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Genetic Variability Analysis for Plant Selection in Pigeonpea [*Cajanus cajan* (L.) Millsp.] under Different Environments

**Ajay Tiwari, R. N. Sharma, N. K. Markam, Harsh Mishra,
A. K. Sarawgi**

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Abstract Three field experiments were conducted during *kharif* 2013-14 to study the genetic variability analysis for plant selection on various yield and yield related components. Findings of analysis of variance revealed significant mean squares due to genotypes for all the traits in all three environments under the study indicated the existence of sufficient genetic variability for the traits. The highest GCV and PCV estimates were observed for seed yield per plant in environment I, number of pod clusters per plant in environment II and number of pods per plant in environment III. The high genetic advance in environment I, II and III were observed for number of pods per plant. High heritability coupled with high genetic advance as percentage of mean was found for number of pods per plant in all the three environments. The indicated the role of additive genetic variance in their expression. Hence, selection of genotypes for these characters may be beneficial for possible improvement in the crop under respective environments. In this study total seed yield per plant, number of pod per plant and number of pod clusters per plant have been identified as selection criteria for obtaining good parental lines in a pigeonpea breeding program.

Keywords Pigeonpea, GCV, PCV, Genetic advance, Heritability.

Introduction

Pigeonpea [*Cajanus cajan* (L.) Millsp.] is one of the most important food legumes grown in over 82 countries across the globe, it ranks as the world's fifth most important pulse crop. The crop is cultivated in an estimated area of 4.92 million hectares in the world with an average of 898 kg/ha [1]. India with a total area of 2.65 million tones with average yield of 741 kg/ha [1] produces nearly 92% of the world's entire pigeonpea crop, though the average seed yields are relatively low, the crop can yield 1600-2900 kg/ha under favorable management [2]; while an exceptional yield of over 8,000 kg/ha of dry has been reported in the first harvest in Australia by [3], pigeonpea as field crop was grown on 4.36 ha, with a production of 3.24 million tones and an average productivity of 0.74 [4]. The success of recombination breeding depends on parental variability or diversity to obtain progressive segregates. Crop yield is one of the complex characters controlled by several interacting genotypic and environmental factors. There are quite few yield components which are less complex, highly inherited and less influenced by the environmental changes [5]. Determination of genetic variability of any given crop

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A. Tiwari*, R. N. Sharma, N. K. Markam, H. Mishra,
A. K. Sarawgi
Department of Genetics and Plant Breeding, Indira Gandhi Krishi Vishwavidyalaya, Raipur, CG, 492012, India
e-mail: tiwariajay064@gmail.com
*Correspondence

species is necessary for improvement of the crop because it generates baseline data to guide selection of parental lines and design of breeding scheme. In the present study, the genetic variation among pigeonpea genotypes was studied, for improvement of the crop yield based on the available breeding strategies for selection of parental lines in different environments.

