

**Study of genetic variability parameters in cowpea (*Vigna unguiculata* L.)
germplasm lines**

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ABSTRACT

The present investigation was carried out on 60 genotypes to study genetic parameters for sixteen characters. The materials collected from, R.A.R.I. Durgapura were evaluated during Kharif season of 2015 at the Research Farm Rajasthan College of Agriculture, Udaipur. The estimates of genotypic parameters revealed that differences between the estimates of GCV and PCV were found least for most of the characters. Higher estimates of GCV and PCV were observed for seed yield /plant, biological yield/ plant, plant height, primary branches /plant and pods / plant. Maximum heritability and maximum genetic gain was found for test weight followed by plant height, biological yield/ plant, seed protein content, primary branches / plant and pods / plant. These characters are governed by additive gene action and one should go for direct selection for these traits to improve breeding programme in future.

Keyword: GCV, PCV, heritability, genetic gain.

INTRODUCTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous crop belongs to family Leguminosae with a diploid chromosome number of $2n=2x=22$. It is native to India but tropical and central Africa is also considered as secondary centre of origin where wild races are found even now. Cowpea has been referred to as "Poor man's meat" because of its high protein content (20-25%). Cowpea young leaves, pods and beans contain vitamins and minerals which have fuelled its usage for human consumption and animal feeding and considered as one of agriculture's oldest legume used as protein source for humans and livestock. Assessment of genetic variability is usually made through the estimates of genetic parameters of variation such as range, genotypic and phenotypic variance and genotypic and phenotypic coefficient of variance of the characters under consideration. Heritability is an index of the transmission of characters from parents to their off-spring. It is generally expressed in percentage. The estimation of heritability helps the plant breeder in selection of elite genotypes. It also measures the degree of resemblance between relatives and correspondence between phenotype and breeding value. Genetic advance is the measure of genetic gain under selection. Heritability estimates along with genetic advance

are more helpful in predicting the gain under selection than heritability estimates alone. Allard (1960) expressed the genetic advance as the product of selection intensity, heritability and phenotypic standard deviation of a character.

MATERIALS AND METHODS

The present investigation was carried out during *Kharif* 2015 at the Research Farm of Plant Breeding and Genetics, Rajasthan college of Agriculture, MPUAT, Udaipur. The experimental material comprised of sixty diverse genotypes including three checks *viz.*, RC-101, RC-19 and RCV-7 of cowpea. The experimental materials of cowpea were sown in randomized block design in three replications. Two rows of each genotype were sown in a plot of 4 m length. The row to row and plant to plant distances were kept at 30 cm and 10 cm, respectively. All the recommended packages of practices were followed to raise a healthy crop. The observations were recorded for 16 characters *viz.*, days to 50% flowering, number of flowers/ plant, number of flowers/ cluster, days to maturity, plant height, number of primary branches/ plant, number of pods/plant, number of clusters/plant, number of pods/cluster, pod length, number of seeds/pod, test weight, seed yield /plant, biological yield/plant, harvest index and seed protein content on five randomly

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selected plants from each genotypes in all the replications while days to 50% flowering and days to maturity which were recorded on plot basis. Genotypic coefficients of variance (GCV), phenotypic coefficients of variance (PCV), heritability (broad sense) and genetic advance was worked out as per (Johnson *et al.*, 1955).

RESULTS AND DISCUSSION

Analysis of variance revealed that the genotypes recorded highly significant variation for all the characters and it indicated the presence of sufficient variability for these characters (Table 1), thus there is a lot of scope for selection. One of the ways of assessing the variability is through examining the range of variation. The phenotypic variance and phenotypic coefficient of variation were slightly higher than corresponding genotypic variance and genotypic coefficient of variation for most of the characters indicated the presence of less

environmental effect upon the concerned characters. This is an agreement with finding of Shahid *et al.*(2005), Tamgadge *et al.*,(2008), and Suganthi, and Murugan, (2008) in cow pea. In the present study the genotypes exhibited considerable amount of variation for sixteen characters viz., , days to 50% flowering, number of flowers / plant, number of flowers/cluster, days to maturity , plant height, number of primary branches / plant, number of pods/ plant, number of clusters / plant, number of pods/ cluster, pod length, number of seeds/pod , test weight, seed yield/plant, biological yield/plant, harvest index and seed protein content (Table 2). The present finding are in accordance with the finding of Khan *et al.* (2015) recorded higher range for these characters, which was in accordance to the present study. The high range of values indicated the good scope for selection of suitable basic material for breeders for further improvement.

