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Variability studies in M₃ generation of pigeon pea (*Cajanus cajan* L. Millsp.)

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Abstract

The present investigation, entitled "Variability studies in M₃ generation of Pigeon pea (*Cajanus cajan* L. Millsp.)", was conducted at Research and Education farm, Department of Agriculture Botany, College of Agriculture, Dapoli during *Kharif* 2021. As a result of the current investigation, it is clear that a wide range of variability exists for various traits, along with high heritability and high genetic advance as percentage of the mean for significant yield traits. Five of the ten quantitative character the number of primary branches per plant, plant height, pod length, number of pods per plant and 100 seed weight were highly significant and positively correlated with seed yield per plant at simple level Based on the findings, the mutants viz., T3(6)16, T2(29)1, T1(47)3 and T1(51)11 can be used for further varietal improvement.

Keywords: Pigeon pea, mutant, variability, heritability, genetic advance

Introduction

Pigeon pea (*Cajanus cajan* (L.) Millsp) (2n=2x=22) popularly known as 'tur, arhar or red gram' is important pulse crop of the tropics and subtropics (Sangle, 2016)^[10]. India is reported as primary center of origin of pigeon pea. Pigeon pea is member of Fabaceae family.

Pigeon pea plants are erect, tall having deep taproot with lateral branches is produced, young stem is angular and pubescent, leaves are spirally arranged. The leaves are trifoliate and spirally arranged. Pigeon pea is self-compatible and are most frequently pollinated by insects. Pigeon pea flowers are bisexual, zygomorphic and predominantly yellow (Sundaraj and Thulasidas, 1980)^[12]. Pigeon pea possesses cleistogamous flowers which favour self pollination. The flowers are visited by insects and depending on the frequency of their visits, 5 to 40 percent of crossing can occur.

Most farmers from Konkan region growing this crop on rice bunds. Farmers are hesitant to grow this crop because of a lack of irrigation facilities during the *Rabi* season. As a result, there is a demand for pigeon pea genotypes that mature at 150 days. There is a scarcity of early duration varieties suitable for Konkan conditions during *Kharif* season in the available germplasm. Mutation breeding is effective means in the hands of plant breeder for evolving a new better forms increasing genetic variability. Mutation induce desired characters in short time which cumbersome by hybridization. Early maturing, tolerance to pod borer and high yielding cultivars are needed by farmers to grow in the areas where season length is of limited duration.

Material and Methods

The experiment was evaluated at Educational and Research farm Department of Agricultural Botany, College of Agriculture, Dapoli, Dr. Balasaheb Sawant Konkan Krishi Vidyapeeth, Dapoli, Dist. Ratnagiri during *Kharif* 2021. The experiment conducted in Augmented design. The experimental material consisted of 156 mutants lines selected from M₂ generation of Pigeon pea (*Cajanus cajan* L.) which were developed by irradiation of variety Konkan Tur-1. Thus, M₃ generation of 156 mutants lines are raised along with check Konkan Tur-1 and BDN 2013-41. Five plants were randomly selected from each line to record the data. The observations were taken on characters like days to flower initiation, plant height (cm), number of branches per plant, pod length (cm), number of pods per plant, number of seeds per pod, days to maturity, 100 Seed weight(g), percent pod borer damage (%), and seed yield per plant (g). The data was statistically analysed as method suggested by Federer (1956)^[12].

Results and Discussion

The experimental results of present investigation entitled are

presented under the following table:

Table 1: Different variability parameters for different quantitative characters in M₃ generation of pigeon Pea

Sr. No.	Characters	Range		Mean	GCV %	PCV %	h ² (bs) %	GA	GA %
		Min	Max						
1.	Days to initiation of flowering	108.2	138.8	131.87	4.02	4.02	99.83	10.93	8.29
2.	Days to maturity	158.6	188.6	181.89	2.87	2.88	99.14	10.71	5.89
3.	Plant height (cm)	81.1	191.7	142.3	13.52	13.52	99.91	39.66	27.87
4.	No. of primary branches	3.2	7.9	4.76	16.92	16.98	99.3	1.66	34.78
5.	Pod length(cm)	3.9	6.4	5.19	7.84	8.76	80.04	0.75	14.46
6.	No. of pods/ plant	46.0	217.9	93.45	35.63	35.64	99.97	68.68	73.49
7.	No. of seeds/pod	2.6	3.6	3.33	6.9	7.11	94.05	0.46	13.8
8.	100 seed weight(g)	6.9	10.7	8.13	8.59	8.63	99.07	1.43	17.65
9.	Seed yield/ plant	14.6	59.1	29.67	33.37	33.37	99.97	20.42	68.83
10.	Pod borer damage %	20.5	57.6	35.39	22.28	22.32	99.7	16.24	45.9

GCV = Genetic coefficient of variation,

PCV = Phenotypic coefficient of variation,

h²(bs) = Heritability (broad sense),

GA = Genetic advance, GA % = Genetic advance as % mean.

