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Research Article

Genetic analysis and trait association in F_2 populations of four different crosses in pigeonpea (*Cajanus cajan* L. Millsp.)

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Abstract

Pigeonpea, a predominant protein source for vast vegetarian population is constrained by numerous biotic and abiotic stresses. Inefficient exploitation of pigeonpea germplasm has limited its utilization. Therefore it is important to identify and select breeding material from germplasm with sufficient genetic variability to utilize in hybridization programmes. In this regard ~200 F_2 plants each from four different crosses were evaluated in *Kharif*-2019 at University of Agricultural Sciences Bengaluru. They were assessed for genetic variability, heritability, genetic advance as *per cent* of mean and trait association. High phenotypic and genotypic coefficient of variation was noticed for pods plant^{-1}, clusters plant^{-1} and seed yield plant^{-1}. High heritability coupled with higher genetic advance as *per cent* mean was noticed for secondary branches plant^{-1}, clusters plant^{-1} and pods plant^{-1}. Seed yield plant^{-1} showed highest significant positive correlation with pods plant^{-1} and clusters plant^{-1}, indicating these traits were the primary yield determinants in pigeonpea. Path coefficient analysis revealed that secondary branches plant^{-1} showed highest positive direct effect on seed yield plant^{-1} followed by pods plant^{-1} and clusters plant^{-1}, thus selection based on these traits would be rewarding. Among the four crosses evaluated, highest numbers of transgressive segregants were identified from the cross BRG-1 × BDN-2 followed by HY3C × BDN-2 for yield and its related traits. The identified transgressive segregants could be evaluated for further exploitation.

Keywords: Genetic variability, heritability, trait association, path coefficient, pigeonpea

INTRODUCTION

Pigeon pea (*Cajanus cajana. (L.)* Millsp.) is one of the major food legume crops of both tropics and subtropics. It belongs to the cajaninae sub-tribe of the economically important leguminous tribe phaseoleae. Based on the natural genetic variability in local germplasm and the presence of numerous wild relatives, Van der Maesen (1990) concluded that India is the probable primary centre of origin. It performs well in semi-arid tropics where moisture availability is unreliable or inadequate (Reddy et al 1993). Productivity of pulses worldwide in comparison to cereals is very low, it may be attributed to its low harvest index and limited man-made selections (Ganapathy *et al.,* 2012). Progress of any breeding programme depends on the amount of variability generated during hybridization. The presence of genetic variation in the basic genetic material is the primary requirement for any crop improvement programme. Hybridization between inbreds harbouring genes governing desirable traits aids in creation of genetic variability in desirable direction that helps to isolate superior genotypes in advanced generations. Time, land and human resource constraints makes it possible to advance only a few crosses. Comparison of means and variances in early segregating generations derived from the crosses is a commonly used practice to assess the relative breeding potential of cross combinations to discern superior recombinant inbred lines (Roy, 2000) in advanced generations.

Besides, to identify promising transgressive segregants, studies on genetic variability, heritability and genetic advance becomes important for effective selection and utilization of genotypes in breeding programme. The major aim of plant breeding is to achieve a higher level of seed yield which is a complex trait. It has generally been accepted that correlation between different traits represents a coordination of physiological processes, which is often achieved through gene linkages. The complex nature of seed yield is largely influenced by number of component traits. Hence, information on the strength and direction of association of these component traits with seed yield and also inter association among them would be very useful in formulating an effective and viable breeding programme for improvement of seed yield. Trait association studies are of great significance during selection by which simultaneous improvement of more than one trait is possible. However, the correlation coefficients between any two traits would not give a complete picture of a complex situation like yield of plant which is jointly determined by a number of traits influencing it either directly or indirectly. In such instances, path coefficient would be a useful approach as it permits the separation of direct effect from indirect effects through other related traits by partitioning the genotypic correlation coefficient (Dewey and Lu, 1959).Therefore, the present study sheds light on the extent of genetic variability, heritability, genetic advance and extent of trait association between yield and its component traits in the F_2 populations generated from four crosses of pigeonpea.

MATERIALS AND METHODS

The experimental material for the study consisted of 236, 208, 153 and 187 F_2 plants derived from four cross combinations namely, BRG-1 × BDN-2, BRG-1 × WRP-1, HY3C × BDN-2 and HY3C × WRP-1, referred as C1, C2, C3 and C4 respectively for the sake of ease. The F_2 plants derived from each of the four crosses and their parents with F_1s were planted in rows of 3.60 m length with a spacing of 0.20 m between plants and 0.90 m between rows during *Kharif* 2019 at experimental plots of All India Co-ordinated Research Project (AICRP) on pigeonpea, Zonal Agricultural Research Station (ZARS), University of Agricultural Sciences (UAS), Bangalore. All the recommended agronomic practices were followed to raise a good crop. Observations were recorded on each of the F_2 population for traits *viz*., days to first flowering, days to maturity, plant height, primary branches plant^{-1}, secondary branches plant^{-1}, pod bearing length (cm), seeds pod^{-1}, pod length (cm), clusters plant^{-1}, pods plant^{-1}, test weight (g) and seed yield plant^{-1}.

