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Studies on character association and causal relationship of seed yield and its components traits in pigeonpea (*Cajanus cajan* (L.) Millsp.)

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Abstract

Correlation between seed yield and yield attribute component traits in forty-eight genotypes of pigeonpea revealed that seed yield per plant was found highly significant and positively correlated with the number of pods per plant and number of primary branches per plant at genotypic and phenotypic levels. The genotypic path analysis showed that there was a high and positive direct effect of days to 50% flowering followed by 100 seed weight, number of pods per plant and number of seeds per pod on seed yield per plant. This revealed that for the improvement of seed yield through selection programme, more emphasis should be given to these traits. The phenotypic path analysis indicated that high and positive direct effect of number of pods per plant and 100-seeds weight on seed yield per plant.

Keywords: Pigeonpea, correlation coefficient analysis, path coefficient analysis

Introduction

Global population explosion is triggering the serious problem of malnutrition. Pulses are one of the reliable options to overcome malnutrition. They are major sources of inexpensive plant-based proteins, vitamins, minerals and dietary fibers, besides having low fat content, zero cholesterol and gluten and consequently have got significant place in the human meal where vegetarian diet is predominant. Pulses with 22-24% protein, have almost twice the protein than wheat and thrice that of rice.

Pigeonpea [*Cajanus cajan*] is one of the important pulse crop with rich dietary protein in its seed satisfying the protein requirements of human. The seed contains 18-29% protein on dry weight basis which is of excellent quality, being high in lysine. The crop is, therefore; an important complement to cereal and root-based diet. Pigeonpea occupies second place after chickpea in India and has been rated the best as far as its biological value is concerned. It has been recommended for a balanced diet with cereals, especially to fill the nutritional gap for proteins. In fact, this crop also possesses medicinal properties used as traditional medicine and has diversified uses such as food, feed, fodder and fuel wood. Also act as a check for soil erosion and maintain soil fertility. It is hard, widely adapted and drought tolerant crop. Productivity of pigeonpea worldwide in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. This low productivity is attributed to its low harvest index because of limited man-made selections (Varshney *et al*., 2010) [25].

Pigeonpea is the fourth most important pulse crop in the world where in India alone accounts for 85 percent of the world supply (Ashutosh *et al*, 2017) [4]. In India, it is cultivated on 4.54 million hectares area with an annual production of 3.31 million tonnes with productivity around 729 kg per ha. In Gujarat, it is cultivated on 0.215 million hectares area with an annual production of 0.285 million tonnes with productivity around 1324 kg per ha (Anon., 2020) [3]. Maharashtra is the single largest producer in the country, accounting for about 32% of total production. Karnataka, Madhya Pradesh, Uttar Pradesh, Gujarat, Andhra Pradesh and Jharkhand contribution about 17%, 15%, 11%, 10%, 8% and 6%, respectively.

At the end of this year, 2020 Pandemic of COVID- 19 falls all over the world and this pandemic is growing very fast in India. For cope up of hunger during such pandemic conditions and to increase pulses production, one has to exploit maximum yield potential of crops. To overcome such situation, genetically stable genotypes having high yield potential are required straightaway.

Materials and Methods

The study was conducted during *kharif* 2020 at the Pulses Research Station, Junagadh Agricultural University, Junagadh. Geographically Junagadh is situated at 21.5^0 N latitude and 70^0 E longitudes with an altitude of 107 meters above the mean sea level. The soil of experimental site was medium black and medium in organic matter. The climate of the area represents tropical and semiarid. Forty-Eight genotypes of pigeonpea were sown in a Randomized Block Design (RBD) with three replications during *kharif* 2020 at Pulses Research Station, Junagadh Agricultural University, Junagadh. Each genotype was accommodated in a single row of 4 m length with a spacing of 90 cm × 20 cm. One row was sown around each replication to remove the border effects. The observations were recorded for nine characters *viz.*, days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seeds weight (g) and seed yield per plant (g).