Materials and Methods

The field experiment was conducted during the *kharif* 2012-13 and 2013-14 at Department of Genetics and Plant Breeding at Research cum Instructional Farm, Indira Gandhi Krishi Viswavidyalaya, Raipur, CG. In hybridization program 5 male parents were crossed to each of the 7 female to generate a set of hybrids in a line × tester fashion as proposed by Kempthorne [6]. A total of 35 hybrids were synthesized by hand emasculation and pollination. Sufficient numbers of hand pollinated seeds were produced during 2012-13 rainy season. The experimental material consisted 12 genotypes (Lines ICP7004, ICP7373, ICP7376, ICP7382, ICP7391, ICP7393, ICP7406 and testers ICPL 87119, BDN-2, UPAS-120, ICPL-87, JKM-189) and their 35 crosses (ICP7004 × ICPL 87119, ICP7004 × BDN-2, ICP7004 × UPA-120, ICP7004 × ICPL-87, ICP7004 × JKM-189, ICP7373 × ICPL 87119, ICP7373 ×BDN-2, ICP7373 × UPAS-120, ICP7373 × ICPL-87, ICP7373 × JKM-189, ICP7376 × ICPL 87119, ICP7376 × BDN-2, ICP7376 × UPAS-120, ICP7376 × ICPL-87, ICP7376 × JKM-189, ICP7382 × ICPL 87119, ICP7382 × BDN-2, ICP7382 × UPAS-120, ICP7382 × ICPL-87, ICP7382 × JKM-189, ICP7391 × ICPL87119, ICP7391 × BDN-2, ICP7391 × UPAS-120, ICP7391 ×ICPL-87, ICP7391 × JKM-189, ICP7393 × ICPL 87119, ICP7393 × BDN-2, ICP7393 × UPAS-120, ICP7393 × ICPL-87, ICP7393 × JKM-189, ICP7406 × ICPL 87119, ICP7406 ×BDN-2, ICP7406 × UPAS-120, ICP7406 × ICPL-87 and ICP7406 × JKM-189. The experiment was laid out in a randomized complete block design (RCBD) with three replications during *kharif* 2013-14. The material was sown in single rows of 4.0 m length and 60 cm apart with 20 cm plant to plant spacing. Sowing of material 12 parents and 35 crosses was done in three dates viz; first week of July, August and September. Recommended dose of fertilizer of 20:50:20 kg per ha of NPK was applied in the rows before sowing. All the recommended package of practices were followed to raise a healthy crop. Five plants were randomly selected and tagged in each genotype per replication for recording the observations for the 13 characters viz: days to flowering initiation, days to 50% flowering, days to maturity, plant height, number of primary branches per plant, number of pod clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, 100 seed weight, seed yield per plant and protein content. The statistical analysis for genetic variability was done as per the method given by Burton [7]. Heritability in broad sense was calculated by Hanson et al. [8]. Whereas genetic advance was calculated by the method given by Johnson et al. [9].

Results and Discussion

Variability parameters

Analysis of variance indicated that the mean sum of squares due to genotypes were highly significant for all the characters in all three environments present in Table 1. Thus, indicating that there was considerable genetic variability present in parents and crosses. The measurement of existing variability in genetic material has been the basic requirement of a breeding program. The wide range of variability was observed for nearly all the traits viz., number of pods per plant, seed yield per plant, number of pod clusters per plant, plant height, days to flowering initiation, days to maturity and days to 50% flowering in environment I,. number of pods per plant, number of pod clusters per plant, plant height, seed yield per plant, days to maturity, days to flowering initiation and days to 50% flowering in environment II and plant height, number of pods per plant, number of pod clusters per plant, days to flowering initiation, days to 50% flowering, number of primary branches per plant, seed yield per plant and protein content in environment III. Similar findings were also reported earlier [1, 10]. The total gene pool, indicating the existence of sufficient variability among the genotypes for the traits.

Genotypic and phenotypic coefficient of variation under different environments

The genotypic and phenotypic coefficients of variations (GCV and PCV) were worked out for all the 13

Table 1. Analysis of variance for seed yield and its components in pigeonpea under three environments (E-I, E-II and E-III). *Significant at 5% probability level,**Significant at 1% probability level.

		Mean sum of squares					
Source variation	DF	Days to flowering initiation			Days to 50% flowering		
		E-I	E-II	E-III	E-1	E-II	E-III
Replication	2	9.45	12.65	2.13	3.51	2.43	4.09
Treatment	46	172.60**	28.88**	35.27**	211.77**	24.80**	17.39**
Error	92	6.57	7.44	5.26	9.21	6.87	3.99
Total	140						

Table 1. Continued.

		Mean sum of squares					
Source of variation	DF	No. of primary branches per plant			No. of pod clusters per plant		
		E-I	E-II	E-II	E-I	E-II	E-III
Replication	2	0.55	0.56	0.31	8.57	6.79	1.48
Treatment	46	12.45**	9.90**	2.57**	1048.25**	844.15**	42.77**
Error	92	0.68	0.54	0.25	7.09	8.51	1.72
Total	140						

Table 1. Continued.

		Mean sum of squares								
Source of variation	DF	Pod length (cm)			No. of seeds per pod			100 seed weight (g)		
		E-I	E-II	E-III	E-I	E-II	E-III	E-I	E-II	E-III
Replication	2	0.02	0.07	0.03	0.02	0.00	0.06	0.23	0.12	0.00
Treatment	46	0.30**	0.20**	0.41**	0.09**	0.04**	0.08**	2.44**	2.22**	1.79**
Error	92	0.06	0.06	0.06	0.04	0.02	0.04	0.11	0.14	0.11
Total	140									

Table 1. Continued.