Statistical analysis: The individual F_2 plant data on the above mentioned traits was used to calculate descriptive statistics such as mean, absolute range (highest-lowest) and standardized range [(highest-lowest)/mean]. The estimates of phenotypic co-efficient of variation (PCV), genotypic co-efficient of variation (GCV) , heritability (h^2), genetic advance as *per cent* mean (GAM), correlation and path co-efficient were calculated using R software *version* 4.0.3. Further, one-way ANOVA and F-test were carried out to determine significant differences among the trait means and variances, respectively. The mean performance of the individual progenies of the F_2 segregating populations derived from the four crosses were compared with the superior parental mean for days to first flowering, yield and yield attributing traits to identify superior transgressive segregants and the frequency of such recombinants was worked out. Transgressive segregation index (TSI) was estimated as [absolute range/trait mean difference between parents].

RESULTS AND DISCUSSION

First degree statistics: The F_2 generations derived from the four crosses differed significantly for all the traits studied except pod bearing length, primary branches plant^{-1} and clusters plant^{-1} (**Table 1**). The F_2 population of the cross C1 had the shortest mean time to 50% flowering, highest mean number of primary branches plant^{-1} and highest mean seed yield plant^{-1}, indicating its potential use in isolating productive short-duration RILs in advanced generations (**Table 1**). Subsequently F_2 descendants from the cross C4 displayed greater primary and secondary branches plant^{-1}, increased pod bearing length and increased seeds pod^{-1} designating and hence could be considered as the second best cross of the study for yield with late maturity. Bernardo 2020, suggested that higher traits' mean indicate the presence of genes that enhances the phenotype and accelerates the probability of recovering superior RILs in advanced generations.
The estimates of standardized and absolute range were higher in the cross C4 than the other crosses for most of the traits studied (**Table 1**).

Second degree statistics: Variance of any segregating population such as those being discussed here (F_2) indicates the degree of scope for selection of genotypes with desired combination of traits. Higher the variance, higher will be the scope for selection. As indicated by F-test, there exists no significant differences between the crosses for the traits evaluated except test weight (**Table 1**). However, the PCV (%) in the cross C4 was higher than the other three crosses (**Table 2**) for days to first flowering, days to 50 % maturity and pod bearing length. The PCV (%) represented an unbiased and true reflection of variability. The GCV for various characters varied from 6.35 (days to 50% maturity) to 94.94 (clusters plant^{-1}) per cent. Further low GCV (%) estimates were observed for Narrow difference between GCV (%) and PCV (%) for days to first flowering, seeds pod^{-1}, days to 50% maturity, and primary branches plant^{-1} in F_2 populations of all the four crosses (**Table 2**) indicated less influence of environment on expression of these

Table 1. Estimates of trait means, variance, standardized range & absolute range of F_2 population derived from four different crosses of pigeonpea in this study

Trait	Mean						Variance						Standardized Range				Absolute Range			
	C1	C2	C3	C4	F-val.	Prb.	C1	C2	C3	C4	F-val.	Prb.	C1	C2	C3	C4	C1	C2	C3	C4
Days to first flowering	113.84	118.89	118.51	116.16	8.57	0.00	0.33	0.66	0.62	0.60	1.04	0.78	0.53	0.44	0.72	0.80	61.00	53.00	86.00	94.00
Days to 50% maturity	152.17	155.72	154.77	157.36	6.95	0.00	0.44	0.60	0.88	0.11	2.32	0.50	0.49	0.37	0.58	0.57	76.00	59.00	90.00	91.00
Plant height (cm)	168.10	173.72	179.45	173.68	7.27	0.00	46.84	124.22	145.40	156.60	6.43	0.09	0.82	0.84	0.87	0.88	139.00	147.00	157.00	153.00
Primary branches plant^{-1}	3.46	3.17	3.15	3.29	3.32	0.19	5.60	5.80	6.20	5.70	5.41	0.14	1.73	1.57	1.26	1.82	6.00	5.00	4.00	6.00
Secondary branches plant^{-1}	16.04	13.25	13.69	16.19	5.41	0.00	23.30	18.60	21.80	18.20	6.14	0.10	2.55	3.62	3.14	3.15	41.00	48.00	43.00	51.00
Pod bearing length (cm)	39.37	38.65	39.97	40.76	1.29	0.28	21.82	29.95	57.60	24.00	2.69	0.44	1.47	1.47	1.32	1.76	58.00	57.00	53.00	56.00
Seeds pod^{-1}	4.30	4.42	4.32	4.46	4.08	0.01	0.10	0.23	0.23	0.10	2.99	0.39	0.69	0.67	0.69	0.44	3.00	3.00	3.00	2.00
Pod length (cm)	5.12	5.41	5.05	5.06	11.29	0.00	0.05	0.07	0.02	0.06	1.98	0.57	0.60	0.79	0.55	0.65	2.00	2.00	2.00	2.00
Clusters plant^{-1}	39.28	37.04	48.96	42.75	3.37	0.18	0.15	0.18	0.24	0.23	0.63	0.88	6.18	4.50	4.33	9.49	243.00	167.00	212.00	406.00
Pods plant^{-1}	76.72	49.97	78.71	69.78	9.28	0.00	0.70	0.19	0.14	0.25	2.97	0.39	5.94	5.82	5.14	7.88	456.00	291.00	405.00	550.00
Test weight (g)	11.89	12.07	10.41	10.73	41.22	0.00	0.48	0.11	0.19	0.28	2.14	0.00	1.00	0.86	0.81	0.83	12.00	10.50	8.50	11.00
Seed yield plant^{-1} (g)	19.45	14.34	18.88	14.77	5.67	0.00	0.25	0.17	0.10	0.69	4.06	0.25	4.80	6.27	6.91	8.39	93.50	94.00	130.50	124.00

