

*Full Length Research Paper*

# Genetic variability, stability and relationship among some Cowpea, *Vigna unguiculata* (L.) Walp breeding lines

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The contribution of cowpea to food security in the sub-Sahara Africa is incontestably obvious. Ten genotypes of cowpea were evaluated in different environments to assess their variability and stability. The genotypes differed significantly ( $P \leq 0.05$ ) with respect to all the eight phenotypic traits studied. Days from planting to first flower production and to first ripe pod showed the least coefficient of variations (CV) in all environments. The number of branches per plant consistently had the highest genotypic and phenotypic CV in all the three environments. The mean proportion of the phenotypic variation due to genetics was 92.9%. The ten genotypes varied considerably in their stability for the studied morphometric traits. The most stable genotype for days to first flowering (DFF) and days to first pod ripening (DPRP) was IBS9193. However, 25026-2 and 24893-2 were most stable for pod length (PL) and peduncle length (PDL), respectively. Significant genetic and phenotypic correlation existed among the variables; implying typical association among the tested traits. For example, the number of pods per plant negatively but significantly ( $P \leq 0.01$ ) correlated with DFF and DPRP. This study indicated that a meaningful selection of genotypes is possible for multi-trait improvement through hybridization.

**Key words:** Heritability, stability, selection, variances, correlation coefficients.

## INTRODUCTION

Cowpea, *Vigna unguiculata* (L.) Walp is an important crop in sub-Sahara Africa, where it is grown for forage, green pods and grains. It is a cheaper source of protein than meat for the rural and urban poor (Fawole et al., 2006). Farmers obtain up to 25% of their income through sales of cowpea fodders. Moreover, cowpea is also very important for soil nutrient maintenance.

World production of cowpea dry grain in 2009 was estimated as 5.3 million tonnes (FAO, 2009). That year, Nigeria produced 2.4 million tonnes, followed by 1.6 tonnes from Niger and 105376 tonnes from Mali. Nigeria is the world largest producer of the cowpea grains (FAO, 2009).

In Nigeria, most varieties under cultivation are unimproved land races which are photoperiodically sensitive and poor productive. Grain and fodder production in cowpea had been inconsistent due to genotypic sensitivity (Mukhtar and Singh, 2006; Umar et al., 2010). Several other causes have been attributed to low yields in cowpea. Among such are poor edaphic environment, excessive or inadequate moisture, inappropriate cultural practices, pests, diseases and poor genetic potential of genotypes for yield.

Among factors for advancing crop improvement will necessarily include: understanding of the genetic potential of genotypes, the stability of the desirable trait to micro and macro environment and the relationship of the quantitative traits among each other. Building a conceptual breeding strategy on these would facilitate selection of genotypes.

Cowpea thrives well within an extensive environment covering 40°N to 30°S and the temperature range

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between 20 and 35°C (Rachie, 1985). Being a major staple, its sustainable production can be enhanced by increasing its productive scope in wider ecologies through breeding for genotypes with neutral photoperiodic sensitivity.

The environment (Aremu et al., 2007; Adewale et al., 2010) influences the genetic performances of many quantitative traits. Analysis of the genotype  $\times$  environment interaction provides unbiased estimates of yield and other morphometric characteristics of a crop. It is also used to determine stability of the traits in different environments (Kamdi, 2001).

The objective of this study therefore was to evaluate ten cowpea genotypes in different environments for their variability and stability. Moreover, genetic estimates of broad sense heritability and correlation among some traits may be understood which will assist the selection of genotypes for breeding programmes.

## MATERIALS AND METHODS

An experiment was conducted to evaluate ten cowpea genotypes in two successive seasons (wet and dry) on the roof top and on the field during the dry season in the Department of Crop Protection and Environmental Biology of the University of Ibadan, Nigeria. On the roof top, the experiment was laid out in a randomised complete block design with three replicates. Each replicate consisted of one hundred plastic pots; a plot contained 10 pots per genotype. The 25 cm size plastic pots were filled with well-mixed garden soils and two seeds were planted per pot. The ten cowpea lines were randomly assigned to each of the three replicates. The field experiment was laid out in a randomised complete block design with three replicates. Each replicate consisted of ten row plots of ten genotypes. A plot had 15 plants. Distance between rows and plants along the rows were 60 and 20 cm, respectively. Weeding for the potted and field experiment was done as at when due and Monocrotophos (Nuvacron) was used to control insect pests at every two weeks.

