



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2019; 8(4): 1271-1274
Received: 13-05-2019
Accepted: 15-06-2019

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Genetic analysis in cowpea (*Vigna unguiculata* (L.) Walp.) under Prayagraj agro climatic conditions

Imandi Swathi and Deepanshu

Abstract

An experiment was conducted on Genetic variability, heritability, correlation, path coefficient, genetic advance and divergence in the twenty-seven genotypes in Cowpea during 2018-19 at the Research Field of Department of Horticulture, Sam Higginbottom University of Agriculture, Technology and Sciences, Prayagraj. The observations were recorded on various yield and yield contributing characters. The results from the present investigation revealed that in Cowpea Genotype Kamini identified as desirable with maximum pod yield. Maximum protein content (25.79%) was recorded in genotype IC - 2022801. Highest GCV and PCV were recorded for Length of Pod (Cm) (50.20, 50.21 respectively), followed by Protein content (46.12, 46.12). Lowest GCV and PCV were recorded for TSS content in pod (%) (0.90, 0.91 respectively) followed by Fibre percentage (3.36, 3.45). Analysis of variance showed significant difference for all the characters under study, indicates that there was ample scope for selection of promising genotypes for yield improvement. At genotypic and phenotypic level No of seeds / plant, Height of plant at flowering (cm), Days to 1st pod emergence (Days), No of Pods / peduncle, Length of Pod (cm), No of Branches, Days to 1st flowering, No of Leaves / plant, had direct positive effect on pod yield per plant. The genotypes included in cluster VII and cluster I are identified as distant genotypes which may serve as potential genotypes for hybridization programme.

Keywords: Cowpea, genotypes, genetic variability, heritability

Introduction

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous vegetable crop of India belongs to family leguminosae (Mackie and Smith, 1935) [3] with a chromosome number of $2n=2x=22$ (Darlington and Wylie, 1955) [2]. It is native to India (Vavilov, 1949) [10] but tropical and central Africa is also considered as secondary centre of origin where wild races are found (Ng and Marechal, 1985) [5].

Cowpea is also known as black-eyed pea, kaffir pea, China pea, southern bean, asparagus bean, snake bean, yard long bean and catjang bean. It is also known internationally as lubia, niebe coupe or frijol. However, they are all species of [*Vigna unguiculata* (L.) Walp.], which in older reference may be identified as [*Vignasinensis* (L.)Walp.] (Quinn, 1999). There are mainly two types of cowpeas growing in India for grain and vegetable purposes. Generally grain type cowpea varieties produce short pods with more number of seeds and mature early whereas vegetable type varieties produce long pods with less number of seeds and mature late and the pods remain tender and soft for longer period. Its young leaves, pods and grains contain vitamins and minerals which have fuelled its usage for human consumption and animal feeding (Nielson *et al.*, 1997) [6].

Flowers are self-pollinating and may be white, dirty yellow, pink, pale blue or purple in color. They are arranged in raceme or intermediate inflorescences in alternate pairs. Flowers open in the early day and close at approximately midday, after blooming they wilt and collapse. Pollinating insect activities are beneficial in increasing the number of pod set, the number of seeds per pod or both; however, there are no recommendations for the use of pollinating insects on cowpeas.

The success of any crop improvement programme largely depends upon the nature and magnitude of genetic variability existing in the breeding material. This study on genetic variability and divergence elucidates information on genetic parameters. Further, path-coefficient technique provides the information on the direct and indirect contribution of individual characters towards yield. Based on these studies, the importance of individual character is marked to facilitate the selection programme for larger gains. Generally, diverse germplasm are expected to give high hybrid vigour. Hence, it necessitates studying the genetic divergence among the existing genotypes for identification of parents for hybridization programme.

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Materials and Method

The present research work entitled, “Genetic analysis in Cowpea (*Vigna unguiculata* (L.) Walp.)” was undertaken to study the variability, heritability, genetic advance, and correlation and their effect on yield and yield contributing traits. On 27 genotypes of Cowpea collected from different institutes, research stations and private seed companies.

Experimental site

The study was conducted in the Research Field of Department of Horticulture, Naini Agriculture Institute, SHUATS, Prayagraj, located between 25. 87° North latitude 81.15° Eastlatitude. The altitude is 78 meters above the mean sea level.

