

Full Length Research Paper

# Genotypic variability and stability of some grain yield components of Cowpea

B. D. Adewale<sup>1\*</sup>, C. Okonji<sup>2</sup>, A. A. Oyekanmi<sup>2</sup>, D. A. C. Akintobi<sup>1</sup> and C. O. Aremu<sup>3</sup>

<sup>1</sup>Department of Plant Breeding and Seed Technology, University of Agriculture, Abeokuta, Ogun State, Nigeria.

<sup>2</sup>Department of Plant Physiology and Crop Production, University of Agriculture, Abeokuta, Ogun State, Nigeria.

<sup>3</sup>Department of Agronomy, Ladoké Akintola University of Technology, Ogbomosho, Oyo State, Nigeria.

Accepted 10 March, 2010

The grain yield components of eleven cowpea genotypes were studied in 2006 and 2007 at Abeokuta, Nigeria, to understand the sensitivity of the quantitative traits to heterogeneous environments. The genotypes differ significantly ( $p \leq 0.05$ ) in grain yield; the pods/plant and Dfodyld equally differed significantly for the two years. Significant ( $p \leq 0.05$ ) genotypic variation in pod length was only in 2007. DT50F, DT95M, 100 seed weight and pod yield were significantly ( $p \leq 0.05$ ) influenced by the effect of genotype, year and their interactions. Seeds/pod, 100 seed weight and pod length had fairly high relative genetic gain resulting from high GCV: PCV, heritability and repeatability; indicating their low sensitivity to G × E. Loss of potential genetic gain was 26% in pod yield and 24% in seeds/pod. IT97K - 499 - 35, IT97 - 568 - 18 and IT95K - 2011 - 11 were identified in this study as the genotypes with high productivity and good genetic stability for pod yield, seeds/pod and 100 seed weight respectively.

**Key words:** Variances, heritability, repeatability, loss of potential genetic gain, stability.

## INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp) remains a leading legume in the recipe of the people in sub-Sahara Africa, supplying majority of the plant protein for human nutrition. The crop is essentially grown for the seed grains although the use of the green pods as vegetable cowpea is becoming important too. The protein content in cowpea is about 25%; and the digestibility of the protein is much higher than that of other legumes (Ologhobo and Fetuga, 1983). The use of other parts of the crop for live stocks feed is very important in animal nutrition. The assessment of the variation in the yield-determining quantitative traits of crop has become primary in the breeding for yield. Yield improvements have been achieved through

directional selections for yield - contributing traits (Akbar and Kamran, 2006). Pods, seeds yield and 100 seed weight have been reported among the prominent grain-yield determinants of cowpea (Brolmann and Stoffella, 1986; Siddique and Gupta, 1991). They have been found to have reliable predictability on grain yields in grain legumes, such as: mungbean, pea and pigeon pea (Singh and Malhotra, 1970; Narsinghani et al., 1978; Dani, 1979).

The magnitude of the coefficient of variation (the ratio of the standard deviation to the mean), heritability (the proportion of phenotypic variation in a population that is attributable to genetic variation) and repeatability (the proportion of total variance in multiple measurements of a trait that is due to differences among individuals) of traits are important guides to selecting polygenic yield determining traits (Ortiz and Ng, 2000).

Many past studies on stability have often been on polygenic traits, most especially, the yield; the genetic performances of other quantitative traits are likewise influenced by the environment (Siddique and Gupta, 1991; Aremu et al., 2007). G × E cannot be avoided, in fact, it is an important limiting factor for testing the efficiency of any breeding programme. The occurrence of

\*Corresponding author. E-mail: [d.adewale@gmail.com](mailto:d.adewale@gmail.com). Tel: +234-803-9228-085.

**Abbreviations:** Ffodyld, Fresh fodder yield; Dfodyld, dry fodder yield; DT50F, days to 50% flowering; DT95M, days to 95% maturity; G×E, genotype x environment; PCV, phenotypic coefficient of variation; GCV, genotypic coefficient of variation.

large genotype x environment (G x E) interaction affects the recommendations of the breeders in selecting genotypes for specific environment. Genotype x environment analysis is used to provide unbiased estimates of yield and other agronomic characteristics and to determine yield stability or the ability to withstand both predictable and unpredictable environmental variation (Kamdi, 2001). Therefore, a good understanding of the genetic stability of those yield determining traits would be prerequisite for any reliable prediction for grain yield in cowpea. Since grain yield improvement through breeding for yield components would be most effective if their variability, heritability and genetic advances are understood; this study therefore aim at revealing: the variability, the broad sense heritability, repeatability and genetic advances of some quantitative traits of cowpea. Moreover, the stability of three grain yield determining traits in the two consecutive years was evaluated.

