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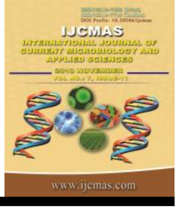

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Character Association and Path Coefficient Analysis for Yield and Its Components in Pigeonpea (*Cajanus cajan* (L.) Mill sp.)

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ABSTRACT

Keywords

Correlation coefficient, Path analysis, Pollen fertility and pigeonpea

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The estimates of genotypic correlation coefficients in general were higher than their corresponding phenotypic correlation coefficients indicating strong inherent association among the traits. The seed yield per plant had significant and positive association with number of primary branches plant$^{-1,}$ number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, biological yield plant^{-1}, seed yield (kg/ha) harvest index and 100-seed weight at both genotypic as well as phenotypic levels. Characters *viz*., pollen fertility%, biological yield plant^{-1}, harvest index, number of secondary branches plant^{-1} and dal recovery% exerted high direct effects on seed yield. 100-seed weight and pods plant^{-1} also contributed indirectly towards seed yield per plant through most of the characters. Thus, based on the present study number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, biological yield plant^{-1}, seed yield (kg/ha) harvest index and 100-seed weight were emerged as the most important components of seed yield.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Mill sp.] is the most important pulse crop of our country, though its productivity is very low. Yield is a complex and multiplicative trait, which is highly influenced by environment. The information on correlation coefficient of yield and yield attributes will assist the breeders whether to give due importance on each of the traits to make significant genetic gain. Path coefficient analysis aids partitioning of the correlation coefficient into direct and indirect effects and thus provides a better insight on the characters and their relationship with yield. The correlation and path analysis thus help in identifying suitable traits for improving the seed yield. The present investigation was under taken to assess the association of yield and yield attributes and to estimate the direct and indirect effects of each character on seed yield in pigeonpea.

Materials and Methods

A total of 28 genotypes including 3 varietal checks (Asha, Maruti, Rajeevlochan) and 2 hybrid checks (ICPH 2740 and ICPH 2671) were grown in randomized complete block design (RCBD) with three replications and two rows per plot each of 4 meter length with a spacing of 75 and 50 cm between and within rows respectively at International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), Patancheru. The recommended agronomic practices were followed for raising a good and healthy crop. In each replication five plants were selected randomly in each genotype for recording observations on days to 50% flowering, pollen fertility%, days to maturity, plant height (cm), number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds pod^{-1}, number of seeds plant^{-1}, 100-seed weight (g), seed yield plant^{-1} (g), biological yield plant^{-1}, seed yield (kg ha^{-1}), harvest index (%) and seed protein content were recorded. The data were statistically analyzed to estimate the phenotypic correlation coefficients of yield, yield attributes, Path coefficient analysis was done for yield, and yield attributes to estimate the direct and indirect effects of various characters on seed yield by using the software INDOSTAT.

Results and Discussion

The analysis of variance indicated significant differences among genotypes for all the characters. The correlation coefficients between seed yield and yield attributes are presented in Table 1. Genotypic correlations (Table 1) were higher in magnitude than the phenotypic correlation indicting strong inherent relationship among the characters except few, which could be due to modifying effects in the environment studied. Pandey and Singh (2002) reported similar findings. Genotypic correlation provides a measure of genotypic association among different traits and helps in identifying the traits in selection. In the present study, seed yield per plant recorded significant and positive association with seed yield plant^{-1} was observed to be significantly and positively associated with number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, biological yield plant^{-1} and seed yield (kg/ha) at both phenotypic and genotypic levels and harvest index showed positive association both phenotypic and genotypic but significant only genotypic level. However, seed yield plant^{-1} was also observed to be significantly and negatively associated with days to 50% flowering, days to maturity and pollen fertility%. Association of seed yield plant^{-1} with other characters, *viz.*, plant height, number of seeds pod^{-1}, 100-seed weight and at both phenotypic and genotypic levels was found but non-significant. However, it recorded negative and significant association with plant height, days to 50% flowering, days to maturity and straw yield at phenotypic level (Table 1). The results of the present study are in conformity with the reports of Aher *et al.*, (1998); Musaana and Nahdy (1998) and Chandirakala and Subbaraman (2010). Among the yield contributing traits, positive and significant association were evident for days to maturity with plant height, days to 50%flowering with days from flowering to maturity; seeds per pod with number of primary branches and pod length; days to50% flowering with plant height as well as specific gravity with test weight; which are in conformity with earlier reports (Salunke *et al.*, 1995, Vikas and Singh, 1998, Baskaran and Muthiah, 2006, Sodavadiya *et al.*, 2009, Sawant *et al.,* 2009). However, VasanthaRao *et al.,* (2010) reported non-significant but positive association of test weight with seed yield.

