



ISSN (E): 2277-7695  
ISSN (P): 2349-8242  
NAAS Rating: 5.23  
TPI 2022; 11(12): 4618-4621  
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[www.thepharmajournal.com](http://www.thepharmajournal.com)  
Received: 07-10-2022  
Accepted: 10-11-2022

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## Studies on correlation and path analysis for yield and yield attributing traits in extra early genotypes of Pigeonpea [*Cajanus Cajan* (L.) Millsp.]

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### Abstract

Pigeonpea also known as red gram or archer is second important pulse crop of India. It is perennial in nature and has indeterminate growth habit but typically cultivated as an annual crop. It is cultivated for seeds for human consumption which contains about 22% of protein. In Haryana Paras, Manak, PAU 881, VLA-1 varieties are grown by farmers which are indeterminate and mature late. By introducing extra-early (110-120days) and dwarf genotypes, pigeonpea can replace rice/cotton crop in *kharif* season and help farmers to fetch better price and add to soil health. At Pulses section of Dept. of Genetics & Plant Breeding, CCS HAU, Hisar; two parents AL-1484 x ICPL 85024 were crossed and pedigree method was used to handle the segregating generations, progenies showing earliness for Days to flowering (50-70 days) and Days to maturity (110-120 days) were selected. The newly developed ten genotypes were evaluated in LST-trial along with check varieties during *kharif* 2019. These ten lines were showing earliness for days to flowering (52-70 days) and days to maturity (110-122 days). Phenotypic correlation coefficients indicated that seed yield showed significantly positive correlation with days to 50% flowering (0.465), plant height (0.482), number of branches (0.536) and pods per plant (0.706). The highest positive direct effect on seed yield per plot was of number of pods per plant (0.54), number of branches (0.27), days to maturity (0.24) and 100-seed weight (0.30). The selection for these traits will be helpful for the development of high yielding extra early genotypes. The genotypes AH 16-36, AH 16-41, AH 16-42, AH 16-43, AH 16-44, AH 16-45, AH 16-47, AH 16-48, AH 16-49 and AH 16-50 can be used in crossing programme for the development of extra early and dwarf varieties that may fit well in new cropping systems (pigeonpea-wheat). It will enhance the diversified farming; in addition, it will solve the labour problem in pigeon pea by reducing the cost of production through mechanical operations.

**Keywords:** Extra-early, correlation, path analysis, pigeon pea

### Introduction

Pigeonpea [*Cajanus Cajan* (L.) Millsp.] ( $2n=2x=22$ ) also known as *Arhar*, Redgram and *Tur* is an important pulse crop grown in tropical and subtropical countries. It belongs to the family Fabaceae. Pigeonpea is the second most important *kharif* grain legume after chickpea in India and grown predominantly under rainfed conditions. The seeds are nutritionally rich containing 20-22% protein (Sarkar *et al.*, 2020) <sup>[16]</sup>, crude fibre between 1.2-8.1% and lipid between 0.6-3.8%. The calcium, copper and iron content of pigeonpea, are 1.39, 1.32 and 5.37mg/100g respectively. Some of the anti-nutritional factors present are cyanogenic glycosides, trypsin inhibitors *etc.* (Talari and Shakappa, 2018) <sup>[22]</sup>. In India, it occupies an area of 3.81 million hectares with production and productivity of 3.83 million tons and 1005kg/ha, respectively (Anonymous, 2020) <sup>[3]</sup>. Being a legume crop it improves soil health through soil nitrogen fixation due to the presence of rhizobium in its root nodules. It is mainly consumed as decorticated split peas known as 'dal'. The plant finds other uses as feed and fodder.

Pigeonpea is an important *kharif* crop mainly sown in June-July and harvested as per the maturity duration. On the basis of maturity duration this crop can be grouped into five *viz.* extra early which matures in less than 130 days, early group which matures in 130-150 days, mid-early group which matures in 151-165 days, medium group maturing in 166-180 days and long duration group taking > 200 to 270 days to mature. Extra early group has its scope only in NWPZ while early group of pigeonpea can be grown all over the country but mid early and medium maturity groups can be grown well in Central Zone and Southern Zone only. The objective of present investigation is to develop extra-early and early genotypes with short plant height and good yield potential for NWPZ of the country which fits well in pigeonpea-wheat cropping system and also allow mechanical harvesting.