## Data collection and analysis

In the two experiments, data were collected on five randomly selected plants per plot. The variables measured included: plant height at four weeks (PH4W), number of days from planting to first flower appearance (DFF), number of days from planting to first ripe pod (DPRP), number of branches per plant (BPP), number of peduncle per plant (PDPP), mean peduncle length per plant (PDL), number of pods per plant (PodPP) and pod length (PL).

Data were analysed using the statistical analysis system, SAS-V9.2 (SAS Institute Inc., 2007). Analysis of variance (ANOVA) was computed using the procedure of the general linear model. The resulting components of variances from ANOVA were used to compute the phenotypic and genotypic coefficient of variation, heritability and genetic advances following the approach of Adewale et al. (2010). Six among the eight variables studied exhibited genotype by environment (GXE) interaction. They were further studied to understand their stability using the stability parameter of Wricke's Ecovalence (Wricke, 1962). Analysis of covariance (ANCOVA) was employed to understand the co-variability among pairs of variables following the approach of Singh and Chaudhary (1985). The genotypic and phenotypic correlation coefficients for pairs of variables were estimated from the variance component of

both ANOVA and ANCOVA following the approach of Singh and Chaudhary (1985).

## RESULTS AND DISCUSSION

In season 1, six of the eight traits (PH4W, PL, DFF, DPRP, PDL and BPP) differed significantly ( $P \leq 0.001$ ) among the ten cowpea genotypes (Table 1). PH4W, PodPP, DPRP, PDL and BPP showed significant ( $P \leq 0.001$ ) differences among the genotypes in season 2 while all the eight traits significantly ( $P \leq 0.001$ ) varied among the ten cowpea genotypes on the field (Table 1).

Number of days from planting to first flowering and number of days from planting to first ripe pod showed the least coefficient of variation (CV) in all environments. This depicted high level of uniformity in the traits compared to number of pods per plant and number of branches per plant, which exhibited least level of uniformity due to high CV values in season 1 and field environments, respectively.

In the combined environments (Table 1), there were significant ( $P \leq 0.001$ ) main effects of genotypes for all the eight traits. Seven traits except BPP exhibited significant ( $P \leq 0.001$ ) environmental main effects. Thus, the variability in BPP was not environmentally dependent.

Genotype  $\times$  environment interaction was significant ( $P \leq 0.001$ ) for PH4W, PL, DFF, DPRP, PDPP, and PDL. The performance of the genotypes with respect to the six variables was environmentally influenced. Differential behaviour of cowpea genotypes to varying environments also has been previously reported (Ariyo and Okeleye, 1998; Akande, 2007).

From Table 2, PCV was higher than GCV in all the traits, with lowest values observed in DPRP and highest in BPP. The GCV ranged from 9.25 to 140.04, while PCV ranged from 9.78 to 152.82. High proportion of GCV to PCV is desirable in selection process because it depicts that the traits are much under the genetic control rather than the environment (Kaushik et al., 2007). The proportion of GCV in PCV observed in this study was generally high with the mean of 92.93% for all the traits. It ranged from 85.50% in PDPP to 97.86% in PH4W. These traits are reliable for selection in genetic improvement of the cowpea genotypes. Traits whose expressions are environmentally dependent may not be reliable descriptors for morphological characterization (Samaee et al., 2003; Pandey et al., 2008). However, in this study, the proportion of genetic contribution to the overall phenotypic expression of most of the traits was very high. Therefore, their use as important discriminatory variable for cowpea classification studies seems relatively reliable.

