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Estimation of genetic advance, heritability, genetic gain and genetic diversity of elite genotypes of grain cowpea [*Vigna unguiculata* (L.) walp.]

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Abstract

The present investigation was conducted during *kharif* 2018 to evaluate forty-two genotypes including five checks, Pant Lobia 1, Pant Lobia 2, Pant Lobia 3, Pant Lobia 4 and Pant Lobia 5 of grain cowpea at Breeder Seed Production Centre to estimate genetic divergence, variability, heritability, genetic advance. Analysis of variance showed the presence of significant amount of variability in all the characters studied. Genetic divergence was performed by D-square statistics. Genotypes were divided into 8 clusters. Maximum inter-cluster distance was observed between cluster VI and VII while maximum intra-cluster distance was observed in cluster V. Mean values of different characters between different clusters was observed maximum for number of seeds per pod. Inter-cluster distance was higher than intra-cluster distance. High estimates phenotypic and genotypic variance was observed for yield per hectare. High estimate of PCV and GCV was observed for yield per plot. High heritability with high genetic advance was observed for plant height, yield per hectare and yield per plant. Moderate heritability and genetic advance were observed for days to 50% flowering while low heritability with low genetic advance was observed for leaf length. In the present investigation, on the basis of mean performance of genotypes PGCP 24, GCP 219 and GCP 378 were found superior of all the genotypes. Earliest 50% flowering was observed in Phule PCP 1124 and GCP-360 which is considered most important and desirable character in cowpea. Three genotypes namely, GCP 345 and GC 3 were identified as the most diversified and could be utilized in future crop improvement programmes.

Keywords: Heritability, genetic advance, genetic divergence, variability, genotypes, PCV and GCV, inter-cluster distance, intra-cluster distance, D-square

Introduction

Grain cowpea [*Vigna unguiculata* (L.) Walp.] is one of the most important pulse crops native to central Africa, belongs to family Fabaceae. It is called as vegetable meat due to high amount of protein in grain with better biological value on dry weight basis. On dry weight basis, Cowpea grain contains more than 25 percent protein, 1.8 percent fat and 60.3 percent carbohydrates and also it is a good source of vitamins and phosphorus, calcium and iron. It is widely adapted and capable of producing grains even in low land and semi-arid regions. However, yield of grain cowpea varies widely when grown at different location. It plays a key role in many farming systems. It possesses the ability to fix atmospheric nitrogen through its root nodules, and grows well in poor soils with more than 85 percent sand and with less than 0.2 percent organic matter and low levels of phosphorus (Singh, 2003) [16]. Total global area of grain cowpea under production is about 12.5 million hectares out of which Africa possess 9.3 million hectares. Global production of grain cowpea is 3 million tonnes. Global production of grain cowpea is 3 million tonnes. It is distributed throughout the tropics but Central and West Africa contributes to 64 percent of area with about 8 million hectares which is followed by about 2.4 million hectares in Central and South America, 1.3 million hectares in Asia and about 0.8 million hectares in East and Southern Africa (Ngalamu *et al.*, 2014).

Before initiating crop improvement programme in any crop, breeder should minutely evaluate, screen and understand the genetic make-up of the germplasm being handled. Estimating the parameters of genetic variability is the major step to be adopted in the source population, if the

goal of breeding program is to improve characters of economic importance. Useful selection depends on the extent of genetic variability available in the base material. Variation is one of the primary tools for improvement of any crop. Genetic variability is the interest of plant breeder because it is easily noticed by the breeder. Variation is requisite for any crop improvement programme. Hereditary changes mainly determined by the sum of hereditary variability and the germplasm serves as an important source of base population and gives scope for wider variability (Gavade and Ghadage, 2015) [17].

