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Dhruv D Patel

Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India

SD Solanki

Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India

Apurv Kumar M Patel

Department of Plant Pathology, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India

Ravi D Patel

Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India

Corresponding Author:

Dhruv D Patel

Department of Genetics and Plant Breeding, C. P. College of Agriculture, S. D. Agricultural University, Sardarkrushinagar, Gujarat, India

Variability, correlation, path analysis and screening for yellow mosaic virus in cowpea

Dhruv D Patel, SD Solanki, Apurv Kumar M Patel and Ravi D Patel

Abstract

Genetic variability, correlation and path analysis was studied for yield and its attributing traits in thirty-two cowpea genotypes. The estimates revealed that highest GCV and PCV values were observed for seed yield per plant followed by plant height, 100 seed weight and number of pod per plant. Among all the traits plant height recorded maximum heritability and seed yield per plant exhibited maximum genetic advance as percent of mean compared to other traits. The character like plant height, number of branch per plant, number of pod per plant, 100 seed weight, harvest index and seed yield per plant exhibited high heritability with high genetic advance as percent of mean. The traits *viz.*, number of pods per plant, number of seed per pod, 100 seed weight, and harvest index showed positive and significant correlation with seed yield per plant. Two genotypes *viz.* GC 3 and PCP 1123 were found resistant against Yellow Mosaic Virus (YMV) disease.

Keywords: GCV, PCV, heritability, correlation, path analysis, yellow mosaic virus

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is grown throughout the India for its long green pods, seed and foliage as fodder. Cowpea, belong to family *Fabaceae/ Papilionaceae* with a chromosome number of $2n=2x=22$. It is commonly known as black-eyed bean or southern pea. Cowpea is excellent forage crop and it is a very good source of high quality protein, carbohydrates, low amounts of fat, fiber, amino acids and minerals. Cowpea being a self-pollinated crop, variability existing is limited. Hence, the effort of the breeder is to evolve better yielding genotypes by exercising selection in segregating generation. Generally direct selection for yield is not effective due to its low heritability, hence it is desirable to adopt indirect selection of component traits for yield improvements. Selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability indicates the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates suggests the extent to which improvement is possible through selection. Study of correlation in combination with path coefficient analysis which will partition the correlation value in to direct and indirect effects of component traits is very much helpful for implementation of any selection programme.

Material and Methods

The present study was conducted during *Kharif* 2020 at Pulse Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The experimental materials consisted thirty-two diverse genotypes of cowpea which were sown in a randomized block design (RBD) with three replications. Each genotype was accommodated in a single row of 4 m length with a spacing 45 cm between row and 15 cm between plants. All the recommended crop production and protection practices were followed to raise the healthy crop. The observations were recorded for characters *viz.*, days to flowering, days to maturity, plant height (cm), number of branch per plant, number of pod per plant, number of seed per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g), harvest index (%) and protein content (%) on five randomly selected plants from each genotypes in all the replications while days to flowering and days to maturity which were recorded on plot basis. For the screening purpose, One set of experiment was sown at Botanical Garden, Department genetics and plant breeding, C. P. College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University. This set of experiment planted in 45×10 cm spacing and use genotype GC 1501 (highly susceptible to YMV) as a infector row after every 3 rows. Total five plants

were randomly selected per genotype and from each randomly selected plant five leaf selected for assessment of YMV scale. P.D.I (Percent Disease Intensity) was measured with the help of formula

$$\text{P.D.I. (\%)} = \frac{\text{Summation of numerical disease rating}}{(\text{Number of leaves observed}) \times (\text{Maximum disease grade})} \times 100$$

Statistical analysis

The analysis of variance was carried out as the procedure suggested by Panse and Sukhatme (1978) [15]. Coefficients of variation were calculated by the formulae suggested by Burton (1952) [4]. Heritability in the broad sense and Genetic advance as expressed in percent of mean was calculated by the method suggested by Johnson *et al.* (1955) [10]. Correlation study was conducted as per Al-Jibouri *et al.* (1958) [1]. Whereas, construction of Path coefficient analysis suggested by Dewey and Lu (1959) [7].