## MATERIALS AND METHODS

### The experiment

A trial was conducted during the late cropping seasons of 2006 and 2007 at the University of Agriculture, Abeokuta research farms (7° 15'N, 3°23'E) on eleven genotypes of cowpea. The results of the soil sample are as follows: total N (0.31%), P (7.51), organic matter (1.24%), CEC 5.9 meq 100 mg<sup>-1</sup> and Ph 5.46. Abeokuta is located in wet savanna/forest transition zone with an annual rainfall of 900 - 1650 mm and a wet season of 130 - 250 days. The field was ploughed and harrowed two weeks later. The experiment was laid out in a randomized complete block design of three replicates. The study involved 11 varieties of cowpea, one of which was a local cultivar. Three to four seeds of each variety were planted per hole at a distance of 75 x 25cm on the 4<sup>th</sup> and 10<sup>th</sup> of September 2006 and 2007 respectively. The plants were thinned down to two plants per hole after emergence. Weeding was done twice (3<sup>rd</sup> and 6<sup>th</sup> weeks after planting) by hoeing during the experiments. Insect pests were controlled with cyper force four weeks after planting, thereafter repeated treatment continued at 10 days interval until pod maturity.

### Data collection and analysis

Data were collected on: days to 50% flowering (the number of days from planting to when 50% of the plants in a plot flowered), days to 95% pod maturity (the number of days from planting to when 95% of the pods on plants in the plot turned brown). The fresh fodder yield was the weight of fresh sample of whole plant before oven drying and the dry fodder yield was the resultant weight of the same sample after oven drying at 70°C for 48 h. The yield component measured includes: pods per plant - which is the mean number of pods from five random plants in a plot, seeds per pod - the mean number of seeds/pod from ten uniform pods, pod length - distance in centimeter from the receptacle to the beak tip of the pod, pod yield - total weight of pods harvested/plot, 100 seed weight - mass of 100 uniform seed from the seed lot of a variety in a replicate and grain yield - the threshed weight of seeds/plot converted to Kg/ha.

All the above data were subjected to analysis of variance (ANOVA). For traits whose genotypic variance were significant in the ANOVA, the means of the genotypes were separated using the Duncan's new multiple range test as suggested by Gomez and Gomez (1984). The resulting components of variances were used

to compute the phenotypic and genotypic coefficient of variation and genetic advances as:

Phenotypic coefficient of variation (PCV) =  $100\sqrt{\sigma_p^2}/X$ ,  
Genotypic coefficient of variation (GCV) =  $100\sqrt{\sigma_g^2}/X$ , according to Singh and Chaudhary (1985) and Genetic Advances (as % of mean) =  $[i.\sigma_g^2/\sqrt{\sigma_p^2}] 100/x$ , according to Allard (1960).

Where;

X = the mean,

$\sigma_g^2$  = (genotypic mean square – error mean square)/number of replications,

$\sigma_p^2$  = genotype mean square/number of replications,

i = standard selection differential for 5% selection intensity (= 2.06).

Annual broad sense heritability was estimated as the proportion of phenotypic variances that is due to genetic differences among genotypes; the broad sense heritability for the combined years was estimated according to Tenkouano et al. (2002) as:

$$H^2 = \sigma_g^2 / \sigma_g^2 + \sigma_{gy}^2/y + \sigma_e^2/ry \quad (1)$$

where;

$H^2$  = the broad sense heritability,

$\sigma_g^2$  = the genetic variance,

$\sigma_{gy}^2$  = the variance associated with genotype x year interaction

$\sigma_e^2$  = the experimental error.

The terms g, y and r indicates the number of genotypes, years and replication.