Developing cultivars with early maturity, acceptable grain quality, resistance for important diseases and pests causes remarkable increase in the yield and cultivated area (Ehlers and Hall, 1997) [16]. Yield being a complex trait, is determined by many other important yield contributing characters which are controlled by polygenes and also by environmental factors. The overall effect of plant breeding on genetic diversity has been a major concern in the evolutionary biology of crop plants (Simmonds, 1962) [15]. The loss of genetic diversity has been notable for many cultivated species (Wikes, 1983) [20]. Better knowledge of the genetic dissimilarity of breeding materials can help to perpetuate genetic diversity and sustain the long-term selection gain. The significance of plant genetic resources and the need for screening adaptive traits cannot be overlooked. Their

indispensable significance for maintenance of genetic improvement and biodiversity has been acknowledged worldwide (Lester *et al.*, 1986) [9]. Keeping these aspects in view, the present study was initiated for evaluating the extent of genetic variability existing for different characters in grain cowpea germplasm collected from different environments which is of immense practical use for plant breeders to choose the plant of interest for different breeding programmes

Material and Methods

The present investigation was conducted at Govind Ballabh Pant University of Agriculture & Technology, Pantnagar (Udham Singh Nagar). Pantnagar is located in the foothills of Shivalik range of Himalayas popularly called as “Tarai” region. Tarai region falls in humid subtropical zone at 29° North latitude, 79.30° East longitude at height of 243.84 m above mean sea level. All genotypes were sown on *kharif*, 25-03-2018 in Randomized Block Design (RBD) with three replications. Each genotypes were accommodated in 2 rows of 4 meters in length having spacing of 45 x 10 centimeters. The experimental material consists of thirty-seven genotypes of grain cowpea with five checks. The genotypes which are selected were highly distinct from each other and they also showed significant amount of variation for both qualitative and quantitative traits.

Table 1: List of genotypes grain cowpea

1.	GC 3	CST 1
2.	PGCP 36	CST 2
3.	RC 101	CST 3
4.	PGCP 24	CST 4
5.	Phule PCP 1124	CST 5
6.	PGCP 28	CST 6
7.	VCP 09-024	CST 7
8.	VCP 12-005	CST 8
9.	CPD 262	CST 9
10.	CPD 275	CST 10
11.	Bidoli Local	CST 11
12.	TC 1801 E	CST 12
13.	PGCP 64	CST 13
14.	VCP 13-001	CST 14
15.	CPD 291	CST 15
16.	CPD 271	CST 16
17.	CPD 277	CST 17
18.	GCP 219	Pantnagar selection
19.	GCP 232	Pantnagar selection
20.	GCP 234	Pantnagar selection
21.	GCP 286	Pantnagar selection
22.	GCP 297	Pantnagar selection
23.	GCP 320	Pantnagar selection
24.	GCP 345	Pantnagar selection
25.	GCP 346	Pantnagar selection
26.	PGCP 29	Pantnagar selection
27.	PGCP 65	Pantnagar selection
28.	GCP 350	Pantnagar selection
29.	GCP 351	Pantnagar selection
30.	GCP 354	Pantnagar selection
31.	GCP 356	Pantnagar selection
32.	GCP 357	Pantnagar selection
33.	GCP 358	Pantnagar selection
34.	GCP 369	Pantnagar selection
35.	GCP 360	Pantnagar selection
36.	GCP 372	Pantnagar selection
37.	GCP 378	Pantnagar selection

Checks: Pant Lobia 1, Pant Lobia 2, Pant Lobia 3, Pant Lobia 4, Pant Lobia 5

Observations were recorded as average of randomly selected five plants from each genotype and then average of five plants were taken for estimation of data. Observations were recorded for the following qualitative and quantitative characters

Genetic Divergence

Mahalanobis (1936) D^2 statistical analysis was used for calculating the genetic divergence between different genotypes in population. The values of D^2 were obtained as the corresponding uncorrelated (Y_s) values of any two uncorrelated genotypes (Rao, 1952). Group constellations- D^2 is treated as the square of generalized distance, all genotypes were divided into clusters according to Tocher method.

Estimation of variability Heritability and Genetic Advance

Mean: The general mean was computed by summing the data of all the treatments over all the three replications for each character

Range: The lowest and highest mean value for each character was taken as range.

