Original Research Article

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

ABSTRACT:

Aims: To study genetic parameters for yield and its components among pigeonpea genotypes which provides in developing an apt selection index to be included in the 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 investigation entitled was carried out on 200 pigeonpea genotypes over seven characters. The data was analyzed to compute analysis of variance (ANOVA), phenotypic coefficient of variance (PCV)*,* genotypic coefficient of variance (GCV), heritability in broad sense (h^2_{bs}) and estimated genetic advance as per cent mean using R software v 4.3.1.

Results The analysis of variation revealed highly significant difference 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 coefficient of variance for all the traits under selection. Higher extent of genotypic coefficient of variation is manifested by days to 50% flowering, plant height, seeds per pod, hundred seed weight and seed yield per plant. High heritability coupled with genetic advance as per cent mean was observed in seed yield per plant, days to 50% flowering and plant height.

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

Keywords:*Pigeonpea, Genetic variability,Heritability, Genetic advance as per cent mean*

1. INTRODUCTION:

Pigeonpea is the versatile crop cultivated across the arid and semi-arid tracts of the world. It belongs to the Family Fabaceae, Genus Cajanus, species Cajan, Tribe *Phaseoleae*, and Sub-tribe *Cajaninae*[1]. It is an often-cross pollinated species with 11 pairs of chromosomes (2n = 2x = 22) and a genome size of 833.07Mbp [2]. Commonly known as Tur or Arhar in India, it is the second important pulse crop in the country after gram (chana). It is well-regarded for its multiple 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. Globally, redgram is grown in an area of 63.57 lakh hectares with a production

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Comment [M2]: ABSTRACT:
A field trial was carried out at the International Crop Research Institute for the Semi-Arid Tropics, Patcheru, Hyderabad during Kharif, 2023-24, with the aim of studying genetic parameters for yield and its components among pigeonpea genotypes which provides in developing an apt selection index to be included in the breeding programs. This research was conducted on 200 genotypes of Indian pigeon pea on seven traits. Data were analyzed to calculate analysis of variance (ANOVA), phenotypic coefficient of variation (PCV), genetic coefficient of variation (GCV), broad sense heritability (h2bs) and estimated genetic progression as percentage mean using R software v 4.3.1. The results of the analysis of variance showed that there was a significant differencefor 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 coefficient of variance for all the traits under selection. Higher extent of genotypic coefficient of variation is manifested by days to 50% flowering, plant height, seeds per pod, hundred seed weight and seed yield per plant. High heritability coupled with genetic advance as per cent mean was observed in seed yield per plant, number of days to 50% flowering and plant height. The results concluded that seed yield per plant, number of days to flowering up to 50%, and plant height are the traits that should be emphasized as selection indicator in Indian pigeonpea breeding programs.

Comment [M3]: Notes on the introduction
1- All three references are about the meaning and importance of the topic. There are no references that refer to the research problem and the importance of this study.
2 - Previous studies and references must be added that highlight the importance of this study.
3- Rephrasing the last sentence to indicate the goal of this study and not to explain the research methodology.

of 54.75 lakh tonnes and productivity of 861.25 kg/ha. In India, total area coverage and production of pigeon pea was recorded at 4.23 million hectares and 3.89 million tons, respectively with 919 kg per ha productivity [3].

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Yield being a complex trait is togetherstimulated by multiple component characters, which are polygenically inherited and tremendously influenced by environmental variations. Development 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, it should be essential to analyse the existing variability in the population. By isolating genetic variance from environmental variance, this would improve the genotype's breeding value for accurate assessment.

~~Therefore, in this present study, the components of variance such as phenotypic coefficient of variance (PCV), genotypic coefficient of variance (GCV), heritability in broad sense (h^2_{BS}) and estimated genetic advance as per cent mean were computed.Thus, theanalysis was done over six characters among 200 genotypes to assess the genetic variability, heritability, genetic advance and diversity among pigeonpea genotypes.~~Therefore, this study aimed to study genetic parameters such as phenotypic variation (PCV) and genotypic variation (GCV) of the crop and its components for 200 Indian pigeon pea genotypes, which helps to develop a suitable selection indicator for inclusion in breeding programmes.