Repeatability ( $r_c$ ) was estimated using the formula described by Ortiz and Ng (2000), as follows:

$$r_c = \sigma_g^c / (\sigma_g^c + \sigma_{gy}^c) \quad (2)$$

Where;

$\sigma_g^2$  = variance of the genotypes

$\sigma_y^2$  = variance of the environment (year)

$\sigma_{gy}^2$  = variance of the genotype and the environment (year)

Loss of potential genetic gain (C) due to G by E effect was estimated using the formula by Matheson and Cotterill (1990) as:

$$C = 1 - [(\sigma_g^2 + \sigma_e^2)^{1/2} / (\sigma_g^2 + \sigma_{gy}^2 + \sigma_e^2)^{1/2}] \quad \text{Equation 3}$$

Where;

C = Loss of potential genetic gain

$\sigma_g^2$  = genetic variance component

$\sigma_e^2$  = error variance

$\sigma_{gy}^2$  = Genotype by year variance component

Notations are presented in Table 1.

The significance of the genotype by year interaction for three yield components (Pod yield, seeds/pod and 100 seed weight) in the ANOVA demanded further investigation.

This was done using two univariate stability parameters:

(1). Wricke's ecovalence ( $W_i$ ) of Wricke (1962)

$$W_i = \sum (Y_{ij} - Y_i - Y_j + Y_{..})^2$$

Where;

$W_i$  = ecovalence of the i-th cultivar

$Y_{ij}$  = the observed phenotypic value of the i-th cultivar in the j-th environment

$Y_i$  = mean of i-th cultivar across the entire environment,  $y_j$  = mean of

**Table 1.** Components of the variances in the ANOVA.

| Sources of variation | Degrees of freedom | Expected mean square (EMS)                  |
|----------------------|--------------------|---|
| Year                 | (y-1)              | $\sigma_e^2 + r\sigma_{gy}^2 + r\sigma_y^2$ |
| Genotypes            | (g-1)              | $\sigma_e^2 + r\sigma_{gy}^2 + r\sigma_g^2$ |
| Genotype X Year      | (g-1)(y-1)         | $\sigma_e^2 + r\sigma_{gy}^2$               |
| Error                | (gy-1)(r-1)        | $\sigma_e^2$                                |

j-th environment  
 $y_{..}$  = grand mean;  
 and (2). Superiority parameter ( $P_i$ ) of Lin and Binns (1988)

$$P_i = \sum_{j=1}^n (X_{ij} - M_j)^2 / 2n$$

Where;  
 $P_i$  = superiority index of the i-th cultivar,  
 $X_{ij}$  = yield of the i-th cultivar in the j-th environment,  
 $M_j$  = maximum response obtained among all the cultivars in the j-th environment,  
 and n = number of environments (years).

## RESULTS AND DISCUSSION

In Table 2, five of the ten traits (DT50F, DT95M, Pods/plant, Seeds/pod and 100 seed weight) differ significantly among the eleven genotypes of cowpea in 2006. In 2007, DT50F, DT95M, 100 seed weight, pod yield and grain yield were the variables with significance differences. All the above traits exhibited very high level of uniformity due to their low coefficient of variation except for pods/plant (in 2006) and pod and grain yield (in 2007). The main and interaction effects were not significant on pod length; however, the eleven genotypes differ significantly for the same trait in 2007. In the pooled ANOVA, there were significant main effects of year and genotype on nine and seven traits respectively. The variability of the seeds/pod and pod length were not determined by the year effect, pods/plant, dry fodder yield and pod length were not different among the eleven genotypes. Genotype by environment (year) interaction effect was significant on: DT50F, DT95M, Seeds/pod, 100seed weight and pod yield (Table 2).

There was no significant variation for fresh and dry fodder yield of cowpea in each of the two consecutive years of experimentation. However, the pooled analysis revealed that the year effect on the fodder yields was highly significant; the mean yield of fresh and dry fodders was higher in 2007 than in 2006. The economic yield that is grain yield and pod yield, were higher significantly in 2006 than 2007, 100seed weight was significantly higher in 2007. The inherent environmental conditions in the two years tested were significant to producing these variations; however, the interaction of the year with genotypic effect is very important in this study. The number of seeds/pod is rather under genetic and its interaction with environmental influence only. The proportion of the geno-

