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S Rajamani
Regional Agricultural Research
Station, Acharya N G Ranga
Agricultural University,
Lam, Guntur, Andhra Pradesh,
India

M Sreekanth
Regional Agricultural Research
Station, Acharya N G Ranga
Agricultural University,
Lam, Guntur, Andhra Pradesh,
India

MV Ramana
Regional Agricultural Research
Station, Acharya N G Ranga
Agricultural University,
Lam, Guntur, Andhra Pradesh,
India

Corresponding Author
S Rajamani
Regional Agricultural Research
Station, Acharya N G Ranga
Agricultural University,
Lam, Guntur, Andhra Pradesh,
India

Genetic analysis in pigeonpea

S Rajamani, M Sreekanth and MV Ramana

Abstract

An experiment was carried out in the experimental field located at Regional Agricultural Research station, Lam, Acharya N G Ranga Agricultural University, Lam, A.P. Study was conducted on Genetic variability, character association and path analysis between yield and its contributing traits with seventeen Pigeonpea [*Cajanus cajan* (L.) Mill sp.] genotypes. Analysis of variance revealed that existence of significant differences among genotypes for all characters studied. The magnitude of PCV and GCV was moderate to high for number of pods per plant, number of primary branches per plant and yield. High heritability was recorded for test weight, days to maturity, days to 50% flowering, and number of pods per plant. High heritability combined with high genetic advance was recorded for test weight, yield and days to 50% flowering, indicating that these characters are controlled by additive gene effect and phenotypic selection of these characters would be effective for further breeding purpose. Yield was positively correlated with Plant height, number of primary branches per plant and number of pods per plant.

Keywords: Pigeon pea, genotypic variance, phenotypic variance, correlation studies

1. Introduction

Pigeon pea [*Cajanus cajan* (L.) Millsp.] is the second important pulse crop after chickpea in India. India is the largest producer and consumer of pigeon pea. Pigeonpea is an often cross pollinated (20-70%) crop with $2n = 2x = 22$ diploid chromosome number. Pigeonpea is a hardy, widely adapted, and drought tolerant crop. It has a wide range of maturity which helps in its adaption in a wide range of environments and cropping systems. But the average productivity is remains low due to most of the area in is cultivated under rainfed area of poor fertile soils. The major pigeon pea producing countries in the world are India, Eastern Africa, Central and South America, The Caribbean and West Indies. Unlike other grain legumes, Pigeonpea production is concentrated in developing countries particularly in South and South East Asia and eastern and southern African countries. Pigeonpea plants have high nutritional, medicinal and economic values. It is contributes to improving the soil fertility (Olawuyi and Fawole, 2005) [10]. Pigeonpea play a significant role to fullfill the need of Indian diet nutritional requirement due to its high nutritional value with high protein content that ranges from 21% to 25%. Besides its rich nutritional value, it also helps in sustaining the soil productivity through symbiotic fixation of atmospheric nitrogen into the soil as well as the leaf fall helps in recycling of nutrients in the soil. The green revolution has been confined by and large to the cereals while the production of pulses has remained stagnant. Pigeonpea plays an important role by virtue of its multipurpose use in food, feed, fuel and farming.

The crop suffers from yield losses due to various biotic stresses like wilt, Sterility Mosaic disease, helioverpa pod borer etc. Therefore, it is necessary to increase the production of pigeonpea by developing pest resistant varieties. To develop high yielding varieties, knowledge on the existing genetic variability in the crop needs to be studied. Yield is a complex trait that is highly influenced by environment. Genetic parameters like genotypic and phenotypic coefficient of variation, heritability and genetic advance are highly reliable making effective selection in the breeding material. The information on correlation of yield with yield attributes will assist the breeders in the identification of traits contributing to yield to make significant genetic gain. The present investigation was carried out to analyze the genetic divergence existing in the crop, phenotypic and genotypic variability, heritability in broad sense and genetic advance. This information is highly useful for breeders in the selection of parents and breeding material for the development of high yielding varieties of pigeon pea suited to rain fed conditions. Lack of genetic variability is one of the major constraints is any crop improvement programme. Correlation studies helps in determination of the interrelationship between various traits and give a better understanding of the contribution of

each trait in the genetic makeup of the crop (Kimani, 2000). The present study was carried out to estimate the genetic variability, heritability, genetic advance and correlation between yield and related characters in pigeon pea

2. Materials and Methods

The present studies was carried out with 17 genotypes viz., LRG 609, LRG 616, LRG 623, LRG 618, LRG 621, LRG 105, LRG 52, LRG 602, LRG 613, LRG 617, LRG 608, LRG 601, LRG 620, LRG 606, LRG 611 and LRG 614. These genotypes were developed at Regional Agricultural Research Station, Lam, Guntur, Andhra Pradesh in 2020-21. The accessions were grown on the field using randomized block design with two replications. Each plot consisted of two rows spaced at 1.50 m between and 0.3m within rows. Two seeds from each accession were planted at 5 cm depth from the soil, and thinned to one three to four weeks after planting. All recommended agronomic practices were duly carried out to raise successful crop. Observation were recorder on five randomly selected plants in each replication for seven characters viz., plant height (cm), days to 50 per cent flowering, number of primary branches per plant, number of secondary branches per plant, number of pods per plant, test weight (g) and seed yield per hectare (Kg). The data were subjected to analysis of variance with Statistical Analysis System package (SAS, 1999) [10]. The formula given by Robinsion and Comstock (1956) [7] was used for estimating the heritability in broad sense. Genetic advance under selection was calculated by the formula given Robinson *et al.*, (1949) [8]. Correlation was calculated as per method suggested by Searle (1961).

