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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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Twenty three pigeonpea genotypes were evaluated in a randomized block design during *Kharif* 2012-13. The aim of this research was to estimate genetic variability utilizing various quantitative traits for overall improvement in pigeonpea crop. Results showed that sufficient amount of variability was present in entire gene pool for all the characters. Based on mean performance for yield along with some of the component traits the most promising genotypes identified were NDA 5-14, NDA 8-6, NDA 96-6, ICP 2155 and NDACMS 1-6B. Secondary branches per plant showed highest phenotypic as well as genotypic coefficient of variation followed by seed yield per plant and biological yield. High heritability coupled with high genetic advance as per cent of mean were observed by 100-seed weight, pods per plant, seed yield per plant, biological yield per plant; and secondary branches per plant indicate that these traits are highly heritable and governed by additive gene action. While, plant height, primary branches per plant, pods per plant, seeds per pod and harvest index showed high heritability with moderate genetic advance as per cent of mean suggesting greater role of non-additive gene action in their inheritance. It may be concluded that the characters 100-seed weight, pods per plant, seed yield per plant, biological yield per plant and secondary branches per plant, were identified as the most important direct selection criterion intended at developing high yielding pigeonpea cultivars.

Key words: Pigeonpea, genetic variability, yield and yield attributes.

INTRODUCTION

Pigeonpea [*Cajanus cajan* (L.) Millsp.], also known as red gram, is the second most important pulse crop of India after chickpea. It is a rich source of protein, carbohydrate, vitamins, lipids and certain minerals. Pigeonpea is a hard, widely adapted and drought tolerant crop. It is cultivated in more than 25 tropical and sub-tropical countries, either as a sole crop or intermixed with such cereals as sorghum, pearl millet or maize or with legumes, e.g., groundnut. Globally, pigeonpea is grown on about 5.54 million ha of land mass, producing 3.22 million tonnes of grain with average yield of 708 kg per hectare. It contributes about 5.6 percent share in global pulse production (Gowda et al., 2009). The Indian sub-continent, Eastern Africa, and Central America, in that

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Table 1. Analysis of variance for 11 quantitative characters in pigeonpea.

Characters	Source of variation		
	Replication [2]	Treatment [22]	Error [44]
Days to 50 % flowering	3.435	45.802**	1.621
Days to maturity	3.522	45.515**	2.082
Plant height (cm)	1.609	411.407**	9.705
Primary branches/ plant	0.339	1.703*	0.646
Secondary branches/ plant	12.192	101.907**	7.530
Pods/ plant	105.33	2245.566**	28.107
Seeds/ pod	0.024	0.345**	0.020
100-seed weight (g)	0.026	9.875**	0.061
Seed yield/ plant (g)	3.399	494.780**	6.784
Biological yield/ plant (g)	80.46	4732.801**	71.474
Harvest-index (%)	0.214	17.090**	0.684

*,** significant at 5% and 1% probability levels, respectively, [ ] value in parenthesis represents degree of freedom

order, are the world's three main pigeonpea producing regions.

Productivity of pigeonpea worldwide in comparison to cereals is very low and stagnant due to several biotic and abiotic stresses. This low productivity is attributed to its low harvest index because of limited man made selections (Varshney et al., 2010). Compared to other food legumes breeding, pigeonpea has been more challenging due to various crop specific traits and highly sensitive nature. Significant progress has been made over the last few decades through breeding for reducing crop duration, improving seed quality and overcoming the constraints of major diseases like wilt and sterility mosaic.

To accumulate optimum combination of yield contributing traits in single genotype, it is essential to understand the implication of the inter-relationships of various traits using correlation and path coefficients. Being an often cross-pollinated crop, pigeonpea has very high genetic variability but yield potential is very low. Seed yield is a very complex character whose manifestation results from multiplicative interactions of several yield components and environmental factors. Improvement in yield primarily depends on the extent of genetic variability present in the population. The systematic breeding programme involves the steps like creating genetic variability practicing selection and utilization of selected genotypes to evolve promising varieties. It is necessary to find out the relative magnitude of additive and non additive genetic variances, heritability and genetic gain with regard to the characters of concern to the breeder. Estimates of Genotypic coefficient of variation (GCV), Phenotypic coefficient of variation (PCV), heritability and genetic advance will play an important role in exploiting future research projections of pigeonpea improvement.