1. Days to initiation of flowering

Among M₃ generation T3 (6)16 (108.2) showed earliest flowering and T6(14)1 (138.8) showed late flowering. The general mean for this character was 131.8 days. Estimated GCV and PCV values for days to initiation of flowering were similar i.e 4.02%. Hence, it is placed in low magnitude. Similar results were obtained by Rao and Rao (2020) [7], Thanga *et al.* (2019) [13] and Rekha *et al.* (2013) [8]. The value of genetic advance as percent mean was low (8.29%) coupled with high heritability (99.83%) which indicated the predominance of non-additive gene effects in the expression of the character. Rekha *et al.* (2013) [8] reported high heritability with high genetic advance for days to initiation of flowering.

2. Days to maturity

The mutant T3 (6)16 (158.6) showed early maturity. On the other hand mutant T2 (29) 12 (188.6) showed late maturity. The general mean for this character was 181.9 days. The estimates of GCV (2.87%) and PCV (2.88%) were low in magnitude for days to maturity. Similar result was obtained by Rao and Rao (2020) [7] for days to maturity. The genetic advance as percent of mean was low (5.89%), which was accompanied with high heritability (99.14%) which indicated the predominance of non-additive gene effects in the expression of the character. These results were in agreement with the findings of Rekha *et al.* (2013) [8], Thanga *et al.* (2019) [13] and Vanirajan *et al.* (2021) [14].

3. Plant height (cm)

The minimum plant height was observed with mutant T2 (29) 1 (81.1 cm), while the maximum plant height was recorded by mutant T9 (30) 5 (191.7 cm). The mean for this trait was (142.3). The estimates of GCV (13.52%) and PCV (13.52%) were moderate indicating moderate variability for plant height in the population. Similar results were obtained by Thanga *et al.* (2019) [13] and Rekha *et al.* (2013) [8] for plant height. The genetic advance (% of mean) was high (27.87%), accompanied with high heritability (99.91%) indicating the additive gene effects was responsible for the expression of this trait. Similar result were observed by Thanga *et al.* (2019) [13] and Rekha *et al.* (2013) [8] for plant height.

4. Number of primary branches per plant

The mean values of number of primary branches per plant ranged from 3.2 (T7 (4) 2) to 7.9 (T1 (8) 1) with an overall mean of (4.76). The values of GCV (16.92%) and PCV (16.98%) were moderate indicating medium variability for number of primary branches per plant in the population. Similar results were obtained by Thanga *et al.* (2019) [13] for this trait. The genetic advance as percent of mean was high (34.78%) coupled with high heritability (99.3%). Similar results were recorded by Rekha *et al.* (2013) [8], Thanga *et al.* (2019) [13] and Vanirajan *et al.* (2021) [14] for number of primary branches per plant.

5. Pod length (cm)

The mutant T9 (30) 5 registered the maximum pod length (6.4 cm) and the mutant T1 (16) 6 had the minimum pod length (3.9 cm). The mean for this trait was (5.19). The estimates of GCV (7.84%) and PCV (8.76%) were low indicating low variability for pod length in the population. Similar results was obtained by Sharma *et al.* (2020) [11] for pod length. The genetic advance as percent of mean was moderate (14.46%) which was accompanied with high heritability (80.04%), While Gupta *et al.* (1975) [4] reported high heritability with high genetic advance for pod length.

6. Number of pods per plant

The mutant T3 (19) 8 (217.9) had the highest number of pods per plant. The mutant T7(4) 2 (46.0) recorded the least number of pods per plant with an overall mean of (93.45). The values of GCV (35.63%) and PCV (35.64%) were high suggesting potential of variability available for this trait and narrow difference between then indicated that the environment had little effect on the expression of this trait. Similar result were obtained by Rao and Rao (2020) [7], Thanga *et al.* (2019) [13] and Rekha *et al.* (2013) [8] for number of pods per plant. The genetic advance as percent of mean was high (73.49%), accompanied with high heritability (99.97%) suggesting that predominance of additive gene action for this trait. The broad sense heritability (99.97%) was high indicating additive gene action responsible for inheritance of character. The results are in accordance with the findings Rao and Rao (2020) [7], Thanga *et al.* (2019) [13] and Sharma *et al.* (2020) [11] for number of pod per plant.