Statistical Analysis

The mean values for each character over three replications were subjected to following statistical analysis: genotypic and phenotypic correlation coefficients for all the pair wise characters were worked out as per Al-Jibouri *et al.* (1958) [2]. Path coefficient analysis was carried out according to the procedure suggested by Dewey and Lu, 1959 [7]. All the statistical analysis was carried with help of INDOSTAT Statistical software.

Results and Discussion

In plant breeding programme, where the aim is for improving seed yield, it becomes necessary to gather the detailed information regarding the association of various components with seed yield and among themselves. Seed yield is a complex trait and is determined by the interactive effects of many component traits, which are in turn influenced by their genetic structures and the environment where the plant is grown. The estimation of correlation coefficient can be done at both genotypic and phenotypic levels. The simple correlation is an important tool for this purpose as knowledge of correlation is essential when selection is to be made on several characters at a time through some simultaneous selection model. True association can only be known through genotypic correlation since phenotypic correlation includes the interaction between genotype and environment.

In the present investigation magnitude of genotypic correlation was found slightly higher than phenotypic correlation for most of the traits. This indicated a greater role of genetic factors in determining these associations which reflected that the environment could not deviate the expression of phenotypic association (Table 1). The difference between genotypic and phenotypic correlation was found very less. The occurrence of higher estimates of genotypic correlation than the corresponding phenotypic correlation between seed yield and yield components in pigeonpea has also been reported by Kumar *et al.* (2018) [12] and Alaka *et al.* (2020) [1].

In the present investigation, seed yield per plant had highly significant and positive correlation with number of pods per plant and primary branches per plant at both genotypic and phenotypic level indicating any improvement of the traits with positive correlation with seed yield will results in a substantial increment of seed yield. Such result also reported by Rao and Rao (2020) [16], Rathore *et al.* (2020) [17] and Sharma *et al.* (2020). The positive genotypic and phenotypic association in pigeonpea has been reported between seed yield per plant with days to 50% flowering (Alaka *et al*., 2020 and Rathore *et al.*,2020) [1, 17], Days to maturity (Singh *et al*., 2013; Kumar *et al.*, 2018 [19, 12] and Alaka *et al*., 2020) [1], plant height (Saroj *et al*., 2013) [19] and 100-seeds weight (Hemavathy *et al.*, 2019 and Alaka *et al*., 2020) [9, 1]. Days to 50% flowering had a positive and significant association at both phenotypic and genotypic levels with days to maturity as well as number of pods per plant. Similar relationship among days to 50% flowering and days to maturity has been reported by Kumar *et al.* (2018) [12], Tharageshwari and Hemavanthy (2020) [23].

Plant height exhibited highly significant and positive correlation with 100-seeds weight at both genotypic and phenotypic levels. Similar findings were reported by Vanisree *et al.* (2013) [24] and Rathore *et al.* (2020) [17]. Number of primary branches per plant showed positive and significant correlation with number of pods per plant at both genotypic and phenotypic levels. Similar finding confounded by Verma *et al.* (2018) [26] and Maher and Kumari (2020) [27]. Number of primary branches per plant showed negative and significant correlation with length of pod at genotypic level. Similar results were obtained by Maher and Kumari (2020) [27]. Number of seed per pod had a positive and significant association at with length of pod at both genotypic and phenotypic levels. Whereas, it showed significant and positive correlation with 100-seeds weight at genotypic level only. Similar results were obtained by Patel *et al.* (2018) [14] for both levels with length of pod and 100-seeds weight at genotypic by Kesha Ram *et al.* (2016) [11] and Ekka *et al.* (2017) [8]. Length of pod showed positive and significant correlation with 100-seeds weight at both genotypic and phenotypic levels confirming earlier report of Saroj *et al.* (2013) [19], Kesha Ram *et al.* (2016) [11] and Rathore *et al.* (2020) [17].