Genotypic variance (σ^2_g): The genotypic variance σ^2_g is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was,

Genotypic variance (σ^2_g) = (MSt-MSe)/r

Where,

MSt = Mean square due to genotypes

MSe = Mean square due to error

r = Number of replications

Phenotypic variance (σ^2_p): Phenotypic variance (σ^2_p) denotes the total variance present in a population for particular character and was calculated by following formula
Phenotypic variance (σ^2_p) = $\sigma^2_g + \sigma^2_e$

Where,

σ^2_g = Genotypic variance

σ^2_e = Mean sum of squares due to error/Environment variance

Environmental variance: The environmental variance (σ^2_e) is the variance due to environmental deviation.

σ^2_e = MSe

Estimation of Heritability

Heritability in broad sense was calculated for each character as described by Johnson *et al.* (1955) [8] as follows.

$$h^2_{(b)} = \frac{\sigma^2_g}{\sigma^2_p}$$

Where,

$h^2_{(b)}$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The genotypic and phenotypic variances are obtained from the expectation of mean squares of analysis of variance of RBD.

Estimation of Expected Genetic Advance

The expected genetic advance from (G.A) straight selection as per Allard (1960).

$$G.A = h^2_{(b)} \times \sigma_p \times K$$

Where,

GA = expected genetic advance

$h^2_{(b)}$ = heritability in broad sense

σ_p = phenotypic standard deviation

K = constant for which the value is given as 2.06 which is the expected in the case of 5% selection intensity.

Genetic advance was expressed as percent of population mean.

$$\text{Genetic advance as per cent of mean} = \frac{\text{Genetic Advance} \times 100}{GM}$$

Result and Discussion

Table 2: Analysis of variance (mean sum of squares) of different characters of grain cowpea genotypes

S. No.	Characters	Source of variation	Mean squares		
			Replications	Treatments	Error
			2	41	82
1	Days to 50% flowering		16.29**	31.00**	0.98
2	Plant height		0.52	174.84**	0.91
3	Leaf length		0.48	1.92**	0.21
4	Leaf width		0.14	2.24**	0.12
5	Peduncle length		0.08	39.15**	0.67
6	Pod length		0.14	8.60**	0.10
7	Number of pods per cluster		0.01	0.52**	0.03
8	Number of pods per plant		0.06	43.58**	0.10
9	Number of seeds per pod		0.001	9.93**	0.04
10	100-grain weight		0.01	16.85**	0.01
11	Protein %		0.12*	27.42**	0.03
12	Yield/plant (gm)		0.77	116.35**	0.56
13	Yield/plot (kg)		0.001	0.31**	0.005
14	Yield/hectare (qtl)		0.02	213.43**	0.53

* & ** Significant at 5% & 1% respectively

The analysis of variance was carried out for all the 14 characters, plant height (cm), leaf length (cm), leaf width (cm), peduncle length (cm), pod length (cm), number of pod per cluster, number of pods per plant, number of seeds per

pod, 100-seed weight, days to 50% flowering, protein %, yield per plant(gm), yield per plot (kg), yield per hectare (qtl) are shown in Table 2. Mean squares were found highly significant for all the studied characters, showing that there

was high amount of differences among the genotypes making them appropriate for estimating other parameters.

The knowledge of genetic divergence provides a basis for the selection of genotypes which could be used in hybridization programme for further improvement. The D^2 analysis was conducted to estimate genetic divergence among the 42 genotypes (including 5 checks) of grain cowpea. The breeders sometimes, makes selection of good parents based on their visual examination of desirable characters but, a more rational approach is selection based on combining ability effects and

F_1 heterosis (Arunchalam, 1981). Maximum heterosis is expressed in F_1 hybrid when parents are genetically more divergent. The generalized D^2 values were estimated for each pair of genotypes in all possible combinations.