MATERIALS AND METHODS

Twenty three pigeonpea genotypes were evaluated in a randomized block design for various agronomical and physiological characters during *Kharif* 2012-13 at Research Farm of Genetics and Plant Breeding, Narendra Deva University of Agriculture and Technology, Kumarganj, Faizabad. The experimental site is located at 26.47 °N latitude, 82.12 °E longitudes and an altitude of 113 m above mean sea level. Each genotype was raised in single row plots of 4 m length with intra-row and inter-row spacing of 25 cm and 75 cm, respectively.

The recommended agronomic practices followed to raise good crop stand. The observations were recorded on five randomly selected competitive plants of a genotype in a plot in each replication for eleven characters viz., days to 50% flowering, days to maturity, number of primary branches per plant, number of secondary branches per plant, plant height (cm), pods per plant, seeds per pod, 100-seed weight, seed yield per plant (g), biological yield per plant (g) and harvest index (%). Mean values were subjected to analysis of variance to test the significance for each character as per methodology advocated by Panse and Sukhatme, (1967). PCV and GCV were calculated by the formula given by Burton (1952), heritability in broad sense (h^2) by Burton and De Vane (1953) and genetic advance, that is, the expected genetic gain were calculated by using the procedure given by Johnson et al. (1955).

RESULTS AND DISCUSSION

The analysis of variance (Table 1) revealed highly significant difference for all the characters under study among the genotypes, indicating that the parents included in this investigation exhibit sufficient variability for the entire characters studied. The presence of large amount of variability might be due to diverse source of materials taken as well as environmental influence affecting the phenotypes. Similar findings were also reported by Srinivas et al. (1999), Basavarajaiah et al.

Table 2. Mean performances for 11 quantitative characters in pigeonpea.

Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/ plant	Secondary branches/ plant	Pods/ plant	Seeds/ pod	100-Seed wt (g)	Seed yield/ plant (g)	Biological yield/ plant (g)	Harvest index (%)
NDA 2	141.00	250.00	172.33	6.45	27.03	165.05	3.60	13.16	69.46	236.45	29.40
NDA 3	137.33	243.33	170.33	4.97	17.85	167.52	3.80	9.67	54.87	192.40	28.52
NDA 3-3	143.67	250.33	169.33	5.30	15.66	163.57	2.80	13.33	53.87	180.78	29.79
NDA 5-14	139.00	248.67	181.67	5.55	22.56	183.33	3.13	15.14	82.39	292.98	28.14
NDA 8-6	137.67	246.00	187.50	5.80	16.97	219.53	3.43	11.47	78.77	264.37	29.79
NDA 96-1	147.33	252.33	166.93	5.34	16.08	174.01	3.42	10.56	56.40	206.22	27.35
NDA 96-6	142.33	246.00	171.00	6.52	20.36	231.62	3.17	11.41	77.07	250.83	30.75
NDA 98-6	141.33	248.00	181.74	4.92	17.40	158.32	3.25	12.58	58.24	195.34	29.81
NDA 98-7	146.00	252.00	170.97	5.73	15.15	172.02	3.00	7.99	32.24	128.16	25.16
NDA 7-11	135.67	247.33	171.29	4.97	14.84	147.83	3.78	11.38	57.74	200.60	28.80
NDA 7-15	147.00	254.67	155.04	5.40	15.28	153.80	3.53	9.57	43.97	147.85	29.72
NDAGC 31	146.67	254.00	183.85	4.87	19.30	206.04	3.35	10.56	70.88	245.69	28.87
NDAGC 1010	143.67	254.33	190.02	5.21	30.04	245.08	3.10	9.54	64.58	204.71	31.55
ICP 2309	147.00	251.00	166.84	4.63	21.30	196.37	3.00	9.17	52.21	173.75	30.04
ICP 2155	146.33	251.00	167.53	4.18	25.18	241.64	3.00	11.30	74.63	240.91	31.01
ICP 870	137.00	245.00	198.91	6.61	34.63	181.18	3.22	8.76	43.59	199.71	21.82
ICP 7353	145.00	256.67	184.41	3.98	19.36	170.46	3.60	8.83	45.83	183.20	25.04
IPA 208	141.33	256.00	166.07	3.62	24.86	181.08	3.00	12.42	62.78	210.40	29.83
Bahar	147.00	258.00	182.33	5.10	27.48	169.53	3.03	10.26	54.39	171.79	31.66
Amar	143.00	252.67	171.66	4.87	16.83	167.63	2.98	11.67	51.24	164.12	31.22
NDACMS 1-3A/B	146.00	251.00	184.67	5.13	15.56	165.13	2.53	13.72	47.95	181.50	26.43
NDACMS 1-4A/B	148.67	254.67	197.67	5.14	26.51	181.25	3.57	9.60	61.22	228.66	26.77
NDACMS 1-6A/B	147.00	250.00	198.42	5.98	30.45	189.74	3.82	9.87	71.94	250.12	28.77
Mean	143.35	251.00	177.85	5.23	21.33	183.99	3.27	10.96	59.40	206.54	28.71
CV	0.75	0.57	1.75	15.36	12.86	2.88	4.36	2.25	4.38	4.09	2.88
CD 5%	1.77	2.37	5.13	1.32	4.52	8.72	0.23	0.41	4.29	13.91	1.36

