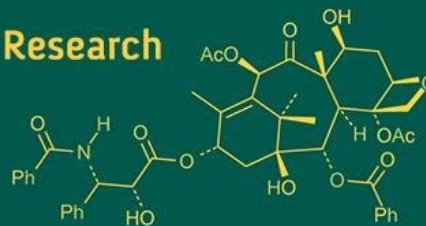


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Genetic variability studies in pigeonpea

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Abstract

Fourty two genotypes were evaluated for variability, heritability and genetic advance during 2023 at College of Agriculture, Badnapur. The analysis of variance showed significant differences among the genotypes for all the characters studied, indicating that there was high variability among the genotypes. Grain yield (t ha⁻¹) has exhibited high genotypic and phenotypic coefficient of variation, thus indicates that this character is governed by genetic factors and possible improvement through selection. Whereas, 100 seed weight (g), Number of pods/ Plant, Number of secondary branches/ Plant and Number of primary branches/ Plant obtained moderate estimate at both level. High heritability showed at character and high genetic advance showed at characters Number of pods/ Plant, Seed yield /Plant, 100 seed weight (g), Number of secondary branches/ Plant and Plant Height (cm). This indicates that the heritability was due to additive gene effects and selection would be promising for these characters.

Keywords: Pigeonpea, genetic variability, heritability, genetic advance

Introduction

Pulses constitute the main source of protein in vegeterians diet. Because of its high protein content and balanced amino acid composition, it is an essential component of the daily diet of humans. In the semi-arid tropics, pigeon pea (*Cajanus cajan* (L). Millisp) is a significant grain legume crop grown through rainfed agriculture. Because of its natural diversity of genes found in the local germplasm and the existence of its wild relatives there, India is regarded as the origin of the pigeonpea. In world pigeonpea cultivated under the area 5.4 million hectare with annual production of 4.49 million tons.

It is grown in eighty two countries in the world. In India pigeonpea is grown in an area 47.17 lakh hectares with production 41.37 lakh tonnes. Pigeonpea contribute 17 percent in total pulses production in India. Karnataka ranked first in area and production followed by Maharashtra (Anonymous 2021) [1].

The estimate of genetic parameters such as genotypic variability, phenotypic variability, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h²) and genetic advance (GA) are useful for the efficient selection and improvement in any of breeding program. Thus, this study was conducted to assess the importance of phenotypic and genotypic variability, phenotypic and genotypic coefficient of variation, heritability in broad sense h² (bs) and expected genetic advance to provide more information that may improve yield characters.

Materials and Methods

The present investigation on Pigeonpea for was conducted Genetic variability, Heritability, Genetic Advance at College of Agriculture, Badnapur, during *kharif* season of 2022-23. Experimental material comprising 42 genotypes lines with wider variability for different characters received from ARS, Badnapur.

Fourty two genotypes of Pigeonpea were evaluated in a randomized block design with two replications during *kharif* season of 2022-23. Each genotype was sown in one rows of 4 m length with spacing of 90 cm between rows and 20 cm within rows. The data were recorded on five randomly selected plants of each replication for all characters such as days to 50% of flowering, days to maturity, plant height (cm), number of primary branches per plant, number of secondary branches per plant, number of pods per plant, number of seeds per pod, 100 seed weight and seed yield.