All the grain cowpea genotypes were divided into clusters/groups according to Tocher method as shown in Table 3. Genotypes were divided into eight clusters. Cluster I contain maximum genotypes i.e. 17 genotypes followed by cluster III and V having 10 genotypes followed by cluster II, IV, VI, VII and VIII having only one genotype each.

Table 3: Analysis of variance (mean sum of squares) of different characters of grain cowpea genotypes

S. No.	Characters	Source of variation	Mean squares		
			Replications	Treatments	Error
			2	41	82
1	Days to 50% flowering		16.29**	31.00**	0.98
2	Plant height		0.52	174.84**	0.91
3	Leaf length		0.48	1.92**	0.21
4	Leaf width		0.14	2.24**	0.12
5	Peduncle length		0.08	39.15**	0.67
6	Pod length		0.14	8.60**	0.10
7	Number of pods per cluster		0.01	0.52**	0.03
8	Number of pods per plant		0.06	43.58**	0.10
9	Number of seeds per pod		0.001	9.93**	0.04
10	100-grain weight		0.01	16.85**	0.01
11	Protein %		0.12*	27.42**	0.03
12	Yield/plant (gm)		0.77	116.35**	0.56
13	Yield/plot (kg)		0.001	0.31**	0.005
14	Yield/hectare (qtl)		0.02	213.43**	0.53

* & ** Significant at 5% & 1% respectively

Table 4: Distribution of 37 grain cowpea genotypes in eight different clusters

Clusters	Number of genotypes	Genotypes
I	17	RC 101, CPD 291, PGCP 24, Phule PCP 1124, GCP 354, GCP 346, GCP 351, GCP 358, GCP 360, PGCP 64, GCP 356, PGCP 36, CPD 277, PGCP 28, GCP 234, GCP 219, TC 1801 E
II	1	GCP 378
III	10	GCP 369, Pant Lobia 2, Pant Lobia 5, Pant Lobia 1, PGCP 65, GCP 357, GCP 286, GCP 297, GCP 350, GCP 232,
IV	1	CPD 271
V	10	VCP 09-024, CPD 262, VCP 13-001, CPD 275, Bidoli Local, GCP 320, VCP 12-005, PGCP 29, GCP 372, Pant Lobia 3
VI	1	GCP 345
VII	1	GC 3
VIII	1	Pant Lobia 4

The inter-cluster distance varied between 36.42 to 177.60. The maximum inter-cluster distance was observed between cluster VI and cluster VII while minimum inter-cluster-distance was observed between cluster II and IV as shown in Table 4.

The intra-cluster distance varied between 0.00 to 72.08. The maximum intra-cluster distance was observed in cluster V while minimum intra-cluster distance was observed in cluster II, IV, VI, VII and VIII.

Mean values of days to 50% flowering it varied between 45 days (cluster VIII) to 53.67 days (cluster VII), for plant height varied between 39.07 cm (cluster IV) to 49.13 cm (cluster V). Mean values of leaf length varied between 7.03 cm (cluster VII) to 9.07 cm (cluster VI), for leaf width it varied between 3.63 cm (cluster VII) to 5.57 cm (cluster VI), for peduncle length it varied between 17.07 cm (cluster VII) to 25.43 cm (cluster VI), for pod length it varied between 12.13 cm (cluster IV) to 17.80 cm (cluster II), for number of pods per

cluster it varied between 1.50 (cluster VI) to 2.83 (cluster VIII), for number of pods per plant it varied between 8.22 (cluster III) to 19.80 (cluster VII), for number of seeds per pod it varied between 6.85 (cluster VIII) to 14.25 (cluster II), for 100-grain weight it varied between 8.43 gm (cluster V) to 15.15 gm (cluster VIII) for protein % it varied between 20.07% (cluster VI) to 28.23% (cluster VII), for yield per plant it varied between 6.62 gm (cluster VIII) to 21.50 gm (cluster VII), for yield per plot it varied between 0.32 kg (cluster VIII) to 1.02 kg (cluster VII), for yield per hectare it varied between 8.65 qtl (cluster VIII) to 28.70 qtl (cluster VII). as shown in Table 5.