type by year interaction in the total phenotypic variation for DT50F, DT95M, seeds/pod, 100 seed weight and pod yield are as follows: 11.12, 0.71, 41.28, 11.35 and 4.31% respectively. The reliability of a trait to be selected for breeding programme among other factors is dependent on the magnitude of its coefficient of variation especially the genotypic coefficient of variation. While a lower value of coefficient of variation (CV) gene-rally depicts low variability among the tested sample; a high proportion genotypic CV to the phenotypic CV is desirable in breeding works. The PCV was higher than the GCV in all the traits; both were moderately low, ranging from 3.86 - 27.15 and 3.72 - 20.56 respectively. In this study, the proportion of GCV in the PCV ranged between 68.42 (in pod length) - 99.88 (in 100 seed weight). Most of the traits exhibited fairly high to high GCV: PCV (Table 3). Higher GCV: PCV denotes that the trait is much under the influence of genetic rather than environmental Kaushik et al. (2007).

The heritability estimates for all the traits are recorded in Table 3. The paired estimate of heritability for the same trait in the two environments (2006 and 2007) was consistently different from each other. The broad sense heritability for DT95M, pods/plant, seeds/pod, 100 seed weight, Ffodyld and Dfodyld was higher in 2006 while the heritability for DT50F, pod yield, grain yield and pod length were superior in 2007. The magnitude of heritability varies with environment, Link et al. (1999) had higher heritability for yield in improved (well-watered) environment and Toker (2004) obtained higher heritability for some quantitative traits in the high yielding years. Heritability estimation on individual year basis ignores G x E variance; the resultant estimate will be unreliable for any genetic predictions. The heritability estimates over pooled environments eliminates biases from G x E interaction; such estimates though low in magnitude is most reliable for genetic gain prediction of traits in any breeding programme (Mudler and Bijma, 2005). This study concurs with the above assertion; the percentages of reduction measured as C are in Table 3. The actual loss of potential genetic gain was an appropriate indicator of the genetic gain reduction arising from the importance of G x E (Matheson and Cotterill, 1990, Yan and Kang, 2003). In this study, the trait with the least value (11%) for loss of potential genetic gain was days to 50% flowering between heritability and loss of potential genetic gain for this population of cowpea was inversely proportional. According to Benin et al. (2005), the concept of repeatability can be

**Table 2.** Summary of annual and combined years ANOVA for ten quantitative traits of Cowpea.

| Sources of variation  | df | Mean squares |           |            |           |                  |                |                  |              |              |                 |
|-----------------------|----|--------------|-----------|------------|-----------|------------------|----------------|------------------|--------------|--------------|-----------------|
|                       |    | DT50F        | DT95M     | Pods/plant | Seeds/pod | 100 seed wt. (g) | Pod yield (kg) | Grain yield (kg) | Ffodyld (kg) | Dfodyld (kg) | Pod length (cm) |
| <b>2006</b>           |    |              |           |            |           |                  |                |                  |              |              |                 |
| Genotypes             | 10 | 25.2*        | 21.9***   | 120.3*     | 7.6**     | 28.8***          | 3109.1         | 718.4            | 15.7         | 2.4          | 2.8             |
| Error                 | 20 | 6.2          | 0.29      | 49.8       | 1.9       | 0.06             | 1652.4         | 569.5            | 6.8          | 1.1          | 4.2             |
| Mean                  |    | 49.6         | 72        | 23.9       | 11.8      | 17.03            | 4.5            | 2.5              | 0.4          | 0.09         | 15.9            |
| CV (%)                |    | 5.02         | 0.75      | 29.5       | 11.7      | 1.5              | 28.2           | 30.9             | 19.6         | 35.1         | 13              |
| <b>2007</b>           |    |              |           |            |           |                  |                |                  |              |              |                 |
| Genotypes             | 10 | 18.1***      | 15.1**    | 18.7       | 1.6       | 6.1***           | 1852.9**       | 842.6**          | 95.6         | 1.5          | 6.4**           |
| Error                 | 20 | 1.4          | 3.5       | 51.4       | 1.02      | 0.07             | 428.9          | 224.7            | 58.5         | 1.7          | 1.4             |
| Mean                  |    | 47.9         | 81.4      | 17.3       | 11.5      | 18.2             | 2.7            | 1.8              | 0.7          | 0.2          | 15.5            |
| CV (%)                |    | 2.5          | 2.3       | 41.4       | 8.8       | 1.4              | 24.5           | 25.3             | 33.9         | 25.4         | 7.7             |
| <b>Combined years</b> |    |              |           |            |           |                  |                |                  |              |              |                 |
| Years                 | 1  | 44.2**       | 1471.9*** | 726.7***   | 1.8       | 53.2***          | 58580.9***     | 5332.9***        | 1413.9***    | 76.5***      | 2.1             |
| Genotypes             | 10 | 34.1***      | 26.2***   | 64.7       | 4.6**     | 24.9***          | 2224.7*        | 798.1*           | 7.1*         | 2.1          | 5.1             |
| Gen. x Yr.            | 10 | 9.8*         | 10.7*     | 74.4       | 4.5**     | 10***            | 2737.3*        | 763              | 40.2         | 1.8          | 4               |
| Error                 | 42 | 4.5          | 1.8       | 49.4       | 1.5       | 0.07             | 1004.9         | 379.3            | 32.8         | 1.4          | 2.7             |
| Mean                  |    | 48.7         | 76.7      | 20.6       | 11.65     | 17.9             | 3.6            | 2.2              | 0.6          | 0.1          | 15.7            |
| CV (%)                |    | 4.4          | 1.8       | 34.1       | 10.6      | 1.4              | 27.8           | 28.6             | 31.9         | 29.8         | 10.5            |