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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. Each entry was accommodated in a two row of 3m each with a spacing of 75 cm X 15 cm. The observations were recorded on five randomly selected plants from each line in each replication except for days to 50 per cent flowering where all plants of plot were considered. All cultural practices were followed and timely plant protection measures were taken to avoid damage through pests and diseases.Observations were carried out on seven characters 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) andseed yield per plant (g).The data recorded for different characters were subjected to various statistical analysis.

The analysis of variance for alpha lattice design was done for each character with the method byusing residual maximum likelihood (REML) procedure using ASREML-R v4 in R software v 4.3.1 [4].From ANOVA table, environmental, genotypic and phenotypic variances were estimated [5]. Phenotypic and genotypic coefficient of variation was calculated from ANOVA table [6]. The GCV (%) and PCV (%) values were classified as described by Sivasubramanian and Madhava Menon (1973) [7]. The heritability in broad sense was estimated according to method given by Allard (1960)[8]. Expected genetic advance represents the shift in a population towards superior side under some selection pressure after single generation of selection. It could be calculated by using the methodology suggested by Allard (1960) at 5 per cent selection intensity using constant ‘K’ as 2.06

[8]. The expected genetic advance expressed as per cent of mean was calculated by the method suggested by Johnson et al., (1955) [5].

3. RESULTS AND DISCUSSION:

3.1 Mean performance of the genotypes:

The morphological characterisation of the genotypes for seven different traits namely days to % 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) displayed vast variation. Days to 50% flowering, Plant height (cm). Hundred seed weight(g)and seed yield per plant(g) displayed significant genotypic variation (Table-1). This evidently shows presence of sufficient amount of variation among the genotypes and ample scope for improvement.

The mean performance of genotypes assessed for days to 50% flowering showed ICP 14936 (51 days) to be earliest to flower while ICP 4231 (180.5 days) being the late 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 restricted range from 3.42 (ICP 7803) to 4 (ICPL 20201) with a mean of 3.72. Hundred seed weight spread vastly across the genotypes from 6.75g (ICP 14900) to 14.5g (ICP 2405) with a mean of 10.2g among the panel. Yield per plant also ranged widely from a minimum of 0.72g (ICP 14294) to 61.44g (ICP 655) with an average of 15.49g (Table 2).

The values of genotypic coefficient of variation were lower than phenotypic coefficient of variation showing an effect of environment over all the characters (Table 2). High values of GCV wereobserved in 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 extent of variability present in these characters, thereby suggesting good scope for improvement through selection. Low values were recorded for number of primary branches per plant, number of secondary branches per plant and seeds per pod, thus indicated the need to create variability either by hybridization followed by selection. Similar results were observed 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~~number of primary branches per plant and number of secondary branches per plant [13].

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

Heritability value alone cannot provide information on amount of genetic progress that would result from selection of best individuals.~~Johnson et al.,(1955)~~[5]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 genetic progress is calculated for all the attribute.

The genetic advance as per cent mean was recorded highest foryield per plant followed bydays to 50% flowering and plant height. Moderate genetic advance as per cent mean is observed for hundred seed weight followed by low genetic advance as per cent mean was observed for number of primary branches per plant, number of secondary branches per plant and seeds per podindicating higher non additive gene action over the characters. The results were similar to the observations by~~Vanishree et al. (2013), Saroj et al. (2013)~~[17,18];~~Galian et al. (2015)for ~~yield per plant [9], 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 and~~,~~ number of secondary branches per plant and seeds per pod [13,15].

Higher heritability coupled with high genetic advance as per cent mean is observed for yield per plant, days to 50% flowering and plant height. This confirms higher additive gene action and thus improvement could be brought about by direct phenotypic selection over the genotypes.Higher heritability with moderate genetic advance as per cent mean is observed hundred seed weightand 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 cent mean was depicted in number of primary branches per plant, while low heritability with low genetic advance as per cent mean was represented in number of secondary branches per plant. These traits confirm a higher non-additive gene action over the trait referring their lower potential in selection index (Table 2).

4. CONCLUSION:

The findings so suggest that all pigeonpeagenotypes 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 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 cent mean yield per plant followed by days to 50% flowering and plant height indicating that phenotypic selection would be worthwhile. Thus, according to the results, yield per plant, days to 50% flowering and plant height are the qualities that need to be prioritised for the development of the pigeonpea selection index.

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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)

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 (%)