Traits with high broad sense heritability estimate suggest that they have high genetic potential; the effect of the environment in determining them is low. Additive gene effect could be playing predominant role on their expression. In Table 2, PH4W had the highest heritability estimates (94.41) in season 1, while PDL had the highest

**Table 1.** ANOVA summary of seasonal, field and combined environments of eight quantitative traits of cowpea.

| Source of variation          | Df | Mean squares |           |          |           |           |           |           |          |
|------------------------------|----|--------------|-----------|----------|-----------|-----------|-----------|-----------|----------|
|                              |    | PH4W (cm)    | Pod PP    | PL (cm)  | DFF       | DPRP      | PDPP      | PDL (cm)  | BPP      |
| <b>Season 1</b>              |    |              |           |          |           |           |           |           |          |
| Genotype                     | 9  | 757.29***    | 71.61     | 12.84**  | 103.10*** | 69.06***  | 6.53      | 162.32*** | 13.04*** |
| Error                        | 18 | 28.16        | 30.69     | 3.62     | 8.95      | 5.52      | 4.93      | 21.77     | 1.89     |
| Mean                         |    | 29.63        | 11.73     | 16.06    | 46.40     | 62.83     | 8.13      | 19.62     | 6.33     |
| CV (%)                       |    | 17.91        | 47.22     | 11.84    | 6.45      | 3.74      | 27.31     | 23.78     | 21.72    |
| <b>Season 2</b>              |    |              |           |          |           |           |           |           |          |
| Genotype                     | 9  | 67.66***     | 23.07**   | 13.49    | 48.26     | 57.72*    | 5.72*     | 55.39***  | 8.63*    |
| Error                        | 18 | 8.75         | 5.34      | 6.93     | 21.68     | 21.82     | 1.65      | 5.99      | 2.73     |
| Mean                         |    | 24.30        | 7.30      | 16.00    | 49.63     | 66.80     | 6.80      | 19.03     | 6.62     |
| CV (%)                       |    | 12.17        | 31.65     | 16.45    | 9.38      | 6.99      | 18.90     | 12.87     | 24.97    |
| <b>Field (dry season)</b>    |    |              |           |          |           |           |           |           |          |
| Genotype                     | 9  | 153.39***    | 64.97***  | 10.79*** | 40.67***  | 69.56***  | 39.74**   | 66.61***  | 1.37*    |
| Error                        | 18 | 26.54        | 11.90     | 1.27     | 10.21     | 11.96     | 10.51     | 8.06      | 1.01     |
| Mean                         |    | 30.37        | 11.77     | 14.79    | 46.00     | 62.90     | 10.70     | 21.42     | 0.97     |
| CV (%)                       |    | 16.79        | 29.32     | 7.62     | 6.95      | 5.50      | 30.31     | 13.25     | 104.02   |
| <b>Combined environments</b> |    |              |           |          |           |           |           |           |          |
| Genotype                     | 9  | 606.38***    | 129.86*** | 21.68*** | 111.71*** | 118.33*** | 22.65***  | 223.21*** | 5.93***  |
| Environment.                 | 2  | 328.93***    | 198.03*** | 15.40*   | 119.08*** | 154.74*** | 117.88*** | 46.69*    | 0.34     |
| Geno. x Env.                 | 18 | 185.97***    | 14.90     | 7.72*    | 40.15***  | 39.00***  | 14.45**   | 30.56**   | 1.06     |
| Error                        | 58 | 25.74        | 17.36     | 4.18     | 12.90     | 12.51     | 6.08      | 13.66     | 0.95     |
| Mean                         |    | 28.10        | 10.27     | 15.62    | 47.34     | 64.18     | 8.55      | 20.02     | 0.92     |
| CV (%)                       |    | 18.05        | 40.58     | 13.08    | 7.59      | 5.51      | 28.85     | 18.46     | 105.63   |

PH4W - plant height at four weeks, PodPP – number of pods per plant, PL – pod length, DFF – number of days from planting to first flowering, DPRP – number of days from planting to first ripe pod, PDPP – number of peduncle per plant, PDL – peduncle length per plant, BPP – number of branches per plant. \*, \*\*, \*\*\*, significant at  $P \leq 0.05$ , 0.01, and 0.001, respectively.

