

Research Article HARNESSING THE GENETIC VARIABILITY IN COWPEA [*Vigna unguiculata* (L.) Walp]

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Abstract: Cowpea [*Vigna unguiculata* (L.) Walp] is an important protein rich pulse crop produced globally, with high nutritional and economic value. Estimation of the genetic variation is key to any crop improvement program. The findings reported here would serve cowpea research and breeding programs including germplasm management, selection of appropriate genotypes to generate new breeding materials for cultivar improvement. These traits showed variability for biological yield per plant, plant height, seed yield per plant, days to maturity, pod/plant, pod length, peduncle length, days to 50 % flowering, seeds /pod, seed index, terminal leaf length, cluster/plant, no. of main branches, fresh pod weight, harvest index, terminal leaf width, no. of node on main stem, pod/cluster and no. of pods per peduncle. The traits with high magnitude of variability can be manipulates for its improvement. High heritability with high genetic advance was recorded for plant height followed by peduncle length, biological yield per plant, pod/plant, pod length, seed yield per plant, days to 50 % flowering, seeds /pod, seed index, no. of main branches, terminal leaf length, terminal leaf width, cluster/plant and fresh pod weight.

Keywords: Cowpea, Genetic variability, Heritability, Crop improvement

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Introduction

Cowpea [Vigna unguiculata (L.) Walp], is among the most important grain legumes in India. Its chromosome number is (2n=22, 24). It is known as snaps bean, snapdragon bean, yard long bean, southern pea, black eyed pea, asparagus bean, chinese long bean, crowder pea, sow pea, catjang, lobia, and snake bean [1]. Cowpea originated in Africa and is widely Africa, Latin America, and Southeast Asia and in the southern united states. It is chiefly used as a grain crop, for animal fodder, or as a vegetable. Its value lies in its high protein content (23-29%, with potential for perhaps 35%); the protein of cowpea is rich in the amino acids, lysine and tryptophan, compared to cereal grains, however it is deficient in methionine and cystine when compared to animal protein. Its ability to fix atmospheric nitrogen, which allows it to grow on, and improve poor soils. Yield is polygenetically controlled quantitative character and is highly influenced by the environment. Thus, for any crop improvement programme, the magnitude and extent of genetic variability, its heritable component and genetic progress expected should be known to formulate an efficient plant breeding programme. Heritability (Narrow sense) and genetic advance are important selection parameters [2]. Heritability estimates can be grouped as broad sense heritability or narrow sense heritability [3]. Broad sense heritability provides information on the relative magnitude of genetic and environmental variation in specific population [4]. Genetic advance is the measure of genetic gain under selection and depends on genetic variability, heritability, and selection intensity. Genetic advance also indicates the mode of gene action in the expression of traits and helps in choosing breeding methods [5]. Thus, heritability estimates coupled with genetic advance are more reliable and helpful in predicting the gain under selection than individual consideration of the parameters.

Materials and Methods

The field experiment was conducted for two year 2016-17 and 2017-18 during

Kharif season. The 15 germplasm of cow pea crop were evaluated for quantitative traits at Field Experimentation Centre, Rajoula, Mahatma Gandhi Chitrakoot Gramodaya Vishwavidhyalaya, Chitrakoot, 485334, Madhya Pradesh, India. The land was ploughed with mould board plough followed by two harrowing with Disc harrow to bring the soil to fine tilth and for proper pulverization so as to facilitate sowing. The land was levelled with the help of leveller. The crop was provided with recommended protective irrigations. Manual hand weeding and row cleaning operations with the help of hand hoe was also carried out at regular intervals during crop growth period. The recommended package and practices were followed to raise the healthy crop.

Result and discussion Mean performance and range of different characters Days to 50% Heading

Days to 50% heading ranged from 30.77to 43.55with an overall mean performance of 35.722. The maximum days to 50% heading was observed in genotype Ujjain AC (43.55) and minimum in RCV 395 (30.78) [6]. Days to 50% flowering ranged from 34.67to 47.55with an overall mean performance of 39.666. The maximum days to 50% flowering was observed in genotype Ujjain AC (47.553) and minimum in RCV 395 (34.67). Days to maturity varied from 75.28to 103.28with an overall mean performance of 94.73. The maximum days to maturity was observed in genotype Selection 2-1 (103.28) and minimum in Arkagarima (75.28). Terminal Leaf length (cm) varied from 9.89 to 17.39 with an overall mean performance of 14.05. The maximum terminal leaf length (cm) was observed in genotype Kashi gouri (17.39) and minimum in Bangal AC (9.89). Terminal leaf width (cm) varied from 4.66to 8.51 with an overall mean performance of 6.88. The maximum terminal leaf width (cm) was observed in genotype RCV 395 (8.51) and minimum in Bangal AC (4.66). No. of main branches varied from 3.89to 8.39 with an overall mean performance of 5.83.

