



E-ISSN: 2278-4136
P-ISSN: 2349-8234
JPP 2017; 6(4): 1384-1387
Received: 19-05-2017
Accepted: 20-06-2017

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Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] Germplasm lines

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Abstract

The present investigation was carried out on 30 genotypes to study genetic parameters for ten characters. 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 plant height, primary branches per plant, seed yield per plant and test weight. Maximum heritability and maximum genetic gain was found for test weight followed by plant height, primary branches per plant, seed yield per plant and harvest index. These characters are governed by additive gene action and one should go for direct selection for these traits to improve in future.

Keywords: Cowpea, genetic advance, heritability, variability

Introduction

Cowpea (*Vigna unguiculata* L. Walp.) is an important leguminous vegetable crop mainly grown both in Kharif and spring summer season crop in most parts of India. It is early, multi seasonal and multipurpose crop. It has multifarious uses like as fodder, cover crop and green manure and provides high quality protein in the form of vegetable and pulse to human diet. For planned breeding programme to improve yield potential. Development of high yielding early varieties and study on biotic and abiotic stresses has to receive much attention in cowpea research. Before initiating crop improvement program in any crop, breeder should thoroughly evaluate, screen and understand the genetic architecture of the germplasm he is handling. Estimation of genetic variability parameters is the foremost step to be adopted in the source population, if the breeding program is aimed at improving economically important traits. The success of a crop improvement program depends on the ability of the breeder to define and assemble the required genetic variability and select for yield indirectly through yield associated and highly heritable characters after eliminating the environmental component of phenotypic variation (Mather and Jinks, 1983) [10].

Materials and methods

The present investigation was carried out during Kharif 2015-16 at the Research Farm of Plant Breeding and Genetics, Rajasthan college of Agriculture, MPUAT, Udaipur. This experiment material comprised of thirty 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 distance was kept at 30 cm and 10 cm, respectively. All the recommended package of practices was followed to raise a healthy crop. The observations were recorded for 10 characters viz, Days to 50% flowering, Number of flowers per plant, Days to maturity, Plant height (cm), Primary branches per plant, Pods per plant, Number of clusters per plant, Test weight (g), Seed yield/ plant (g.), Harvest index (%) on five randomly 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) [5].

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) [24], Tamgadge, *et al.*, (2008) [27], and Suganthi, and Murugan, (2008) [26] in cow pea. In the present study the genotypes exhibited considerable amount of variation for ten characters viz., Days to 50% flowering, Number of flowers per plant, Days to maturity, Plant height, Number of primary branches per plant, Number of pods per plant, Number of clusters per plant, Test weight, Seed yield per plant and Harvest index (Table-2). The present findings are in accordance with the finding of Sawant (1994) [22] and Khan (2015) [6] 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. Genetic variability is a basic information needed for the breeders to improve the crops by adopting appropriate method of selection based on variability that exist in the material. In this regard, it is necessary to partition the total variability into heritable and non-heritable components viz., genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV) and further to compute heritability and genetic advances for various metric traits. In the maximum time the GCV value is lower than PCV for all the characters indicating environmental variations, if the GCV and PCV value is show less or minimum difference it means the characters are less affected by environmental variations. In the present study the genotypic coefficient of variations (GCV) and phenotypic coefficient of variations (PCV) high for plant height, primary branches per plant, seed yield per plant and test weight indicating greater scope for improvement of these characters by simple selection. Several earlier workers also reported high GCV and PCV for plant height (Marappa *et al.*, 2004 and Khan *et al.* 2015) [12, 6], seed yield per plant (Resmi *et al.*, 2004, Meshram *et al.*, 2013, Rakesh *et al.*, 2013 and Ravishanker *et al.*, 2013) [20, 13, 18, 19] and primary branches per plant (Marappa *et al.* 2007 and Khan *et al.* 2015) [12, 6]. However harvest index, pods per plant, clusters per plant and flowers per plant showed moderate GCV and PCV value, while days to 50% flowering and days to maturity exhibited low GCV and PCV value. Moderate PCV and GCV value were reported for pods per plant (Tyagi *et al.* 2000 and Khan *et al.* 2015) [31, 6], cluster per plant (Selvam *et al.* 2000, Kumari *et al.* 2003 and Nwosu *et al.* 2013) [23, 7, 16] and flowers per plant (Nausherwan *et al.* 2008 and Manggol *et al.* 2012) [14, 9]. While low GCV and

PCV were also report for days to 50% flowering (Singh and Verma 2002, Venkatesen *et al.* 2003, Zergar *et al.* 2005, Manggol *et al.* 2012 and Chattopadhyay *et al.* 2014) [24, 32, 33, 9, 1], seed protein content and days to maturity (Thiyagarajan 1989 and Khan *et al.* 2015) [29, 6].