Table 1: Analysis of variance for quantitative characters studied in cow pea

| S.No. | Characters | Mean sum of square | | |
|-------|------------------------------|--------------------|------------|-----------|
| | | Replications | Genotypes | Error |
| | | d.f. =02 | d.f. =59 | d.f.= 118 |
| 1 | Days to 50% flowering | 0.350 | 17.056** | 3.254 |
| 2 | Flowers / plant | 3.613 | 40.634** | 3.546 |
| 3 | Flowers /cluster | 0.215 | 0.830** | 0.306 |
| 4 | Days to maturity | 0.017 | 5.419** | 0.186 |
| 5 | Plant height (cm) | 1.413 | 4290.140** | 5.830 |
| 6 | Primary branches /plant | 0.141 | 25.850** | 0.276 |
| 7 | Pods /plant | 1.982 | 19.450** | 1.337 |
| 8 | Clusters/ plant | 1.279 | 3.888** | 0.464 |
| 9 | Pods / clusters | 0.199 | 0.160** | 0.080 |
| 10 | Pod length (cm) | 0.090 | 6.074** | 0.562 |
| 11 | Seeds / pod | 0.000 | 8.189** | 0.313 |
| 12 | Test weight (g) | 0.001 | 13.152** | 0.000 |
| 13 | Seed yield /plant (g) | 40.289 | 940.261** | 17.311 |
| 14 | Biological yield / plant (g) | 12.422 | 7545.192** | 16.326 |
| 15 | Harvest index % | 6.474 | 173.444** | 7.187 |
| 16 | Seed protein content % | 0.000 | 1.872** | 0.008 |

** significance levels of 1%

In the present study, the genotypic coefficient of variations (GCV) and phenotypic coefficient of variations (PCV) were higher for plant height, biological yield/ plant, seed yield / plant and primary branches /plant indicating greater scope for improvement of these characters by simple selection. Several earlier workers also reported high GCV and PCV for plant height (Khan *et al.* 2015), biological yield/

plant (Eswaran *et al.* 2007), seed yield /plant (kumar *et al.*, 2013 and Ravishanker *et al.*, 2013) and primary branches /plant (Khan *et al.* 2015). However harvest index, test weight, pods/plant, clusters/plant, seeds/pod and flowers/plant showed moderate GCV and PCV value, while flowers/clusters, pod length, pods/ clusters, days to 50% flowering, seed protein content and days to maturity exhibited low GCV and PCV value.

Moderate PCV and GCV value were reported for test weight (Marappa *et al.* 2007), pods / plant (Khan *et al.* 2015), cluster/plant (Nwosu *et al.* 2013), seeds/ pod (Nwosu *et al.* 2013 and Khan *et al.* 2015) and flowers/plant (Manggol *et al.* 2012). While low GCV and PCV were also report for pod length (Chauhan *et al.*, 2003), pods / cluster (Nwosu *et al.* 2013), days to 50% flowering (Manggol *et al.* 2012 and Chattopadhyay *et al.* 2014), seed protein content (Sharma *et al.* 2015) and days to maturity (Khan *et al.* 2015).

Table 2: Grand Mean, range, coefficient of variation, genotypic and phenotypic variation for quantitative characters of cow pea

| S.No. | Characters | Grand mean | Range | C.V.% | VG | VP |
|-------|----------------------------|------------|--------------|-------|---------|---------|
| 1 | Days to 50% flowering | 44.52 | 37.33-50.00 | 4.05 | 4.60 | 7.85 |
| 2 | Flowers /plant | 25.02 | 18.53-35.93 | 7.53 | 12.36 | 15.91 |
| 3 | Flowers/ cluster | 3.96 | 2.90-6.01 | 13.97 | 0.17 | 0.48 |
| 4 | Days to maturity | 63.75 | 61.00-66.00 | 0.68 | 1.74 | 1.93 |
| 5 | Plant height (cm) | 68.87 | 34.40-157.83 | 3.51 | 1428.10 | 1433.93 |
| 6 | Primary branches/ plant | 12.40 | 8.60-20.73 | 4.24 | 8.52 | 8.80 |
| 7 | Pods / plant | 13.43 | 9.93-19.87 | 8.61 | 6.04 | 7.37 |
| 8 | Clusters/ plant | 6.42 | 4.60-9.67 | 10.61 | 1.14 | 1.61 |
| 9 | Pods/clusters | 2.11 | 1.58-2.85 | 13.42 | 0.03 | 0.11 |
| 10 | Pod length (cm) | 12.92 | 10.27-17.40 | 5.80 | 1.84 | 2.40 |
| 11 | Seeds/ pod | 10.91 | 6.87-15.33 | 5.13 | 2.63 | 2.94 |
| 12 | Test weight (g) | 10.68 | 6.95-17.59 | 0.20 | 4.38 | 4.39 |
| 13 | Seed yield/ plant (g) | 66.54 | 26.00-110.00 | 6.25 | 307.65 | 324.96 |
| 14 | Biological yield/plant (g) | 182.17 | 85.67-312.33 | 2.22 | 2509.62 | 2525.95 |
| 15 | Harvest index % | 37.33 | 20.63-54.02 | 7.18 | 55.42 | 62.61 |
| 16 | Seed protein content % | 24.45 | 22.64-25.92 | 0.35 | 0.62 | 0.63 |

