic and genotypic coefficient of variation was calculated from the ANOVA table [6]. The GCV (%) and PCV (%) values were classified as described by Sivasubramanian and Madhava Menon (1973) [7]. The broad sense heritability in broad sense was estimated according to method given by Allard (1960) [8]. The Eexpected genetic advance represents the shift in a population towards the superior side under a certainsome selection pressure after a single generation of selection. It can be could be calculated according to the method proposed by using the methodology suggested by Allard (1960) with a selection intensity ofat 5 per-cent selection andintensity using constant 'K' as of 2.06 [8]. The expected genetic advance expressed as per centage of mean, was calculated according to by the method proposed suggested by Johnson et al., (1955) [5].

3. RESULTS AND DISCUSSION:

3.1 Mean performance of the genotypes:

The mMorphological characterizsation of the genotypes for seven different traits, namely days to 50 % flowering (DF), plant height (cm) (PH), number of primary branches per plant (PB), number of secondary branches per plant (SB), seeds per pod (SPP), hundred seed weight (g) (HSW), yield per plant (g) (YLD) showed a wide displayed vast variation. Days to 50% flowering, Pplant height (cm),. Hhundred seed weight (g) and seed yield per plant (g) displayed significant genotypic variation (Table 1). This clearly indicates that there is evidently shows presence of sufficient amount of variation among the genotypes and there is ample scope for improvement.

The mean performance of genotypes assessed evaluated for days to 50% flowering showed that ICP 14936 (51 days) was the to be earliest to flower, while ICP 4231 (180.5 days) was being the latest entry with a mean of 126.12 days across the panel. Plant height ranged from 88.3 (ICP 11627) to 256.6 (ICP 11833) with an average height of 191.4 cm. The number of primary and secondary branches per plant ranged from 6.1 (TS3R) to 10.2 (ICP 10276, ICP 2577), 7.9 (ICP 6892, GRG 152) to 15.6 (BSMR 736) with a mean of 8.16 and 11.74, respectively. Seeds per pod across the panel had a limited restricted range from 3.42 (ICP 7803) to 4 (ICPL 20201) with a mean of 3.72. Hundred seed weight rangedspread vastly across the genotypes from 6.75 g (ICP 14900) to 14.5 g (ICP 2405) with a mean of 10.2 g among in the panel for all genotypes. The Yyield per plant also varied greatlyranged widely from a minimum of 0.72 g (ICP 14294) to 61.44 g (ICP 655) with an average of 15.49 g (Table 2).

The values of the genotypic coefficient of variation were lower than those of the phenotypic coefficient of variation, indicating showing an effect of environment over all traitsthe characters (Table 2). High values of GCV were observed forin yield per plant, while a moderate variance was reported for days to 50% flowering, plant height (cm), and hundred seed weight (g) thus indicating a greater

Comment [IĆ1]:

1.
The data in the text of this section are not the same as in table 2. It is necessary to correct either the numbers in the text or the data in the table.

2.
The names of the genotypes, which are not given in the table, are also given in this section.
Maybe :a) to write the names of those genotypes in the min and max columns OR
b) delete the names of the genotypes from the text of this section OR
c) give supplementary table with all data

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degree~~extent~~ of variability ~~present~~ in these ~~characters~~traits~~,~~ and ~~thereby~~ thus suggesting a good scope for improvement through selection. Low values were recorded for the number of primary branches per plant, the number of secondary branches per plant and seeds per pod, suggesting that variability needs ~~thus indicated the need~~ to be created ~~variability either~~ by hybridization followed by selection. Similar results were ~~observed~~ reported by Galian et al. (2015) [9]; for yield per plant and plant height (cm) by Pushpavalli et al. (2018) [10]; for days to 50% flowering by Naik et al.~~,~~ (2013) [11]; Sahu and Ekka, (2020) for hundred seed weight (g) and seeds per pod [12]; Pashwan et al. (2021) for the number of primary branches per plant and the number of secondary branches per plant [13].

The present study showed a wide~~vast~~ range of variability for all ~~the characters~~traits. The presence of genotypic variation alone does not~~cannot give the idea of~~ indicate an improvement that could be achieved by ~~obtained through~~ selection. The estimation of heritability of the trait shows the relative per~~-~~centage of heritable variability that allows~~allowing for~~ efficient selection. ~~-~~High heritability was ~~observed~~ found for all ~~the~~ traits except the number of primary and secondary branches per plant, indicating that all ~~the~~ traits are mainly ~~majorly governed~~determined ~~-~~by additive genes and thus have the least environmental influence. The results were in accordance with those of Galian et al. (2015)~~;~~, Gaur et al, (2020)~~;~~ Patel et al. (2021) and Bhagat et al. (2022) for all ~~the~~ traits with~~having~~ high heritability [9,14,15,16]. ~~While~~ The number of primary branches per plant and the number of secondary branches per plant showed~~had~~ moderate and low heritability, respectively, indicating a ~~larger environmental play over the characters~~ greater influence of the environment on the traits, which is also explained by Pushpavalli et al. (2018) and Patel et al. (2021) ~~respectively~~ [10,15].

The ~~H~~heritability value alone cannot provide information on the amount of genetic progress that would result from the selection of the best individuals. Johnson et al.~~,~~ (1955) suggested that the heritability estimates along with genetic gain would be more successful in forecasting the success of selecting the best individuals [5]. In order to improve the effectiveness of the selection process, it was crucial to take the expected genetic advance into account alongside the heritability estimate. As a result, ~~projected~~ the expected genetic progress is calculated for all ~~the~~ attributes.

