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Correlation and Path Analysis Studies in Pigeon Pea (*Cajanus cajan* (L.) Millsp.) Genotypes under Foothill Conditions of Nagaland

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Abstract

Correlation coefficient and Path coefficient analysis were evaluated in eleven Pigeon Pea genotypes along with one check variety under the research field of Genetics and Plant Breeding Medziphema, Nagaland, India during *kharif* season 2017-2018 and the data were recorded on nine quantitative characters. The correlation studies showed that, seed yield plant^{-1} showed significant and positive correlation with secondary branches plant^{-1} both at phenotypic and genotypic level and at genotypic level with number primary branches plant^{-1}, number of secondary branches plant^{-1}, number of pods plant^{-1} and test weight respectively. In path coefficient analysis, number of pods plant^{-1} exhibited high and positive direct effect on seed yield plant^{-1} followed by number of secondary branches plant^{-1} and days to maturity. Negative direct effect was exhibited by number of primary branches plant^{-1} for seed yield plant^{-1}. Number of primary branches plant^{-1} and number of seeds pod^{-1} showed high indirect effect through number of pods plant^{-1}. The study on the correlation and path analysis concluded that out of the eleven genotypes, PA-291 can be used as a promising genotype since it exhibited high number of primary and secondary branches, high number of pods plant^{-1}, high test weight and high seed yield plant^{-1}. And the genotypes *viz.* UPAS-120 which takes the least days to flower and shortest height, PA-421 which has the maximum test weight and PA-441 which have the maximum pods plant^{-1} may be considered as potential genotypes for incorporation in pigeon pea breeding programme.

Keywords: Pigeon Pea, correlation coefficient, path coefficient

1. Introduction

Pigeon pea (*Cajanus cajan* (L.) Millsp.) is one of the major grain legume (pulse) crops grown in about 50 countries in the tropics and subtropics. India is considered as the native of pigeon pea (Van der Maesen, 1980) and it is the second important pulse crop of India which has diversified uses as food, feed, fodder and fuel. It is tolerant to water deficit, can be helpful in recovering degraded areas and in soil fertility maintenance (Singh et al., 2013) and is mainly used as Daal in the vast majority of the vegetarian diet, and also serves as a back bone of nutritional security as its grain is of high nutritional value with high protein content (Chaithanya et al., 2014). 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. Seeds of arhar are also rich in iron and iodine. They are rich in essential

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amino acids like lycine, tyrosine, cystine and arginine. The world production of pigeon pea was 4.68 million tons in an area of 4.23 million hectares. Although India leads the world both in area and production of pigeon pea, its productivity is lower (671 kg ha^{-1}) than the world average (742 kg ha^{-1}) (Anonymous, 2013). One of the factors responsible for the poor productivity of pigeon pea is the lack of improved cultivars. Research for genetic improvement of this crop to raise yield levels effectively has to be strengthened countering biotic stresses and through widening genetic base. In order to study it properly, different factors affecting the yield must be considered and evaluated with regard to their contribution to yield. Study of character association and path analysis helps the breeder in fixing the selection criteria for higher grain yield which is the main variable, so that selection will be effective in isolating the genotypes with desirable combination of characters (Vange & Moses, 2009; Devi et al., 2012; Birhan et al., 2013; Cruz 2013; Singh et al., 2013; Chaithanya et al., 2014). Accordingly, the present study was carried out to estimate relationship between yield and its component characters and to assess the direct and indirect influence of the various components on yield.

2. Materials and Methods

The investigation was carried out in the experimental field of Genetics and Plant Breeding Department, Nagaland University; School of Agricultural Sciences and Rural Development, Medziphema campus during *Kharif* season of 2017 with 11 early varieties of Pigeon pea alone with one check variety. Details of genotypes are as follows: AL- 1849, AL-1756, AL-2025, AL-1871, AL-2021, AL-1760, AL- 1758, PA-440, PA-421, PA-441, PA-291 and UPAS-120 used as check variety. The varieties were designated as G1,G2,G3,G4,G5,G6,G7,G8,G9,G1 0,G11 and G12 respectively for the research purpose. The site is located at 23°45’’49’’”N latitude, 90°33’’04’’”S longitude at an altitude of 305 m above sea level. The experimental farm lies in the humid sub tropical zone with an average rainfall ranging from 2000 to 2500 mm per annum where the mean temperature ranges from 21 to 32° C during summer and rarely goes below 8 °C in the winter season. The soil is acidic in nature with pH varying from 4.5-6.2. The organic matter content is low which varied from 1.2-2.9%. N.P.K availability was 100.35 kg, 20.45 kg and 196.68 kg ha^{-1} respectively. The genotypes along with the check variety were collected from AICRP on pigeon pea Nagaland University, SASRD Medziphema and were evaluated under randomized block design with three replications with spacing of 60×30 cm^2 between rows and plants respectively. The data recording was done on five randomly selected tagged plants from each plot in each replication and the average value was recorded for statistical analysis. Observations were recorded on nine quantitative characters viz, days to 50% flowering, 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}, test weight and seed yield plant^{-1}. The details of the genotypes are given in Table 1. The correlation between the characters under study and genotypic, phenotypic and environmental levels were estimated by using the method given by Singh and Chaudhury (1979) and the path coefficient analysis was worked out by the formula applied by Dewey and Lu (1959).

