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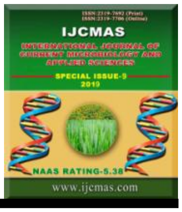

Original Research Article

Estimation of Variance and its Component for Different Quantitative Characters in Pigeon pea [*Cajanus cajan* (L.) Millsp.] Germplasm

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ABSTRACT

The present investigation was carried out at the Birsa Agricultural University Research farm (Dryland Section), Kanke, Ranchi during Kharif season 2016-17 utilizing 104 genotypes of Pigeonpea along with 4 checks viz. ASHA, BA-1, BAHAR and ICPB 2078, evaluated in a Augmented Block Design-II with 4 blocks with the spacing 1.5 m X 20 cm. observation were recorded from randomly selected five plants and checks for fourteen quantitative characters viz. Number of initial plant stand plot,$^{-1}$ Number of final plant stands plot^{-1} Days to first flowering, Days to 50 % flowering, Days to maturity, Number of primary branches plant^{-1}, Number of secondary branches plant^{-1}, Plant height (cm), Number of pods plant^{-1}, Pod size (cm), Wilt (%), Sterility Mosaic Disease (%), 100 seed weight (g) and Yield (kg/ha). Analysis of variance revealed that, out of fourteen characters the significant treatment (eliminating block effect) differences were for only five traits i.e. initial plant stand plot^{-1} wilt (%), days to maturity, pod size and yield (kg/ha). Most of the characters showed a wide range in their gross variability. The coefficient of variation was the highest for sterility mosaic disease (267.79%), wilt % (156.47%), and number of primary branches plant^{-1} (140.69%). High heritability estimates was observed for initial plant stands plot^{-1}, wilt (%), days to maturity, pod size(cm), and yield (kg/ha) whereas high value of genetic advance as mean was found wilt (%), pod size(cm), and yield (kg/ha). Relatively high GCV, PCV heritability (broad sense) and genetic advance as percent of mean, wilt percent, pod size (cm) and yield (kg/ha) which suggested that these characters could be transmitted to the progeny when hybridization would be conducted and phenotypic based selection would be effective.

Keywords

Augmented design, Pigeonpea, Variance, Heritability, Genetic advance, Germplasm.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] also known as Arhar, Red gram, Tur, Cango Pea, Angole, Rahar etc. is often cross pollinated (20-70%) crop belonging to the family Leguminoseae. India is considered as the native of Pigeonpea (Van der Maesen, 1980) because of its natural genetic variability available in the local germplasm and the presence of its wild relatives in the country. It is a deep rooted and drought-tolerant leguminous food crop which can grow in any warm climate well suited for tropical and sub-tropical regions. In India, Pigeonpea is second most important pulse crop after Chickpea (Sodavadiya *et al.*, 2009 and Vijayalakshmi *et al.*, 2013) and is the world's largest pigeon pea producer accounting for 90 per cent of the world production (Rangare *et al.*, 2013). In India, Pigeonpea is grown in 5.13 million ha area with the production and productivity of 4.23 million tonnes and 824 kg/ha respectively (Anon, 2016-17). In Jharkhand, Pigeonpea area, production and productivity occupies about 193.7 thousand ha, 202.0 thousand tonnes and 1045 kg/ha respectively (Anon, 2016-17). Pigeon pea is highly proteinaceous 18-29 % which is about three times the value found in cereals (Techale *et al.*, 2013). 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. The productivity of Pigeonpea is constant since last decades, which is mainly due to lack of high yielding variety grown in the region and also because of susceptibility of biotic (Pod borer and wilt) and abiotic (Drought and acidity) stresses. The wild relatives of cultivated species are important source of genetic variability for various desired agronomic traits including seed quality, resistance to various biotic and abiotic stresses. Utilization of crop wild relatives in Pigeonpea improvement is generally envisaged from its secondary pool. Systematic study and characterization of germplasm is not only important for utilizing the appropriate attribute based donors, but also essential in the present era for protecting the unique Pigeonpea genotypes.