						Ta	ble-1 Me	an perfo	ormance	e and ra	inge of	differen	t charac	ters					
Genotype	DFH	DFF	DM	TLL	TLW	NMB	NNMS	NPPP	PPC	CPP	PiL	PPP	PL	PH	FPW	SPP	SI	BYPP	HI
Kashi kanchan	35.44	39.17	98.39	15.61	7.82	6.78	3.83	4.28	3.89	12.39	15.38	42.39	34.57	65.74	9.99	23.89	12.55	329.01	42.61
Ujjain AC	43.55	47.55	97.67	13.01	6.52	4.33	4.39	4.33	3.83	7.78	9.18	25.22	36.93	160.34	6.74	18.11	14.00	180.81	39.05
Kashi gouri	31.94	36.16	95.00	17.39	7.73	4.94	3.89	3.45	3.94	8.83	10.51	36.11	28.34	75.70	8.19	16.39	15.06	256.05	38.48
Kashi nidhi	32.33	36.17	94.78	15.23	7.49	5.67	4.44	3.78	3.61	11.17	10.64	39.16	40.01	66.79	10.42	21.67	15.22	335.16	39.80
Selection 2 - 1	38.28	42.28	103.28	15.22	6.66	3.89	4.61	3.44	2.89	8.05	22.82	23.45	22.22	71.71	10.11	14.78	15.89	151.39	39.15
Arkagarima	30.95	34.78	75.28	16.16	6.46	6.39	4.05	3.44	3.39	8.84	14.99	29.72	19.21	128.93	9.76	23.17	14.11	267.78	38.22
Kashi shyamal	31.89	35.89	88.89	11.28	6.71	4.78	3.78	4.11	3.44	8.28	8.71	34.72	30.16	169.81	10.72	12.28	16.39	188.94	39.71
Indra lal	40.56	44.61	89.83	16.17	5.67	4.05	3.50	4.06	3.61	6.61	28.70	22.17	24.99	179.32	9.53	15.67	13.33	122.90	38.84
NDCP13	37.44	41.44	96.39	12.49	7.20	7.95	4.61	3.17	2.89	8.83	12.89	29.94	27.18	122.44	9.87	22.67	15.97	294.02	40.21
BCKV1	37.83	41.61	94.22	14.92	7.25	5.00	3.28	3.61	2.95	9.61	14.87	32.45	25.41	94.13	10.30	20.56	15.50	271.34	40.45
Kashi Shudha	30.94	34.78	101.39	12.91	6.40	5.55	4.05	3.39	2.50	11.33	13.83	26.00	31.25	76.47	10.72	13.89	13.00	122.87	41.11
RCCP1	39.83	43.89	101.78	13.60	7.00	8.39	4.61	3.61	2.67	10.33	14.95	26.78	28.16	132.76	10.23	22.11	12.11	192.78	36.91
Kashi unnati	31.72	35.78	94.44	13.24	7.06	7.00	4.83	4.22	3.72	10.89	13.27	40.50	35.70	72.63	11.85	16.95	16.17	311.18	39.56
RCV 395	30.78	34.67	94.55	13.57	8.51	8.17	3.83	3.83	3.33	10.61	8.66	35.95	30.46	110.63	6.49	21.11	16.94	330.35	38.58
Bangal AC	42.33	46.22	95.06	9.89	4.66	4.61	5.00	4.11	3.61	7.78	13.35	27.33	38.14	193.79	9.17	15.44	7.67	86.85	38.95
Mean	35.72	39.67	94.73	14.05	6.88	5.83	4.18	3.79	3.35	9.42	14.18	31.46	30.18	114.75	9.61	18.58	14.26	229.43	39.44
S.E.	0.32	0.34	0.45	0.37	0.18	0.27	0.29	0.23	0.25	0.32	0.28	0.39	0.37	0.67	0.31	0.33	0.24	4.57	0.49
Range Lowest	30.78	34.67	75.28	9.89	4.66	3.89	3.28	3.17	2.50	6.61	8.66	22.17	19.21	65.74	6.49	12.28	7.67	86.85	36.91
Range Highest	43.55	47.55	103.28	17.39	8.51	8.39	5.00	4.33	3.94	12.39	28.70	42.39	40.01	193.79	11.85	23.89	16.94	335.16	42.61
C.D. @ 5%	0.93	0.98	1.30	1.06	0.51	0.77	0.85	0.68	0.73	0.93	0.82	1.12	1.06	1.95	0.91	0.94	0.68	13.23	1.41
C.V. @ 5%	1.55	1.48	0.82	4.53	4.44	7.92	12.19	10.65	13.08	5.90	3.47	2.12	2.11	1.02	5.64	3.04	2.86	3.45	2.13