7. Number of seeds per pod

The mutant T1 (67) 11 (3.6) was recorded maximum number of seed per pod. On the other hand, T5 (5) 5 (2.65) was showed the least number of seed per pod. The mean for this trait found was 3.33. The estimates of GCV (6.9%) and PCV (7.11%) were low, indicating low variability for number of seeds per pod in the population. This were also reported by Thanga *et al.* (2019) [13] and Sharma *et al.* (2020) [11] for number of seeds per pod. The value of genetic advance as % of mean was moderate (13.8%) coupled with high heritability (94.05%), whereas high heritability coupled with moderate genetic advance as percent of mean for this trait was reported by Thanga *et al.* (2019) [13].

8. 100 seed weight (g)

The highest value of 100 seed weight was recorded by mutant T1 (82) 6 (10.66 g). The mutant T1 (53) 1 (6.96 g) had a lowest value for 100 seed weight with overall mean (8.13 g). The values of GCV (8.59%) and PCV (8.63%) were low magnitude for this trait in the population. Similar result was obtained by Gaur *et al.* (2020) [3] for 100 seed weight. The genetic advance as percent of mean was moderate (17.65%) coupled with high heritability (99.07%). Similar findings was reported by Gaur *et al.* (2020) [3] for 100 seed weight.

9. Seed yield per plant (g)

The mutant T1 (47) 3 (60.35 g) had the highest seed yield per

plant, whereas mutant T1 (16) 6 (14.65 g) recorded the least seed yield per plant. The high estimates of GCV (33.37%) and PCV (33.37%) revealed sufficient variability in the population under investigation. Similar results were obtained by Thanga *et al.* (2019) [13] and Rekha *et al.* (2013) [8] for seed yield per plant. The genetic advance as percent of mean was high (68.83%) coupled with high heritability (99.97%). Rao and Rao (2020) [7], Thanga *et al.* (2019) [13], Rekha *et al.* (2013) [8] and Sharma *et al.* (2020) [11] reported high heritability with high genetic advance as percent of mean for seed yield per plant.

10. Percent pod borer damage (%)

The mutant T1 (53) 1 (57.6%) showed maximum percent pod borer damage, while mutant T2 (1) 13 (20.55%) showed minimum percent pod borer damage with overall mean (35.39).The values of GCV (22.28%) and PCV (22.32%) were high in magnitude indicated the presence of wide genetic variability with little effect of environment on the expression of this trait. Similar results was obtained by Palshetkar (2021) [6] for percent pod borer damage. The value of genetic advance as percent of mean was high (45.9%), coupled with high heritability (99.7%). Similar results was obtained by Palshetkar (2021) [6] for percent pod borer damage.