(2000), Venkateswarlu (2001), Baskaran and Muthiah (2006), Bhadru (2008), Bhadru (2011) and Yerimani et al. (2013).

The mean performance of 23 parents of pigeonpea for 11 characters is presented in Table 2. Highest mean performance for seed yield per plant along with some of the component traits was exhibited by NDA 5-14 (82.39 g) followed by NDA 8-6 (78.77 g), NDA 96-6 (77.07 g), ICP 2155 (74.63 g) and NDACMS 1-6B (71.94 g). The above mentioned genotypes may be used as donor parents in hybridization programme for developing high yielding varieties of respective groups. Some other genotypes exhibiting very high mean performance for characters other than seed yield per plant are also listed in Table 4. These lines merit consideration as promising parents for hybridization programme for bringing over all improvement in plant architecture in a component breeding approach ultimately leading to high yielding pigeonpea genotypes even if they

Table 3. Genetic variability parameters for 11 quantitative characters in pigeonpea

Characters	General Mean ± SE	Range		Coefficient of variation		h² (BS)	GA as % of mean
		Lowest	Highest	GCV	PCV		
Days to 50 % flowering	143.35± 0.62	135.67	148.67	2.69	2.79	92.76	5.34
Days to maturity	251.00± 0.83	243.33	258.00	1.52	1.62	87.43	2.92
Plant height (cm)	177.85±1.80	155.04	198.91	6.51	6.74	93.24	12.94
Primary branches/ plant	5.23±0.46	3.62	6.61	11.36	19.11	35.34	13.91
Secondary branches/ plant	21.33±1.58	14.84	34.63	26.29	29.27	80.69	48.65
Pods/ plant	183.99±3.06	147.83	245.08	14.78	15.05	96.34	29.88
Seeds/ pod	3.27±0.08	2.53	3.82	10.07	10.97	84.24	19.04
100-seed weight (g)	10.96±0.14	7.99	15.14	16.51	16.66	98.18	33.7
Seed yield/ plant (g)	59.40±1.50	32.24	82.39	21.47	21.91	96.00	43.34
Biological yield/ plant (g)	206.54±4.88	128.16	292.98	19.08	19.52	95.60	38.44
Harvest-index (%)	28.71±0.48	21.82	31.66	8.15	8.64	88.88	15.82

*h^2 (BS) = Heritability broad sense, GCV = Genotypic coefficient of variation, PCV = Phenotypic coefficient of variation, GA = Genetic advance, S.E. = standard error.

have moderate or low seed yield.