F-val. = F-Value; Prb. = Probability; C1- BRG-1 × BDN-2; C2- BRG-1 × WRP-1; C3- HY3C × BDN-2; C4- HY3C × WRP-1

traits. Highest difference between PCV (%) and GCV (%) was noticed for grain yield plant^{-1} and pods plant^{-1}, indicating that environment had greater influence on the expression of these two traits. (**Table 2**). Similar results were observed by Rao and Rao (2015), Pushpavalli *et al.* (2018), Anuradha and Patro (2019) and Linge *et al.* (2010) in pigeonpea.

The PCV for various characters varied from 6.72 (days to 50% maturity) to 98.64 (clusters plant^{-1}) per cent. High PCV was observed for primary branches plant^{-1}, secondary branches plant^{-1}, pod bearing length, clusters plant^{-1}, pods plant^{-1}and seed yield plant^{-1} indicating that expression of these trait is much influenced by the environment. Low PCV was observed for days to 1st flower opening and days to 50% maturity indicating less influence of environment on expression of these traits (**Table 2**). Similar results were also observed by Rao and Rao (2015) and Linge *et al.* (2010) in pigeonpea.

Higher estimate of heritability was exhibited by all the traits under evaluation except primary branches plant^{-1} and seed yield plant^{-1}. Seed yield plant^{-1} exhibited low to high heritability (broad sense) and high GAM (%) whereas, primary branches plant^{-1} exhibited a low heritability and low to moderately higher GAM (**Table 2**). High heritability (broad sense) andhigher GAM was observed, indicating these traits were governed by additive genes. Hence, simple selection may be practiced on these traits to develop superior RILs with superior yield performance. Similar results were reported by Sreelakshmi *et al.* (2010), Rao and Rao (2015) and Rao *et al.* (2016).

Low GAM (%) was reported for days to first flowering, primary branches plant^{-1} and days to 50 *per cent* maturity and seeds pod^{-1} across all the crosses. Higher GAM (%) for seed yield plant^{-1}, pods plant^{-1}, clusters plant^{-1} and secondary branches plant^{-1} indicated that these traits are under the influence of additive gene action. Hence, genetic gain will be rewarding for these traits. Simple selection practice may lead to improvement of these traits. This is in line with the results of Hemavathy *et al.* (2019) and Nair *et al.* (2018).

Table 2. Estimates of genetic variability parameters for growth, yield and yield attributing traits in F_2 population of four pigeonpea crosses in this study

Trait	PCV (%)				GCV (%)				h^2				GAM			
	C1	C2	C3	C4	C1	C2	C3	C4	C1	C2	C3	C4	C1	C2	C3	C4
Days to first flowering	8.89	9.51	10.24	11.43	8.60	9.25	9.87	11.15	93.65	94.69	92.84	95.18	17.15	18.55	19.59	22.41
Days to 50% maturity	6.72	7.87	8.28	8.39	6.35	7.72	8.00	8.08	89.23	90.53	93.31	92.76	12.60	14.68	15.93	16.03
Plant height (cm)	13.94	14.74	12.92	12.74	13.27	13.74	12.46	12.11	90.66	86.83	93.09	90.29	26.04	26.38	24.78	23.07
Primary branches plant^{-1}	33.84	34.19	37.08	33.52	14.70	18.71	7.40	6.24	18.88	29.94	3.98	3.46	13.16	21.09	3.04	2.39
Secondary branches plant^{-1}	62.62	67.87	67.68	53.55	58.42	55.41	61.46	49.66	86.20	66.65	82.45	86.01	111.73	93.19	114.96	94.88
Pod bearing length (cm)	25.85	27.78	26.20	31.23	23.78	24.66	21.93	29.19	84.62	78.80	70.09	87.32	45.06	45.10	37.83	56.19
Seeds pod^{-1}	11.57	13.40	12.06	12.07	10.34	10.96	7.70	9.92	79.88	66.92	40.77	67.53	19.04	18.48	10.13	16.80
Pod length (cm)	14.11	15.31	11.58	12.15	13.25	14.46	10.61	10.90	88.13	89.23	83.96	80.49	25.63	28.14	20.04	20.16
Clusters plant^{-1}	98.64	6.94	74.70	84.34	94.94	61.49	71.85	80.81	92.64	91.93	92.32	91.81	188.25	114.67	142.29	159.52
Pods plant^{-1}	87.13	93.35	85.28	87.60	78.51	63.77	76.72	76.18	81.19	46.66	80.93	75.62	145.75	89.73	145.67	136.47
Test weight (g)	16.62	13.99	15.44	15.68	16.27	13.45	15.03	14.98	95.91	92.33	94.70	91.28	32.84	26.62	30.13	29.49
Seed yield plant-1 (g)	85.41	95.31	79.63	93.04	46.37	49.19	55.95	75.35	29.48	26.63	49.37	65.59	51.87	52.3	80.99	125.72