Result and Discussion

Analysis of variance revealed highly significant differences for all phenotypic traits among the thirty two cowpea genotypes studied (Table 1) indicating a high level of genetic variation. These results suggest opportunity for improvement of cowpea crop by selection of superior genotypes by using suitable breeding methods. The phenotypic variance and phenotypic coefficient of variation were slightly higher than corresponding genotypic variance and genotypic coefficient of variation for all the characters which indicated the presence of environmental effect upon the concerned characters. This is an agreement with finding of Shahid, *et al.* (2005) [17], Sharma *et al.* (2017) [19, 20], Chaudhary *et al.* (2020) [5] in cow pea.

In the present investigation the trend for highest estimates of genotypic and phenotypic coefficient of variation were observed for seed yield per plant (25.99 and 28.03) followed by plant height (21.54 and 22.37), 100 seed weight (20.54 and 21.58) number of pod per plant (19.01 and 21.03) respectively (Table 2). Several earlier workers also reported high GCV and PCV for seed yield per plant (Shahid *et al.* 2005, Sharma *et al.* 2017 and Havaraddi and Deshpande 2018) [17, 19, 20, 9], number of pod per plant (Bhagavati *et al.* 2018) [3], plant height (Khan *et al.* 2015). Moderate estimates of genotypic and phenotypic coefficient of variation were observed for harvest index (18.01 and 18.92), number of branch per plant (13.84 and 16.89), pod length (9.72 and 13.08), respectively. While lowest estimates of genotypic coefficient variation and phenotypic coefficient variation were observed for protein content (3.80 and 4.34), days to maturity (5.53 and 6.00), days to flowering (5.82 and 6.29), number of seed per pod (6.72 and 10.65), respectively. Which indicated selection will be effective among genotypes for seed yield per plant and its contributing traits *viz.*, plant height, 100 seed weight, number of pod per plant, harvest index, number of branch per plant, pod length.

Based on the results, the highest estimates of the genetic advance as percentage of mean were recorded for seed yield per plant (49.63%) followed by plant height (42.72%), 100 seed weight (40.26%), number of pod per plant (35.38%), harvest index (35.34%), number of branch per plant (23.35%), pod length (14.89%) and days to flowering (11.08%). The high values of genetic advance as percentage of mean observed in cowpea had also been reported by Sabale *et al.* (2018) [16], Nair *et al.* (2018) [13] for plant height; Gupta *et al.*

(2019) [8] for number of branch per plant and pod length; Nwosu *et al.* (2013) [14] for number of pod per plant and number of seed per pod; Thorat and Gadewar (2013) [22] for number of branch per plant; Shahid *et al.* (2005) [17], Bhagavati *et al.* (2018) [3] for 100 seed weight; Chaudhary *et al.* (2020) [5] for seed yield per plant; Sharma *et al.* (2017) [19, 20], Nair *et al.* (2018) [13] for harvest index; Sabale *et al.* (2018) [16], Shahid *et al.* (2005) [17] for seed yield per plant.

Table 1: Analysis of variance for different character in cowpea

Sr. No.	Source	Replications	Genotypes	Error
	d.f.	2	31	62
	Characters	Mean squares		
1.	Days to flowering	0.01	20.41**	1.10
2.	Days to maturity	3.13	37.04**	2.04
3.	Plant height	4.76	621.34**	15.86
4.	Number of branch per plant	0.47	2.50**	0.35
5.	Number of pod per plant	1.13	19.81**	1.37
6.	Number of seed per pod	0.63	3.06**	1.02
7.	Length of pod	4.28	6.62**	1.40
8.	100 seed weight	0.49	12.06**	0.40
9.	Harvest index	37.18	359.86**	11.94
10.	Protein content	0.03	2.20**	0.20
11.	Seed yield per plant	9.15	68.86**	3.55

*, ** significant at 5% and 1% level of significance, respectively.