Path Coefficient Analysis

In selection programme when inter- relationship of large number of variables with seed yield and among themselves is studied, the situation become very complex to understand the actual role of a variable for increasing yield. In such a situation, the information of correlation coefficient coupled with the information on path coefficient greatly helps in identification of suitable characters for giving due weightage during selection. The Path coefficient analysis was done for yield and yield attributes to estimate the direct and indirect effects of various characters on seed yield. Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients. In order to understand these effects, genotypic as well as phenotypic correlation coefficient of different characters with seed yield was portioned into their direct and indirect effects (Table 1 and Table 2). This facilitates the selection of genotypes on the basis of those traits which will eventually contribute more towards seeds yield.

Table 1: Genotypic (r_g) and phenotypic (r_p) correlation coefficients among nine characters of pigeonpea

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100-seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	r_g	1.000	0.940**	-0.108	0.167	0.376**	0.022	0.042	-0.185	0.165
	r_p	1.000	0.697**	-0.068	0.124	0.304*	0.047	0.127	-0.124	0.155
Days to maturity	r_g		1.000	-0.022	0.211	0.281	0.017	0.327*	0.119	0.039
	r_p		1.000	-0.019	0.142	0.233	0.061	0.211	0.091	0.045
Plant height (cm)	r_g			1.000	0.155	-0.161	0.225	0.245	0.349*	-0.023
	r_p			1.000	0.133	-0.138	0.220	0.184	0.303*	-0.013
No. of primary branches per plant	r_g				1.000	0.445**	-0.207	-0.296*	-0.103	0.428**
	r_p				1.000	0.371*	-0.204	-0.222	-0.077	0.383**
Number of pods per plant	r_g					1.000	-0.238	-0.205	-0.280	0.726**
	r_p					1.000	-0.221	-0.166	-0.255	0.670**
Number of seeds per pod	r_g						1.000	0.954**	0.324*	-0.072
	r_p						1.000	0.745**	0.254	-0.059
Length of pod (cm)	r_g							1.000	0.632**	-0.119
	r_p							1.000	0.463**	-0.101
100- seeds weight (g)	r_g								1.000	0.083
	r_p								1.000	0.073
Seed yield per plant (g)	r_g									1.000
	r_p									1.000

*, ** Significant at 5 and 1% levels, respectively

Table 2: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 48 genotypes of pigeonpea

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100- seeds weight (g)	Genotypic correlation with Seed yield per plant (g)
Days to 50% flowering	0.950	-0.935	0.011	0.021	0.309	0.013	-0.031	-0.173	0.165
Days to maturity	0.893	-0.994	0.002	0.027	0.230	0.010	-0.241	0.112	0.039
Plant height (cm)	-0.102	0.022	-0.106	0.020	-0.132	0.128	-0.181	0.328	0.023
Number of primary branches per plant	0.159	-0.210	-0.016	0.126	0.365	-0.118	0.218	-0.096	0.428**
Number of pods per plant	0.357	-0.279	0.017	0.056	0.821	-0.136	0.151	-0.263	0.726**
Number of seeds per pod	0.021	-0.017	-0.024	-0.026	-0.196	0.569	-0.704	0.304	-0.072
Length of pod (cm)	0.040	-0.325	-0.026	-0.037	-0.168	0.543	-0.739	0.593	-0.119
100- seeds weight (g)	-0.176	-0.118	-0.037	-0.013	-0.230	0.184	-0.467	0.939	0.083

*, ** Significant at 5 and 1% levels, respectively

Table 3: Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 48 genotypes of pigeonpea

