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

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DOI: https://doi.org/10.22271/chemi.2020.v8.i2j.8839

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) [10]. 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) [7].

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) [6]. 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

| No. | Genotype     | Check Code |
|-----|--------------|------------|
| 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 |
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 (Ys) 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 ($\sigma^2_g$):** The genotypic variance $\sigma^2_g$ is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was,

$$\text{Genotypic variance} = \frac{(\text{MST}-\text{MSE})}{r}$$

Where,

- MST = Mean square due to genotypes
- MSE = Mean square due to error
- $r$ = Number of replications

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

$$\text{Phenotypic variance} = \sigma^2_g + \sigma^2_e$$

Where,

- $\sigma^2_g$ = Genotypic variance
- $\sigma^2_e$ = Mean sum of squares due to error/Environment variance

**Environmental variance:** The environmental variance ($\sigma^2_e$) is the variance due to environmental deviation.

$$\sigma^2_e = \text{MSE}$$

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

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

Where,

- $h^2_{(b)}$ = Heritability in broad sense
- $\sigma^2_g$ = Genotypic variance
- $\sigma^2_p$ = 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).

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

Where,

- G.A = expected genetic advance
- $h^2_{(b)}$ = heritability in broad sense
- $\sigma_p$ = 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**

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

| S. No. | Characters                  | Mean squares       |
|-------|----------------------------|--------------------|
|       | Source of variation        | Replications | Treatments | Error  |
| 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 2: Analysis of variance (mean sum of squares) of different characters of grain cowpea genotypes
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 D² 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 F₁ heterosis (Arunchalam, 1981). Maximum heterosis is expressed in F₁ hybrid when parents are genetically more divergent. The generalized D² 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  |
| 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 intra-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 IV) 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.

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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     | 74.55      | 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      | 0.00       | 76.27       | 150.99     | 129.23    | 176.02     |              |              |
| Cluster V  | 72.08     | 174.09     | 93.85       | 118.09     | 187.09    |            |              |              |
| Cluster VI | 0.00      | 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 observed 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° Contribution % |
|-------------------------|--------------------------------|
| Days to 50% flowering   | 1                              |
| Plant height            | 5                              |
| Leaf length             | 1                              |
| Leaf width              | 1                              |
| Peduncle length         | 3                              |
| Pod length              | 1                              |
| Number of pods per cluster| 2                         |
| Number of pods per plant| 2                              |
| Number of seeds per pod | 301                            |
| 100-grain weight        | 429                            |
| Protein %               | 104                            |
| Yield per plant (gm)    | 3                              |
| Yield per plot (kg)     | 2                              |
| Yield per hectare (qtl) | 13                             |

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) [3]. 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) [14].

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 plant (58.99), yield per plot (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 plant and number of pods per plant (38.55%) and number of seeds per pod (41.13%) followed by yield per hectare (39.17%), yield per plot (58.99) and number of pods per plant (14.59). On the contrary, the lowest PCV was recorded 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 plant followed by yield per plant, number of pods per plant and lowest for yield per plot. Nwosia et al. (2013) [13] also found same result

The highest GCV 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. Nwoou et al. (2013) [13] also found 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.

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%).

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

| Characters                  | Environment variance | 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 | 51.93-68.23 |
| 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                  | h² (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                         |

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 Tamgadge et al. (2008) [17] founded for number of pods per cluster and number of seeds per pod.
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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