The character like plant height, number of branch per plant, number of pod per plant, 100 seed weight, harvest index and seed yield per plant exhibited high heritability with high genetic advance as percent of mean. These traits may be attributed to the preponderance of additive gene action with fixable and selection may be effective for improvement of these traits. Among all the traits plant height recorded maximum heritability (92.71 percent) while seed yield per plant exhibited maximum genetic advance as percent of mean (49.63) compared to other traits. Several earlier workers have also reported high heritability coupled with high genetic advance for plant height Nair *et al.* (2018) [13], Havaraddi and Deshpande (2018) [9]; for number of branch per plant Gupta *et al.* (2019) [8], Verma *et al.* (2019) [24]; for number of pod per plant Chaudhary *et al.* (2020) [5]; for 100 seed weight Shahid *et al.* (2005) [17] Bhagavati *et al.* (2018) [3]; for harvest index Chaudhary *et al.* (2020) [5], Nair *et al.* (2018) [13]; for seed yield per plant Sabale *et al.* (2018) [16], Chaudhary *et al.* (2020) [5]. Moderate values of heritability coupled with lowest values of genetic advance expressed as percentage of mean were recorded in cowpea had been reported by Chaudhary *et al.* (2020) [5] for protein content. High estimate of heritability coupled with moderate values of genetic advance expressed as percentage of mean were recorded in cowpea had been reported by Shanko *et al.* (2014) [18] for days to maturity.

Correlation studies provides the information about degree and direction of traits with grain yield which is useful for selection of elite genotypes from population. Genotypic and phenotypic correlation coefficient among seed yield per plant and its contributing traits are presented in table 3. In present study for all traits genotypic correlation values are higher than phenotypic correlation values which indicates little influence of environment. Number of pods per plant, number of seed per pod, 100 seed weight, and harvest index showed positive and significant correlation with seed yield per plant which is similar to the findings of Manggoel *et al.* (2012) [12], Thorat and Gadewar (2013) [22], Sharma *et al.* (2016) [21], Waghmare *et al.* (2019) [25].

The path coefficient analysis is a statistical device which takes into account the cause and effect relation between the variables which is unique in partitioning the association into direct and indirect effects through other independent variables. The path coefficient analysis also measures the relative importance of causal factors involved. Direct and indirect effects of yield components on seed yield presented in table 4. The path coefficient analysis estimated that number of pod per plant (0.6673), harvest index (0.4199), number of seed per pod (0.3548), days to flowering (0.3564) and 100 seed weight (0.3278) showed high and positive direct effect on seed yield per plant while, protein content exhibited low and positive direct effect (0.2001) on seed yield per plant while, pod length showed negligible and positive direct effect (0.0416) on seed yield per plant which exhibited to be the most important yield components. Number of pod per plant exhibited positive indirect effects on seed yield per plant via number of branch per plant. Harvest index exhibited high and positive indirect effect on seed yield per plant via number of

pod per plant (0.4119) while low and positive indirect effects on seed yield per plant via days to maturity (0.0537). These findings are in confirmation with Udensi and Ikpeme (2012)^[23], Anamika and Tajane (2014)^[2], Sharma *et al.* (2016)^[21], Cyrus (2019)^[6], Waghmare *et al.* (2019)^[25], Chaudhary *et al.* (2020)^[5].

The genotypes were also evaluated against the Yellow Mosaic Virus (YMV) disease (Table 5). The range for P.D.I. was observed from 21.11% (GC 3) to 77.70% (GC 1501). Lower P.D.I., indicates the less infection of YMV in plant leaves and its better for plant growth and pod formation. The maximum P.D.I. showed in genotype GC 1501 (72.44%) followed by GDVC 2 (73.33%), GC 1805 (68.82%), RC 101 (63.22%) and GC 1601 (62.22%) while the minimum P.D.I. was observed in genotype GC 3 (21.11%) followed by PCP 1123 (24.44%), GC 1603 (31.08%), Pant Lobia 3 (32.19%) and GC 1506 (34.44%) respectively. GC 3 is best among the all-other genotypes with higher resistance in YMV disease rating scale (21.11%).