DT50F – Days to 50% flowering, DT95M – Days to 95% maturity, Ffodyld – Fresh fodder yield, Dfodyld – Dry fodder yield. \*, \*\*, and \*\*\* - Significant levels at P ≤ 0.05, 0.01 and 0.001 respectively.

**Table 3.** Annual and pooled estimates of heritability, repeatability and loss of potential genetic gain of some traits of Cowpea.

| Traits           | PCV (%) | GCV (%) | H <sup>2</sup> (%) - 2006 | H <sup>2</sup> (%) - 2007 | H <sup>2</sup> (%) - Pooled | C (%)          | r <sub>c</sub> |
|------------------|---------|---------|---------------------------|---------------------------|-----------------------------|----------------|----------------|
| DT50F            | 06.92   | 06.45   | 80.25                     | 92.82                     | 85.77                       | 10.69          | 0.125          |
| DT95M            | 03.86   | 03.72   | 98.69                     | 81.18                     | 82.21                       | 14.94          | 0.018          |
| Pod/plant        | 22.52   | 18.95   | 70.60                     | 26.68                     | 58.75                       | G x Y not sig. | 0.081          |
| Seeds/pod        | 10.65   | 08.73   | 80.00                     | 61.07                     | 64.84                       | 24.14          | 0.730          |
| 100seed wt. (g.) | 16.07   | 16.05   | 99.79                     | 98.87                     | 83.19                       | 15.50          | 0.394          |
| Pod yield (Kg.)  | 23.85   | 17.66   | 65.30                     | 81.20                     | 59.16                       | 26.43          | 0.036          |
| Grain yield(Kg.) | 23.93   | 17.34   | 55.78                     | 78.95                     | 64.22                       | G x Y not sig. | 0.131          |
| Ffodyld (Kg.)    | 27.15   | 19.93   | 69.78                     | 62.03                     | 21.74                       | G x Y not sig. | 0.003          |
| Dfodyld (Kg.)    | 20.88   | 20.56   | 68.57                     | 46.87                     | 64.84                       | G x Y not sig. | 0.027          |
| Pod length (cm.) | 08.33   | 05.70   | 40.00                     | 82.05                     | 67.67                       | G x Y not sig. | 0.836          |

PCV – Phenotypic coefficient of variation, GCV – Genotypic coefficient of variation, H<sup>2</sup> – Broad sense heritability, r<sub>c</sub> – Repeatability and C – Loss of potential genetic gain.