(value) in season 2. The highest broad sense heritability both in the field (89.47) and combined data (95.02) were in PL and PDL, respectively. Heritability estimate over pooled environments eliminates biases from  $G \times E$  interactions, important for genetic gain prediction of traits

(Toker, 2004; Mulder and Bijma, 2005). Pooled heritability estimate was higher than in the three environments for traits: PodPP, PDPP, PDL and BPP. Hence, reliable selection of genotypes can be made based on these traits with high and unbiased broad sense heritability estimates.

Table 3 represents means of some traits and the Wricke's stability statistics (that is,  $W_i$ ). Wricke's ecovalence expresses stability of traits across certain environments; its value is an indicator of how stably or unstably a genotype responds to certain environment (Wricke, 1962).

**Table 2.** Coefficient of variation and broad sense heritability for each of the three and combined environments.

| Traits    | PCV (%) | GCV (%) | GCV:PCV | H <sup>2</sup> (%) - S <sub>1</sub> | H <sup>2</sup> (%) - S <sub>2</sub> | H <sup>2</sup> (%) - FLD | H <sup>2</sup> (%) - (Pooled) |
|-----------|---------|---------|---------|-------------------------------------|-------------------------------------|--------------------------|-------------------------------|
| PH4W (cm) | 50.59   | 49.51   | 97.87   | 94.41                               | 88.55                               | 85.25                    | 90.34                         |
| Pod PP    | 64.06   | 59.62   | 93.07   | 70.00                               | 81.20                               | 84.52                    | 94.96                         |
| PL (cm)   | 17.21   | 15.46   | 89.83   | 78.00                               | 66.06                               | 89.47                    | 87.71                         |
| DFF       | 12.89   | 12.12   | 94.03   | 92.01                               | 69.00                               | 79.93                    | 88.29                         |
| DPRP      | 9.78    | 9.25    | 94.58   | 92.60                               | 72.57                               | 85.33                    | 89.16                         |
| PDPP      | 32.16   | 27.50   | 85.51   | 56.98                               | 76.16                               | 79.08                    | 80.49                         |
| PDL (cm)  | 43.08   | 41.75   | 96.91   | 88.17                               | 90.24                               | 89.21                    | 95.02                         |
| BPP       | 152.82  | 140.04  | 91.64   | 87.34                               | 75.97                               | 57.56                    | 92.82                         |
| Mean      | 47.82   | 44.41   | 92.93   | 82.44                               | 77.47                               | 81.29                    | 89.85                         |

\*PCV – phenotypic coefficient of variation, GCV – genotypic coefficient of variation, S<sub>1</sub> – season one, S<sub>2</sub> – season 2, H<sup>2</sup> – broad sense heritability, \*PH4W - plant height at four weeks, PodPP – number of pods per plant, PL – pod length, DFF – number of days from planting to first flowering, DPRP – number of days from planting to first ripe pod, PDPP – number of peduncle per plant, PDL – peduncle length per plant, BPP – number of branches per plant.