Table 2: Genetic parameters of variation for seed yield and its contributing characters in cowpea

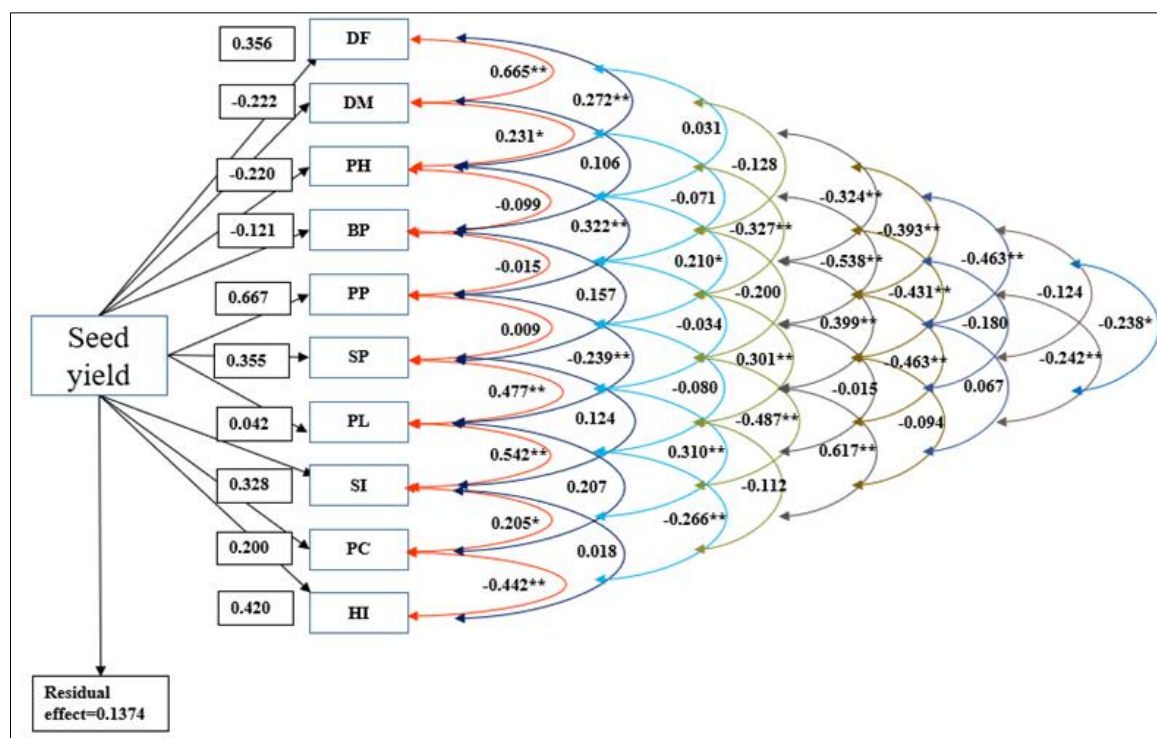
Sr. No.	Characters	Genetic parameters										
		Mean	Range	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	ECV (%)	h ² (%)	GA	GAM (%)
1.	Days to flowering	43.61	39.67-54.00	6.44	7.53	1.10	5.82	6.29	2.40	85.45	4.83	11.08
2.	Days to maturity	61.73	54.33-71.33	11.67	13.71	2.04	5.53	6.00	2.31	85.13	6.49	10.52
3.	Plant height (cm)	65.96	34.79-86.95	201.83	217.68	15.86	21.54	22.37	6.04	92.71	28.18	42.72
4.	Number of branch per plant	6.12	4.53-7.80	0.72	1.07	0.35	13.84	16.89	9.68	67.14	1.43	23.35
5.	Number of pod per plant	13.04	7.07-16.53	6.14	7.52	1.38	19.01	21.03	9.01	81.66	4.61	35.38
6.	Number of seed per pod	12.26	11.0-15.40	0.68	1.71	1.03	6.72	10.65	8.26	39.87	1.07	8.75
7.	Pod length (cm)	13.56	11.30-17.37	1.74	3.15	1.41	9.72	13.08	8.75	55.58	2.02	14.89
8.	100 seed weight (g)	9.60	6.99-15.61	3.89	4.29	0.41	20.54	21.58	6.63	90.56	3.86	40.26
9.	Harvest Index (%)	59.78	32.98-72.44	115.98	127.91	11.94	18.01	18.92	5.78	90.67	21.12	35.34
10.	Protein content (%)	21.48	19.32-23.30	0.67	0.87	0.20	3.80	4.34	2.10	76.60	1.47	6.85
11.	Seed yield per plant (g)	17.95	10.07-26.60	21.77	25.32	3.56	25.99	28.03	10.50	85.96	8.91	49.63