3. Result and Discussion

The analysis of variance revealed that all the treatments were

significantly different from each other (Table-1). The estimation of parameters of statistical and genetical variability viz., Range, grand mean, phenotypic and genotypic coefficient of variation, heritability and genetic advance as per cent mean in respect of all the seven attributes under study are presented in (Table-2). A wide range of variation was found for almost all the traits. High estimates of coefficient of variation was noticed in character number of primary branches per plant, yield and number of pods per plant. In general phenotypic coefficient of variation was found higher than the genotypic coefficient of variation. But differences were more for the traits viz. plant height, days to 50% flower, days to maturity, number of primary branches and number of secondary branches per plant and yield/ha. There by indicating the influence of environment. Higher phenotypic variance than genotypic variance in traits due to the interaction of environmental components as similarly observed by (Oseni and Khadir., 1994 and Nguru., 1995) [3]. High estimation of heritability was recorded for test weight, yield, days to 50% flowering, number of primary branches per plant and pods per plant. High estimation of genetic advance as per cent mean was recorded for yield, number of pods per plant and plant height. Therefore selection would be beneficial for those characters having high heritability coupled with high genetic advance. The nature and magnitude of all possible correlation coefficients, both at genotypic, phenotypic levels, among the seven attributes were worked out and are presented in table 3. From the correlation studies it is evident that seed yield was positively correlated with number of pods per plant and number of primary branches per plant. Therefore, these traits would be suitable selection criteria for improvement of yield in pigeonpea.

Table 1: Analysis of variance for different characters in pigeonpea Mean Sum of Squares (MSS)

Sources of variation	DF	Days to 50% flowering	Plant height (cm)	No of primary branches/plant	No of secondary branches/plant	Pods /plant	Test weight (g)	Yield (Kg/ha)
Replications	1	6.618	44.735	0.169	0.058	125503.059	0.011	15544.971
Treatments	16	10.750*	188.217*	0.665*	5.758*	10501.504*	4.199*	244798.452*
Error	16	0.493	48.923	0.104	1.305	1895.371	0.037	6811.908

Table 2: Mean range, grand mean, coefficient of variation, standard error, critical difference heritability and genetic advance as per cent of mean for seven characters in pigeonpea.

S. No	Character	Range	Grand Mean	PCV	GCV	SE	CD	h ²	GA as Per cent mean
1	Days to 50% flower	121-126	124.7	1.904	1.819	0.702	1.8954	91.236	3.579
2	Plant height (cm)	207-238	218.0	4.996	3.829	6.994	18.8838	58.739	6.045
3	No. of primary branches/plant	1.7-3.6	2.58	23.959	20.450	0.323	0.8721	72.849	35.956
4	No. of secondary branches/plant	13.4-20.3	17.65	10.645	9.452	1.142	3.0834	63.042	13.825
5	Pods/plant	422-627	511.35	15.398	12.830	43.536	117.5472	69.422	22.021
6	Test weight (g)	10.0-15.7	12.53	11.638	11.535	0.194	0.5238	98.232	23.551
7	Yield (Kg/ha)	1290-2350	1497.61	20.598	19.983	82.534	222.8418	94.118	39.936

Table 3: Correlation between seven character combinations in Pigeon pea

	DF	Plant height (cm)	No of pri.br/plant	No of sec.br/plant	Pods/plant	Test wt (g)	Yield (Kg/ha)
Days to 50% flower G (DF) P		-0.346*	-0.554**	-0.056 NS	0.296 NS	0.186 NS	-0.0167 NS
		-0.190 NS	-0.441**	-0.025 NS	0.241 NS	0.172 NS	-0.173 NS
Plant height GP			0.835**	0.596**	0.255 NS	0.230 NS	0.135 NS
			0.561**	0.398*	0.145 NS	0.182 NS	0.052 NS
No of Pri. Branches GP				0.709**	0.269 NS	0.273 NS	0.233 NS
				0.375*	0.223 NS	0.243 NS	0.209 NS
No of Sec. Branches GP					0.036 NS	0.037 NS	-0.259 NS
					0.027 NS	0.041 NS	-0.176 NS
Pods/plant GP						0.093 NS	0.81 NS
						0.096 NS	0.056 NS

Test weight GP								-0.114 NS -0.104 NS
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