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HERITABILITY AND GENETIC ADVANCE IN PIGEONPEA (CAJANUS *CAJAN* L.) MILLSP.

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Abstract

Heritability, in narrow sense, and genetic advance in percentage of mean were worked out separately in F_1 *and* F_2 *generations. None of the characters showed high heritability estimates. The moderate value of heritability estimate was observed for number of seeds per pod in* F_2 *generation. However, for rest of the characters, in both the generations, low estimates of heritability were recorded. Regarding genetic advance, none of the characters displayed high value of genetic advance in per cent of mean. However, low magnitude of genetic advance in per cent of mean was observed for all the characters.*

Keywords: *Heritability, Genetic advance, pigeon pea, (Cajanus cajan (L.) Millsp.)*

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Introduction

Pulses occupy an indispensable place in our daily diet as a source of protein. Pulse crops also have an unique potentiality to associate symbiotically with Rhizobium spp. and fix atmospheric nitrogen. This has helped in maintaining the fertility level of soils .Pulse crops had received little attention at the hands of agricultural scientists in the past. This was probably because as late as in the Third Five Year Plan, the per-capita availability of pulses was 60 g/day which could be considered as adequate. Subsequently, with a sharp increase in the population and continued stagnation in the pulse production, the pre-capita availability of pulses has come down to less than 40 g/day at present. India is the major pulse-growing country of the world accounting roughly for one-third of the total world acreage and one-fourth of the total world production. The annual production of pulses has fluctuated in the range of between 11 and 13 million tones. india, pigeonpea or arhar or red gram Cajanus cajan (L.) Mill sp. 2n=22) is an important pulse crop next to chickpea. The major countries growing pigeonpea are India, Uganda, Kenya, West Indies, Puerto Rico, Dominican Republic in the Carebbean region and Burma. In India, Its area and production have shown upward trend over the years. The crop is extensively grown in Uttar Pradesh, Madhya Pradesh, Maharashtra, Karnataka, Andhra Pradesh and Gujarat. These six states account for about 85 per cent of the total Indian acreage and production. Pigeonpea is a rich source of protein and supplies a major share of the protein requirement of the vegetarian population. It is mainly consumed as split dal and is considered as 'meat' for Hindu priest as well as for poor people. The husk of pods along with the dried green leaves are very nutritive cattle feed. The dried stalk of pigeonpea is very good fuel and is more precious now a days when the fuel wood is scarcely available. It is also used for thatching the temporary mud house by poor persons besides various other purposes like broom, baskets, temporary partition wall etc. being a legume, it fixes atmospheric nitrogen in to the soil. Its deep root system is reported to break the plough pans, thus improving the soil structure. No wonder the pigeonpea is often called a "biological plough". Heritability is an important estimate and is used as an index of transmissibility of characters from parents to offsprings. It has indicates the relative importance of heredity and environment on the expression of characters. Heritability estimates were grouped according to Robinson (1966) as low (less than 10%), moderate (above 10 % and less than 30 %) and high (30 % and above).

Material and Methods

The experiment comprised of 19 parents (16 lines and 3 testers), their 48 F1s and 48 F28 which were grown in randomized complete block design with three replication. The observations were recorded for thirteen quantitative traits namely, days to initial flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of seeds per pod, pod length, days to maturity, 100-seed weight, seed density, grain yield per plant and protein content. The data gathered were subjected to 'line x tester analysis (Kempthorne, 1957) and various other biometrical analysis. Present investigation involved 16 lines as females and 3 testers as male parents of pigeonpea (Cajanus cajan (L.) Millsp.) selected on the basis of genetic Variability in respect of yield and its contributing characters. All the 16 lines were crossed with 3 testers to obtain sufficient F0 seed of all the 48 crosses. The final experiment was laid out with 115 treatments consisting 19 parents (16 lines and 3testers), 48 F1s and 48 F2s in a Randomized Complete Block Design with 3 replications. The non-segregating population (Parents and F1 s) were sown in single row and segregation population (F2 s) in two rows each of 5 m length. The inter and intra-row spacing were 60 cm and 20 cm, respectively. All the recommended agronomic practices were adopted for growing a good crop. Individual plant data in respect of the following characters were recorded on five randomly taken plants in each parents and F1s, and ten plants in each F2's in each replication.

Results and Discussion

Heritability estimate is a useful tool and has been widely used in estimating the expected genetic gain. It indicates the relative importance of heredity and environment in the expression of character. The population expressing large variability for the character(s) can give the desirable genotypes more frequently but in case of large environmental influences on the character, a large population will have to be raised for making effective selections. Besides this, it also helps in deciding the intensity of selection to be placed on the character under improvement. Hanson (1963) critically reviewed the heritability estimates in biometrical studies and pointed out that the heritability estimates are influenced by method of estimation, generation of study, sample size and the environments.

In the present case, the estimates of heritability in narrow sense and genetic advance in percentage of mean (Table 1.) were calculated for 13 characters. It is clear that heritability estimates were comparatively low for almost all the characters under study. This Indicates that these characters are governed by non-additive gene effects and significant advance may not be possible through selection.