3. Results and Discussion

The correlation coefficient between seed yield plant^{-1} and its

Table 1: Genotypic (r_g) and phenotypic (r_p) correlation coefficient of yield and its contributing characters

Characters		Days to maturity	Plant height	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Test weight	Seed yield plant^{-1}
Days to 50% flowering	r_g	0.8817**	0.2993	0.4387	-0.1167	-0.1126	-0.4935*	-0.3599	0.2500
	r_p	0.6066*	0.1675	0.3085	-0.1087	-0.0822	-0.2085	-0.1618	-0.0659
Days to maturity	r_g		0.4822	0.6358*	0.0065	0.0854	-0.1316	0.2186	0.1154
	r_p		0.2383	0.4628	0.0014	0.0083	-0.1051	0.0027	0.0754
Plant height	r_g			0.7611**	0.1319	-0.0035	0.2716	0.0536	0.1021
	r_p			0.3849	0.1225	0.1100	0.0206	-0.0818	-0.2546
Primary branches plant^{-1}	r_g				0.7131**	0.4915*	0.3318	0.5815*	0.8873**
	r_p				0.5727*	0.2656	0.0699	0.4598	0.3642
Secondary branches plant^{-1}	r_g					0.3656	0.0858	0.6498*	0.9969**
	r_p					0.3198	0.0607	0.4231	0.5123*
No. of pods plant^{-1}	r_g						0.5791*	0.7234**	0.7524**
	r_p						0.2693	0.4383	0.4609
No.of seeds pod^{-1}	r_g							0.6893**	-0.1204
	r_p							0.3510	-0.0697
Test weight	r_g								0.6746**
	r_p								0.2977

component characters are presented in Table 1. At phenotypic level seed yield plant^{-1} exhibited significant and positive correlation with number of secondary branches plant^{-1} (0.5123). Whereas at genotypic level, it exhibited significant and positive correlation with number of primary branches plant^{-1} (0.8873) and number of secondary branches plant^{-1} (0.9969) respectively. It also showed significant and positive correlation with number of pods plant^{-1} (0.7524) and test weight (0.6746) respectively.

For the component characters, at genotypic level, days to 50% flowering showed significant and positive correlation with days to maturity (0.8817), while it showed negative significant correlation with number of seeds pod^{-1} (-0.4935) . Days to maturity showed significant and positive correlation with number of primary branches plant^{-1} (0.6358) and plant height exhibited significant positive correlation with number of primary branches plant^{-1} (0.7611). Also number of primary branches plant^{-1} showed positive and significant correlation with number of secondary branches plant^{-1} (0.7131), number of pods plant^{-1} (0.4915) and test weight (0.5815) respectively. Number of secondary branches plant^{-1} showed positively correlated with test weight (0.6498) while number of pods plant^{-1} showed significant correlation with number of seeds pod^{-1} (0.5791) and test weight (0.7234) respectively. Number of seeds pod^{-1} was also found to be significantly correlated with test weight (0.6893) at genotypic level.

At phenotypic level, days to 50% flowering was found to be significantly positively correlated with days to maturity (0.6066) whereas number of primary branches plant^{-1} with number of secondary branches plant^{-1} (0.5727) respectively.

In the present investigation, seed yield plant^{-1}exhibited significant positive correlation with number of secondary branches plant^{-1} both at phenotypic and genotypic level. The same was recorded by Bhadru (2010) on his investigation in white seed coated pigeon pea lines. And at genotypic level seed yield plant^{-1}exhibited significant positive correlation with for characters such as number of primary branches plant^{-1}, number of pods plant^{-1} and test weight. The result are in agreement with Sawant et al. (2009), Sodavadiya et al. (2009), Kumara et al. (2014) and Kanade et al. (2013).