Studies on inter-character associations among the yield components studied had revealed significant and positive association of days to 50% flowering with days to maturity, pollen fertility % and 100-seed weight; days to maturity with pollen fertility and seed yield (kg/ha); number of primary branches plant^{-1} with number of secondary branches plant^{-1}, plant height, biological yield plant^{-1}and seed yield (kg/ha).

Number of secondary branches per plant with number of pods plant^{-1}; number of seeds plant^{-1}, biological yield plant^{-1} and seed yield (kg/ha); plant height with 100-seed weight; number of pods plant^{-1} with number of seeds plant^{-1}, biological yield plant^{-1} and seed yield (kg/ha); Number of seeds plant^{-1} with biological yield plant^{-1} and seed yield (kg/ha); biological yield plant^{-1} with seed yield (kg/ha) similarly, seed yield (kg/ha) with harvest index positive and significant at both the phenotypic and genotypic level indicating the possibility of simultaneous improvement of these characters through selection.

However significant and negative inter character association was observed for days to 50% flowering with number of primary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, biological yield plant^{-1} and seed yield (kg/ha); days to maturity with number of primary branches plant^{-1}, number of pods plant^{-1} and biological yield plant^{-1}; biological yield plant^{-1} with harvest index at phenotypic and genotypic levels, indicating competition for a common possibility, such as nutrient supply (Adams, 1967; Adams and Grafius, 1971) and the need for balanced selection, while attempting for improvement of these traits.

The characters *viz.,* number of primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}, biological yield plant^{-1}, seed yield (kg/ha) harvest index and 100-seed weight recorded positive association with seed yield, which indicated that these are major yield contributing traits in pigeonpea. Hence, laying stress on these traits will aid in making significant improvement of yield potentiality in pigeonpea.

Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients. The detailed path coefficient analysis (Table 2) showed that pollen fertility % had maximum positive direct effect fallowed by biological yield plant^{-1}, harvest index, number of secondary branches plant^{-1} and dal recovery%. Whereas, the characters *viz.,* days to 50% flowering, days to maturity, and seed protein content showed negative and high direct effects on grain yield at both genotypic and phenotypic levels. Whereas, number of seeds plant^{-1}, number of primary branches, 100-seed weight and number of seeds pod^{-1} in these cases genotypic had showed negative direct effect but phenotypic had showed positive and direct effects on the seed yield plant^{-1}.

Plant height and number of pods plant^{-1} at genotypic level had showed positive direct effect but negative direct effect on the grain yield at phenotypic level. The highly significant and positive correlation of pollen fertility % had found with grain yield due to their maximum direct and indirect effect via days to 50% flowering and days to maturity respectively. Number of seeds pod^{-1} showed medium positive direct effect and their genotypic correlation with grain yield was significant. Similar results were also reported by Rao *et al.,* (2013) for number of primary branches, pods plant$^{-1,}$ seeds pod^{-1}, days to 50% flowering and harvest index.

Table.1 Phenotypic and Genotypic correlations for yield and yield components in pigeonpea genotypes

Character	Corre. Coeffi.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16
1	**G** **P**	1 1	0.861*** 0.733***	0.977*** 0.941***	-0.201 -0.134	-0.53*** -0.257*	0.11 0.046	-0.350** -0.242*	-0.38*** -0.143	-0.263* -0.223*	0.243* 0.339**	-0.31** -0.264*	-0.357*** -0.317**	0.060 0.021	-0.244* -0.164	0.102 0.051	**-0.297**** **-0.254***
2	**G** **P**		1 1	0.951*** 0.910***	-0.59*** -0.315**	-0.785*** -0.312***	0.182 0.019	-0.38*** -0.241*	-0.47*** -0.175	-0.33** -0.208	0.185 0.101	-0.474*** -0.328**	-0.503*** 0.405***	0.057 -0.022	0.057 -0.082	0.011 -0.001	**-0.453***** **-0.298****
3	**G** **P**			1 1	-0.39*** -0.236*	-0.670*** -0.297**	0.142 0.049	-0.37*** -0.256*	-0.43*** -0.169	-0.299** -0.224*	0.28** 0.195	-0.390*** -0.299**	-0.438*** -0.385***	0.049 -0.009	-0.101 -0.140	0.079 0.044	**-0.379***** **-0.284****
4	**G** **P**				1 1	1.074*** 0.353***	0.26* 0.257*	-0.099 0.064	0.52*** 0.021	0.351** 0.132	0.133 0.125	0.836*** 0.394***	0.861*** 0.319**	0.183 0.006	-0.259* -0.109	0.293** 0.041	**0.735***** **0.260****
5	**G** **P**					1 1	-0.073 -0.057	0.594*** 0.395***	0.212* -0.053	0.619*** 0.404***	0.018 0.080	1.013*** 0.504***	0.761*** 0.376***	0.176 -0.102	0.181 -0.046	0.271* 0.076	**0.971***** **0.579*****
6	**G** **P**						1 1	0.015 0.081	0.73*** 0.184	-0.029 0.002	0.334** 0.296**	-0.062 0.060	0.0938 0.089	0.201 0.098	0.042 0.105	0.197 0.129	**-0.221*** **-0.154**
7	**G** **P**							1 1	0.49*** -0.019	0.909*** 0.641***	-0.37*** -0.173	0.291** 0.271*	0.323** 0.302**	0.045 0.045	0.271* 0.087	0.40*** 0.152	**0.663***** **0.579*****
8	**G** **P**								1 1	0.0286 -0.061	0.47*** 0.156	-0.016 0.0347	-0.024 0.010	-0.187 -0.116	0.306** 0.107	-0.192 -0.032	**-0.022** **-0.093**
9	**G** **P**									1 1	-0.38*** -0.20	0.641*** 0.432***	0.386*** 0.330**	0.117 -0.024	0.245* 0.039	0.353*** 0.223*	**0.809***** **0.59******
10	**G** **P**										1 1	-0.054 0.029	-0.122 -0.065	0.017 0.047	0.441*** 0.13	0.021 -0.002	**-0.323**** **-0.136**
11	**G** **P**											1 1	0.349** 0.330 **	-0.318** -0.245*	0.099 0.044	0.097 0.132	**0.542***** **0.497*****
12	**G** **P**												1 1	0.520 0.459***	0.039 0.083	0.154 0.106	**0.636***** **0.527*****
13	**G** **P**													1 1	0.009 0.047	0.362 0.109	**0.273*** **0.170**
14	**G** **P**														1 1	0.421*** 0.118	**0.124** **-0.004**
15	**G** **P**															1 1	**0.326**** **0.201**