Soil type

The soil type of experimental field was sandy loam with average fertility level and pH in the range of 7.0 to 8.0.

Climate

Department of Horticulture, Naini Agricultural Institute, SHUATS, Prayagraj, falls under the humid subtropical zone. Maximum rainfall received during the period between July to the end of September. However, occasional showers are also very common in the month of June, December and January. The winter month will usually cool and dry. The summer is hot and dry western hot winds start from April and end at onset of monsoon.

Table 1: List of genotypes were used in the present investigation

S. No.	Genotypes	Source
1.	Kashi Shyamal	IIVR, Varanasi, Uttar Pradesh, India.
2.	Kashi Kanchan	IIVR, Varanasi, Uttar Pradesh, India.
3.	Kashi Gauri	IIVR, Varanasi, Uttar Pradesh, India.
4.	Kashi Nidhi	IIVR, Varanasi, Uttar Pradesh, India.
5.	Kashi Unnati	IIVR, Varanasi, Uttar Pradesh, India.
6.	EC 1738	IIVR, Varanasi, Uttar Pradesh, India.
7.	EC 399251	IIVR, Varanasi, Uttar Pradesh, India.
8.	EC 390213	IIVR, Varanasi, Uttar Pradesh, India.
9.	EC 572715	IIVR, Varanasi, Uttar Pradesh, India.
10.	EC 9738	IIVR, Varanasi, Uttar Pradesh, India.
11.	IC 58905	IIVR, Varanasi, Uttar Pradesh, India.
12.	IC 202804	IIVR, Varanasi, Uttar Pradesh, India.
13.	IC 209711	IIVR, Varanasi, Uttar Pradesh, India.
14.	IC 249588	IIVR, Varanasi, Uttar Pradesh, India.
15.	IC 97797	IIVR, Varanasi, Uttar Pradesh, India.
16.	IC 201098	IIVR, Varanasi, Uttar Pradesh, India.
17.	IC 337932	IIVR, Varanasi, Uttar Pradesh, India.
18.	IC 202280	IIVR, Varanasi, Uttar Pradesh, India.
19.	IC 202526	IIVR, Varanasi, Uttar Pradesh, India.
20.	IC 34009	IIVR, Varanasi, Uttar Pradesh, India.
21.	NS620	Local variety, Karnataka
22.	Nikitha	Local variety, Karnataka
23.	Kamini	Local variety, Karnataka
24.	USM Konark	Local variety, Karnataka
25.	Canara 77	Local variety, Karnataka
26.	Anant	Local variety, Karnataka
27.	Bhagya lakshmi	KAU, kerela

Result and Discussion

The analysis of variance revealed significant differences among the 27 genotypes for 17 characters under study. Thus indicating the ample scope for selection of promising genotypes from the present gene pool.

The maximum pod yield was recorded in variety Highest was recorded for Kamini (16223.2), followed by variety USM

Konark (9676.17), NS620 (9577.01), whereas the minimum pod yield was recorded in variety EC 1738 (3731.08), and Bhagyalakshmi (3228.2).

The estimation of phenotypic coefficient of variance was higher than the genotypic coefficient of variance for all the traits.

Highest GCV and PCV were recorded for Length of Pod (Cm) (50.20, 50.21 respectively), followed by Protein content (46.12, 46.12). Lowest GCV and PCV were recorded for TSS content in pod (%) (0.90, 0.91 respectively) followed by Fiber percentage (3.36, 3.45).

Higher genotypic variance and phenotypic variance were observed for pod yield per hectare and seed yield per hectare indicating more contribution of genetic components of these characters. The present findings are in accordance with the findings of Nath *et al.* (2009)^[4].

Heritability in broad sense was noticed high for all the characters, *i.e.*; 100% for Protein content, Length of Pod (Cm), Height of plant at flowering (Cm), No of seeds / plant and No of Pods.

High genetic advance at 5 % were observed for the characters like Protein content (5704.72kg), No of seeds / plant(322.19), Height of plant at Maturity (cm)(88.42)., whereas low genetic advance at 5 % was observed for characters like TSS content in pod (%) (0.52), No of Pods / peduncle(0.56) &No. of Days to germination of 1st seedling (0.64).