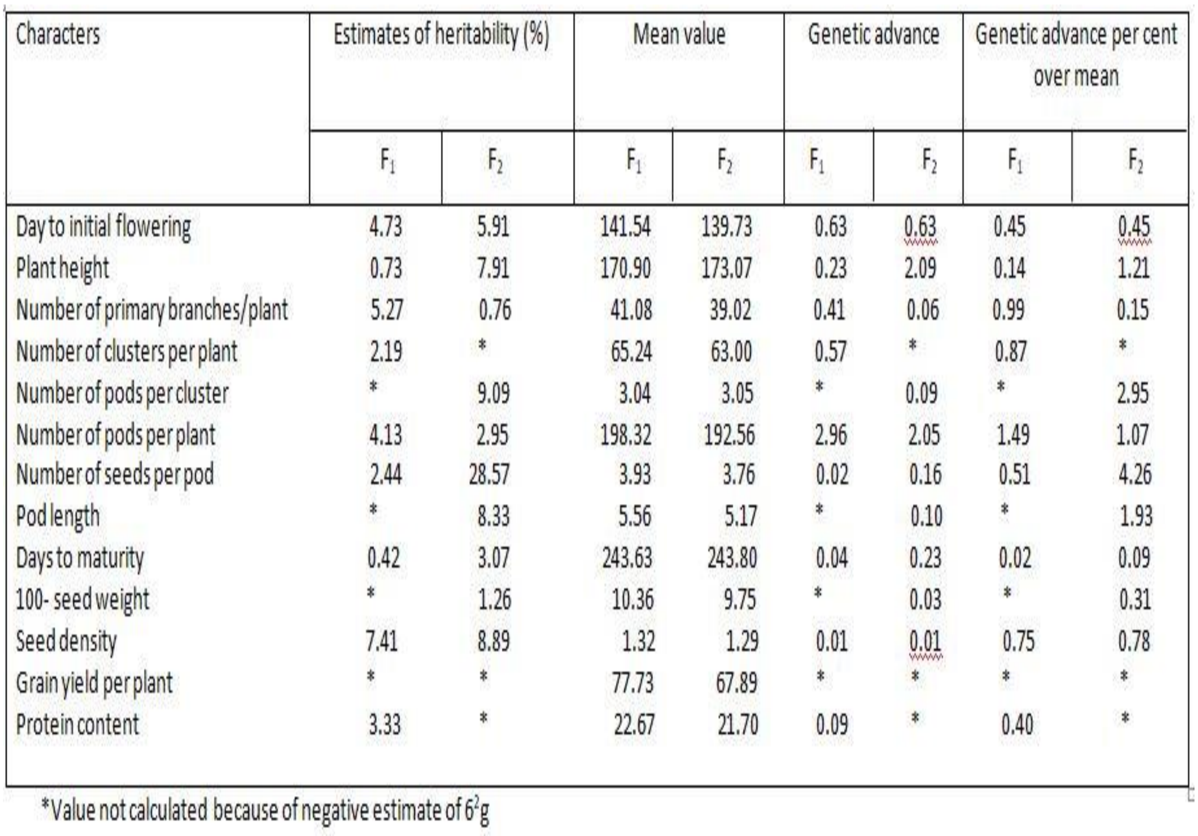
Only the character number of seeds per pod showed moderate heritability estimates in F2 generation with low value of genetic advance indicating that this trait is influenced by the environment, and thus required small selection intensity for improving this character. Regarding other characters, there is no need of selection for improving these traits.

Sagar and Jatasra (1984) reported high value of heritability and genetic advance for number of pods per plant and grain yield per plant. Khapre and Nerkar (1992) observed high heritability for grain yield per plant, Konwar and Hazarika (1988) reported heritability estimates being high for days to maturity, days to flowering and plant height.

Githiri et al. (1991) reported high heritability estimates for days to 50 per cent flowering. These findings, however, do not tally with the results obtained in the present investigation which may be due to environmental effects. But the low estimates of heritability for number of seeds per pod and seed size, as reported by Sandhu (1994), have been confirmed by the results obtained during the course of present study.

The indirect selection is more appropriate and effective tool than the direct selection when the particular character under selection has low heritability or is not easily or precisely measured. Under such circumstances, some criteria of early assessment have to be used to rationalize the selection breeding programme.

Table1. Estimates of heritability (h2) in per cent and genetic advance (per cent over mean) for 13 characters in a 16x3-parent-line X tester crosses of pigeonpea



Characters	Estimates of heritability (%)		Mean value		Genetic advance		Genetic advance per cent over mean	
	F_1	F_2	F_1	F_2	F_1	F_2	F_1	F_2
Day to initial flowering	4.73	5.91	141.54	139.73	0.63	0.63	0.45	0.45
Plant height	0.73	7.91	170.90	173.07	0.23	2.09	0.14	1.21
Number of primary branches/plant	5.27	0.76	41.08	39.02	0.41	0.06	0.99	0.15
Number of clusters per plant	2.19	*	65.24	63.00	0.57	*	0.87	*
Number of pods per cluster	*	9.09	3.04	3.05	*	0.09	*	2.95
Number of pods per plant	4.13	2.95	198.32	192.56	2.96	2.05	1.49	1.07
Number of seeds per pod	2.44	28.57	3.93	3.76	0.02	0.16	0.51	4.26
Pod length	*	8.33	5.56	5.17	*	0.10	*	1.93
Days to maturity	0.42	3.07	243.63	243.80	0.04	0.23	0.02	0.09
100- seed weight	*	1.26	10.36	9.75	*	0.03	*	0.31
Seed density	7.41	8.89	1.32	1.29	0.01	0.01	0.75	0.78
Grain yield per plant	*	*	77.73	67.89	*	*	*	*
Protein content	3.33	*	22.67	21.70	0.09	*	0.40	*

*Value not calculated because of negative estimate of 6^2g

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