**Table 4.** Wricke's ecovalence ( $W_i$ ) and the superiority Index ( $P_i$ ) for grain yield components of cowpea.

| Genotypes                  | Mean yield | Rank | $W_i$   | Rank | $P_i$  | Rank |
|----------------------------|------------|------|---------|------|--------|------|
| <b>Pod yield (Kg)</b>      |            |      |         |      |        |      |
| IT98K - 356 - 1            | 14.7a      | 1    | 0.924   | 7    | 0.848  | 1    |
| IT97K -499 - 35            | 12.2ab     | 2    | 0.610   | 4    | 8.007  | 2    |
| IT95K - 193 - 12           | 12.0ab     | 3    | 0.784   | 6    | 8.826  | 3    |
| Oloyin                     | 11.8abc    | 4    | 50.214  | 11   | 13.882 | 5    |
| IT97 - 568 - 18            | 11.0abc    | 5    | 4.124   | 9    | 15.167 | 6    |
| IT96D – 610                | 10.6bc     | 6    | 0.002   | 1    | 13.772 | 4    |
| IT93K – 452 – 1            | 10.2bc     | 7    | 0.315   | 3    | 15.170 | 7    |
| IT99K – 491 – 7            | 10.0bc     | 8    | 16.064  | 10   | 25.319 | 10   |
| IT95K - 2011 - 11          | 9.9bc      | 9    | 0.294   | 2    | 17.916 | 8    |
| IT98K - 506 - 1            | 9.0bc      | 10   | 1.957   | 8    | 25.270 | 9    |
| IT95K - 1072 - 57          | 7.8bc      | 11   | 0.624   | 5    | 30.648 | 11   |
| <b>Seeds per pod</b>       |            |      |         |      |        |      |
| IT98K - 506 - 1            | 39a        | 1    | 12.5    | 7    | 1.0    | 1    |
| IT95K - 193 - 12           | 37.5ab     | 2    | 18.0    | 8    | 4.3    | 2    |
| IT97 - 568 - 18            | 37ab       | 3    | 0.5     | 1    | 5.0    | 3    |
| IT97K -499 - 35            | 36.5ab     | 4    | 2.0     | 4    | 6.3    | 4    |
| IT95K - 2011 - 11          | 36ab       | 5    | 0.5     | 1    | 8.5    | 5    |
| IT96D – 610                | 35.5ab     | 6    | 32.0    | 10   | 13.3   | 6    |
| IT95K - 1072 - 57          | 34.5abc    | 7    | 32.0    | 10   | 30.3   | 8    |
| IT98K - 356 - 1            | 33bc       | 8    | 24.5    | 9    | 37.0   | 10   |
| IT93K – 452 – 1            | 33bc       | 8    | 0.5     | 1    | 26.5   | 7    |
| IT99K – 491 – 7            | 32.5bc     | 10   | 8.0     | 5    | 34.3   | 9    |
| Oloyin                     | 30bc       | 11   | 8.5     | 6    | 54.5   | 11   |
| <b>100 seed weight (g)</b> |            |      |         |      |        |      |
| IT95K - 1072 - 57          | 65.6a      | 1    | 195.228 | 11   | 6.3    | 1    |
| Oloyin                     | 58.9b      | 2    | 10.811  | 7    | 54.5   | 2    |
| IT95K - 2011 - 11          | 57.9c      | 3    | 0.130   | 3    | 80.5   | 3    |
| IT98K - 356 - 1            | 55.9d      | 4    | 0.076   | 2    | 99.8   | 4    |
| IT95K - 193 - 12           | 55.1d      | 5    | 61.938  | 10   | 167.4  | 8    |
| IT93K – 452 – 1            | 53.0e      | 6    | 0.423   | 4    | 143.7  | 5    |
| IT97K -499 - 35            | 52.7e      | 7    | 0.003   | 1    | 145.0  | 6    |
| IT98K - 506 – 1            | 52.5e      | 8    | 0.471   | 5    | 145.4  | 7    |
| IT97 - 568 – 18            | 49.1f      | 9    | 3.303   | 6    | 216.7  | 9    |
| IT96D – 610                | 48.2g      | 10   | 14.961  | 9    | 249.5  | 10   |
| IT99K – 491 – 7            | 42.1h      | 11   | 13.520  | 8    | 377.1  | 11   |

Note: There is no significant difference between values with the same alphabet.