		Mean sum of squares					
Source of variation	DF	Days to maturity			Plant height (cm)		
		E-I	E-II	E-III	E-I	E-II	E-III
Replication	2	10.48	1.94	0.99	3.33	11.82	5.04
Treatment	46	181.49**	29.89**	6.46*	618.43**	486.39**	249.09**
Error	92	14.90	9.44	4.29	8.65	9.40	17.43
Total	140						

Table 1. Continued.

		Mean sum of squares					
Source of variation	DF	No.of pods per cluster			No. of pods per plant		
		E-I	E-II	E-III	E-I	E-II	E-III
Replication	2	0.04	0.07	0.05	14.57	1.69	1.63
Treatment	46	0.41**	0.48**	0.47**	6787.71**	3875.71**	207.96**
Error	92	0.04	0.04	0.12	17.89	14.40	4.12
Total	140						

Table 1. Continued.

		Mean sum of squares					
Source of variation	DF	Seed yield per plant (g)			Protein content (%)		
		E-I	E-II	E-III	E-I	E-II	E-III
Replication	2	18.72	2.06	0.26	0.26	0.05	1.46
Treatment	46	884.26**	541.78**	13.77**	12.49**	21.49**	13.89**
Error	92	6.79	4.72	1.22	0.82	0.22	0.84
Total	140						

Table 2. Estimates genetic parameters of variations for seed yield and its components in pigeonpea under three environments (E-I, E-II and E-III).

Sl. No.	Parameters characters	Environment	Grand mean (X)	Range		GCV	PCV	Heritability (%)	Genetic advance	Genetic advance as % of mean
				Min	Max					
1	Days to flowering initiation	E-I	123.53	104.00	135.00	6.02	6.37	89.40	14.49	13.73
		E-II	103.84	97.00	109.00	2.57	3.68	49.00	3.85	3.71
		E-III	89.20	79.33	95.33	3.54	4.38	65.50	5.27	5.91
2	Days to 50% flowering	E-I	139.58	121.33	151.00	5.89	6.27	88.00	15.88	11.38
		E-II	116.64	111.33	121.67	2.09	3.07	46.50	3.43	2.94
		E-III	99.17	92.33	104.33	2.13	2.93	52.80	3.16	3.19
3	Days to maturity	E-I	192.95	174.67	204.67	3.86	4.35	78.80	13.63	7.06
		E-II	177.02	171.33	184.67	1.48	2.78	41.90	3.48	1.97
		E-III	161.28	158.00	163.67	0.52	1.39	14.40	0.66	0.41
4	Plant height (cm)	E-I	147.51	120.45	181.50	9.67	9.87	95.90	28.76	19.50
		E-II	117.37	88.20	141.57	10.74	11.06	94.40	25.24	21.51
		E-III	78.93	62.93	102.83	11.13	12.33	81.60	16.35	20.71
5	No. of primary branches per plant	E-I	10.77	6.47	15.33	18.38	19.92	85.20	3.77	34.95
		E-II	9.65	6.00	12.41	19.48	21.12	85.10	3.36	37.02
		E-III	6.02	4.31	7.92	14.61	16.84	75.20	1.57	26.10
6	No. of pod clusters per plant	E-I	67.69	28.17	94.60	27.52	27.80	98.00	37.99	56.12
		E-II	46.31	16.33	87.35	36.03	36.58	97.00	33.87	73.13
		E-III	15.32	8.80	25.14	24.15	25.62	88.80	7.18	46.88
7	No. of pods per clusters	E-I	3.91	3.08	4.80	9.05	10.47	78.90	0.63	16.14
		E-II	3.41	2.58	4.32	11.13	12.69	76.90	0.69	20.10
		E-III	2.23	1.67	3.17	15.19	22.11	47.20	0.48	21.48
8	No. of pods per plant	E-I	163.06	86.87	290.83	29.13	29.24	99.20	97.47	59.78
		E-II	119.59	63.93	187.37	29.99	30.17	98.90	73.50	61.46
		E-III	34.00	25.27	57.47	24.24	24.97	98.30	16.49	48.49
9	Pod length (cm)	E-I	6.02	5.37	6.55	4.67	6.25	55.80	0.43	7.19
		E-II	5.65	5.07	6.33	3.80	5.85	42.30	0.29	5.10
		E-III	5.25	4.29	5.94	6.54	7.98	67.20	0.58	11.04
10	No of seeds per pod	E-I	4.07	3.77	4.80	2.92	6.17	22.50	0.12	2.86
		E-II	3.93	3.67	4.20	1.94	4.21	21.20	0.07	1.84
		E-III	3.76	3.17	4.07	3.00	6.43	21.80	0.11	2.89
11.	100 seed weight (g)`	E-I	10.25	8.46	12.61	8.60	9.19	87.50	1.70	16.57
		E-II	9.99	8.30	11.98	8.34	12.73	82.80	1.56	25.42
		E-III	8.93	7.39	10.51	8.37	9.17	83.20	3.93	15.72
12.	Seed yield per plant (g)	E-I	52.99	24.59	96.25	32.27	32.64	97.70	34.83	65.72
		E-II	40.71	21.27	73.91	32.86	33.29	97.40	27.21	66.82
		E-III	15.29	12.23	20.56	13.38	15.21	77.40	3.70	24.24
13.	Protein content (%)	E-I	21.74	17.91	26.08	9.07	9.98	82.50	3.69	16.96
		E-II	40.71	21.27	73.91	32.86	33.29	97.40	27.21	66.82
		E-III	21.02	17.47	25.82	9.92	10.84	83.70	1.40	18.71