Results and Discussion

The analysis of variance revealed significant genotypic differences for all the characters indicating the presence of considerable amount of variability in the experimental material showed in Table No 1. Analysis of variance of genotype highest for number of pods per plant this similar result found by Baldaniya *et al.* (2018) [2]. Similar result were obtained by Baria *et al.* (2023) [3] and Chetana *et al.* (2015) [5] for analysis of variance of replication, genotype and error showed highest value of number of pods per plant. The estimates of variability (genotypic and phenotypic coefficient of variation), heritability (broad sense), genetic advance as percent of mean for seed yield and its component characters in forty two genotypes of pigeonpea were presented in Table No 2. Genotypic variance (43.95) was lower than phenotypic variance (50.28). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 5.59 and 5.98 per cent respectively. Higher estimates of heritability (87.4) coupled with medium genetic advance as percent of mean (10.77) was observed. The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 5.09 and 5.28 per cent respectively. Higher estimates of heritability (92.9) coupled with medium genetic advance as percent of mean (10.11) was observed. Genotypic variance (79.52) was lower than phenotypic variance (85.63). Similar result found by Sarkar lowest GCV and PCV was shown by days to 50% flowering and days to maturity. Higher estimates of heritability (81.7) coupled with medium genetic advance as percent of mean (21.11) was observed. Genotypic variance (646.28) was lower than phenotypic variance (790.84). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 11.34 and 12.54 per cent respectively. Genotypic variance (2.83) was lower than phenotypic variance (3.64). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 18.74 and 21.25 per cent respectively. Higher estimates of heritability (77.8) coupled with high genetic advance as percent mean (34.05) was observed. Higher

estimates of heritability (86.1) coupled with high genetic advance as percent mean (55.62) was observed. Genotypic variance (30.58) was lower than phenotypic variance (35.53). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 29.10 and 31.37 per cent respectively. The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 34.17 and 35.20 per cent respectively. Genotypic variance (5825.14) was lower than phenotypic variance (6178.75). Higher estimates of heritability (94.3) coupled with high genetic advance as percent mean (68.36) was observed. Similar result shown highest genetic advance of number of pods per plant were obtained by Sarkar *et al.* (2020). Genotypic variance (0.21) was lower than phenotypic variance (0.23). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 11.00 and 11.53 per cent respectively. Higher estimates of heritability (91.0) coupled with high genetic advance as percent mean (21.62) was observed. The higher estimates of heritability (98.9) coupled with high genetic advance as percent mean (42.90) was observed. Genotypic variance (4.56) was lower than phenotypic variance (4.61). The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 20.93 and 21.05 per cent respectively. According to earlier research by Reddy and Jayamani (2019) [8] high heritability found in 100 seed weight. The genotypic coefficient of variation (GCV) and phenotypic coefficient variation (PCV) were 39.78 and 41.16 per cent respectively. Genotypic variance (806.17) was lower than phenotypic variance (863.21). Higher estimates of heritability (93.4) coupled with high genetic advance as percent mean (79.19) was observed. Highest GCV and PCV for seed yield were recorded earlier by Bhagat *et al.* (2022) [4] and Patel *et al.* (2021) [6]. According to earlier research by Reddy and Jayamani (2019) [8] high genetic advance found in yield per plant. Phenotypic coefficient of variance were found higher than genotypic coefficient of variance for all characters similar result found by Reddy *et al.* (2020) [9], Rao and Rao (2020) [7].

Table. 4.1: Analysis of variance for yield and its component characters in pigeonpea

Sr. No	Character	Sum of squares		
		Replication (d.f.1)	Genotype (d.f.41)	Error (d.f.41)
1	Days to 50% flowering	13.76	94.24**	6.32
2	Days to maturity	6.29	165.18**	6.07
3	Plant height (cm)	210.90	1437.13**	144.55
4	Number of primary branches	2.89	6.47**	0.80
5	Number of secondary branches per plant	20.01	66.11**	4.95
6	Number of pods per plant	960.19	12003.90**	353.60
7	Number of seeds per pod	0.03	0.44**	0.02
8	100 seed weight (g)	0.09	9.18**	0.04
9	Seed yield per plant.	107.80	1669.38**	57.04

*,**indicates significance at 5 and 1 percent Level

Table.2: Estimates of variability parameters for yield and its component characters of Pigeonpea