The maximum no. of main branches was observed in genotype RCCP1 (8.39) and minimum in Selection 2-1 (3.89). No. of node on main stem varied from 3.28to 5.00 with an overall mean performance of 4.18. The maximum no. of node on main stem was observed in genotype Bangal AC (5.00) and minimum in BCKV1 (3.28). No. of pods per peduncle varied from 3.17 to 4.33 with an overall mean performance of 3.79. The maximum no. of pods per peduncle was observed in genotype Ujjain AC (4.33) and minimum in NDCP13 (3.17). Pod/cluster varied from 2.50 to 3.94 with an overall mean performance of 3.35. The maximum pod/cluster was observed in genotype Kashi gouri (3.94) and minimum in Kashi Shudha (2.50). Cluster/plant varied from 6.61 to 12.39 with an overall mean performance of 9.42. The maximum cluster/plant was observed in genotype Kashikanchan (12.39) and minimum in Indralal (6.61). Peduncle length varied from 8.66 to 28.70 with an overall mean performance of 14.18. The maximum peduncle length was observed in genotype Indra lal (28.70) and minimum in RCV 395 (8.66). Pod/plant varied from 22.17 to 42.39 with an overall mean performance of 31.46. The maximum pod/plant was observed in genotype Kashi kanchan (42.39) and minimum in Indra Ial (22.17). Pod length varied from 19.21 to 40.01 with an overall mean performance of 30.18. The maximum pod length was observed in genotype Kashi nidhi (40.01) and minimum in Arkagarima (19.21). Plant height (cm) varied from 65.737 to 193.790 with an overall mean performance of 114.75. The maximum plant height (cm) was observed in genotype Bangal AC (193.79) and minimum in Kashi kanchan (65.74). Fresh pod weight varied from 6.49 to 11.85 with an overall mean performance of 9.61. The maximum fresh pod weight was observed in genotype Kashiunnati (11.85) and minimum in RCV 395 (6.49). Seeds/pod varied from 12.28 to 23.89 with an overall mean performance of 18.58.

The maximum seeds/pod was observed in genotype Kashi kanchan (23.89) and minimum in Kashi shyamal (12.28). Seed index varied from 7.67 to 16.94 with an overall mean performance of 14.26. The maximum seed index was observed in genotype RCV395 (16.94) and minimum in BangalAC (7.67). Biological yield per plant varied from 86.85 to 335.16 with an overall mean performance of 229.43. The maximum biological yield per plant was observed in genotype Kashinidhi (335.16) and minimum in BangalAC (86.85). Harvest index varied from 36.91 to 42.61 with an overall mean performance of 39.44. The maximum harvest index was observed in genotype Kashi kanchan (42.61) and minimum in RCCP1(36.91). Seed yield per plant varied from 33.86 to 136.79 with an overall mean performance of 90.59. The maximum seed yield per plant was observed in genotype Kashi kanchan (136.79) and minimum in Bangal AC (33.86) [7].

Genotypic and phenotypic coefficient of variation (GCV & PCV %)

Genotypic variation is the heritable portion of phenotypic or total variation. It gives the variation between genotypes. Environmental variation is the non-heritable portion of observable variation. Phenotypic variance refers to the total variation in a population. It is sum of genotypic and environment variance[8]. The estimation of genotypic and phenotypic coefficient of variation (GCV & PCV) for yield and yield attributing traits of pooled over environments were computed and results are presented in [Table-2].

Table-2 Genetic parameters for yield and yield attributing traits of cowpea genotypes pooled over environments

136.79 71 69

100.95

134.46

58.50 103.41

73.45

48.31

114.34

107.62

49.15

72.13

123.83

130.37 33.86

90 59 2.33

33.86

136.79

6.74 4.45

SN	Traits	GCV (%)	PCV (%)	h² (bs) (%)	GA	GA (%)
1	DFH	12.62	12.71	98.51	9.22	25.8
2	DFF	11.41	11.5	98.35	9.24	23.3
3	DM	7.06	7.11	98.61	13.68	14.45
4	TLL	14.12	14.83	90.66	3.89	27.7
5	TLW	13.19	13.92	89.85	1.77	25.76
6	NMB	25.69	26.88	91.33	2.95	50.57
7	NNMS	9.82	15.66	39.32	0.53	12.68
8	NPPP	7.75	13.17	34.58	0.36	9.38
9	PPC	11.59	17.48	43.97	0.53	15.83
10	CPP	17.01	18	89.26	3.12	33.1
11	PiL	37.8	37.95	99.16	11	77.53
12	PPP	20.38	20.49	98.93	13.14	41.75
13	PL	19.89	20	98.89	12.3	40.74
14	PH	38.88	38.89	99.93	91.87	80.07
15	FPW	14.81	15.84	87.34	2.74	28.51
16	SPP	20.29	20.52	97.81	7.68	41.34
17	SI	16.42	16.67	97.05	4.75	33.33
18	BYPP	36.88	37.04	99.13	173.56	75.65
19	HI	3.16	3.81	68.7	2.13	5.4
20	SYPP	37.94	38.2	98.65	70.33	77.63

Result indicated that the value of phenotypic coefficient of variation were higher than the genotypic coefficient of variation for all the characters in pooled data over various environments.