Note: Significant at *- 5% level, ** - 1% and*** - 0.1% level of significance

Note: 1- Days to 50% flowering, 2- Days to maturity, 3- Pollen fertility, 4- No. of primary branches plant^{-1},5-No.of secondary branches plant^{-1}, 6- Plant height, 7- Pods plant^{-1}, 8-Seeds pod^{-1},9-Seeds plant^{-1}, 10- 100-seed weight, 11-Biological yield plant^{-1}, 12- Yield (kg/ha), 13- Harvest index, 14- seed protein content, 15- Dal recovery% and 16-Yield plant^{-1}.

Table.2 Genotypic and Phenotypic path co-efficient for yield and yield components in pigeonpea

Character	Pathcoeff.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	r_g and r_p
1	**G** **P**	**-13.13** **-0.362**	-10.121 -0.388	23.331 -0.499	0.182 0.071	-0.068 0.136	0.023 -0.024	-0.353 0.128	0.072 0.076	0.325 0.118	-0.083 -0.129	-0.577 0.139	0.071 -0.011	0.000 -0.027	0.034 0.087	**-0.297**** **-0.254***
2	**G** **P**	-11.309 -0.275	**-11.752** **-0.223**	22.814 -0.341	0.609 0.118	-0.099 0.117	0.038 -0.007	-0.384 0.090	0.089 0.066	0.408 0.078	-0.045 -0.038	-0.883 0.123	0.068 0.008	0.000 0.001	-0.008 0.031	**-0.453***** **-0.298****
3	**G** **P**	-12.804 0.837	-11.206 0.809	**23.942** **0.547**	0.381 -0.210	-0.085 -0.265	0.030 0.043	-0.379 -0.228	0.080 -0.151	0.377 -0.199	-0.069 0.173	-0.728 -0.266	0.066 -0.008	0.000 0.039	0.015 -0.125	**-0.379***** **-0.284****
4	**G** **P**	2.380 -0.012	7.132 -0.029	-9.083 -0.022	**-1.014** **0.122**	0.138 0.033	0.049 0.024	-0.064 0.006	-0.102 0.002	-0.452 0.012	-0.032 0.012	1.565 0.037	0.215 0.001	0.001 0.004	0.044 -0.010	**0.735***** **0.260****
5	**G** **P**	7.072 -0.056	9.333 -0.067	-16.277 -0.064	-1.108 0.076	**0.117** **0.297**	-0.017 -0.013	0.599 0.085	-0.042 -0.011	-0.774 0.087	-0.005 0.017	1.894 0.108	0.209 -0.022	0.001 0.016	-0.026 -0.010	**0.971***** **0.579*****
6	**G** **P**	-1.433 -0.011	-2.126 -0.005	3.419 -0.012	-0.234 -0.063	-0.01 0.014	**0.212** **-0.270**	0.014 -0.020	-0.138 -0.046	0.037 -0.000	-0.081 -0.074	-0.115 -0.015	0.239 -0.024	0.001 -0.032	-0.006 -0.026	**-0.221*** **-0.154**
7	**G** **P**	4.593 -0.073	4.472 -0.072	-8.984 -0.077	0.064 0.019	0.074 0.118	0.003 0.024	1.008 -0.390	-0.095 -0.006	-1.122 0.192	0.090 -0.051	0.542 0.081	0.054 0.014	0.002 0.046	-0.038 0.026	**0.663***** **0.579*****
8	**G** **P**	4.951 -0.001	5.524 -0.001	-10.008 -0.001	-0.537 0.000	0.027 -0.000	0.154 0.001	0.505 -0.000	**-0.191** **0.007**	-0.035 -0.001	-0.114 0.001	-0.031 0.000	-0.222 -0.001	-0.001 -0.000	-0.043 0.001	**-0.022** **-0.093**
9	**G** **P**	3.457 -0.032	3.885 -0.03	-7.306 -0.033	-0.368 0.019	0.079 0.059	-0.006 0.000	0.918 0.093	-0.006 -0.009	**-1.238** **0.195**	0.092 -0.029	1.193 0.063	0.139 -0.004	0.001 0.033	-0.034 0.006	**0.809***** **0.59******
10	**G** **P**	-4.448 -0.005	-2.179 -0.002	6.74 -0.004	-0.134 -0.003	0.002 -0.002	0.071 -0.006	-0.374 0.004	-0.089 -0.003	0.474 0.004	**-0.242** **0.288**	-0.101 -0.001	0.019 -0.001	0.000 0.000	-0.062 -0.003	**-0.323**** **-0.136**