Materials and Methods

A total of 104 genotypes of Pigeonpea along with 4 checks viz; ASHA, BA-1, BAHAR and ICPB 2078 were evaluated in a Augmented Block Design-II with 4 blocks with a spacing of 1.5 m X 20 cm at the Birsa Agricultural University Research farm (Dryland Section), Kanke, Ranchi during Kharif season 2016-17. Observation was recorded from five random selected plants and checks for 14 quantitative characters viz. Number of initial plant stand plot,$^{-1}$ Number of final plant stands plot,$^{-1}$ Days to first flowering, Days to 50 % flowering, Days to maturity, Number of primary branches plant$^{-1,}$ Number of secondary branches plant^{-1} , Plant height (cm), Number of pods plant^{-1}, Pod size (cm), Wilt (%), Sterility Mosaic Disease (%),100 seed weight (gm) and Yield (kg/ha) selected plants for quantitative characters. The data recorded was subjected to analysis of variance for Augmented Randomized Block Design (Federer, 1956), genotypic variance and phenotypic variance (Nadarajan and Gunasekaran, 2005), Genotypic Coefficient of variation, Phenotypic Coefficient of variation, Heritability (Singh and Choudhary, 1977) and genetic advance (Johnson *et al.*, 1955).

Results and Discussion

Analysis of variance revealed that, out of fourteen characters the significant treatment (eliminating block effect) differences were for only five traits i.e. initial plant stand plot^{-1} wilt (%), days to maturity, pod size and yield (kg/ha). The check's mean sum of square value was found significant for days to maturity while block's mean sum of square was found significant for six traits whereas, the mean sum of square due to check versus varieties were found to be significant for only two characters (Table 1).

As indicated in Table-2, most of the characters showed a wide range in their gross variability. These characters were grain yield (18.94-1813.04) kg/ha, number of pods plant^{-1} (0.68-177.43), plant height (81.67-183.57) cm, wilt% (-2.88-72.11), number of secondary branches plant^{-1} (5.85-44.50), days to first flowering (77.56-111.31), days to 50% flowering (87.75-121.00) and number of primary branches plant^{-1} (-2.91-24.23) .However, pod size (0, 03-6.75) cm, initial plant stand plot^{-1} (13.12-21.37) and 100 seed weight (-0.05-11.54) gm showed lowest range of variability.

The coefficient of variation was the highest for sterility mosaic disease (267.79%), wilt % (156.47%), and number of primary branches plant^{-1}(140.69%).The lowest coefficient of variation was shown by the character, pod size (1.66%), days to maturity (1.77%), initial plant stand per plot(6.60%), days to 50% flowering (7.58%) and followed by 100 seed weight (8.51%).

The genetic coefficient of variation (table 3) provides a measure to compare the genetic variability present among the various quantitative traits.The genotypic coefficient of variation for different quantitative character ranged from (2.60) days to maturity to (267.00) for wilt. The characters namely, pod size (35.05) and grain yield (18.56) also recorded high value of phenotypic coefficient of variation. The other characters, initial plant stands plot^{-1} gave moderate to low values of phenotypic coefficient of variation.

Similar results obtained by Islam *et al.,* (1985), Nimbalkar (2000), Basir *et al.,* (2001), Saukat *et al., (*2002) and Kumar *et al.,* (2014) who observed low value of GCV and PCV for days to maturity Prashant *et al.,* (1990), Kavita and Reddy (2002), Saukat *et al.,* (2002), Sandhu and Mandal (1989), Singh *et al.,* (2000), Kumar *et al.,* (2010) who observed moderate GCV and PCV of grain yield in Pigeonpea.

High heritability estimates was observed for initial plant stands plot^{-1}, wilt(%), days to maturity, pod size(cm), and yield (kg/ha) which is clearly indicate that these characters were least influence by environment. The results are in accordance with reports of earlier work reported by, Manyasa *et al.,* (2007), Singh *et al.,* (2009), Khan *et al., (*2011), Sharma *et al.,* (2012), Chetukuri *et al.,* (2013), Mustaq and Saleem (2013), Shuney *et al.,* (2013), Rangare *et al.,* (2013) and Patel *et al.,* (2014) for days to maturity, Dasgupta *et al.,* (1992), Tripathi *et al.,* (1998), Kumar *et al.,* (1999), Altinbas *et al.,* (2002), Sable *et al.,* (2003), Durga *et al.,* (2007), Canci *et al.,* (2007), Vange and Moses (2009), Khan *et al., (*2011), Mustaq and Saleem (2013), Birhan *et al.,* (2013), Saroj *et al.,* (2013), Shuney *et al.,* (2013), Rangare *et al.,* (2013), Patel *et al.,* (2014), Priyanka *et al.,* (2016) and Sharma *et al.,* (2017) for Yield.