*, ** significant at 0.05% and 0.01% level of significance, respectively.

Table 3: Genotypic correlation and phenotypic correlation coefficient for different characters in cow pea

Sr. No.	Characters		DF	DM	PH	BP	PP	SP	PL	SI	PC	HI	SYP
1.	DF	r _g	1.000	0.665**	0.272**	0.031	-0.128	-0.324**	-0.393**	-0.463**	-0.124	-0.238*	-0.348**
		r _p	1.000	0.642**	-0.224*	0.047	-0.113	-0.220*	-0.261*	-0.421**	-0.116	-0.211*	-0.290**
2.	DM	r _g		1.000	0.231*	0.106	-0.071	-0.327**	-0.538**	-0.431**	-0.180	-0.242*	-0.419**
		r _p		1.000	0.196	0.143	0.052	-0.182	-0.330**	-0.375**	-0.139	-0.217*	-0.370**
3.	PH	r _g			1.000	-0.099	0.322**	0.210*	-0.200	-0.399**	-0.463**	0.067	-0.077
		r _p			1.000	-0.044	0.276**	0.129	-0.140	-0.374**	-0.377**	0.046	-0.087
4.	BP	r _g				1.000	-0.015	0.157	-0.034	0.301**	-0.015	-0.094	-0.011
		r _p				1.000	0.038	0.085	0.023	0.237*	0.020	-0.091	-0.059
5.	PP	r _g					1.000	0.009	-0.239*	-0.080	-0.487**	0.617**	0.666**
		r _p					1.000	0.067	-0.176	-0.074	-0.363**	0.528**	0.549**
6.	SP	r _g						1.000	0.477**	0.124	-0.310**	-0.112	0.204*
		r _p						1.000	0.132	0.015	-0.041	-0.045	0.152
7.	PL	r _g							1.000	0.542**	0.207*	-0.266**	0.187
		r _p							1.000	0.381**	0.080	-0.203*	0.101**
8.	SI	r _g								1.000	0.205*	0.018	0.372**
		r _p								1.000	0.187	-0.004	0.324**
9.	PC	r _g									1.000	-0.442**	-0.246
		r _p									1.000	-0.372**	-0.223*
10.	HI	r _g										1.000	0.666**
		r _p										1.000	0.653**
11.	SYP	r _g											1.000
		r _p											

(DF: Days to flowering, DM: Days to maturity, PH: Plant height, BP: Number of branch per plant, PP: Number of pod per plant, SP: Number of seed per pod, PL: Pod length, SI: 100 seed weight, PC: Protein content, HI: Harvest Index, SYP: Seed yield per plant)



(DF: Days to Flowering, DM: Days to Maturity, PH: Plant Height, BP: Number of Branch Per Plant, PP: Pods Per Plant, SP: Seeds Per Pod, PL: Pod Length, SI: 100 Seed Weight, PC: Protein Content, HI: Harvest Index)