PCV=Phenotypic Coefficient of Variation; GCV= Genotypic Coefficient of Variation; h2=Heritability; GAM=Genetic Advance per cent Mean; C1- BRG-1 × BDN-2; C2- BRG-1 × WRP-1; C3- HY3C × BDN-2; C4- HY3C × WRP-1

Heritability along with genetic advance is useful and reliable in predicting the resultant effects of selection. Selection can only be achieved when high heritability is accompanied with high genetic advance (Burton 1952).

Identification of desirable transgressive segregants for earliness and increased seed yield and its attributing traits in F_2 population of the four pigeonpea crosses.

Harnessing transgressive segregants: Transgressive segregants for early maturity and seed yield and its attributing traits were identified in the F_2 generation of all the four crosses. A higher number of transgressive segregants with early flowering (5.35%), increased pod bearing length (10.16 %) and higher number of clusters plant^{-1} (96.79 %) were obtained in C4 (**Table 3**). This result was similar with the observations of Anantharaju and Muthiah, (2008) & Ajay *et al.* (2014) in pigeonpea and Chauhan *et al.* (2018) in black gram. Higher frequency of transgressive segregants in F_2 population of the cross C4 could be attributed to dispersion of parental linked (repulsion phase) genes controlling the said traits (Kearsey and Pooni 1996; Bernardo, 2020). It is engrossing to observe that none of the crosses produced transgressive segregants higher than their respective higher parent for seed yield plant^{-1}. Low frequency of transgression may be caused by genes linked in coupling phase in the parents (Choo *et al.,* 1986).

Higher number of transgressive segregants were recorded in the cross C1 followed by C3 for various combination of traits indicating superiority of these two crosses over other crosses. Across the four cross, higher number of transgressive segregants were identified for the traits pod length and pod bearing length whereas, lower for seed yield plant^{-1} followed by pods plant^{-1} (**Table 3A; 3B; 3C & 3D**). Superior performance of transgressive segregants is attributed to the recombination of favorable genes (positive alleles) from both parents in addition to additive gene action and due to contribution of component traits. This result was similar to the observations of Anantharaju and Muthiah, (2008) & Ajay *et al.* (2014) in pigeonpea and Chauhan *et al.* (2018) in black gram.

The transgressive segregation index (TSI): Without transgressive segregation (TS), plant breeding does not work; plant breeding does work, therefore TS occurs (Mackay et al 2020). The cross C4 displayed higher TSI than other crosses for days to 50% maturity, clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1}. While, the cross C1 displayed higher TSI than other crosses for days to first flowering and pod bearing length (**Table 3**). Jambormias *et al.* (2015) in mung bean, Shreya *et al.* (2017) in groundnut, Suresh *et al.* (2017) in dolichos bean and Guindon *et al.* (2018) in pea have also reported TS for economically important traits. Theoretical investigations have indicated that TS results from

Table 3. Estimates of frequency (%) of transgressive segregants (%) & TSI for significantly positive correlated traits obtained in F$_2$ generation of the four crosses of pigeonpea used in the study

Trait	Per cent transgressive segregants obtained in F$_2$ in the desirable direction				Transgression index in F$_2$ populations			
	C1	C2	C3	C4	C1	C2	C3	C4
Days to first flowering	2.54	0.96	1.31	5.35	30.50	13.25	28.66	18.80
Days to 50% maturity	48.72	44.71	46.41	22.99	15.20	19.66	45.00	91.00
Pod bearing length (cm)	9.75	10.09	7.19	10.16	2.23	1.61	1.92	1.52
Clusters plant^{-1}	94.92	96.15	94.12	96.79	11.14	22.87	7.53	30.25
Pods plant^{-1}	81.35	0.00	0.65	0.53	7.29	1.82	3.75	35.71
Seed yield plant^{-1} (g)	0.00	0.00	0.00	0.00	2.36	2.71	1.80	5.24