Sr. No	Name of the characters	Range	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	h^2 (b. s) (%)	G.A	G.A. as % of mean
1	Days to 50% Flowering.	98 - 138	43.95	50.28	6.32	5.59	5.98	87.40	12.77	10.77
2	Days to Maturity.	146 - 192	79.55	85.63	6.07	5.09	5.28	92.90	17.70	10.11
3	Plant Height (cm).	146.00 - 256.10	646.28	790.84	144.55	11.34	12.54	81.70	47.34	21.11
4	Number of primary branches/ Plant.	5.40 - 11.80	2.83	3.64	0.80	18.74	21.25	77.80	3.05	34.05
5	Number of secondary branches/ Plant.	11.30 - 33.00	30.58	35.53	4.95	29.10	31.37	86.10	10.59	55.62
6	Number of pods/ Plant.	73 - 376	5825.14	6178.75	353.60	34.17	35.20	94.28	152.65	68.36
7	Number of seeds/Pod	3.30 - 4.85	0.21	0.23	0.02	11.00	11.53	90.97	0.90	21.62
8	100 seed weight (g).	7.10 - 15.95	4.56	4.61	0.04	20.93	21.05	98.92	4.37	42.90
9	Seed yield /Plant.	27.15 - 134.00	806.17	863.21	57.04	39.78	41.16	93.39	56.52	79.19

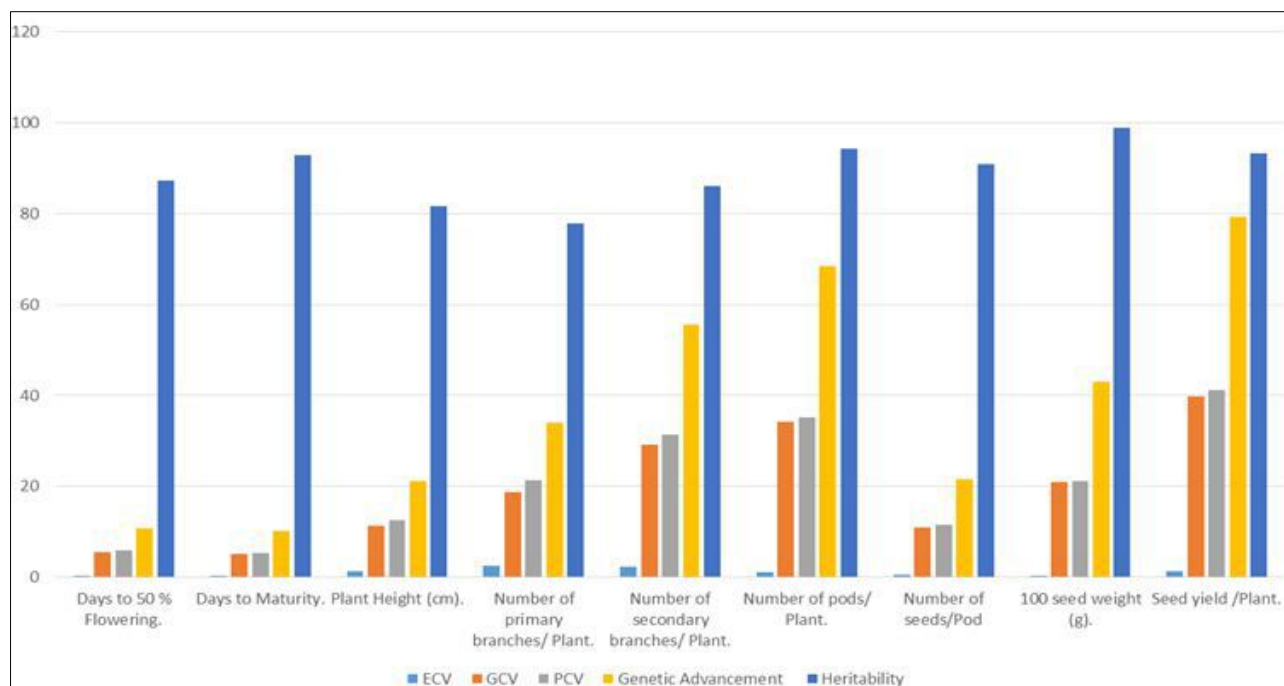


Fig 1: Graphical comparison of GCV, PCV, ECV, Genetic advance and heritability yield and its component characters of Pigeonpea

Conclusion

The character viz. seed yield per plant, number of secondary branches per plant, number of primary branches per plant, number of pods per plant, 100 seed weight and days to 50% flowering showed moderate to high magnitudes of GCV and PCV. Suggested that choosing desirable genotypes for these character could be beneficial for enhancing seed yield in next breeding programme.

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