expressed as the correlation between measures of a given trait in an individual repeated in time or space. This coefficient expresses the proportion of total variation that is explained by variations in function of the genotype and those attributable to the environment. High values of this coefficient for any trait indicate that the genotypes are expressed with high stability (Falconer and Mackay, 1996 and Ortiz and Ng, 2000). From Table 3, the  $r_c$  for seeds per pod and pod length were near unit (0.73 and 0.84 respectively), they could be classified as very stable

traits. The repeatability coefficient for 100 seed weight was 0.4, fresh fodder yield had the least (0.003), making it the most unstable trait of the studied cowpea genotypes. Repeatability is a useful tool for quantifying the extent to which an individual's performance or behaviour remains consistent over time (Arnold, 1994). Selection could be reliable if the choice of genotypes can be based on: high GCV: PCV ratio, high broad sense heritability and high repeatability (Ortiz and Ng, 2000 and Anicchirico, 2002). Table 4 presented the mean yield and ranks

based on the two stability statistics ( $W_i$  and  $P_i$ ) for pod yield, seeds/pod and 100 seed weight. The ecovalence ( $W_i$ ) - the biological valence, express the stability of traits in certain environmental conditions. According to Wricke (1962), smaller ecovalence value depicts high stability.

For pod yield, IT96D - 610 is the most stable genotype ( $W_i = 0.002$ ), Oloyin - a common local variety in south western Nigeria was mostly unstable ( $W_i = 50.214$ ). Three genotypes: IT97 - 568 - 18, IT95K - 2011 - 11 and IT93K - 452 - 1 had good phenotypic stability for seeds/pod with  $W_i = 0.5$  each. They were equally stable with non-significant difference in their mean yield. The highest value ( $W_i = 32$ ) were by IT96D - 610 and IT95K - 1072 - 57, they are most unstable among the eleven genotypes for seeds/pod; their mean yield difference was statistically nil too. The responses to stability of 100 seed weight by the genotypes were in the following fashion: IT97K - 499 - 35 ( $W_i = 0.003$ ) - most stable, followed by IT98K - 356 - 1 ( $W_i = 0.076$ ) and then IT95K - 2011 - 11 ( $W_i = 0.130$ ). IT95K - 1072 - 57 was most unstable with  $W_i$  of 195.23 for 100 seed weight. IT98K - 356 - 1, IT98K - 506 - 1 and IT95K - 1072 - 57 were the genotypes with the highest mean for pod yield, seeds/pod and 100 seed weight respectively; by ecovalence statistics, they ranked 7<sup>th</sup>, 7<sup>th</sup> and 11<sup>th</sup> in terms of stability (Table 4). This result is consistent with the assertion of Kamdi (2001), that most high yielding genotypes are usually unstable. The explanation for stability by the superiority index ( $P_i$ ) of Lin and Binns (1988) was to a large extent in correspondence with mean yield for the three traits. This may be due to its peculiarity of characterizing genotypes by associating stability and productivity.  $P_i$  defines a superior cultivar as one with a performance near the maximum in various environments (Lin and Binns, 1988).

Therefore, small values of this estimator imply the closeness of the yield of a genotype to the maximum and hence its superiority for the overall response. In Table 4, IT98K - 356 - 1, IT98K - 506 - 1 and IT95K - 1072 - 57 were the most stable and superior ( $P_i = 0.85, 1.0$  and  $6.3$ ) genotypes for pod yield, seeds per pod and 100 seed weight respectively. The mean yield of the first six genotypes and their ranking by  $P_i$  statistics for seeds per pod exhibited perfect correlation (Table 4). The seeds/pod of Oloyin was most adversely affected by the environmental variation; however, its weight for a hundred seeds was very encouraging. Moreover, the first four (high yielding, stable and superior) and the last three (poor yielding, unstable and less superior) genotypes equally had perfect correlation with the  $P_i$  statistics ranking for 100 seed weight (Table 4). Just like some other authors (Lin et al., 1986; Aremu et al., 2007) the two stability statistics employed in this study did not agree in the selection of genotypes. However, since the search for most stable and highly productive genotypes is an important objective of the plant breeders, genotypes with the combination of the duo properties would be mostly preferred. Therefore, this study identified IT97K - 499 - 35, IT97 - 568 - 18 and IT95K - 2011 - 11 to combine

bine high productivity with stability for pod yield, seeds/pod and 100 seed weight: respectively. They are better than Oloyin for these three traits and can therefore be recommended along with Oloyin as cowpea varieties with promising high yield with good stability in western Nigeria.