The range of mean values between clusters showed maximum divergence for number of seeds per pod followed by number of pods per plant, 100-grain weight, pod length, number of pods per cluster, protein %, plant height, leaf length, leaf width, peduncle length, yield per plot, yield per hectare and yield per plant.

Table 5: Inter and Intra cluster distance for thirty-seven grain cowpea genotypes

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Cluster I	61.73	74.35	100.48	89.88	93.69	116.03	93.31	130.01
Cluster II		0.00	97.50	36.42	62.28	149.43	101.26	169.62
Cluster III			68.57	92.09	127.96	95.52	155.57	117.94
Cluster IV				0.00	76.27	150.99	129.23	176.02
Cluster V					72.08	174.09	93.85	187.09
Cluster VI						0.00	177.60	53.36
Cluster VII							0.00	175.09
Cluster VIII								0.00

Table 6: Cluster mean values for various quantitative characters in grain cowpea

Characters	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50% flowering	48.80	51.33	49.53	51.00	50.30	49.67	53.67	45.00
Plant Height	44.04	42.17	41.59	39.07	49.13	43.67	45.20	43.30
Leaf length	7.79	7.50	7.76	7.90	7.34	9.07	7.03	7.63
Leaf width	4.99	5.17	4.58	4.33	5.21	5.57	3.63	4.60
Peduncle length	23.95	19.90	23.76	21.33	23.84	25.43	17.07	21.67
Pod length	14.25	17.80	15.00	12.13	13.88	14.60	13.20	14.40
Number of pods per cluster	2.29	2.73	2.01	2.50	1.87	1.50	2.30	2.83
Number of pods per plant	15.14	14.17	8.22	12.65	13.07	10.80	19.80	6.40
Number of seeds per pod	11.86	14.25	12.72	14.85	11.70	11.30	11.10	6.85
100-grain weight	11.82	10.35	13.24	10.31	8.43	16.70	9.94	15.15
Protein %	21.76	21.80	23.13	20.90	23.74	20.07	28.23	24.30
Yield/plant (gm)	0.99	1.02	0.63	0.88	0.60	0.94	1.02	0.32
Yield/plot (kg)	26.79	27.20	17.65	23.95	15.95	26.53	28.70	8.65
Yield/hect (qtl)	20.24	20.45	12.95	18.00	12.21	19.55	21.50	6.62

Contribution of individual character to divergence

The maximum contribution towards divergence was shown by 100-grain weight followed by number of seeds per pod and protein % while leaf contribution was shown by leaf width and pod length.

Table 7: Contribution of each character towards divergence

Source	Times ranked 1 st	Contribution %
Days to 50% flowering	1	0.15
Plant height	5	0.58
Leaf length	1	0.13
Leaf width	1	0.12
Peduncle length	3	0.35
Pod length	1	0.12
Number of pods per cluster	2	0.20
Number of pods per plant	2	0.23
Number of seeds per pod	301	34.96
100-grain weight	429	49.83
Protein %	104	12.08
Yield per plant (gm)	3	0.30
Yield per plot (kg)	2	0.23
Yield per hectare (qtl)	13	1.51

In selecting genotypes from already chosen cluster, important characters such as disease resistance, earliness, quality or performance of particular trait etc. should also be taken into consideration (Choudhary *et al.*, 1975) [5]. The mean performance of already formed clusters could not be considered simultaneously. It was, therefore, vital to consider characters having high contribution to total divergence.

In the present investigation mean values of the clusters showed that number of seeds per pod followed by number of pods per plant followed by 100-grain weight contributed maximum towards divergence. These observations agreed with Umaharan *et al.* (1997), Amanullah *et al.* (2000) [1], Nehru *et al.* (2001) [11], Bezerra *et al.* (2001) [4].