From the study of genetic advance as per cent of mean for different characters, it was observed that the high value of genetic advance as mean was found wilt (%), pod size (cm), and yield (kg/ha). Moderate value of genetic advance was found for initial plant stands plot^{-1} and low value was found for days to maturity. The above results indicated that the characters wilt (%), pod size and yield show high heritability coupled high genetic advance as percent of mean due to predominance of the additive gene action. Therefore, selection may be effective for further improvement of these traits. These results are in agreement with the findings reported by, Dasgupta *et al.,* (1992),Kumar *et al.,* (1999), Basavarajaijah *et al., (*2000), Durga *et al.,* (2007), Vange and Moses (2009), Birhan *et al.,* (2013), Saroj *et al.,* (2013), Shuney *et al., (*2013), Rangare *et al.,* (2013), Priyanka *et al.,* (2016), and Sharma *et al.,* (2017). The characters like initial plant stands per plot and days to maturity exhibit high heritability coupled with moderate to low genetic advance as percent of mean, suggesting predominance of non-additive gene action in the inheritance of these characters; in this case selection may not be effective.

Table.1 Mean Sum of Squares of Analysis of Variance (ANOVA) for fourteen quantitative traits of Pigeonpea genotypes

Source of variation	**DF**	**Initial plant stands plot-1(No.)**	**Days to first flowering**	**Days to 50 % flowering**	**No. of Pr. Branches plant^{-1}**	**No. of Sec. branches Plant^{-1}**	**Plant Height (cm)**	**Days to Maturity**
Block(Ignoring Treatment)	3	18.14**	127.32	126.36	43.55	18.46	2169.96**	98.05**
Treatment (Eliminating Block)	107	3.33*	23.21	24.41	25.87	27.73	331.82	140.23**
Entries(Ignoring Block)	107	3.63	23.18	24.53	15.83	17.60	390.73	142.67**
Checks	3	1.75	119.89	152.33	390.69	415.20	240.15	2953.50**
Varieties	103	3.72	20.59	21.04	1.90	2.67	393.38	37.72*
Checks *vs.* Varieties	1	0.01	0.11	0.28	326.30	362.44	569.68	2520.00**
Error	9	1.36	61.50	59.94	417.94	418.16	188.49	111.89
Block(Ignoring Treatment)	**DF**	**No. of Pods plant^{-1}**	**Wilt (%)**	**Sterility mosaic disease (%)**	**Final plant stands plot^{-1}(No.)**	**Pod size (cm)**	**100seed weight (g)**	**Yield (kg/ha)**
Treatment (Eliminating Block)	3	869.69	217.72**	31.56	5.75	14.39**	4.76**	1081101.64**
Entries(Ignoring Block)	107	381.93	68.29*	14.91	4.94	4.09**	1.28	33845.32*
Checks	107	400.90	73.44*	15.61	4.97	4.46**	1.41	36771.50*
Varieties	3	125.77	37.07	6.79	3.72	2.30	0.35	13919.21
Checks *vs.* Varieties	103	412.80	75.19*	16.01	5.05	4.45**	1.44	37709.93*
Error	1	0.70	2.18	0.02	0.09	11.84**	0.79	8669.66
Block(Ignoring Treatment)	9	19.06	2.61	20.98	20.98	0.80	0.63	9945.40

*Significant at 5%, **Significant at 1%

Table.2 Estimation and original value of range and grand mean for fourteen quantitative traits of Pigeonpea genotypes

Sl. No.	Characters	Range		Mean	S.Em(±)	CV (%)	CD at 5%
		Lowest	Highest				
1	Initial plant stand plot^{-1} (No.)	13.12(15.0)	21.37(20)	17.65	0.58	6.60	1.86
2	Days to first flowering	77.56(85.0)	111.31(125.0)	91.97	3.92	8.52	12.53
3	Days to 50 % flowering	87.75(97.0)	121.00(136.0)	102.10	3.87	7.58	12.37
4	No. of primary branches	-2.91(11.0)	24.23(18.0)	14.53	10.22	140.69	32.67
5	No. of secondary branches	5.85(20.0)	44.50(28.0)	24.13	10.22	84.74	32.67
6	Plant height(cm)	81.67(86.0)	183.57(227.0)	139.30	6.86	9.85	21.94
7	Days to maturity	181.00(181.0)	247.00(248.0)	194.01	1.72	1.77	5.51
8	No. of pods plant^{-1}	0.68(25.0)	177.43(184.0)	135.01	9.05	13.40	28.92
9	Wilt (%)	-2.88(0.0)	72.11(75.0)	2.79	2.18	156.47	6.97
10	Sterility mosaic disease (%)	-1.19(0.0)	23.80(25.0)	1.71	2.28	267.79	7.31
11	Final plant stand plot^{-1} (No.)	5.56(15.0)	21.06(20)	17.14	0.80	9.42	2.58
12	Pod Size((cm)	0.03(4.0)	6.76(7.0)	5.42	0.45	1.66	1.44
13	100 Seed weight (g)	-0.05(8.0)	11.54(11.3)	9.32	0.39	8.51	1.26
14	Yield (kg/ha)	18.94(90.0)	1813.04(1833.0)	893.29	49.86	11.16	159.36