C1- BRG-1 × BDN-2; C2- BRG-1 × WRP-1; C3- HY3C × BDN-2; C4- HY3C × WRP-1

Table 3A. Transgressive segregants (TS) identified for combination of traits in F$_2$ population of pigeonpea derived from the cross BRG-1 × BDN-2 used in the study

Trait	BRG-1 × BDN-2										Check (Mean of Parents)		
Identity of TS	P-338	P-372	P-516	P-483	P-14	P-445	P-32	P-9	P-6	P-316	BRG-1	BDN-2	Mean F$_2$
Days to first flowering	111.00	111.00	107.00	110.00	97.00	85.00	85.00	85.00	90.00	109.00	98.00	96.00	113.84
Days to 50% maturity	161.00	154.00	153.00	142.00	136.00	126.00	123.00	120.00	126.00	151.00	156.00	151.00	152.17
Pod bearing length (cm)	60.00	30.00	80.00	58.00	55.00	50.00	68.00	50.00	50.00	70.00	28.40	54.40	39.37
Clusters plant^{-1}	245.00	230.00	200.00	200.00	100.00	80.00	70.00	49.00	45.00	74.00	118.00	139.80	41.73
Pods plant^{-1}	460.00	330.00	275.00	270.00	225.00	210.00	200.00	113.00	111.00	155.00	134.30	417.20	76.72
Seed yield plant^{-1} (g)	85.00	71.50	69.00	64.00	95.00	47.50	43.50	25.00	19.00	29.50	102.12	141.58	19.45

Table 3B. Transgressive segregants (TS) identified for combination of traits in F$_2$ population of pigeonpea derived from the cross BRG-1 × WRP-1 used in the study

Trait	BRG-1 × WRP-1							Check (Mean of Parents)		
Identity of TS	P-388	P-351	P-510	P-775	P-35	P-583	P-198	BRG-1	WRP-1	Mean F$_2$
Days to first flowering	104.00	108.00	112.00	102.00	99.00	113.00	113.00	98.00	94.00	118.89
Days to 50% maturity	144.00	146.00	149.00	136.00	136.00	140.00	159.00	156.00	153.00	155.72
Pod bearing length (cm)	37.00	47.00	53.00	50.00	78.00	45.00	47.00	28.40	63.60	38.56
Clusters plant^{-1}	187.00	158.00	142.00	153.00	125.00	119.00	185.00	118.00	110.70	27.10
Pods plant^{-1}	294.00	202.00	180.00	195.00	190.00	220.00	280.00	134.30	294.00	49.97
Seed yield plant^{-1} (g)	86.50	68.00	92.00	62.50	61.50	58.00	56.50	102.12	69.98	14.34

Table 3C. Transgressive segregants (TS) identified for combination of traits in F$_2$ population of pigeonpea derived from the cross HY3C × BDN-2 used in the study

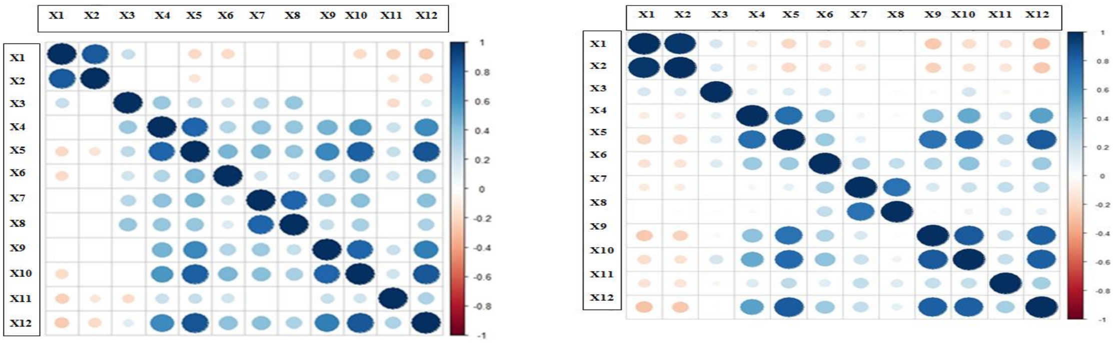
Trait	HY3C × BDN-2									Check (Mean of Parents)		
Identity of TS	P-586	P-3	P-142	P-585	P-898	P-966	P-1141	P-1145	P-816	HY3C	BDN-2	Mean F$_2$
Days to first flowering	102.00	115.00	135.00	107.00	111.00	114.00	102.00	123.00	90.00	99.00	96.00	154.77
Days to 50% maturity	139.00	150.00	165.00	140.00	145.00	152.00	146.00	157.00	128.00	153.00	151.00	179.45
Pod bearing length (cm)	75.00	50.00	37.00	53.00	68.00	60.00	35.00	78.00	32.00	26.80	54.40	39.97
Clusters plant^{-1}	195.00	145.00	160.00	225.00	220.00	170.00	215.00	45.00	42.00	111.40	139.80	38.09
Pods plant^{-1}	425.00	200.00	180.00	365.00	315.00	290.00	235.00	60.00	45.00	309.40	417.20	70.06
Seed yield plant^{-1} (g)	70.50	39.00	38.00	34.50	69.00	47.00	44.00	21.00	16.50	69.32	141.58	14.05

