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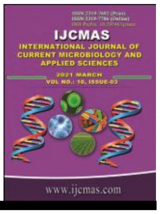

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Studies on Direct Selection Parameters for Seed Yield and its Component Traits in Pigeonpea [*Cajanus cajan* (L.) Millsp.]

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ABSTRACT

Pigeonpea [*Cajanus cajan* (L.) Millsp.] commonly known as arhar, red gram and tur is the second most important pulse crop of India after chickpea. It is. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian foods. Assessment of genetic variability present in the population and knowledge of association between yield and its components helps in formulating strong selection programme. Correlation studies would provide estimates of degree of association between grain yield and its various components and also among the components. While, path co-efficient analysis further elucidates the intrinsic nature of association of component traits by determining direct or indirect contribution of these traits to yield. Therefore**,** twenty one genotypes of pigeonpea were evaluated under rainfed conditions at Agricultural Research Station, Ummedganj, Agriculture University, Kota, Rajasthan, during *Kharif*, 2019-20. In the present study, high heritability accompanied with high genetic gain (GG) was recorded for days to flowering, pods per plant and grain yield. Grain yield was found to be highly significant and positively correlated with plant height, number of branches per plant, number of pods per plant, and test weight in pigeonpea. This indicated that selection for these traits would be effective to improve total grain yield in pigeonpea. In path analysis highest positive direct effect on grain yield was recorded for pods per pant, followed by number of branches per plant. Over all study showed that selection may effective for the pods per plant, branches par plant, test weight, and days to 80% maturity for development of early maturing and high yielding genotypes in pigeonpea.

Keywords

GCV, PCV, heritability, Genetic Gain, Correlation, Path Analysis, Pigeonpea

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Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is the second most important pulse crop of India after chickpea. It is commonly known as Arhar, Red gram and Tur. It has been recognized as a good source of vegetarian protein particularly in the developing countries where majority of the population depends on the low priced vegetarian foods. In fact, this crop has diversified uses such as food, feed, fodder and fuel. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals.

Assessment of genetic variability present in the population and the extent to which it is heritable are important factors to have effective selection in any breeding programme. Yield, being a complex character, is composed of several components some of which affect the yield directly, while, others affect indirectly. However, inheritance of quantitative characters is often influenced by variation in other characters which may be due to pleiotrophy or genetic linkage. Hence, knowledge of association between yield and its components helps in formulating selection programme. Correlation studies would provide estimates of degree of association between grain yield and its various components and also among the components. While, path co-efficient analysis further elucidates the intrinsic nature of association of component traits by determining direct or indirect contribution of these traits to yield (Baldaniya *et al*, 2018).

Materials and Methods

Twenty one genotypes of pigeonpea were evaluated under rainfed conditions at Agricultural Research Station, Ummedganj, Kota, Agriculture University, Kota, Rajasthan, during *Kharif*, 2019-20. The genotypes were grown in 6 rows of 3.6m length spaced 90 cm apart with the plant to plant distance of 25 cm. Each genotype was planted in three replications in Randomized Block Design. Observations were recorded on days to 50% flowering, days to 80% maturity, plant height (cm), branches per plant, pods per plant, 100-seed weight (g) and seed yield per plot (g). Recommended and uniform agronomical practices as well as plant protection measures were followed to raise the healthy crop. The genetic variability parameters, correlation (Singh and Chaudhary, 1985) and direct and indirect effects (Dewey and Lu, 1959) between seven characters were estimated in pigeonpea genotypes.

Results and Discussion

Mean squares due to genotypes revealed that genotypes had significant differences for the all the characters in pigeonpea. These results indicated that the genotypes exhibited sufficient amount of variability for grain yield and related traits. High estimates of phenotypic and genotypic coefficient of variation were recorded for grain yield, whereas moderate estimates of these were observed for pods per plant. The overall range of phenotypic coefficient variation (PCV) revealed relatively high values in comparison to corresponding genotypic coefficient of variation (GCV) for all the traits studied**,** indicating that all these traits were influenced by environment (Table 1). These finding are similar in agreement with earlier reported by Rao *et al.*, (2013), Pandey *et al.*, (2015), Kumar *et al.*, (2018) and Sharma *et al.*, (2020).

Higher heritability was observed for the characters like days to 50% flowering, days to 80% maturity, pods per plant, test weight and grain yield, suggesting that the highly heritable characters were least affected by environmental variation and selection for these characters based on phenotypic performance may be more effective for pigeonpea improvement. Similar results were also reported by Birhan *et al.*, (2013), Kumar *et al.*, (2018) and Sharma *et al.*, (2020). In the present study, high heritability accompanied along with high genetic gain (GG) was recorded for days to flowering, pods per plant and grain yield. The characters showing high heritability estimates coupled with high genetic gain (GG) indicates the preponderance of additive gene action and greater scope for improvement in these traits through selection. Similar finding were also reported by Rao *et al.*, (2013) and Kumar *et al.*, (2018).