The experimental material used in present investigation consisted of ten advanced extra early genotypes of pigeonpea. At Pulses section, Dept. of Genetics & Plant Breeding, CCS HAU, Hisar; two parents AL-1484 x ICPL 85024 were crossed and pedigree method was used to handle the segregating generations, few spontaneous mutants were observed in the population and progenies showing earliness for Days to flowering (50-70 days) and Days to maturity (110-120 days) were selected. The newly developed ten advanced genotypes were evaluated in LST-trial along with check varieties Manak and Pusa 992 during *kharif* 2019. These genotypes were sown in a randomized block design (RBD) with three replications in the field area of Pulses section of Dept. of Genetics and Plant Breeding CCS HAU, Hisar. Each genotype was sown in a plot consisting of 6 rows with 4m row length and 30 cm row to row spacing. Five randomly competitive plants were selected for taking the observations in each genotype from each replication. The data was recorded for seven different traits *viz.*, days to 50% flowering, Days to maturity, number of branches/plant, plant height(cm), number of pods/plant, 100- seed weight and seed yield/plot (kg/ha).

The Phenotypic and genotypic coefficient of variations were calculated as per formula given by Burton (1952) [5]. Heritability and genetic advance was measured for all the traits by the method described by Allard (1960) [2]. Phenotypic and genotypic correlation coefficient for yield and yield attributing characters were also calculated as suggested by Searle (1961) [17]. Path coefficient analysis to study direct and indirect effects of various characters on seed yield were estimated as suggested by Wright (1921) [24] and Dewey and Lu (1959) [8]. Statistical analysis was performed using OPSTAT software available online at: <http://www.hau.ac.in>. Genetic variability studies provide information regarding genetic makeup of the population, based on such studies breeding methods are formulated for crop improvement and superior genotypes having expression of desired traits were selected. The average performance of ten extra early pigeonpea genotypes is presented in Table 1. Days to fifty per cent flowering ranged from 52 days in genotype AH 16-36 to 76 days in Manak variety of pigeonpea and days to maturity ranged from 102 days in AH 16-42 to 138 days in Pusa 992. Thus genotypes AH 16-36, AH 16-41, AH 16-42, AH 16-43, AH 16-44, AH 16-45, AH 16-47, AH 16-48, AH 16-49 and AH 16-50 are extra-early genotypes. Plant height ranges 135 cm to 248 cm, genotypes AH 16-36, AH 16-41, AH 16-42, AH 16-43 and AH 16-44 are shorter in height (< 2m) as compared to other genotypes under study. Number of pods/plant ranged from 85 in genotype AH 16-36 to 313 in genotype AH 16-50. Similarly, a wide range of values was observed for 100-seed weight (5.93-9.83) and yield kg/ha (1049.98-1791.3). The estimates of mean values with wider range were observed for all the traits under study. These results suggested adequate variability among pigeonpea genotypes. To estimate the variability existing in the population genotypic and phenotypic coefficient of variation are utilized. PCV could be designated into three classes namely low (< 20%), moderate (20-30%) and high (> 30%) as proposed by Siva Subramanian and Menon (1973) [21]. Highest PCV was observed for number of pods per plant (43.61%) followed by plant height (26.46%), number of branches (22.23%) and yield per plot (19.39%) (Table 2). The GCV ranged from 5.62% to 41.72 %. High value of GCV was

observed for number of pods per plant (41.73%) and plant height (25.76%). In the present investigation, phenotypic coefficient of variation is slightly higher than genotypic coefficient of variation for all the characters. Thus, the narrow gap between PCV and GCV revealed low influence of environment in the expression of these characters. Al-Aysh (2014) [11], Hussan *et al.* (2018) [11] and Kumar *et al.* (2020) [13] also found PCV values to be slightly higher than that of GCV for all the characters.

Heritability could be designated as low (0-30%), moderate (30-60%) and high (60% and above) as proposed by Johnson *et al.*, (1955) [12]. The significance of estimation of heritability comes from the fact that it helps in the prediction of transmissibility of character from one generation to the next generation. Higher heritability suggests single plant selection in early generation could be effective to yield better gain for a trait as compared to a trait with low heritability. The magnitude of heritability in broad sense in genotypes under study ranged from 97.50% to 67.06%. Higher heritability estimates in broad sense were observed for 100- seed weight (97.50%), days to 50% flowering (95.92%), plant height (94.80%), number of pods per plant (91.53%), seed yield kg/ha (89.60 %) and days to maturity (67.76%) (Table 2). High heritability for pods per plants and 100- seed weight was earlier reported by Sharma *et al.*, (2014) [18] and Pushpavalli *et al.* (2018) [15].