Table 3D. Transgressive segregants (TS) identified for combination of traits in F_2 population of pigeonpea derived from the cross HY3C × WRP-1 used in the study

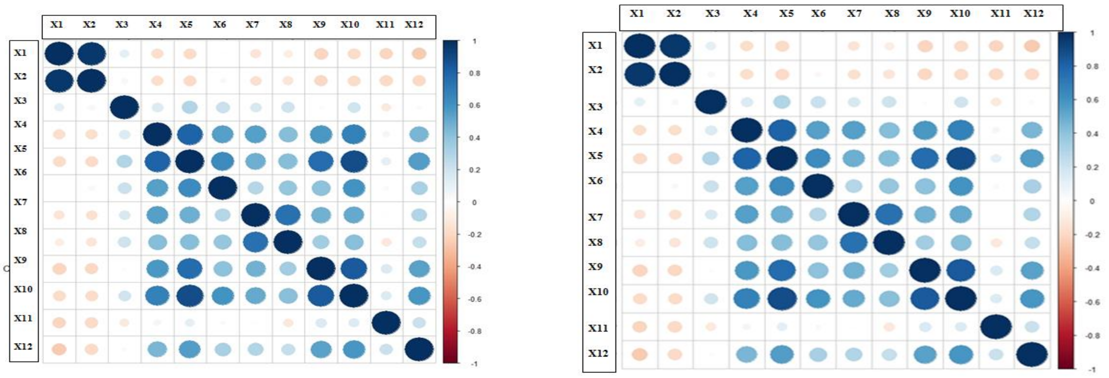
Trait	HY3C × WRP-1					Check (Mean of Parents)		
Identity of T.S.	**P-550**	**P-626**	**P-589**	**P-90**	**P-459**	**HY3C**	**WRP-1**	**Mean F_2**
Days to first flowering	116.00	114.00	116.00	87.00	115.00	99.00	94.00	116.17
Days to 50% maturity	156.00	159.00	159.00	120.00	150.00	153.00	153.00	157.36
Pod bearing length (cm)	33.00	94.00	69.00	55.00	82.00	26.80	63.60	40.76
Clusters plant^{-1}	435.00	60.00	60.00	200.00	50.00	111.40	110.70	31.59
Pods plant^{-1}	560.00	300.00	350.00	235.00	180.00	309.40	294.00	63.57
Seed yield plant^{-1} (g)	126.00	77.00	36.50	66.50	48.50	69.32	69.98	14.77

dispersion of favourable complementary alleles between the parents from which segregating population are derived (Bernardo, 2020; Mackay *et al.,* 2020). These theoretical studies suggests that alleles that increase days to 50% maturity, clusters plant^{-1}, pods plant^{-1}, and seed yield plant^{-1} are dispersed between HY3C and WRP-1, while those that increase days to first flowering and pod bearing length are dispersed between BRG-1 and BDN-2.

Correlation and Path coefficient: Correlation coefficients at genotypic level were generally of higher magnitude than the corresponding phenotypic level indicating the strong association between the characters. Estimation of correlation coefficients between different pairs of traits in this study revealed that not all traits were correlated to each other or with seed yield. The traits pods plant^{-1}, clusters plant^{-1} and secondary branches plant^{-1}exhibited highly significant and high degree of positive correlation with seed yield plant^{-1}. Whereas, test weight, pod bearing length, pod length, primary branches plant^{-1} and seeds pod^{-1} expressed positively significant correlation with seed yield plant^{-1} (**Fig.1**). Hence, practicing direct selection for



BRG-1 × BDN-2 BRG-1 × WRP-1



HY3C × BDN-2 HY3C × WRP-1

X1 = Days to first flowering, X2 = Days to maturity, X3 = Plant height, X4 = Primary branches plant-1,
X5 = Secondary branches plant-1, X6 = Pod bearing length X7 = Seeds pod-1 X8 = Pod length
X9 = Clusters plant-1 X10 = Pods plant-1 X11 = Test weight X12 = Seed yield plant-1

Fig.1. Correlogram depicting phenotypic correlation coefficient for yield and yield attributing traits in F_2 population of four pigeonpea crosses used in the study

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Table 4. Estimates of path coefficient of various traits on seed yield plant^{-1} in F_2 population derived from four pigeonpea crosses used in the study