The genetic advance as per~~-~~centage of mean was ~~recorded~~ highest for yield per plant, followed by days to 50% flowering and plant height. Moderate genetic advance as per~~-~~centage of mean was~~is~~ observed for hundred seed weight followed by low genetic advance as per~~-~~centage of mean ~~was observed~~ for number of primary branches per plant, number of secondary branches per plant and seeds per pod indicating higher non~~-~~additive gene action in these traits~~over the characters~~. The results were similar to the observations ~~by~~ of Vanishree et al. (2013), Saroj et al. (2013) [17,18]; Galian et al. (2015) for yield per plant [9], Gaur et al. (2020) for days to 50% flowering and plant height~~, Gaur et al, (2020)~~; Bhagat et al. (2022) for hundred seed weight [14,16]; Pashwan et al. (2021) and Patel et al. (2021) for number of primary branches per plant, number of secondary branches per plant and seeds per pod [13,15].

A ~~H~~higher heritability coupled with a high genetic advance as per~~-~~centage of mean is observed for yield per plant, days to 50% flowering and plant height. This confirms higher additive gene ~~action~~ effects and thus improvement could be ~~brought about~~achieved by direct phenotypic

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selection ~~over the genotypes~~. A ~~H~~higher heritability with a moderate genetic advance as per~~-~~centage of mean is observed for hundred seed weight and ~~I~~ a higher heritability with low genetic advance in seeds per pod, indicating ~~that~~ the effect of non-additive gene action. The higher heritability might be due to the favourable environment rather than the genotype. Moderate heritability with low genetic advance as per~~-~~centage of mean was ~~depicted~~ observed in the number of primary branches per plant, while low heritability with low genetic advance as per~~-~~centage of mean was ~~represented~~ observed in the number of secondary branches per plant. These traits confirm a higher non-additive gene action ~~over the trait referring~~ and their lower potential for improvement ~~in~~by selection ~~index~~ (Table 2).

4. CONCLUSION:

The findings ~~so~~ suggest that all pigeonpea genotypes have enough variation to account for the seven variables under investigation. The value of PCV was ~~just a~~ higher than GCV, indicating a considerable influence of the environment on phenotypic expression. High heritability was observed for all ~~the~~ traits except number of primary and secondary branches per plant, while high genetic advance as a per centage of mean for yield per plant, followed by days to 50% flowering and plant height indicat~~ing~~ed that phenotypic selection would be worthwhile. Thus, according to the results, yield per plant, days to 50% flowering and plant height are the ~~qualities~~ traits that need to be prioritised for the development of the pigeonpea selection index.

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Comment [IĆ2]: More recent data could be found. It could be the following paper :

Gargi, B.; Semwal, P.; Jameel Pasha, S.B.; Singh, P.; Painuli, S.; Thapliyal, A.; Cruz-Martins, N. Revisiting the Nutritional, Chemical and Biological Potential of Cajanus cajan (L.) Millsp.. Molecules **2022**, 27, 6877. https://doi.org/10.3390/molecules27206877

and there is reference no 7 (Orni, P.R.; Ahmed, S.Z.; Monefa, M.; Khan, T.; Dash, P.R. Pharmacological and phytochemical properties of Cajanus cajan (L.) Huth.(Fabaceae): A review. Int. J. Pharm. Sci. Res. **2018**, 3, 27–37.)**.**

Or some another, fresher reference could be cited.

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Table 1: Combined analysis of variance for different traits in Pigeonpea

DESCRIPTION	DF	PH	PB	SB	SPP	HSW	YLD
Genotype	1508.30**	732.58**	1.303	5.240	0.019	5.141**	231.012**
Replication	0.520	374.91	1.368	1.270	0.003	0.083	12.185
Residuals	8.481	91.163	1.523	7.149	0.025	0.780	27.596

DF= Days to 50% flowering; PH= Plant height (cm); PB= Number of primary branches per plant; SB=Number of secondary branches per plant; SPP= Seeds per pod; HSW= Hundred seed weight (g); YLD= Seed yield per plant (g)

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Table 2: Genetic components of variance for pigeonpea genotypes

TRAIT	MIN	MAX	MEAN	PCV	GCV	Trend of GCV	h^2 (B.S)	Trend of h^2(B.S)	GAM (%)	Trend of GAM (%)
DF	51	180.5	126.12	17.70	17.54	Mod	0.982	High	35.82	High
PH	88.8	256.6	191.39	12.77	11.77	Mod	0.849	High	22.34	High
PB	6.2	11.6	8.16	15.72	4.83	Low	0.059	Mod	1.81	Low
SB	7	18.8	11.74	22.38	7.10	Low	0.111	Low	4.89	Low
SPP	3.32	4.28	3.73	3.86	1.07	Low	0.077	High	0.61	Low
HSW	6.80	14.80	10.20	15.30	11.95	Mod	0.610	High	19.25	Mod
YLD	0.64	77.05	15.49	67.87	61.82	High	0.829	High	115.99	High

DF= Days to 50% flowering; PH= Plant height (cm); PB= Number of primary branches per plant; SB=Number of secondary branches per plant; SPP= Seeds per pod; HSW= Hundred seed weight (g); YLD= Seed yield per plant (g)

MIN= Minimum; MAX= Maximum; GCV= Genotypic coefficient of variation; PCV= Phenotypic coefficient of variation; h^2_{bs} = Heritability (Broad sense); GAM = GA as per cent of mean (%)

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