In the present investigation, genetic advance as percent of mean estimates medium to high (29.40 to 108.14) majority of the characters. The character like plant height, primary branches per plant, pods per plant, test weight, seed yield per plant and harvest index exhibited high heritability with high genetic advance as percent of mean. Test weight recorded maximum heritability (99.99 percent) compared to other traits. Plant height exhibited maximum genetic advance as percent of mean (108.14) compared to other traits. Several earlier workers have also reported high heritability coupled with high genetic advance plant height (Nwosu *et al.* 2013 and Tudu *et al.* 2015) [16, 30], test weight (Venkatesan *et al.* 2003 and Idahosa *et al.* 2010) [32, 4], primary branches per plant (Malarvizhi and Rangasamy 2005 and Khan *et al.* 2015) [8, 6], pods per plant (Gireesh *et al.* 2006 and Khan *et al.* 2015) [3, 6] and seed yield per plant Khan *et al.* 2015) [6], harvest index (Eswaran *et al.* 2007 and Sharma *et al.* 2015) [2, 26], flowers per plant (Makeen *et al.*, 2007, Oyiga and Uguru, 2011, Manggol *et al.* 2012) [11, 17, 9] and cluster per plant (Kumari *et al.* 2003, Nehru *et al.* 2009 and Nwosu. *et al.* 2013) [7, 15, 16].

High heritability and low genetic advance were reported for days to maturity (Sarvamangala 2004 and Khan *et al.* 2015) [21, 6]. Moderate heritability with low genetic advance were exhibited for days to 50% flowering (Tudu *et al.* (2015) [30].

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.

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

| S. No | Characters | Mean sum of square | | |
|-------|--------------------------------------|--------------------|-----------|----------|
| | | Replication | Genotypes | Error |
| | | d.f.= 02 | d.f.= 29 | d.f.= 58 |
| 1 | Days to 50% flowering | 21.03 | 12.03** | 2.55 |
| 2 | Number of flowers/ plant | 4.64 | 50.33** | 4.09 |
| 3 | Days to maturity | 0.21 | 4.98** | 0.19 |
| 4 | Plant height (cm) | 13.75 | 3042.22** | 4.70 |
| 5 | Number of primary branches per plant | 0.09 | 33.45** | 0.30 |
| 6 | Number of pods per plant | 2.59 | 20.38** | 1.05 |
| 7 | Number of clusters per plant | 0.31 | 4.63** | 0.54 |
| 8 | Test weight (g) | 0.00 | 16.66** | 0.00 |
| 9 | Seed yield per plant (g.) | 61.14 | 808.81** | 15.07 |
| 10 | Harvest index % | 15.11 | 160.76** | 7.46 |

** Significance levels of 1%.

Table 2: Genetic parameters of 30 cowpea genotype

| Characters | VG | VP | GCV | PCV | h ² (Broad Sense) % | GA 5% | G.G. |
|-------------------------|---------|---------|-------|-------|--------------------------------|-------|--------|
| Days to 50% flowering | 3.20 | 5.71 | 4.00 | 5.40 | 55.33 | 2.72 | 6.14 |
| Flowers/ plant | 15.41 | 19.50 | 16.04 | 18.05 | 79.02 | 7.20 | 29.40 |
| Days to maturity | 1.60 | 1.59 | 1.98 | 2.10 | 88.90 | 2.45 | 3.90 |
| Plant height (cm) | 1012.50 | 1017.21 | 52.62 | 52.62 | 99.53 | 65.40 | 108.14 |
| Primary branches/ plant | 11.10 | 11.35 | 26.26 | 26.62 | 97.34 | 6.75 | 53.40 |
| Pods/ plant | 6.44 | 7.50 | 19.52 | 21.10 | 85.90 | 4.84 | 37.30 |
| Clusters/ plant | 1.40 | 1.91 | 18.83 | 22.30 | 71.29 | 2.03 | 32.75 |
| Test weight (g) | 5.55 | 5.55 | 21.24 | 21.24 | 99.99 | 4.85 | 43.75 |
| Seed yield/ plant (g.) | 264.60 | 279.65 | 24.10 | 24.75 | 94.60 | 32.60 | 48.25 |
| harvest index % | 51.10 | 58.60 | 18.10 | 19.40 | 87.25 | 13.75 | 34.80 |

VG-Genotypic variance, VP- Phenotypic variance, GCV-Genotypic Coefficient of Variance, PCV- Phenotypic Coefficient of Variance, h²- Heritability, GA- Genetic Advance, GG- Genetic Gain

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