**Table 3.** Wricke's ecovalence of some trait in cowpea.

| Genotypes           | PH4W  |        | DPRP  |       | PL    |       | PDPP  |       | DFF   |        | PDL   |       |
|---------------------|-------|--------|-------|-------|-------|-------|-------|-------|-------|--------|-------|-------|
|                     | Mean  | Wi     | Mean  | Wi    | Mean  | Wi    | Mean  | Wi    | Mean  | Wi     | Mean  | Wi    |
| 24881-2             | 21.33 | 19.71  | 64.22 | 36.38 | 13.20 | 2.11  | 10.11 | 3.10  | 49.33 | 35.43  | 24.83 | 20.33 |
| 24884-1             | 29.33 | 1.04   | 72.44 | 55.09 | 16.17 | 11.54 | 6.67  | 2.50  | 56.00 | 122.69 | 14.17 | 55.55 |
| 24893-2             | 25.78 | 48.09  | 64.44 | 17.69 | 17.33 | 1.22  | 9.89  | 2.13  | 44.56 | 10.85  | 23.19 | 3.18  |
| 24901-1             | 26.56 | 34.67  | 63.33 | 45.18 | 14.66 | 0.20  | 7.56  | 11.08 | 46.78 | 23.64  | 15.07 | 14.69 |
| 25014-1             | 36.11 | 66.00  | 64.56 | 5.54  | 17.56 | 3.41  | 11.22 | 36.84 | 47.78 | 1.24   | 16.70 | 9.56  |
| 25016-2             | 23.22 | 14.31  | 64.78 | 19.62 | 15.56 | 15.07 | 7.78  | 12.61 | 47.11 | 31.82  | 14.01 | 4.77  |
| 25022-4             | 23.00 | 1.00   | 60.00 | 39.76 | 15.93 | 7.46  | 8.11  | 0.23  | 43.44 | 12.38  | 20.32 | 8.80  |
| 25026-2             | 27.67 | 76.51  | 66.44 | 8.89  | 17.22 | 0.57  | 9.89  | 4.93  | 47.22 | 1.07   | 24.02 | 8.21  |
| IBS9193             | 47.56 | 816.94 | 62.00 | 0.16  | 15.21 | 1.51  | 7.00  | 12.17 | 46.89 | 0.07   | 28.26 | 54.12 |
| Ife-brown           | 20.44 | 37.56  | 59.56 | 5.72  | 13.37 | 3.20  | 7.22  | 1.10  | 44.33 | 1.72   | 19.64 | 4.12  |
| Grand Means         | 28.1  |        | 64.18 |       | 15.62 |       | 8.54  |       | 47.34 |        | 20.02 |       |
| LSD <sub>0.05</sub> | 4.79  |        | 3.33  |       | 1.93  |       | 2.33  |       | 3.39  |        | 3.49  |       |

PH4W – plant height at four weeks, DPRP – Days from planting to first ripe pod, PL – pod Length, DPP – peduncles per plant, DFF – days to first flowering and PDL – peduncle length.

Genotypes with lower wi are more stable than those with high magnitude values. IBS9193, 24884-1, 25014-1 and 24884-1 had the highest

mean for PH4W, DPRP, PDPP and DFF, respectively; the four genotypes had the highest wi for each corresponding trait. This observation

concurs with the remark of (Kamdi, 2001) that most productive genotypes are usually very unstable. Moreover, IBS9193 was the most stable

**Table 4.** Phenotypic and genotypic correlation coefficient of eight morphological traits.

|       |     | PodPP  | PL       | DFF      | DPRP      | PDPP     | PDL      | BPP       |
|-------|-----|--------|----------|----------|-----------|----------|----------|-----------|
| PH4W  | PCC | -0.018 | 0.266*   | 0.127    | 0.077     | -0.012   | 0.256*   | -0.339**  |
|       | GCC | -0.082 | 0.232*   | 0.126    | 0.063     | -0.069   | 0.255*   | -0.393*** |
| PodPP | PCC |        | -0.048   | -0.334** | -0.350**  | 0.566*** | 0.537*** | 0.429***  |
|       | GCC |        | -0.286** | -0.296** | -0.360*** | 0.392*** | 0.489*** | 0.400***  |
| PL    | PCC |        |          | -0.082   | 0.177     | 0.405*** | 0.019    | -0.083    |
|       | GCC |        |          | 0.097    | 0.359***  | 0.241*   | -0.123   | -0.202    |
| DFF   | PCC |        |          |          | 0.801***  | -0.114   | -0.314** | 0.016     |
|       | GCC |        |          |          | 0.594***  | -0.136   | -0.209   | 0.052     |
| DPRP  | PCC |        |          |          |           | -0.004   | -0.294** | 0.058     |
|       | GCC |        |          |          |           | 0.016    | -0.245*  | 0.102     |
| PDPP  | PCC |        |          |          |           |          | 0.184    | 0.379***  |
|       | GCC |        |          |          |           |          | 0.163    | 0.335**   |
| PDL   | PCC |        |          |          |           |          |          | 0.292**   |
|       | GCC |        |          |          |           |          |          | 0.300**   |