11	**G** **P**	4.074 -0.057	5.574 -0.071	-9.362 -0.065	-0.845 0.085	0.129 0.109	-0.013 0.013	0.294 0.059	0.003 0.008	-0.791 0.094	0.013 0.006	**1.858** **0.289**	-0.377 -0.053	0.000 0.029	-0.015 0.009	**0.542***** **0.497*****
12	**G** **P**	-0.791 0.004	-0.673 -0.004	1.334 -0.001	-0.182 0.001	0.022 -0.019	0.043 0.019	0.046 0.009	0.036 -0.023	-0.145 -0.005	-0.004 0.009	-0.592 -0.048	**1.184** **0.196**	0.001 0.021	-0.001 0.01	**0.273*** **0.170**
13	**G** **P**	-1.342 0.003	-0.125 0.0001	1.471 0.003	-0.308 0.002	0.035 0.004	0.042 0.008	0.406 0.009	0.037 -0.000	-0.436 0.013	-0.005 -0.000	0.181 0.001	0.428 0.006	**0.004** **0.059**	-0.059 0.007	**0.326**** **0.201**
14	**G** **P**	3.205 0.003	-0.669 0.002	-2.623 0.003	0.318 0.002	0.023 0.000	0.009 -0.002	0.273 -0.001	-0.058 -0.002	-0.303 -0.001	-0.107 -0.003	0.186 -0.001	0.011 0.001	0.002 0.001	**-0.141** **-0.019**	**0.124** **-0.004**

Residual effect=0.4788 for Genotypic path and Residual effect=0.5680 for Phenotypic path coefficients. Diagonal values = direct effects Off-diagonal values = indirect effects.

Note: 1-Days to 50% flowering, 2-Days to maturity, 3-Pollen fertility%, 4-No.of primary branches plant^{-1},5-No.of secondary branches plant^{-1}, 6-Plant height, 7-Pods plant^{-1}, 8-Seeds pod^{-1},9-Seeds plant^{-1}, 10-100-seed weight, 11-Biological yield plant^{-1}, 12-Harvest index, 13-Dal recovery% and 14-seed protein content.

r_g and r_p – Genotypic correlation and Phenotypic correlation

Considering overall observation of path analysis the traits *viz.,* pollen fertility%, biological yield plant^{-1}, harvest index, pods plant^{-1}and number of primary branches plant^{-1} showed considerable positive direct influence on seed yield plant^{-1}.

However, the character pollen fertility% did not exhibit positive correlation on yield due to its high negative indirect effect *via* days to 50% flowering, days to maturity, pods plant^{-1} and biological yield plant^{-1}. Hence, improving seed yield of pigeonpea may be possible through selection for these traits.

From the present investigations here concluded that the estimation of correlation and path analysis are more useful to identification of superior cultivars for yield and yield traits. Based on association studies, improvement in pigeonpea can be attained by isolating individuals possessing high values for the characters like primary branchesplant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1}, number of seeds plant^{-1}and biological yield plant^{-1}.

The character seed yield plant^{-1} had high to moderate positive indirect effects *via* characters *viz.,* pods plant^{-1}, seeds plant^{-1}, number of secondary branches plant^{-1}and biological yield plant^{-1} also exhibited the significant and positive association with seed yield.

These traits may be given more emphasis while selecting high yielding pigeon pea genotypes for drought condition.

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