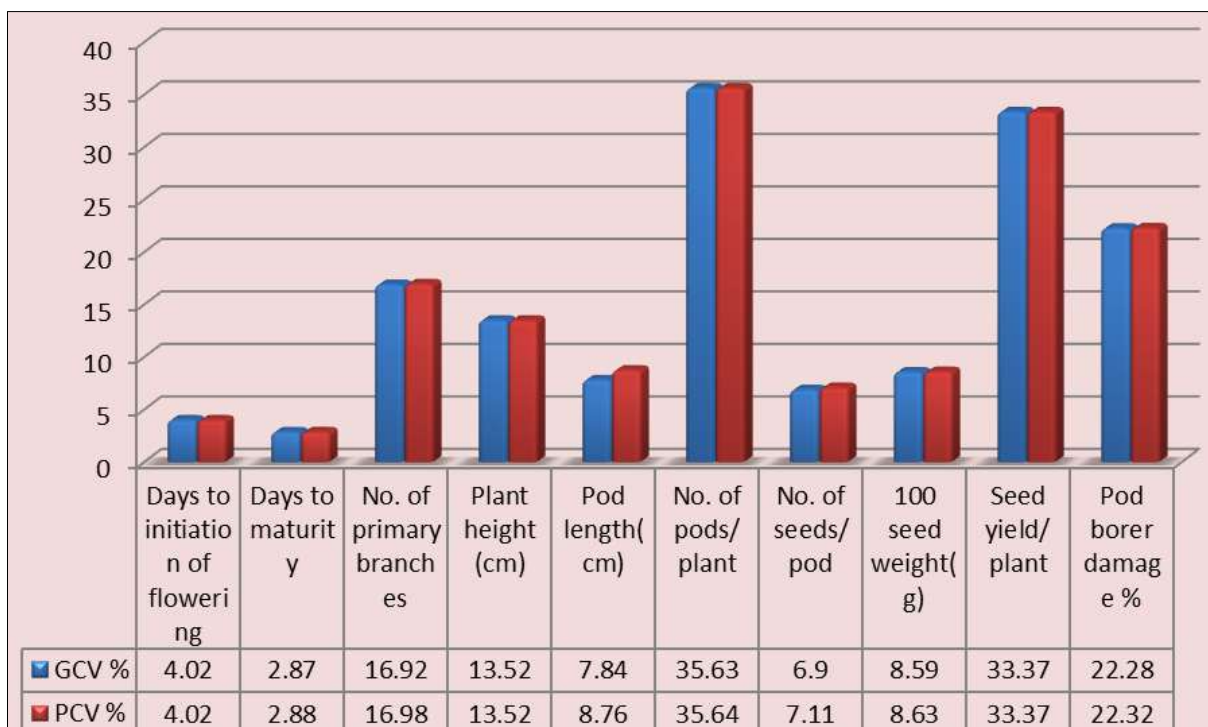


Fig 1: Graphical comparison of GCV, PCV as percent of mean for 10 characters in pigeon pea.

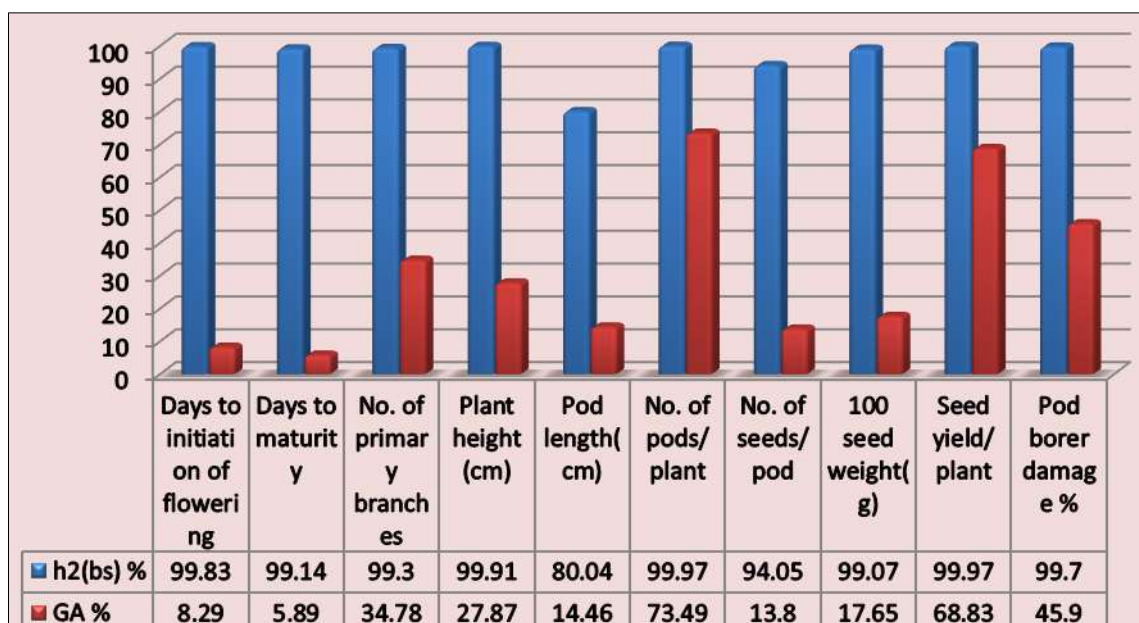


Fig 2: Graphical comparison of heritability (b.s.) and expected genetic advance as percent of mean for 10 characters in pigeon pea

Conclusion

To achieve success in any strategic crop improvement programme depends on extent of variability present and effective skills applied under selection. Therefore, present research was performed for evaluation of the performance of promising mutants by estimating their mean and coefficient of variation, genetic variability, heritability, genetic advance, genetic advance as percent of mean. From the present investigation it is concluded that in a breeding programme aiming to improve seed yield in pigeon pea, more weightage should be given to number of pod per plant, number of branches per plant, number of seed per pod and percent pod borer damage.

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