C.V. - Coefficient of variation, VG- Genotypic variation, VP- Phenotypic variation

The genetic advances as per cent of mean estimates were medium to high (25.52 to 112.80) majority of the characters. The character like plant height, primary branches /plant, pods /plant, test weight, seed yield/plant, biological yield/plant and harvest index exhibited high heritability with high genetic advance as percent of mean. Test weight recorded maximum heritability (99.77 percent) compared to other traits. Plant height exhibited maximum genetic advance as percent of mean (112.80) compared to other traits. Several earlier workers have

Table 3: Genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for quantitative characters of cow pea

| S.No | Characters | GCV | PCV | h^2 (%) | GA | GAM |
|------|-----------------------------|-------|-------|-----------|--------|--------|
| 1 | Days to 50% flowering | 4.82 | 6.30 | 58.59 | 3.38 | 7.60 |
| 2 | Flowers/ plant | 14.06 | 15.94 | 77.68 | 6.38 | 25.52 |
| 3 | Flowers/ cluster | 10.55 | 17.51 | 35.41 | 0.52 | 13.10 |
| 4 | Days to maturity | 2.07 | 2.18 | 90.15 | 2.59 | 4.06 |
| 5 | Plant height (cm) | 54.87 | 54.98 | 99.59 | 77.69 | 112.80 |
| 6 | Primary branches/ plant | 23.54 | 23.92 | 96.81 | 5.92 | 47.72 |
| 7 | Pods/ plant | 18.29 | 20.21 | 81.95 | 4.58 | 34.09 |
| 8 | Clusters/ plant | 16.64 | 19.74 | 70.80 | 1.86 | 28.91 |
| 9 | Pods/ clusters | 7.75 | 15.50 | 27.27 | 0.17 | 7.97 |
| 10 | Pod length (cm) | 10.49 | 11.99 | 76.66 | 2.44 | 18.91 |
| 11 | Seeds/ pod | 14.85 | 15.71 | 89.45 | 3.15 | 28.91 |
| 12 | Test weight (g) | 19.60 | 19.61 | 99.77 | 4.31 | 40.37 |
| 13 | Seed yield/ plant (g) | 26.36 | 27.09 | 94.67 | 35.16 | 52.84 |
| 14 | Biological yield/ plant (g) | 27.50 | 27.59 | 99.35 | 102.86 | 56.47 |
| 15 | Harvest index % | 19.94 | 21.20 | 88.51 | 14.43 | 38.65 |
| 16 | Seed protein content % | 3.22 | 3.24 | 98.41 | 1.61 | 6.60 |

GCV- Genotypic coefficient of variation, PCV – Phenotypic coefficient of variation, h^2 –Heritability, GA- Genetic Advance, GAM- Genetic advance as percentage of mean

also reported high heritability coupled with high genetic advance plant height (Nwosu *et al.* 2013 and Tudu *et al.* 2015), test weight (Idahosa *et al.* 2010), biological yield/plant (Eswaran *et al.* 2007), primary branches/plant (Khan *et al.* 2015), pods / plant (Khan *et al.* 2015) and seed yield /plant (Sughanthi and Muragan 2007 and Khan *et al.* 2015), harvest index (Sharma *et al.* 2015), flowers/plant (Manggoel *et al.* 2012), cluster/plant (Nwosu *et al.* 2013) and seeds/pod (Idahosa *et al.* 2010).

High heritability and low genetic advance were reported for seed protein content (Sharma *et al.* 2015), days to maturity (Khan *et al.* 2015) and pod length (Khan *et al.* 2015). Moderate heritability with low genetic advance were exhibited for days to 50% flowering (Tudu *et al.* (2015). Low heritability with low genetic advance were reported for pods/cluster (Venkatesan *et al.* (2003). High heritability estimate indicates less

influence of environment on respective characters. Hence, direct selection can be followed to improve early maturing genotypes. Low heritability (broad sense) indicates predominance of non additive gene action indicating the scope for breeding. High estimates of GA coupled with substantial amount of heritability indicate that selection for such characters would result in the improvement of characters in the desired direction as the character is governed by additive genes. High heritability coupled with low genetic advance indicates non-additive gene action. The heritability exhibited due to favorable influence of environment rather than genotypes and selection for such traits may not be rewarding. If, low heritability coupled with low genetic advance indicates such character was highly influenced by environment and selection would be ineffective for those traits.

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