Heritability coupled with estimates of genetic advance as percent of mean is more efficient and pragmatic in predicting the genotypes with higher yield values. The magnitude of genetic advance as percent of mean could be categorized as low (0-10%), moderate (10-20%) and high (above 20%) as proposed by Johnson *et al.* (1955) [12]. Values for genetic advance as percent of mean was high for number of pods per plant (82.24%), plant height (51.67%), seed yield per plot (35.78%), number of branches (30.72%), whereas moderate for 100- seed weight (20.12%). Low estimate was recorded for days to maturity (9.53%) (Table 2).

Analysis of correlation coefficient gives a reliable estimation of magnitude and direction of association between pair of characters. It is a handy tool to ascertain the expected response in one character when changes are made in another character. The correlation coefficient was determined for all the quantitative traits with seed yield per plot and among the traits themselves at both phenotypic and genotypic level (Table 3). Study of the values of the phenotypic correlation coefficients indicated that seed yield showed significantly positive correlation with days to 50% flowering (0.465), plant height (0.482), number of branches (0.536) and pods per plant (0.706). There was significant and positive correlation between pods per plant and yield per plant. The results are in agreement with Thanki and Sawargaonkar (2010) [23], Singh *et al.* (2016) [6], Meena *et al.* (2017) [14], Deepak *et al.* (2018) [7] and Kumar *et al.* (2020) [13]. Selection for these traits will be useful in breeding programme. Number of branches was found positively associated with days to 50% flowering (0.739) and pods per plant (0.668). Days to flowering was positively correlated with days to maturity (0.487). 100-seed weight was found significantly positive associated with days to maturity (0.424) whereas it was negatively associated with pod per plant (-0.072).

Path coefficient analysis was originally proposed by Wright (1921) [24] and later utilized in plant breeding by Dewey and Lu (1959) [8]. It is simple standardized partial regression

coefficient which splits genotypic and phenotypic correlation coefficient into series of direct and indirect effect. Analysis of path coefficient was done by using seed yield as a dependent variable and other characters as independent variables. Path coefficient analysis was carried using phenotypic correlation and results are showed in table 4.

The path coefficient analysis on phenotypic basis showed that among seven characters investigated, four characters demonstrated positive direct effect while rest exhibited negative direct effect. The highest positive direct effect on seed yield per plot was of number of pods per plant (0.54), number of branches (0.27), days to maturity (0.24) and 100-seed weight (0.30) (Table 4). Thus number of pods per plant has been identified as an important yield component as it had highest direct effect towards yield per plot. Dahiya and Singh (1994) [6], Thanki *et al.*, (2010) [23], Bhadru *et al.*, (2011) [4] and Hemvati *et al.*, (2019) also reported similar results. Days to 50 % flowering had positive indirect effect on seed yield per plot through days to maturity, number of pods per plant and number of branches whereas negative indirect by plant height and 100-seeds weight. The results of indirect effect of days to maturity on seed yield per plant revealed that number of pods per plant (0.11), number of branches (0.06) had

positive indirect effect whereas plant height (-0.01) and 100-seed weight (-0.13) had negative indirect effect. Plant height exhibited positive indirect effect on seed yield per plot through days to maturity (0.09), number of pods per plant (0.37), number of branches (0.23); whereas negative indirect by days to 50% flowering (-0.11) and 100-seed weight (-0.09). Number of pods per plant exhibited positive indirect effect *via* days to maturity (0.05) and number of branches (0.18); whereas negative indirect effect *via* days to 50% flowering (-0.08).

The present investigation suggested that estimates of genetic variability, correlation and path analysis are important for the identification of superior genotypes for yield and its attributing traits. The genotypes AH 16-36, AH 16-41, AH 16-42, AH 16-43, AH 16-44, AH 16-45, AH 16-47, AH 16-48, AH 16-49 and AH 16-50 are extra-early genotypes developed at Pulses Breeding Section of CCS HAU. These genotypes can be used in breeding programme for the development of early maturing, short stature, and high yielding varieties. It will be helpful in diversified farming and will also solve the labour problem in pigeon pea by reducing the cost of production through mechanical operations.