In this context, the most desirable lines were NDA 7-11, ICP 870, NDA 3 and NDA 8-6 for days to 50% flowering and days to maturity; ICP 870 and NDACMS 1-6A for plant height, primary and secondary branches per plant; NDAGC 1010 and ICP 2155 for pods per plant and NDACMS1-6A, NDA 3, NDA 7-11, ICP 7353 and NDA 2 for seeds per pod. Similarily, the most promising genotypes were NDA 5-14, NDACMS 1-3A, NDA 3-3 and NDA 2 for 100-seed weight; NDA 5-14, NDA 8-6, NDA 96-6 and NDAGC 31 biological yield per plant and Bahar, NDAGC 1010, Amar, ICP 2155 and NDA 96-6 for harvest-index. An earlier work has also reported wide range of variation for various character and have identified superior pigeonpea genotypes for further use in breeding programmes.

The mean range, GCV, PCV, heritability and genetic advance percentage of mean are given in Table 3. The character possessing high genotypic coefficient of variation value has better scope of improvement through selection. The influence of environment on each trade could be determined on the basis of difference between phenotypic coefficient of variation and genotypic coefficient of variation. A perusal of coefficient of variation revealed that the highest estimates of genotypic and phenotypic coefficient of variation were observed in case of secondary branches per plant (26.29 and 29.27%), followed by seed yield per plant (21.47 and 21.91%) which can be considered as high because of being very close to 20%.

Moderate estimates were recorded for biological yield per plant (19.08 and 19.52%), 100-seed weight (16.51 and 16.66%), pods per plant (14.78 and 15.05%), primary branches per plant (11.36 and 19.11%) and seeds per pod (10.07 and 10.97%). The remaining four characters exhibited low estimates of genotypic as well as phenotypic coefficient of variation. The lowest estimates of GCV and PCV were observed for days to maturity (1.52 and 1.62%), followed by days to 50% flowering (2.69 and 2.79%), plant height (6.51 and 6.74%) and harvest index (8.15 and 8.64%). The magnitude of phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the characters which may be due to higher degree of interaction of genotypes with the environment. These findings were in close agreement with the findings of earlier works (Bashkarana and Muthiah, 2006; Bhadru, 2008; 2011; Yerimani et al., 2013).

These values alone are not helpful in determining the heritable portion of variation (Falconer, 1960). The proportion of genetic variability which is transmitted from parents to offspring is reflected by heritability (Lush, 1949). In this context, the high estimates of heritability was recorded by 100 seed weight (98.18%), followed by pods per plant (96.34%), seed yield per plant (96.00%), biological yield per plant (95.60%), plant height (93.24), harvest index (88.88%), days to maturity (87.43%), seeds per pod (84.24%) and secondary branches per plant (80.69%); however primary branches per plant

Table 4. The five most desirable genotypes identified for high mean performance for 11 quantitative characters in pigeonpea

Characters	Genotypes
Days to 50 % flowering	NDA 7-11(135.67 days), ICP 870 (137 days), NDA 3 (137.33 days), NDA 8-6 (137.67 days), NDA 5-14 (139 days)
Days to maturity	NDA 7-11 (243.33 days), ICP 870 (245 days), NDA 8-6 (246 days), NDA 96-6 (246 days), NDA 3 (247.33 days)
Plant height (cm)	ICP 870 (198.91 cm), NDACMS 1-6A (198.42 cm), NDACMS 1-4A (197.67 cm), NDAGC 1010 (190.02 cm), NDA 8-6 (187.50 cm)
Primary branches/ plant	ICP 870 (6.61), NDA 96-6 (6.52), NDA 2 (6.45), NDACMS 1-6A (5.98), NDA 8-6 (5.80)
Secondary branches/ plant	ICP 870 (34.63), NDACMS 1-6A (30.45), NDAGC 1010 (30.04), Bahar (27.48), NDA 2(27.03)
Pods/ plant	NDAGC 1010 (245.08), ICP 2155 (241.64), NDA 96-6 (231.62), NDA 8-6 (219.53), NDAGC 31 (206.04)
Seeds/ pod	NDACMS 1-6A (3.82), NDA 3 (3.80), NDA 7-11 (3.78), ICP 7353 (3.60), NDA 2 (3.60)
100-seed weight (g)	NDA 5-14 (15.14 g), NDACMS 1-3B (13.72 g), NDA 3-3 (13.33 g), NDA 2 (13.16 g), NDA 98-6 (12.58 g)
Seed yield/ plant (g)	NDA 5-14 (82.39 g), NDA 8-6 (78.77 g), NDA 96-6 (77.07 g), ICP 2155 (74.63 g), NDACMS 1-6B (71.94 g)
Biological yield/ plant (g)	NDA 5-14 (292.98 g), NDA 8-6 (264.67 g), NDA 96-6 (250.83 g), NDACMS 1-6B (250.12 g), NDAGC 31 (245.69)
Harvest-index (%)	Bahar (31.66%), NDAGC 1010 (31.55%), Amar (31.22%), ICP 2155 (31.01%), NDA 96-6 (30.75%)