	Cross	X1	X2	X3	X4	X5	X6	X7	X8	X9	X10	X11
X1	**C1**	**-0.0729**	-0.065	-0.0303	-0.0020	0.0074	0.0007	-0.0185	-0.0173	0.0044	0.0077	-0.0032
	C2	**-0.1076**	-0.1047	-0.0406	-0.0046	0.0107	-0.0030	-0.0212	-0.0272	0.0159	0.0101	-0.0170
	C3	**-0.8290**	-0.8065	-0.3368	0.0049	0.0602	-0.1409	-0.2089	-0.2434	0.0871	0.0722	-0.1166
	C4	**-0.0866**	-0.0831	-0.0349	-0.0080	-0.0055	-0.0204	-0.0126	-0.0379	-0.0034	-0.0034	-0.0164
X2	**C1**	-0.0148	**-0.0165**	-0.0060	-0.0007	0.0006	-0.0015	-0.0054	-0.0047	0.0002	0.0005	-0.0028
	C2	0.0484	**0.0498**	0.0191	0.0028	-0.0039	0.0029	0.0119	0.0142	-0.0049	-0.0031	0.0100
	C3	0.7765	**0.7982**	0.3199	0.0195	-0.0437	0.1428	0.2349	0.2546	-0.0574	-0.0551	0.1581
	C4	-0.0214	**-0.0222**	-0.0105	-0.0022	-0.0019	-0.0054	-0.0068	-0.0109	-0.0007	-0.00010	-0.0050
X3	**C1**	0.0105	0.0092	**0.0254**	0.0104	0.0069	0.0069	0.0108	0.0126	0.0026	0.0036	0.0000
	C2	-0.0501	-0.0511	**-0.1327**	-0.0242	-0.0226	-0.0306	-0.0254	-0.0263	-0.0115	-0.0260	-0.0190
	C3	-0.0511	-0.0504	**-0.1257**	-0.0294	-0.0387	-0.0419	-0.0512	-0.0560	-0.0090	-0.0267	-0.0199
	C4	-0.0176	-0.0206	**-0.0438**	-0.0069	-0.0085	-0.0141	-0.0130	-0.0163	-0.0034	-0.0070	-0.0119
X4	**C1**	-0.0015	-0.0025	-0.0232	**-0.0564**	-0.0447	-0.0183	-0.0246	-0.2370	-0.0277	-0.0327	-0.0148
	C2	-0.0035	-0.0047	-0.0151	**-0.0830**	-0.0267	-0.0326	-0.0115	-0.0096	-0.0342	-0.0417	-0.0178
	C3	-0.0002	0.0008	0.0075	**0.0321**	0.0258	0.0182	0.0180	0.0148	0.0187	0.0216	0.0048
	C4	-0.0035	-0.0037	-0.0060	**-0.0377**	-0.0293	-0.0156	-0.0145	-0.0136	-0.0113	-0.0196	-0.0029
X5	**C1**	-0.0515	-0.0178	0.1385	0.4020	**0.5079**	0.2370	0.2283	0.1972	0.3629	0.4153	0.1294
	C2	-0.0520	-0.0412	0.0890	0.3944	**0.5227**	0.1948	0.0715	0.0289	0.3864	0.4049	0.1384
	C3	-0.0149	-0.0112	0.0631	0.1648	**0.2052**	0.1294	0.0955	0.0853	0.1584	0.1809	0.0315
	C4	0.0181	0.0241	0.0550	0.2203	**0.2833**	0.1050	0.0968	0.0944	0.1551	0.2162	0.0260
X6	**C1**	0.0005	-0.0051	-0.0154	-0.0183	-0.0263	**-0.0563**	-0.0165	-0.0131	-0.0234	-0.0259	-0.0151
	C2	0.0005	0.0010	0.0041	0.0070	0.0066	**0.0178**	0.0067	0.0057	0.0056	0.0073	0.0038
	C3	-0.0080	-0.0084	-0.0158	-0.0268	-0.0298	**-0.0472**	-0.0184	-0.0225	-0.0198	-0.0282	-0.0078
	C4	0.0098	0.1001	0.0134	0.0171	-0.0154	**0.0414**	0.0187	0.0209	0.0052	0.0140	-0.0006
X7	**C1**	0.0092	0.0119	0.0153	0.0157	0.0162	0.0106	**0.0361**	0.0302	0.0127	0.0143	0.0073
	C2	0.0091	0.0111	0.0088	0.0064	0.0063	0.0173	**0.0462**	0.0363	0.0090	0.0104	0.0185
	C3	-0.0154	-0.0180	-0.0250	-0.0344	-0.0285	-0.0239	**-0.0612**	-0.0505	-0.0275	-0.0289	-0.0153
	C4	0.0030	0.0036	0.0035	0.0046	0.0041	0.0054	**0.0119**	0.0086	0.0021	0.0031	0.0030
X8	**C1**	-0.0039	-0.0047	-0.0081	-0.0069	-0.0063	-0.0038	-0.0137	**-0.0163**	-0.0043	-0.0053	-0.0009
	C2	0.0119	0.0135	0.0094	0.0054	0.0026	0.0150	0.0370	**0.0472**	0.0010	0.0047	0.0144
	C3	0.0259	0.0282	0.0393	0.0406	0.0367	0.0420	0.0728	**0.0883**	0.0305	0.0348	0.0156
	C4	0.0189	0.0211	0.0161	0.156	0.0144	0.0218	0.0314	**0.0432**	0.0037	0.0097	0.0054
X9	**C1**	-0.0091	-0.0018	0.0158	0.0749	0.1091	0.0634	0.0537	0.0399	**0.1527**	0.1335	0.0381
	C2	-0.0328	-0.0219	0.0193	0.0916	0.1644	0.0700	0.0433	0.0045	**0.2224**	0.1858	0.0557
	C3	0.0008	0.0005	-0.0005	-0.0044	-0.0059	-0.0032	-0.0034	-0.0026	**-0.0076**	-0.0064	-0.0014
	C4	0.0118	0.0097	0.0237	0.0907	0.1656	0.0377	0.0525	0.0258	**0.3026**	0.2428	0.0242
X10	**C1**	-0.0330	-0.0102	0.0442	0.1808	0.2549	0.4136	0.1233	0.1011	0.2726	**0.3117**	0.0649
	C2	-0.0231	-0.0155	0.0481	0.1234	0.1902	0.1008	0.0555	0.0244	0.2051	**0.2455**	0.0596
	C3	-0.0353	-0.0280	0.0860	0.2739	0.3575	0.2419	0.1912	0.1600	0.3410	**0.4056**	0.0686
	C4	0.0163	0.0188	0.0654	0.2127	0.3124	0.1387	0.1054	0.0920	0.3285	**0.4095**	0.0158
X11	**C1**	0.0048	0.0186	0.0001	0.0289	0.0281	0.0296	0.0223	0.0061	0.0275	0.0229	**0.1102**
	C2	0.0131	0.0166	0.0118	0.0177	0.0219	0.0178	0.0330	0.0251	0.0207	0.0201	**0.0825**
	C3	0.0168	0.0237	0.0189	0.0178	0.184	0.0197	0.0298	0.0211	0.0221	0.0202	**0.1196**
	C4	0.0198	0.0233	0.0284	0.0081	0.0096	-0.0015	0.0261	0.0130	0.0084	0.0040	**0.1043**
r value	**C1**	0.0118	0.0014	0.0040	-0.0355	0.4337	-0.0232	0.0143	-0.0051	0.1191	0.2636	0.0345
	C2	0.0200	-0.0073	-0.0028	-0.0446	0.4371	0.0066	0.0114	0.0058	0.1814	0.2008	0.0272
	C3	0.1110	-0.0568	-0.0039	0.0147	0.1144	-0.0159	-0.0183	0.0220	-0.0041	0.2394	0.0284
	C4	0.0027	0.0004	-0.0048	-0.0194	0.2152	0.0121	0.0034	0.0095	0.2381	0.3555	0.0148