High heritability (bs) coupled with high genetic advance at (% of mean) were observed for the characters Protein content (100 & 99.98), Length of Pod (cm), (103.40 & 99.97), No of Pods (99.80 & 89.53).

At genotypic Length of Pod (cm) (0.547**), Days to 1st pod emergence (Days) (0.457**), No. of Nodes (0.378**), Height of plant at flowering (cm), (0.323**), Height of plant at Maturity (cm) (0.278*), No of Pods (0.220*), had positive direct effect on pod yield per plant. High variances are in accordance with the studies of Khanpara *et al.* (2015)

Negative direct effect on pod yield per plant was exerted by No of Pods / peduncle (-0.006), Fibre percentage (-0.062), No of Leaves / plant (-0.067), No of seeds /pod (-0.08), TSS content in pod (%) (-0.087) at genotypic level.

At phenotypic level Length of Pod (Cm), (0.547**), Days to 1st pod emergence (Days), (0.480**), No. of Nodes (0.387**), Height of plant at flowering (Cm), (0.324**), Height of plant at Maturity (cm), (0.280*), No of Pods (0.220*), showed significant positive correlation with seed yield (kg/ha) at phenotypic level had positive direct effect on pod yield per plant.

Negative direct effect on No of Leaves / plant (-1.790**), showed significant negative correlation with seed yield (kg/ha) at phenotypic level while No of Pods / peduncle (-0.006), Fiber percentage (-0.064), TSS content in pod (%), (-0.087), No of seeds /pod (-0.098 at phenotypic level.

Seed Yield at kg/ha (5.905, 1.514) showed maximum positive direct effect on pod yield at both genotypic and phenotypic level.

Maximum intra-cluster distance (D^2) was registered for cluster I (52605.86) followed by cluster III (37672.61), while minimum intra-cluster distance was observed for cluster V (0).

Maximum inter-cluster distance was observed between cluster cluster II and VI (103.00) followed by cluster V and VI (82.5).The minimum inter-cluster distance was found between cluster cluster I and I (9.88).

Cluster I recorded high mean performance for for No.of Days to germination of 1st seedling (2.67), No of Pods / peduncle

(2.74). Cluster II recorded high mean performance for No. of Days to germination of 1st seedling (2.4), No of Pods / peduncle (3.19), Fibre percentage (3.19); and minimum mean value for Height of plant at Maturity (cm) (84.05), No of seeds / plant (564.24).

Genetic advance reflects on the improvement in the performance of the selected lines over the base or original population. High genetic advance gives substantial scope for selection to improve the yield and its attributing characters. A high heritability is not always accompanied by high genetic

advance as reported by (Panse, 1957) [8]. That is why high heritability coupled with high genetic advance is a reliable measure of the genetic gain. High genetic advance at 5 % was observed for the characters like No of Leaves / plant (5704.72), No of Pods (322.19), No of seeds / pod (88.42). As studied by Nwosu *et al.* (2013) [7], whereas low genetic advance at 5 % was observed for characters like dry pod weight (0.94), pods per peduncle (1.05) & TSS⁰ (1.47). High heritability, GCV and genetic advance were reported for the seed weight per plant as reported by Ajayi *et al.* (2014) [1]