(35.34%) had low estimate. The characters with exhibited high heritability, suggests that the selection will be more effective. According to Panse (1957) such characters are governed predominantly by additive gene action and could be improved through individual plant selection. Whereas, low heritability indicated that the characters were highly influenced by environmental factors, genetic improvement through selection will be difficult due to effect of genotypes.

Johnson et al. (1955) have showed that a character exhibiting high heritability may not necessarily give high genetic advance. The highest value of genetic advance in percent of mean was shown by secondary branches per plant (48.65%), while days to maturity (2.92%) had lowest value for this parameter. The characters exhibiting high estimates of genetic advance in percent of mean were seed yield per plant (43.34%), biological yield per plant (38.44%), 100-seed weight (33.70%) and pods per plant (29.04%), along with secondary branches per plant (48.65%). However, the moderate estimates of genetic advance resulted in the case of seeds per pod (19.04%), harvest-index (15.82%), primary branches per plant (13.91%) and plant height (12.94%). In addition to days to maturity (2.93%), the low estimate of genetic advance was also found for days to 50% flowering (5.34%).

It can be find out with greater degree of accuracy when heritability in conjunction with genetic advance is studied (Dudley and Moll, 1969). Thus a character possessing high heritability along with high genetic advance will be valuable in the selection programme. High heritability coupled with high genetic advance as per cent of mean were recorded for secondary branches per plant, seed yield per plant, biological yield per plant, 100-seed weight and pods per plant; suggesting preponderance of additive gene action in the expression of these characters. Therefore, selection may be effective through these characters in segregating generation. High heritability coupled with moderate genetic advance as per cent of mean were observed for plant height, primary branches per plant, seeds per pod and harvest index. However, days to 50% flowering and days to maturity exhibited high heritability coupled with low genetic advance suggesting preponderance on non-additive gene action in the inheritance of these traits; hence, in this case selection may not be effective. Most of the above results in respect to heritability and genetic advance are in agreement with earlier reports on pigeonpea by Basavarajaiah et al. (2000), Venkateswarlu (2001), Bashkarana and Muthiah (2006), Bhadru (2008), Bhadru (2011) and Yerimani et al. (2013).

Conclusion

The highest mean performance for seed yield per plant along with some of the component traits was exhibited by NDA 5-14, NDA 8-6, NDA 96-6, ICP 2155 and NDACMS 1-6B. The above mentioned genotypes may be used as donor parents in hybridization programme for developing high yielding varieties. The characters 100-seed weight, pods per plant, seed yield per plant, plant and secondary branches per plant showed high heritability coupled with high genetic advance as percentage of mean, suggesting preponderance of additive gene action in the expression of these characters. Such traits could be improved by mass selection and other breeding methods based on progeny testing; while, plant height, primary branches per plant, pods per plant, seeds per pod and harvest index showed high heritability with moderate genetic advance as percent of mean suggesting greater role of non-additive gene action in their inheritance; to improve these traits heterosis breeding could be used.

Conflict of Interest

The authors have not declared any conflict of interest.

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