The phenotypic and genotypic variances were studied for all the characters under study as shown in Table 7. Phenotypic

variances were found higher than genotypic variances for all the characters. Range of phenotypic variance was found between 0.11 (yield per plot) to 71.50 (yield per hectare). Phenotypic variance was observed maximum for yield per hectare (71.50) followed by plant height (58.89), yield per plant (39.16) and number of pods per plant (14.59). Range of genotypic variance was found between 0.10 (yield per plot) to 70.97 (yield per hectare). The maximum phenotypic and genotypic variance was estimated for yield per hectare (qtl) and lowest for yield per plot (kg).

PCV and GCV were estimated for all the characters under study. PCV values were higher than GCV values for all the characters. The highest PCV was recorded for yield per plot (41.13%) followed by yield per hectare (39.17%), yield per plant (38.55%) and number of pods per plant (30.04%). Leaf length (11.50%) and days to 50% flowering (6.70%) showed minimum PCV values respectively. The presence of considerable high variability was revealed by higher phenotypic and genotypic variance for all the characters studied. The phenotypic variance was found higher than their respective genotypic variance for all the characters studied and was found highest for yield per hectare followed by plant height, yield per plant, number of pods per plant and lowest for yield per plot. Nwofia *et al.* (2013) [13] also founded same result

The highest GCV value was recorded for yield per plot (40.15%) followed by yield per hectare (39.03%), yield per plant and number of pods per plant (38.27%). Leaf length (9.83%) and days to 50% flowering (6.39%) showed minimum GCV values respectively. Nwosu *et al.* (2013) [13] also founded high PCV and GCV for number of pods per plant.

Knowledge about genetic variation present within the genetic material is important in assessing the potential for successful selection and breeding for increased grain yield per plant since, genetic variability is essential to realize response to selection pressure. Thus, genetic variability was estimated for

grain yield per plant and its components. Analysis of variance indicated significant amount of differences among the genotypes for all the characters under study, which showed that the material studied had considerable genetic variability. Similar findings were also reported by (Vineeta *et al.*, 2003) ^[19] and (Zargar *et al.*, 2005) ^[22]. The significant difference among the genotypes for the characters studied indicated that the genotypes, if crossed could produce better combining segregating generation

Heritability (broad sense) was estimated for all the characters under study as shown in Table 8. It ranged from 73.08% (leaf length) to 99.82% (100-grain weight). High estimate of heritability was recorded for 100-grain weight (99.82%) followed by protein % (99.67%), number of pods per plant (99.31%), yield per hectare (99.26%), number of seeds per pod (98.80%), yield per plant (98.57%), plant height (98.45%), pod length (96.59%), yield per plot (95.28%) and peduncle length (95.04%). Veeraswamy *et al.* (1973) also found high heritability for pod weight, pod length and number of pods per plant, Bapan and Joshi (1973) ^[3] also observed high heritability for 100-seeds weight and seed yield per plant. Pravin *et al.* (2013) ^[14] found high heritability and genetic advance for 100-grain weight and number of seeds per pod. Moderate heritability was recorded for days to 50% flowering. Ubi *et al.* (2001) ^[18] found moderate heritability for days to 50% flowering. Low estimate of heritability was observed for leaf length.

Moderate estimates of heritability was recorded for days to 50% flowering (91.08%) followed by leaf width (85.49%) and number of pods per cluster (84.46%). A low estimate of heritability was observed for leaf length (73.08%). Expected genetic advance varied from 0.64 (yield per plot) to 17.29 (yield per hectare). High expected genetic advance was estimated for yield per hectare (17.29) followed by plant height (15.56) and yield per plant (12.71).

Genetic advance measures genetic gain under selection. It is defined as the product of selection intensity, heritability and phenotypic standard deviation of a trait (Allard, 1960). According to Johnson *et al.* (1955) ^[8] heritability along with genetic advance were more potential rather than considering heritability alone in the prediction of resultant effect for selecting the best individuals. Moderate expected genetic advance was estimated for number of pods per plant (7.82) followed by peduncle length (7.19) and days to 50% flowering (6.22), protein % (6.21), 100-grain weight (4.88), number of seeds per pod (3.72) and pod length (3.41).