S.E m **(±):** Standard Error of Mean
C.V: Coefficient of Variation
C.D: Critical Difference

Table.3 Genetic estimates for only five quantitative traits

Sl. No.	**Characters**	**Phenotypic variance** $(\sigma^2 P)$	**Genotypic variance** $(\sigma^2 G)$	**Error variance** $(\sigma^2 E)$	**GCV (%)**	**PCV (%)**	**h^2 (%)**	**GA (%)**
1.	Initial plant stands plot^{-1}	3.69	2.33	1.36	8.61	10.87	63.14	14.16
2.	Wilt (%)	74.65	55.59	19.06	267.02	309.00	74.46	472
3.	Days to maturity	37.47	25.58	11.89	2.60	3.15	68.26	4.41
4.	Pod Size(cm)	4.41	3.61	0.80	35.05	38.74	81.85	64.45
5.	Yield (Kg/ha)	37442.91	27497.51	9945.40	18.56	21.66	73.43	32.57

GCV: Genotypic Coefficient of Variation, PCV: Phenotypic Coefficient of Variation, h^2: Heritability, GA: Genetic Advance

Table.4 Promising genotypes identified for different quantitative characters in Pigeonpea

S. No	**Different quantitative characters**									
	DF	**DFF**	**DM**	**PB**	**PH**	**PPP**	**W**	**SMD**	**100 SW**	**Y**
1	-	-	-	-	ICPB2051	ICPB2051	-	-	-	-
2	-	-	WRG220	-	-	-	-	WRG220	-	WRG220
3	CRG2012-30	CRG2012-30	-	-	-	-	-	-	-	-
4	-	-	-	-	-	WRG204	-	-	-	WRG204
5	-	-	-	WRG293	-	-	-	-	-	WRG293
6	-	-	WRG260	-	-	-	WRG260	WRG260	-	-
7	-	-	-	-	-	-	WRG283	WRG283	-	-
8	-	-	-	RVSA07-12	-	-	RVSA07-12	-	-	-
9	-	-	WRG197	WRG197	-	WRG197	-	-	-	-
10	BSMR243	BSMR243	-	-	-	BSMR243	-	-	-	BSMR243
11	-	-	-	-	ICP7035	-	-	-	ICP7035	-
12	-	-	-	-	-	-	RVSA-9	RVSA-9	-	-

DF-Days to first flowering, DFF-Days to 50 % flowering, DM-Days to maturity, PB-Primary branches, PH-Plant height, PPP-Pods Plant^{-1}, W-Wilt, SMD-Sterility Mosaic Disease, 100 SW-100 seed weight and Y-Yield

Relatively high GCV, PCV heritability (broad sense) and genetic advance as percent of mean, wilt percent, pod size(cm) and yield(kg/ha) suggested these characters could be transmitted to the progeny when hybridization would be conducted and phenotypic based selection would be effective.

In conclusion, the knowledge of variability for various quantitative characters will provide an estimate in formulating sound breeding programme and will also help breeder in selection of suitable parent for future breeding programme.The result revealed that relatively high GCV, PCV heritability(broad sense) and genetic advance as percent of mean was observed for wilt percent, pod size(cm) and yield (kg/ha), which suggested that these characters could be transmitted to the progeny when hybridization would be conducted and selection based on phenotypic would be effective. Thus selection for these traits would be advantageous for future improvement in Pigeonpea. Five promising genotypes of Pigeonpea (table 4) were selected as donor for multiple traits for utilization in hybridization programme or may be directly used if found stable. High number of pods plant^{-1} were observed for the early ICPB 2051,WRG 204,WRG 197 and BSMR 243, while the genotypes WRG 220, WRG 204, WRG 293 and BSMR 243 were good as far as seed yield plant is concerned. Low incidence of wilt and sterility Mosaic Disease was recorded for the entry, WRG 260,WRG283,and RVSA-9.These genotypes can be used for hybridization programme for disease resistant . From the table 4 it may be concluded that the genotypes WRG 204, WRG260, WRG220, WRG197 and BSMR 243 were identified as good performance for most of the yield attributing traits and hence may be used for further breeding programme.

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