characters studied (Table 2) . The phenotypic coefficient of variation in general was slightly higher than the genotypic coefficient of variation for all the characters.

The highest GCV and PCV was estimated for seed yield per plant (32.27% and 32.64%) followed by number of pod per plant (29.13% and 29.24%), number of pod clusters per plant (27.52% and 27.80%), number of primary branches per plants (18.38% and 19.92%), protein content (9.07% and 9.98%), plant height (9.67% and 9.87%), number of pods per cluster (9.05% and 10.47%) and 100 seed weight (8.60% and 9.19%) in environment I. The environment II highest GCV and PCV was observed for number of pod clusters per plant (36.03% and 36.58%)followed by seed yield per plant (32.36% and 33.29%), number of pods per plant (29.99% and 30.17%), number of primary branches per plant (19.48% and 21.12%), protein content (12.53% and 9.16%), number of pods per cluster (11.13% and 12.69%), plant height (10.74% and 11.06%) and 100 seed weight (8.34% and 12.73%). The highest GCV and PCV was observed for number of pods per plant (24.24% and 24.97%) followed by number of pod clusters per plant (24.15% and 25.62%), number of pods per cluster (15.19% and 22.11%), number of primary branches per plant (14.61% and 16.84%), seed yield per plant (13.38% and 15.21%), plant height (11.13% and 12.33%), protein content (9.92% and 10.84%) and 100 seed weight (8.37% and 9.17%) in environment III.

The results on genotypic and phenotypic coefficient of variation clearly indicated that the phenotypic coefficients of variation in general were slightly higher than the genotypic coefficients of variation for all the characters indicating the substantial influence of environment in the expression of the characters. The high value of genotypic and phenotypic variation suggest that there is good scope for yield improvement through selection for seed yield per plant, number of pod per plant and number of pod clusters per plant in environment I, number of pod clusters per plant, seed yield per plant, number of pods per plant and in environment II and number of pods per plant number of pod clusters per plant, number of pods per cluster, number of primary branches per plant and seed yield per plant in environment III. These findings are in agreement with other reports earlier [11–13], suggested the techniques for estimation of components of genetic variability.