Characters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100- seeds weight (g)	Phenotypic correlation with Seed yield per plant (g)
Days to 50% flowering	0.154	-0.172	0.004	0.020	0.220	0.012	-0.036	-0.048	0.155
Days to maturity	0.108	-0.247	0.001	0.022	0.169	0.016	-0.059	0.035	0.045
Plant height (cm)	-0.011	0.005	-0.052	0.021	-0.100	0.057	-0.051	0.118	-0.013
Number of primary branches per plant	0.019	-0.035	-0.007	0.158	0.269	-0.054	0.062	-0.030	0.383**
Number of pods per plant	0.047	-0.057	0.007	0.059	0.725	-0.058	0.046	-0.099	0.670**
Number of seeds per pod	0.007	-0.015	-0.011	-0.032	-0.160	0.262	-0.208	0.099	-0.059
Length of pod (cm)	0.020	-0.052	-0.010	-0.035	-0.120	0.195	-0.279	0.181	-0.101
100- seeds weight (g)	-0.019	-0.022	-0.016	-0.012	-0.185	0.066	-0.129	0.390	0.073

*, ** Significant at 5 and 1% levels, Residual effect = 0.632

Genotypic path coefficient analysis

The genotypic path coefficient analysis (Table 2) revealed that days to 50% flowering, 100-seeds weight, number of pods per plant and number of seeds per pod expressed positive and higher direct effect on seed yield per plant. These results were in conformity with earlier report of Ravika and Solanki (2017) [18] for days to 50% flowering; Saroj *et al.* (2013) [19] for 100-seeds weight;), Kandarkar *et al*. (2020 b)

[10] for number of pods per plant; Rathore *et al.* (2020) [17] for number of seeds per pod. While, number of primary branches per plant had low and positive direct effect on seed yield. Similar conclusion also derived by Kumar *et al.* (2018) [12]. The characters like days to maturity, length of pod and plant height has negative direct effect on seed yield at genotypic level. These results are in accordance with the reports of Borah *et al.* (2020) [6] for days to maturity; Borah *et al.* (2020) [6] and Alaka *et al.* (2020) [1] for length of pod; Baldaniya *et al.* (2018), Kumar *et al.* (2018) [12], Patel *et al.* (2018) [14], Alaka *et al.* (2020) [1] and Borah *et al.* (2020) [6] for plant height.

Phenotypic path coefficient analysis

The phenotypic path coefficient analysis (Table 3) revealed that number of pods per plant and 100-seeds weight expressed positive and higher direct effect on seed yield. Which coincides earlier reported by Borah *et al.* (2020) [6] and Chaudhary and Chhabra, (2020) [28] for Number of pods per plant; Chaudhary and Chhabra, (2020) [28] for 100-seeds weight.

While, number of seeds per pod, number of primary branches per plant and days to 50% flowering had moderate to low and positive direct effect on seed yield. The similar results were corroborated by Singh *et al.* (2013) [19] for number of seeds per pod; Kumar *et al.* (2018) [12] for number of primary branches per plant; Ravika and Solanki, (2017) [18] for days to 50% flowering. However, negative direct effect on seed yield per plant were contributed through length of pod, days to maturity and plant height at phenotypic level. Similar outcome were also reported by Verma *et al.* (2018) [26] and Alaka *et al.* (2020) [1] for length of pod; Ravika and Solanki (2017) [18] for days to maturity; Saroj *et al.* (2013) [19], Kesha Ram *et al.* (2016) [11], Ravika and Solanki, (2017) [18] and Alaka *et al.* (2020) [1] for plant height.

The residual effect was found to be 0.323 at genotypic path coefficient analysis, while it was 0.632 at phenotypic path coefficient analysis. This indicated that other attributing character were also important and may play a critical role in pigeonpea improvement. These results are in accordance with the reports of Singh *et al.* (2013) [19] and Pushpavalli *et al.* (2018) [15].

Conclusion

Study of correlation coefficient and path analysis clearly indicate that the number of pods per plant was most important trait. Therefore, selection for number of pods per plant, number of primary branches per plant, seed yield per plant and 100-seeds weight would offer the scope for stimulations improvement of contributing characters for improving the yield potential in pigeonpea.

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