Fig 1: Diagrammatic representation of genotypic path analysis

Table 4: Direct and indirect effects of yield components on seed yield in cowpea

Sr. No.	Characters	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of pod per plant	Number of seed per pod	Pod length	100 seed weight	Protein content	Harvest Index	Seed yield per plant
1	Days to flowering	0.3564	-0.1479	-0.0600	-0.0038	-0.0852	-0.1150	-0.0163	-0.1517	-0.0248	-0.1000	-0.3483
2	Days to maturity	0.2371	-0.2224	-0.508	-0.0128	0.0474	-0.1159	-0.0223	-0.1413	-0.0360	-0.1015	-0.4186
3	Plant height	0.0971	-0.0514	-0.2203	0.0119	0.2149	0.0746	-0.0083	-0.1309	-0.0926	0.0283	-0.0767
4	Number of branch per plant	0.0112	-0.0235	0.0217	-0.1208	-0.0103	0.0558	-0.0014	0.0987	-0.0030	-0.0394	-0.0111
5	Number of pod per plant	-0.0455	-0.0158	-0.0708	0.0019	0.6673	0.0032	-0.0099	-0.0263	-0.0975	0.2592	0.6655
6	Number of seed per pod	-0.1155	0.0726	-0.0463	-0.0190	0.0060	0.3548	0.0198	0.0406	-0.0621	-0.0472	0.2037
7	Pod length	-0.1400	0.1197	0.0440	0.0042	-0.1594	0.1691	0.0416	0.1776	0.0415	-0.1116	0.1867
8	100 seed weight	-0.1649	0.0958	0.0880	-0.0364	-0.0536	0.0440	0.0225	0.3278	0.0410	0.0075	0.3717
9	Protein content	-0.0441	0.0400	0.1020	0.0018	-0.3254	-0.1101	0.0086	0.0671	0.2001	-0.1858	-0.2457
10	Harvest Index	-0.0849	0.0537	-0.0148	0.0113	0.4119	-0.0399	-0.0110	0.0059	-0.0885	0.4199	0.6636

Residual effect = 0.1374

Table 5: P.D.I (Percent Disease Intensity) of cowpea genotypes against yellow mosaic virus

Sr. No.	Genotype	YMV PDI	Sr. No.	Genotype	YMV PDI
1	GC 3	21.11	17	GC 1506	34.44
2	GC 4	57.77	18	GC 1802	56.66
3	GC 5	53.32	19	GC 1805	68.82
4	GC 6	41.11	20	GC 1807	40.00
5	GC 1501	77.70	21	Pusa Phalguni	54.39
6	GC 1203	57.72	22	GC 1806	34.62
7	GC 1602	44.44	23	TC 901	55.55
8	GC 1712	55.55	24	Pant lobia 7	42.22
9	GC 901	37.77	25	PGCP 72	34.44
10	GDVC 2	73.33	26	PCP 1123	24.44
11	PGCP 13	55.55	27	VCP 15006	42.22
12	TC 701	50.00	28	PGCP 71	47.77
13	GC 1603	31.08	29	Pant lobia 3	32.19
14	RC 101	63.32	30	CPD 319	45.55
15	GC 1612	41.11	31	CPD 317	48.88
16	GC 1601	62.22	32	GC 1808	41.11

Conclusion

Based on the above result it is concluded that high heritability value indicates less influence of environment on respective characters. Hence direct selection should be followed to improve the genotypes. In the present study, the character like plant height, number of branch per plant, number of pod per plant, 100 seed weight, harvest index and seed yield per plant exhibited high heritability with high genetic advance as percent of mean. So these characters are governed by additive gene action and we should go for direct selection for these traits to improve in future breeding programme. Considering correlation and path coefficient analysis number of pods per plant, number of seed per pod, 100 seed weight, and harvest index showed positive and significant correlation along with high and positive direct effect on seed yield per plant. Therefore selection for these traits can directly be followed for yield improvement in segregating generations of cowpea during selection of breeding lines. Lower P.D.I. is favourable for plant growth and pod development so two genotypes GC 3

and PCP 1123 found resistant against YMV and should be used future breeding programme.

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