## REFERENCES

- Akbar AA, Kamran M (2006). Relationship among yield components and selection criteria for yield improvement of Safflower - *Carthamus tinctorious* L. J. Appl. Sci. 6: 2853-2855.
- Allard RW (1960). Principles of Plant Breeding, John Wiley and Sons, Inc., New York.
- Annicchiarico P (2002). Genotype x environmental interactions: challenges and opportunities for plant breeding and cultivar recommendations - FAO Plant Production and Protection Papers - 174. p. 126.
- Aremu CO, Ariyo OJ, Adewale BD (2007). Assessments of selection techniques in genotype x environment interaction in cowpea *Vigna unguiculata* (L.) Walp. Afr. J. Agric. Res. 2: 352-355.
- Arnold SJ (1994). Multivariate inheritance and evolution: a review of concepts. In: Boake CRB (eds), Quantitative Genetic Studies of Behavioral Evolution. University of Chicago Press, Chicago, pp. 17-48.
- Benin G, Hartwig I, de Carvalho FIF, de Oliveira AC, Vieira EA, Bertan I, da Silva JA, Valério IP, Ribeiro G (2005). Repeatability estimates of genetic, phenotypic and environmental correlations in oats with and without fungicide application. Crop Breeding Appl. Biotechnol. 5: 183-190.
- Brolmann JB, Stoffella PJ (1986). Differences in yield stability among cowpea cultivars. Soil and crop Sci. Soc. Fla. Proc. 45: 118-120.
- Dani RG (1979). Variability and association between yield and yield components in pigeon pea. Indian J. Agric. Sci. 49: 507-510.
- Falconer DS, Mackay TF (1996). Introduction to Quantitative Genetics, Longman, Harlow.
- Gomez AG, Gomez AA (1984). Statistical procedure for Agricultural research, John Wiley and son Inc., New York.
- Kamdi RE (2001). Relative Stability, Performance, and Superiority of Crop Genotypes across Environ. 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 and Bioenergy 31: 497-502.
- Lin CS, Binns MR, Lefkovich LP (1986). Stability Analysis: Where Do We Stand? Crop Sci. 26: 894-900
- Lin CS, Binns MR (1988). A Superiority measure of cultivar performance for cultivar x location data. Can. J. Plant Sci. 68: 193-198.
- Link W, Abdelmula AA, von Kittlitz E (1999). Genotypic variation for draught tolerance in *Vicia faba* L. Plant Breeding 118: 477-483.
- Matheson AC, Cotterill PP (1990). Utility of Genotype x environment interaction. For. Ecol. Manage. 30: 159-174.
- Mulder HA, Bijma P (2005). Effects of genotype x environment interaction on genetic gain in breeding programs. J. Animal Sci. 83: 49-61.
- Narsinghani VG, Kanwal KS, Singh SP (1978). Character correlations in pea. Indian J. Agric. Sci. 48: 390-394.
- Ologhobo AD, Fetuga BL (1983). Investigation on the trypsin inhibitor, hemagglutinin, phytic and tannic acid content of cowpea *Vigna unguiculata* Food Chem. 12: 249-254.
- Ortiz R, Ng NQ (2000). Genotype x Environment Interaction and its Analysis in Germplasm Characterization and Evaluation In: Ekanayake IJ, Ortiz R (eds) Genotype x Environment Interaction Analysis of IITA mandate crops in Sub - Saharan Africa. IITA, Ibadan. 32-40.
- Siddique AKMAR, Gupta SN (1991). Genetic and phenotypic variability for seed yield and other traits in cowpea (*Vigna unguiculata* (L.) Walp) Int. J. Trop. Agric. 9: 144-148.

- Singh RK, Chaudhary SD (1985). Biometrical methods in Quantitative Genetic Analysis, Kalyan Publishers, New Delhi, pp. 205 -214.
- Singh KB, Malhotra RS (1970). Interrelationships between yield and yield components in mung bean. Indian J. Genet. Plant breeding 30: 244-250.
- Tenkouano A, Ortiz R, Baiyeri KP (2002). Phenotypic and Genetic correlations in *Musa* populations in Nigeria. Afr. J. Crop Sci. 10: 121-132.
- Toker G (2004). Estimates of broad sense heritability for Seed yield and yield criteria in faba bean (*Vicia faba* L.). Hereditas 140: 222- 225.
- Wricke G (1962). Über eine Methode zur Erfassung der Ökologischen Streubreite in Feldversuchen. Z Pflanzenzüchtung 47: 92-96.
- Yan W, Kang MS (2003). GGE Biplot Analysis: A graphical tool for breeders, geneticists and Agronomists, CRC Press, Florida, p. 8.