Association analysis provides measures of relationship among the traits and serves to assess the opportunity of mutual improvement of two desirable traits by common selection programme. Prior to any breeding program for the improvement in crops, it is imperative to obtain information regarding the inter-relationship of different plant characters with yield, since it facilitates a quick assessment of high yielding genotypes in selection program. The real or true association could be known only through genotypic correlation which eliminates the environmental influence. In the present investigation, grain yield per plot was found to be highly significant and positively correlated with plant height, number of branches per plant, number of pods per plant, and test weight (Table 2). This indicated that selection for these traits would be effective to improve total yield per plot in pigeonpea. This also suggested that above traits helped to improve total seed yield per. Similar findings of positive association were also reported by Prasanthi *et al.*, (2011) and Kumar *et al.*, (2018) for plant height, number of branches per plant and number of pods per plant. Similarly, Baldaniya *et al.*, (2018), Kumar *et al.*, (2018) and Sharma *et al.*, (2020) also reported same findings for pods per plant and branches per plant. Whereas, Bal *et al.*, (2018), Narayanan *et al.*, (2018) and Pal *et al.*, (2018) showed for pods per plant.

Table.1 Estimates of variability parameters for seed yield and its component traits in pigeonpea

S.No	Characters	Mean	GCV (%)	PCV (%)	Heritability h^2 (%)	GA	GG
1	Days to 50% Flowering	106.27	9.77	9.88	97.79	21.16	19.91
2	Days to 80% Maturity	204.71	4.03	4.06	98.19	16.84	8.22
3	Plant height(cm)	206.70	4.58	9.47	23.38	9.52	4.56
4	Branches/plant	5.90	7.10	11.60	37.47	0.52	8.95
5	Pods/plant	160.16	14.97	17.76	71.00	41.61	25.98
6	Test weight (gm)	10.68	5.15	6.12	70.75	0.95	8.92
7	Yield (gm)/Plot	895.22	50.30	52.31	92.43	891.81	99.61

Table.2 Estimates of genotypic correlation coefficients between seed yield and its component traits in pigeonpea

Characters	DF 50%	DM 80%	Plant height(cm)	Branches/ plant	Pods/ plant	Test weight	Seed Yield/ plot (g)
DF 50%	1.000						
DM 80%	0.757**	1.000					
Plant height(cm)	-0.169^{NS}	-0.136^{NS}	1.000				
Branches/ plant	-0.426**	-0.577**	0.390**	1.000			
Pods/ plant	-0.355**	-0.562**	0.229^{NS}	0.450**	1.000		
Test weight	-0.162^{NS}	-0.440**	-0.073^{NS}	0.239^{NS}	0.370**	1.000	
Seed Yield/ plot (g)	-0.505**	-0.644**	0.262*	0.685**	0.829**	0.381**	1.000

Table.3 Genotypic path coefficients showing direct and indirect effects of different characters on grain yield in pigeonpea

Character	DF 50%	DM 80%	Plant height(cm)	Branches/ plant	Pods/ plant	Test weight	r_g
DF 50%	**-0.187**	0.069	0.007	-0.160	-0.224	-0.010	-0.505^{**}
DM 80%	-0.141	**0.091**	0.005	-0.216	-0.354	-0.028	-0.644^{**}
Plant height(cm)	0.031	-0.012	**-0.043**	0.146	0.144	-0.004	0.262^{*}
Branches/plant	0.079	-0.052	-0.016	**0.375**	0.283	0.015	0.685^{**}
Pods/plant	0.066	-0.051	-0.009	0.169	**0.631**	0.023	0.829^{**}
Test weight	0.030	-0.040	0.003	0.089	0.233	**0.064**	0.381^{**}

Residual = 0.17079; r_g = Genotypic correlation of seed yield with yield components
*, ** Significant correlation with dependent character at 5% and 1%, respectively

In the selection programme, when less number of variable are considered, correlation study alone can serve the purpose. However, when variables are increased, the situation becomes complex. For overcoming this complexity, path analysis method was adopted to partition the genotypic correlation into direct and indirect effects, so that a relative merit of each trait is established and their number is reduced in selection programs. In the present investigation, the highest positive direct effect on grain yield was recorded for pods per pant, followed by number of branches per plant (Table 3). Over all study showed that selection may effective for the pods per plant, branches par plant, test weight, and days to 80% maturity for development of early maturing and high yielding genotypes in pigeonpea. These results were in conformity with of Rao *et al.*, (2013), Rekha *et al.*, (2013), Ram *et al.*, (2016), Verma *et al.*, (2018) and Sharma *et al.*, (2020). Therefore, selection for these traits in pigeonpea would be effective for genetic improvement as these traits may exhibit additive gene effects.

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