X1=Days to first flowering, X2=Days to maturity, X3= Plant height (cm) X4= primary branches plant^{-1},
X5 =Secondary branches plant^{-1}, X6 =Pod bearing length (cm) X7= Seeds pod^{-1} X8 =Pod length
X9 =Clusters plant^{-1} X10 =Pods plant^{-1} X11= Test weight (g)

these traits may lead to increase in seed yield. In contrary, days to first flowering % days to 50 *per cent* maturity and had negative association with seed yield plant^{-1}. This indicates, that these traits are not in association with yield. So, selection based on these characters may lead in isolation of low undesirable genotypes for yield but one can expect early maturing types. Similar report was given by Bhadru (2010).

The correlation coefficient of seed yield with its component traits was further apportioned into direct and indirect effects. The path coefficients to create a good image of the interconnection of the seed yield with other contributory characters, and the direct and indirect effects of them.

Pods plant^{-1}, clusters plant^{-1} and secondary branches plant^{-1} had higher positive direct effect on yield plant^{-1} and moderate direct effect by test weight, seeds pod^{-1}and pod length in all the four crosses (**Table 4**). It indicates selection for these traits may lead to improvement of seed yield. The traits *viz.,* days to first flowering, plant height and number of primary branches exhibited negative but direct effect on seed yield plant^{-1} and these traits have negative impact on seed yield.

High PCV and GCV was noticed for pods plant^{-1}, clusters plant^{-1} and seed yield plant^{-1} while, high h^2 coupled with higher value GAM for secondary branches plant^{-1}, clusters plant^{-1} and pods plant^{-1}. Seed yield plant^{-1} showed highest significant positive correlation with pods plant^{-1} and clusters plant^{-1} indicating that these traits were the primary yield determinants in pigeonpea. Path coefficient revealed that secondary branches plant^{-1} showed highest positive direct effect on seed yield plant^{-1} followed by pods plant^{-1} and clusters plant^{-1}, thus selection based on these traits would be rewarding. Among the four crosses evaluated, C1 followed by C3 are superior over other crosses with respect to transgressive segregants identified for yield and its related traits. The identified transgressive segregants in the study could be evaluated under different agro-climatic conditions to release as a variety.

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