\*PCC – phenotypic correlation coefficient, GCC – genotypic correlation coefficient (in bold). PH4W – plant height at four weeks, PodPP – pods per plant, PL – pod length, DFF – days to first flowering, DPRP – days from planting to first ripe pod, PDPP – peduncles per plant, PDL – peduncle length and BPP - branches per plant. \*, \*\*, \*\*\*, - significant at  $P < 0.05$ , 0.01, and 0.001, respectively.

genotype for DPRP and DFF. The genotype could be a day-neutral responsive; its choice as a parent for hybridization programme could lead to the success of generating hybrids with neutral photoperiodic sensitivity. Hybrids with such genetic potential could enhance high productivity in adverse environment. The genotype 25022-4 was most stable for PH4W and PDPP as very minimal variation occurred in the genotype for the two traits in the three environments. This implies that the vegetative stage of the genotype exhibit high uniformity. The height (at 4 weeks) of 23 cm and 8 peduncles per plant uniformly expressed in the three environments makes a good genotype for mechanical harvest. 25026-2 had a pod length of 17.22 cm; it significantly ( $W_i = 0.57$ ) exhibited a very high stability across the three environments. This genotype exhibited the highest stability ( $W_i = 0.57$ ) for pod length. With the remarked positive link between pod length and seeds per pod in cowpea (Morakinyo and Ajibade, 1998; Bashir, et al., 2001), Lima bean, *Phaseolus lunatus* L. (Akande and Balogun, 2007), 25026-2 is a genotype with a very high and stable grain yield capacity. The most stable genotype for PDL is 24893-2 (Table 3).

Phenotypically and genotypically, PH4W positively and significantly ( $P \leq 0.05$ ) correlated with pod length and peduncle length. The phenotypic and genotypic relationship of the same trait was very significant ( $P \leq 0.01$ ) but negative with the number of branches per

plant. It could be implied that cowpea plants with good height may have fewer number of branches, which could support longer peduncles and pods. The number of pods per plant negatively but significantly ( $P \leq 0.01$ ) correlated with DFF and DPRP. This agrees with the previous assertion by Umar et al. (2010), genotypes which flowered, early produced many pods. Such genotype maximizes the favourable day length to initiate flowering and fruiting. Genotypically, number of pods per plant significantly ( $P \leq 0.01$ ) though negatively correlated with pod length. Efficient assimilate distribution to every initiated pods may lead to the reduction in the length of each of the resultant pod. On the other hand, the number of pods positively and significantly ( $P \leq 0.01$ ) correlated with PDPP, PDL and BPP (Table 4). Phenotypically and genotypically, pod length correlated positively and significantly ( $P \leq 0.05$ ) with PDPP, however, the same variable had a positive and significant ( $P \leq 0.01$ ) relationship with DPRP (Table 4). Genotypes, which flowered earlier, equally had earlier pod maturation. Phenotypically, DFF significantly ( $P \leq 0.01$ ) and negatively correlated with PDL. The phenotypic and genotypic relationship of DPRP and PDL was significant ( $P \leq 0.05$ ) and negative. However, the phenotypic and genotypic relationship of the number of branches per plant with PDPP and PDL was significant ( $P \leq 0.01$ ) and positive (Table 4).

The high broad sense heritability for each trait evidently

indicates the possibility of high genetic gain from selection for these characters. Moreover, pairs of strongly associated variables are disposed to simultaneously selection. Some of the ten studied cowpea-breeding lines have some unique and desirable characteristics, especially days to flowering and pod maturation.

Cowpea productivity can be advanced through the selection and hybridization of genotypes with early flowering/maturity and day-neutral characteristics. Land mass for cowpea cultivation will increase if genotypes with day-neutral photoperiodic sensitivity are bred and made available to farmers for cultivation.