In general the magnitude of genotypic correlation tends to be higher than that of phenotypic correlation. These suggest that a strong genetic association with traits was observed. The critical analysis of characters association revealed that number of secondary branches plant^{-1}, number of primary branches plant^{-1}, number of pods plant^{-1} and test weight are the major yield contributing characters traits as they have positive association with seed yield plant^{-1}. Hence, selection of these traits will be more reliable for obtaining high yielding early genotypes of pigeon pea.

In path coefficient analysis (Table 2), number of pods plant^{-1} exhibited high and positive direct effect on seed yield plant^{-1} (1.1413) followed by number of secondary branches plant^{-1} (1.2258) and days to maturity (0.5315). Plant height exhibited meagre and positive direct effect on seed yield plant^{-1} (0.1483). Test weight exhibited negative direct effect on seed yield plant^{-1} (-0.7594) followed by number of seeds pod^{-1} (-0.4291) and days to 50% flowering (-0.3648). Negative direct effect was exhibited by number of primary branches plant^{-1} for seed yield plant^{-1} (-0.2545). Number of primary branches plant^{-1} (0.5610) and number of seeds pod^{-1} (0.6609) showed high indirect effect through number of pods plant^{-1}. Also test weight showed negative indirect effect through number of seeds pod^{-1} (-0.2958) and number of primary branches plant^{-1} (-0.1480) but positive strong indirect effect through number of pods plant^{-1} (0.8257). Shreelakshmi et al. (2010), Devi et al. (2012), Saroj et al. (2013), Birhan et al.(2013), Mahajan et al. (2007) also reported direct effect of these characters on seed yield as well.

The highest indirect effect was exhibited by number of secondary branches plant^{-1} followed by number of pods plant^{-1}. Mittal et al. (2010) also observed the similar type of result in pigeon pea. It was also observed that a high indirect contribution was also exhibited by most of the yield components and hence these traits may be given emphasis while selecting high yielding pigeon pea genotypes. Number of primary branches plant^{-1} and number of seeds pod^{-1} showed high indirect effect through number of pods plant^{-1}. Mittal et

Table 2: Direct and indirect effect of yield components at genotypic level in Pigeon pea genotypes

Characters	Days to 50% flowering	Days to maturity	Plant height	Primary branches plant^{-1}	Secondary branches plant^{-1}	No. of pods plant^{-1}	No. of seeds pod^{-1}	Test weight	Seed yield plant^{-1}
Days to 50% flowering	-0.3648	0.4687	0.0444	-0.1117	-0.1431	-0.1285	0.2118	0.2734	0.2501
Days to maturity	-0.3217	0.5315	0.0715	-0.1619	0.0081	0.0975	0.0565	-0.1661	0.1154
Plant height	-0.1092	0.2563	0.1483	-0.1937	0.1618	-0.0040	-0.1166	-0.0408	0.1022
Primary branches plant^{-1}	-0.1601	0.3380	0.1129	-0.2545	0.8741	0.5610	-0.1424	-0.4416	0.8874
Secondary branches plant^{-1}	0.0426	0.0035	0.0196	-0.1815	1.2258	0.4173	-0.0368	-0.4935	0.9969
No. of pods plant^{-1}	0.0411	0.0454	-0.0005	-0.1251	0.4482	1.1413	-0.2485	-0.5494	0.7524
No.of seeds pod^{-1}	0.1801	-0.0699	0.0403	-0.0845	0.1052	0.6609	-0.4291	-0.5235	-0.1204
Test weight	0.1313	0.1162	0.0080	-0.1480	0.7966	0.8257	-0.2958	-0.7594	0.6746

Residual effect= 0.616

al. (2010) also reported indirect contribution of number of branches plant^{-1} and number of pods plant^{-1} via each other. Also test weight showed negative indirect effect through number of seeds pod^{-1} and number of primary branches plant^{-1} but positive strong indirect effect through number of pods plant^{-1}. This investigation suggest that for getting higher seed yield there should be more number of secondary branches and number of pods plant^{-1}. The residual effect estimated was 0.616 indicating that the trait under study are not sufficient to account for variability and there might be a few more characters other than those studied in the present investigation thus inclusion of some more characters are necessary.

4. Conclusion

PA-291 can be used as a promising genotype since it exhibited high number of primary and secondary branches, high number of pods plant^{-1}, high test weight and high seed yield. And the genotypes *viz.* UPAS-120 which takes the least days to flower and shortest height, PA-421 which has the maximum test weight and PA-441 which have the maximum pods plant^{-1} may be considered as potential genotypes for incorporation in pigeon pea breeding programme.

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