Low expected genetic advance was estimated for leaf length (1.60) followed by leaf width (1.33), number of pods per cluster (0.76) and yield per plot (0.64). It was observed highest for yield per hectare followed by plant height, yield per plant. Yap *et al.* (1997) also found high genetic advance for seed yield per plant. Bapan and Joshi (1973) ^[3] also found high genetic advance for seed yield per plant. Similarly Tamgadage *et al.* (2008) ^[17] founded for number of pods per cluster and number of seeds per pod.

Table 8: Genetic parameters of variation for various characters in grain cowpea

Characters	Environment variance	ECV	Genotypic variance	GCV	Phenotypic variance	PCV	Mean	Range
Days to 50% flowering	0.98	2.00	10.01	6.39	10.99	6.70	49.49	40.33-54
Plant height	0.91	2.14	57.98	17.11	58.89	17.24	44.51	31.93-68.23
Leaf length	0.21	5.97	0.57	9.83	0.78	11.50	7.68	6.03-9.40
Leaf width	0.12	7.06	0.71	17.14	0.83	18.54	4.91	2.97-7.17
Peduncle length	0.67	3.48	12.83	15.22	13.50	15.61	23.54	15.00-29.00
Pod length	0.10	2.20	2.83	11.72	2.93	11.92	14.36	10.37-17.80
Number of pods per cluster	0.03	8.12	0.16	18.93	0.19	20.60	2.13	1.50-2.83
Number of pods per plant	0.10	2.49	14.49	29.94	14.59	30.04	12.72	5.90-19.80
Number of seeds per pod	0.04	1.67	3.30	15.13	3.34	15.22	12.00	6.85-15.25
100-grain weight	0.01	0.87	5.61	20.73	5.62	20.75	11.43	6.65-16.70
Protein %	0.03	0.76	9.13	13.30	9.16	13.33	22.71	19.70-28.97
Yield/plant(gm)	0.56	4.61	38.60	38.27	39.16	38.55	16.23	5.70-30.90
Yield/plot (kg)	0.005	8.93	0.10	40.15	0.11	41.13	0.79	0.28-1.70
Yield/hectare(qtl)	0.53	3.37	70.97	39.03	71.50	39.17	21.59	7.15-40.97

Table 9: Heritability, genetic advance and genetic advance as percent of mean

Characters	h ² (broad sense)	Genetic advance	Genetic advance as % of mean
Days to 50% flowering	91.08	6.22	12.57
Plant height	98.45	15.56	34.97
Leaf length	73.08	1.33	17.31
Leaf width	85.49	1.60	32.64
Peduncle length	95.04	7.19	30.56
Pod length	96.59	3.41	23.73
Number of pods per cluster	84.46	0.76	35.84
Number of pods per plant	99.31	7.82	61.47
Number of seeds per pod	98.80	3.72	30.98
100-grain weight	99.82	4.88	42.66
Protein %	99.67	6.21	27.36
Yield/plant (gm)	98.57	12.71	78.27
Yield/plot (kg)	95.28	0.64	80.73
Yield/hectare (qtl)	99.26	17.29	80.09

Expected genetic advance as percent of mean was estimated for all the characters under study. It varied from 12.57% (days to 50% flowering) to 80.73% (yield per plot). High expected

genetic advance as percent of mean was observed for yield per plot (80.73%) followed by yield per hectare (80.09%),

yield per plant (78.27%) and number of pods per plant (61.47%).

Moderate expected genetic advance as percent of mean was observed followed by 100-grain weight (42.66%), number of pods per cluster (35.84%), plant height (34.97%), leaf width (32.64%), number of seeds per pod (30.98%), peduncle length (30.56%), protein % (27.36%) and pod length (23.73%). Low expected genetic advance as percent of mean was observed for leaf length (17.31%) and days to 50% flowering (12.57%).

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