## REFERENCES

- Adelele BD, Okonji C, Oyekanmi AA, Akintobi DAC, Aremu CO (2010). Genotypic variability and stability of some grain yield components of cowpea. *Afr. J. Agric. Res.*, 5: 874-880.
- Akande SR (2007). Genotype by environment interaction for cowpea seed yield and disease reactions in the forest and derived savannah agro-ecology of South - West Nigeria. *American-Eurasian J. Agric. Environ. Sci.*, 2: 163-168.
- Akande SR, Balogun MO (2007). Evaluation and heritability studies of local Lima bean (*Phaseolus lunatus* L.) cultivars from South-West Nigeria. *Revista UDO Agrícola*, 7: 22-28.
- Aremu CO, Ariyo OJ, Adelele BD (2007). Assessments of selection techniques in genotype x environment interaction in cowpea *Vigna unguiculata* (L.) Walp. *Afr. J. Agric. Res.*, 2: 352-355.
- Ariyo OJ, Okeleye KA (1998). Performance of cowpea (*Vigna unguiculata* L. Walp) varieties as measured by additive main effects and multiplicative interaction model. *Nig. J. Gen.*, 12: 1-5.
- Bashir S, Ali A, Qamar IA, Arshad M, Sheikh S, Asif M (2001). Correlation of economically important traits in warm season forage legume species. *Online J. Bio. Sci.*, 1: 97-98.
- FAO (2009). Food and Agriculture Organization, Statistics Division <http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567#anc> or [Accessed 15th July, 2011].
- Fawole OB, Ahmed O, Balogun O (2006). Pathogenicity and cell wall-degrading enzyme activities of some fungi isolates from cowpea (*Vigna unguiculata* L. Walp). *Biokemistri.*, 18: 45-51.
- Kamdi RE (2001). Relative Stability, Performance, and Superiority of Crop Genotypes across Environment. *J. Agric. Biol. Environ. Stat.*, 6: 449-460.
- Kaushik N, Kumar K, Kumar S, Kaushik N, Roy S (2007). Genetic variability and divergence studies in seed traits and oil content of *Jatropha* (*Jatropha curcas* L.) accessions. *Biomass Bioenerg.*, 31: 497-502.
- Morakinyo JA, Ajibade SR (1998). Characterization of the segregants of an improved cowpea lines IT84E-124-6. *Nig. J. Sci.*, 32: 27-32.
- Mukhtar FB, Singh BB (2006). Influence of photoperiod and Gibberellic acid (GA3) on the growth and flowering of Cowpea (*Vigna unguiculata* (L.) Walp). *J. Food Agric. Environ.*, 4: 201-203.
- Mulder HA, Bijma P (2005). Effects of genotype x environment interaction on genetic gain in breeding programs. *J. Anim. Sci.*, 83: 49-61.
- Pandey S, Kumar S, Rai M, Mishra U, Singh M (2008). Assessment of genetic diversity in Indian ash gourd (*Benincasa hispida*) accessions using RAPD markers. *1 Cucurbitaceae 2008 (genetics and breeding of Cucurbitaceae)*, Proceedings of the IX<sup>th</sup> EUCARPIA, INRA, Avignon (France), May 21-24th, 2008.
- Rachie KO (1985). Introduction to Cowpea Research, Production and Utilization. John Wiley and Sons, Chichester, pp. 21-26.
- SAS Institute Inc. (2007). SAS OnlineDoc® 9.2. SAS Institute Inc., Cary, NC.
- Samaee SM, Shobbar ZS, Ashrafi H, Hosseini-Mazinani M (2003). Molecular Characterization of Olive Germplasm in Iran by Use of Random Amplified Polymorphic DNA (RAPD): Correlation with Phenotypic Studies. *Proc. XXVI IHC – Plant Genetic Resources - Acta Hort.*, 623: 169-175.
- Singh RK, Chaudhary SD (1985). Biometrical methods in Quantitative Genetic Analysis. Kalyan Publishers, New Delhi, pp. 205-214.
- Toker G (2004). Estimates of broad sense heritability for Seed yield and yield criteria in faba bean (*Vicia faba* L.). *Hereditas*, 140: 222- 225.
- Umar ML, Sanusi MG, Lawan FD (2010). Relationships between some Quantitative Characters in Selected Cowpea Germplasm *Vigna unguiculata* (L.) Walp. *Notulae Scientia Biologicae*, 2: 125-128.
- Wricke G (1962). About a method for measuring the ecological spread in field trials. *Z Plant Breed.*, 47: 92-96.