Heritability under different environments

The highest heritability estimates (Table 2) was observed for number of pods per plant (99.20%) followed by number of pod clusters per plant (98.00%), seed yield per plant (97.70%), plant height (95.90%), days to flowering initiation (89.40%), days to 50% flowering (88.00%), 100 seed weight (87.50%), number of primary branches per plant (85.20%) and protein content (82.50%) in environment I, environment II highest heritability observed for number of pods per plant (98.90%) followed by seed yield per plant (97.40%), number of pod clusters per plant (97.00%), protein content (96.90%), plant height (94.40%), number of primary branches per plant (85.10%), 100 seed weight (82.80%) and number of pods per cluster (76.90%) and environment III highest heritability was observed for number of pods per plant (94.30%) followed by number of pod clusters per plant (88.80%), protein content (83.70%), 100 seed weight (83.20%), plant height (81.60%), seed yield per plant (77.40%), number of primary branches per plant (75.20%), pod length (67.20%) and days to flowering initiation (65.50%). The above findings are in conformity with the earlier reports [11–15]. In this study, number of pods per plant, number of pod clusters per plant and seed yield per plant environment I, number of pods per plant, seed yield per plant and number of pod clusters per plant in environment II and number of pods per plant, number of pod clusters per plant and protein content in the environment III has been identified as selection criteria for obtaining good parental lines in a pigeonpea breeding program.

Genetic advance under different environments

Genetic advance all three environments present in Table 2. In environment I the highest genetic advance was observed for number of pods per plant (97.47) followed by number of pod clusters per plant (37.99), seed yield per plant (34.83), plant height (28.76) and days to 50% flowering (15.88), environment II the highest genetic advance was observed for number of pods per plant (73.50) followed by number of pod clusters per plant (33.87), seed yield per plant (27.21) and plant height (25.24) and environment III the highest genetic advance was observed for number of pods per plant (16.49) followed by plant height (16.35), number of pod clusters per plant (7.18), days to flowering initiation (5.27), 100 seed weight (3.93) and seed yield per plant (3.70).

Genetic advance as percentage of mean
under different environments

Genetic advance as percentage of mean all three environments present in Table 2. In environment I of mean was observed for seed yield per plant (65.72%) followed by number of pods per plant (59.78%), number of pod clusters per plant (56.12%), number of primary branches per plant (34.95%), plant height (19.50%), protein content (16.96%), 100 seed weight

(16.57%) and number of pods per cluster (16.14%), environment II the highest genetic advance as percentage of mean was observed for number of pod clusters per plant (73.13%) followed by seed yield per plant (66.82%), number of pods per plant (61.46%), number of primary branches per plant (37.02%), 100 seed weight (25.42%), plant height (21.51%), number of pods per cluster (20.10%) and protein content (15.62%) and environment III the highest genetic advance as percentage of mean was observed for number of pods per plant (48.49%) followed by number of pod clusters per plant (46.88%), number of primary branches per plant (26.10%), seed yield per plant (24.24%), number of pods per cluster (21.48%), plant height (20.71%), protein content (18.71%), 100 seed weight (15.72%) and pod length (11.04%). The genetic advance and genetic advance as percentage of mean. Similar results are also reported earlier [11, 15–17].

The high heritability coupled with high genetic advance as percentage of mean were observed for number of pods per plant I, II and III followed by number of pod clusters per plant I and II plant height, number of pod clusters per plant III. This indicated the role of additive genetic variance in the expression of these characters. Hence, selection of genotypes for these characters may be beneficial for possible improvement in the crop under respective environments. Other traits had high to moderate heritability coupled with moderate to genetic advance as percentage of mean which is mainly due to the role of non-additive genetic component in their expression Green et al. [18] also reported that the maturity period of pigeonpea lines ranges from 120-270 days and that each specific maturity group is adapted to a specific environment. The found that early, medium and late maturing groups are suitable for areas with low, medium and high rain fall respectively. Therefore, studying the three groups at one location would favor the group most adapted to that location. The medium maturity groups (160-180 days) are best adapted to Raipur conditions where the present investigation was carried out.

Conclusion

The wide range genetic variability observed for most of the characters as evidenced in three environments by significant variances due to genotypes suggesting that, it could be helpful in isolation of better parents and crosses. An overall observation over the environments revealed that high heritability estimates coupled with high genetic advance as percentage of mean were noted for number of primary branches per plant, number of pod clusters per plant, number of pods per plant and seed yield per plant indicated the role of additive genetic variance in their expression.

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