Table 2: Genetic parameters of 27 genotypes for 17 characters of Cowpea

Characters	Genotypic variation	Phenotypic variation	Genotypic Coefficient of Variation	Phenotypic Coefficient of Variation	Heritability	GA	GA AS %
No. of Days to germination of 1st seedling	0.16	0.25	16.71	21.29	61.57	0.64	27.01
Height of plant at flowering (Cm)	1668.71	1669.95	40.78	40.80	99.93	84.12	83.98
Height of plant at Maturity (cm)	1850.55	1859.00	35.78	35.87	99.55	88.42	73.55
No of Branches	30.37	31.02	26.46	26.74	97.91	11.23	53.92
No of Pods	82.16	82.32	43.50	43.55	99.80	18.65	89.53
No of Leaves / plant	1811.57	2004.20	35.93	37.79	90.39	83.36	70.37
Days to 1st flowering	1.31	1.36	3.65	3.72	96.26	2.31	7.38
No. of Nodes	10.05	10.49	22.83	23.34	95.74	6.39	46.03
No of Pods / peduncle	0.12	0.19	11.98	15.04	63.40	0.56	19.65
Length of Pod (Cm)	232.97	233.04	50.20	50.21	99.97	31.44	103.40
Days to 1st pod emergence (Days)	7.08	7.83	6.91	7.26	90.50	5.22	13.53
No of seeds / pod	3.67	5.67	10.48	13.02	64.75	3.18	17.37
No of seeds / plant	24498.99	24535.99	39.65	39.68	99.85	322.19	81.63
Protein content	7670520.64	7672127.61	46.12	46.12	99.98	5704.72	94.99
Fibre percentage	0.6930	0.7309	3.36	3.45	94.81	1.67	6.74
TSS content in pod (%)	0.0652	0.0664	0.90	0.91	98.17	0.52	1.83
Pod Yield / plant (kg /ha)	0.997	1.003	7.79	7.81	99.43	2.05	15.99

Table 3.1: Cluster mean values of 7 clusters for different quantitative characters in cowpeas (continued)

Clusters	Characters							
	No. of Days to germination of 1st seedling	Height of plant at flowering (cm)	Height of plant at Maturity (cm)	No. of Branches	No of Pods	No of Leaves / plant	Days to 1 st flowering	No. of Nodes
1	2.67	116.23	138.38	18.05	17.32	132.75	31.99	15.53
2	2.40	66.06	84.05	18.51	21.23	70.91	30.87	11.12
3	2.04	124.28	148.72	20.00	17.45	145.29	31.55	14.33
4	2.83	121.25	137.70	32.74	28.92	145.47	30.58	17.69
5	2.67	55.63	70.68	27.14	29.05	125.77	26.06	14.79
6	2.33	208.00	224.37	18.87	9.72	208.00	32.27	22.11
7	2.67	131.10	148.67	25.58	33.04	166.90	31.45	17.13
Total	18.60	824.55	955.57	164.89	161.73	1001.08	221.77	120.70

Table 3.2: Cluster mean values of 7 clusters for different qualitative characters in cowpeas

Clusters	Characters								
	No of Pods / peduncle	Length of Pod (Cm)	Days to 1st pod emergence (Days)	No of seeds /pod	No of seeds / plant	Protein content	Fibre percentage	TSS content in pod (%)	Pod Yield / plant (kg /ha)
1	2.74	17.36	37.67	16.75	307.92	25.66	2.74	17.36	37.67
2	3.19	28.70	35.93	17.86	564.24	24.65	3.19	28.70	35.93
3	2.66	26.61	39.92	19.13	345.66	24.60	2.66	26.61	39.92
4	2.64	57.20	42.10	17.45	514.23	25.27	2.64	57.20	42.10
5	2.62	24.88	38.23	20.33	601.78	24.64	2.62	24.88	38.23
6	2.71	51.62	42.62	19.13	287.00	24.53	2.71	51.62	42.62
7	2.69	27.33	43.46	14.99	583.60	25.45	2.69	27.33	43.46
Total	28.25	243.68	290.93	137.62	3217.43	188.81	28.25	243.68	290.93

Conclusion

The results from the present investigation revealed that cowpea variety Kamini identified as desirable with maximum pod yield. Maximum protein content was recorded in variety IC 2022801 (25.79%). Analysis of variance showed

significant difference for all the characters under study, indicates that there was ample scope for selection of promising genotypes for yield improvement. At genotypic and phenotypic level No of seeds / plant, Height of plant at flowering (cm), Days to 1st pod emergence (Days), No of

Pods / peduncle, Length of Pod (Cm), No of Branches, Days to 1st flowering, No of Leaves / plant, No of Pods, Height of plant at flowering (Cm), Length of Pod (Cm) Days to 1st flowering, Days to 1st pod emergence (Days), No of Pods / peduncle, No of Branches had direct positive effect on pod yield per plant.

The genotypes included in cluster VII and cluster I are identified as distant genotypes. Hence, these genotypes can be utilized as parents in further hybridization programme.

Hence it can be concluded that cowpea variety Kamini having highest pod yield can be utilized further for crop improvement programs.

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