High genotypic and phenotypic coefficient of variation observed for Plant height (38.881 and 38.894) followed by seed yield per plant (37.944 and 38.203), peduncle length (37.795 and 37.954), biological yield per plant (36.883 and 37.044), no. of main branches (25.689 and 26.881), seeds /pod (20.292 and 20.519) and pod/plant (20.377 and 20.488). Moderate GCV & PCV % observed for pod length (19.887 and 19.999) followed by cluster/plant (17.009 and 18.003), pod/cluster (11.591 and 17.479), seed index (16.424 and 16.671), fresh pod weight (14.807 and 15.843), terminal leaf length (cm) (14.120 and 14.830), terminal leaf width (cm) (13.194 and 13.919), days to 50% heading (12.618 and 12.714) and days to 50 % flowering (11.406 and 11.501)[2, 5].

The low GCV & PCV % were observed for days to maturity (7.059 and 7.107) and harvest index (3.160 and 3.812). Moderate PCV and low GCV were observed for two traits i.e., no. of node on main stem (9.816 and 15.655) and no. of pods per peduncle (7.745 and 13.17)[9, 10].

Heritability (%) in broad sense

The concept of heritability is important to determine, whether phenotypic differences observed among various individual are due to genetic changes or because of environmental factors. Heritability indicates the possibility and extent to which improvement can be brought through selection. Heritability (broad sense) is an index of transmitting a character from the parents to offspring.

Heritability was recorded for all characters under study varied between 34.58% (No. of pods per peduncle) to 99.93% (Plant height).

High heritability was recorded for plant height (99.93) followed by peduncle length (99.16), biological yield per plant (99.13), pod/plant (98.93), pod length (98.89), seed yield per plant (98.65), days to maturity (98.61), days to 50% heading (98.51), days to 50% flowering (98.35), seeds /pod (97.81), seed index (97.05), no. of main branches (91.33), terminal leaf length (cm) (90.66), terminal leaf width (cm) (89.85), cluster/plant (89.26) and fresh pod weight (87.34).Moderate heritability was recorded for harvest index (68.70) whereas low heritability was recorded for pod/cluster (43.97) followed by no. of node on main stem (39.32) and no. of pods per peduncle (34.58) [11, 12].

Genetic advance as percent of mean

Genetic advance or genetic gain is still a more useful estimate. It is a measure of an improvement in the genotypic value in the new population as compared to the base population.

Genetic advance is the improvement in mean genotypic and phenotypic value of selected population over the parental population. Based on the heritability (broad sense) expected genetic advance was computed on the hypothetical selection at 5% best individual (k=2.06).

The value of genetic advance as percentage of mean estimate POE was highest for plant height (80.068) followed by seed yield per plant (77.632), peduncle length (77.531), biological yield per plant (75.65), no. of main branches (50.572), pod/plant (41.751), seeds/pod (41.342), pod length (40.74), seed index (33.331), cluster/plant (33.104), fresh pod weight (28.506), fresh pod weight (27.697), days to 50% heading (25.799), terminal leaf width (cm) (25.763) and days to 50% flowering (23.302)[13, 14, 15].

Medium genetic advance as percentage of mean were expressed by pod/cluster (15.834), days to maturity (14.445) and no. of node on main stem (12.679). Low genetic advance as percentage of mean were expressed by no. of pods per peduncle (9.382) and harvest index (5.395).

Application of research: This research will be help to the cowpea breeder to improving the traits and find out the suitable genotypes for stable performance in different genotypes.

Research Category: Plant Breeding

Abbreviations: DFH- Days to 50% heading, DFF- Days to 50% flowering, DM-Days to maturity, TLL-Terminal leaf length (cm), TLW-Terminal leaf width (cm), NMB- No. of main branches, NNMS- No. of node on main stem, NPPP- No. of pods per peduncle, PPC- pod/cluster, CPP-cluster/plant, PiL- peduncle length, PPP-pod/plant, PL- pod length, PH-plant height (cm), FPW- fresh pod weight, SPP- seeds /pod, SI- seed index, BYPP- Biological yield per plant, HI- harvest index and SYPP- Seed yield per plant

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Study area / Sample Collection: Field Experimentation Centre, Rajoula

Cultivar / Variety / Breed name: Cowpea [Vigna unguiculata (L.) Walp]

Conflict of Interest: There is no conflict among the authors.

Ethical approval: This article does not contain any studies with human participants or animals performed by any of the authors. Ethical Committee Approval Number: Nil

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