**Table 1:** Mean performance for various characters of extra-early pigeonpea genotypes

S. No	Genotype	Days to 50% flowering	Days to maturity	Plant height (cm)	Branches/Plant	Pods/Plant	100- seed wt. (g)	Yield Kg/ha
1	AH 16-36	52	110	149.00	7.00	85.00	8.53	1181.47
2	AH 16-41	56	123	153.00	6.67	224.33	7.26	1457.39
3	AH 16-42	55	102	146.00	6.00	201.00	5.93	1243.50
4	AH 16-43	56	118	152.67	5.33	109.33	8.54	1085.78
5	AH 16-44	58	127	135.33	9.00	98.67	8.47	1049.98
6	AH 16-45	67	121	225.33	8.33	232.67	8.23	1321.56
7	AH 16-47	69	122	242.00	8.00	266.67	8.53	1282.37
8	AH 16-48	68	123	233.67	9.00	218.00	8.93	1127.12
9	AH 16-49	70	122	243.67	8.67	305.00	9.04	1442.24
10	AH 16-50	69	121	235.33	6.00	313.00	8.03	1791.30
11	Manak	76	135	248.00	9.33	250.00	7.87	1297.80
12	Pusa 992	75	138	246.67	8.00	298.33	9.83	1401.81
	Mean	58.92	119.44	194.46	7.37	212.06	8.26	1206.33
	Range	52-76	102-140	135-248	6-9	85-313	5.93-9.83	1049.98-1791.3
	CV (%)	9.07	9.16	12.33	12.35	2.35	1.59	2.07

**Table 2:** Estimation of Genetic parameters for pigeonpea genotypes

Character	Coefficient of variation		Broad sense heritability%	Genetic advance	Genetic advance as mean (%)
	Genotypic	Phenotypic			
Yield/plot (kg/ha)	18.35	19.39	89.60	486.73	35.78
Plant height (cm)	25.76	26.46	94.80	92.89	51.67
Branches/Plant	18.21	22.23	67.06	2.20	30.72
Pods/Plant	41.73	43.61	91.53	162.09	82.24
Days to Flowering	12.25	12.50	95.92	14.82	24.70
Days to maturity	5.62	6.83	67.76	11.23	9.53
100-seed weight	9.89	10.02	97.50	1.65	20.12

**Table 3:** Genotypic and Phenotypic correlation coefficient for various characters in pigeonpea genotypes

	Yield/plot (kg/ha)	Plant height (cm)	Branches/Plant	Pods/Plant	Days to Flowering	Days to maturity	100-seed weight
Yield/plot (kg/ha)	-	0.499**	0.655**	0.744**	0.508**	0.365*	-0.234 <sup>NS</sup>
Plant height (cm)	0.482**	-	0.948**	0.705**	0.990**	0.465**	0.322*
Branches/Plant	0.536**	0.859**	-	0.801**	0.959**	0.318*	0.223 <sup>NS</sup>
Pods/Plant	0.706**	0.684**	0.668**	-	0.725**	0.268 <sup>NS</sup>	-0.081 <sup>NS</sup>
Days to Flowering	0.465**	0.942**	0.739**	0.671**	-	0.577**	-0.081 <sup>NS</sup>
Days to maturity	0.226 <sup>NS</sup>	0.386*	0.223 <sup>NS</sup>	0.205 <sup>NS</sup>	0.487**	-	0.536**
100-seed weight	-0.226 <sup>NS</sup>	0.306 <sup>NS</sup>	0.176 <sup>NS</sup>	-0.072 <sup>NS</sup>	0.292 <sup>NS</sup>	0.424**	-

\*significant at 5% level \*\*significant at 1% level

Above diagonal values for genotypic correlation coefficient while below diagonal are of phenotypic correlation coefficient

**Table 4:** Path coefficient analysis using phenotypic correlation showing direct (diagonal) and indirect effects of different characters on seed yield

	Plant height (cm)	Branches/ Plant	Pods/Plant	Days to Flowering	Days to maturity	100-seed weight
Plant height	-0.014	0.23	0.37	-0.11	0.09	-0.09
Branches/Plant	-0.01	0.27	0.36	-0.09	0.05	-0.05
Pods/Plant	-0.01	0.18	0.54	-0.08	0.05	0.02
Days to Flowering	-0.01	0.20	0.36	0.12	0.12	-0.09
Days to maturity	-0.01	0.06	0.11	-0.06	0.24	-0.13
100-seed weight	-.004	0.05	-0.04	-0.03	0.10	0.30

Residual effect: 0.411

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