DIVERSITY, SELECTION AND GENOTYPE X ENVIRONMENT INTERACTION IN COWPEA *vigna unguiculata* (L.) WALP

BY

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ABSTRACT

Thirty-one cowpea genotypes from divers eco-geographic origins were planted in the 2000 planting season of derived savanna ecology to determine the genetic diversity, using multivariate analysis. In four location – season environments twenty cultivars were grown to measure genotype x environment interaction and stability. Data were collected on gronomic and yield characters. The first three axes of the Principal Component Analysis (PCA) captured 40.7% of the total variation among the enteries. Height at flowering and maturity, length of peduncle, number of seed per pod, fresh and dry pod colour, number of days to 50 % flowering and maturity contributed most to the variation. The first three axes of the Canonical and Discriminant analyses respectively summarised 58.9% and 74.5% of the total variations. Canonical analysis identified seed characteristics, length of branch and maturity period as the most important characters in the variations in cowpea accessions. The genotype, environment and GXE interaction accounted for 53.7%, 3.1% and 15.1% of the GXE interaction sum of squares. The first and second interaction PCA accounted for 68.2% and 27. % of the total variation; IT97k-499-39, TVx-3236, LDPD, Owode, IT96K-277-2, Ife-brown, AGRIB VI and IT97k-113-6 had a combination of stable and above average yield and suitable for cultivation across seasons using stability parameters. Unlike the deviation mean square, (S^2di) and unbiased estimator (δ_i^2) more genotypes were adjudged unstable with respect to the characters by the ecovalence mean square (WMS). Deviation mean square, unbiased estimator and WMS identified medino I and II and IT90k–1034-34 as unstable and hence unsuitable for cultivation across seasons. IT97K-499-39, TVx-3236, LDPD, Owode, and AGRIBVI adapted to all the seasons using AMMI analysis even as IT97K-499-39, Owode and IT97K-113-6 were adaptable to Ogbomoso environment. Only IT97K-499-39,TVx-3236, AGRIB VI and IT97K-113-6 could adapt to Abeokuta environment. TVx-3236, LDPD

and AGRIB VI which were identified stable by AMMI, were also selected by modified rank-sum method. Six generations of parents, first and second filial generations, back crosses 1 and 2 (P_1, P_2, F_1, F_2, BC_1 and BC_2) were produced from a cross Danilla x Ife-Brown. Additive gene effects were higher than the dominance gene effects for these traits. Number of branches, number of peduncles per plant, days to maturity and 100-seed weight were controlled by complementary gene action. Days to flower, length of peduncle, number of pod and seeds per pod were controlled by duplicate epistatic gene actions, therefore, yield improvement via these traits will be difficult. Two crosses of Ife-brown x Danilla and Ife-brown x IAR48W used in early generation selection identified number of branch, number of pod and number of seeds per pod as having highest heritability estimates during the f_2 generation. Therefore, cowpea selections based on these characters should be carried out in the early generations preferably in the F_2.

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CHAPTER ONE

1.0 INTRODUCTION

Cowpea, *Vigna unquiculata* (L) Walp, is an important source of protein for man in tropical Africa. In fresh form, the young leaves, immature pods and peas are used as vegetables. The grain is used for snacks and main meal dishes. All the plant parts that are used for food are nutritious, providing protein, vitamins and minerals. Cowpea grain contains about 25% protein, 70% starch and 5% vitamins and minerals (Duke, 1990). The insitu decay of root and leaf residues are used as manure while the low or creeping growth habit allow for soil protection against erosion and degradation (Singh and Rachie,1987). Cowpea is pivotal to sustaining animal production in semi arid regions. In Africa, farmers cut and store fodder for sales to obtain about 25% annual income and fodder yields of about 4t /ha can be obtained under crop rotation. Cowpea is grown for one season and followed by inter crop with other cereals such as maize have been found to increase cereal crop yield (FAO 1996). Another important feature of cowpea is that it fixes atmospheric nitrogen through symbiosis with nodule bacteria thereby increasing Nitrogen level in the soil (FAO 1996). Total amount of nitrogen Fixation ranges from 70 – 35 kg / ha which becomes useful for succeeding crops. Cowpea is a single crop specie with constant genome number but the varietal differences in terms of plant type; seed type, maturity and end user needs are extremely diverse from region to region (Singh *et. al,* 1997). In Nigeria, cowpea testing across locations has been fruitful and worthwhile due to the diverse agro climatic zones, which include transition, derived, Guinea, Sudan and Sahel savanna ecologies. The diversity existing in a germplasm collection is equally essential in understanding the genetic variability existing in different cowpea genotypes. This

understanding also enhances successful genotypes selection in breeding programme (Redona and Mackill 1996; Ariyo 1993, Berdahl *et al,*1999). A simple and precise technique for measuring the overall genetic diversity of a crop is not yet available therefore no approach is considered the best for measuring diversity. In summarizing and describing the inherent variation in a population of crop genotypes, a collection of the crop accessions, is needed (Vaillancourt *et al.*1993; Nair *et al*, 1998)

A lot of techniques have been used to analyze variations in crop accessions. These analyses help to classify the range of variability among accessions to facilitate the maintenance and further acquisition of germplasm resources (Ariyo and Odulaja, 1991). The various techniques used include Principal Component Analysis, Principal Co-ordinate Analysis, Coefficient of Racial Likeness, metro-glyph, and Index Score Analysis, Cluster Analysis, Discriminate Canonical Analysis and Mahalanobis D^2 technique. These techniques resolve several phenotypic measurements into fewer, interpretable and more easily visualized dimensions and as such elucidate their patterns of variations. For long-term improvement, genotypes with the potential for better quality characters are needed as parent stocks for the development of improved varieties. The genetic parameters controlling the expression of yield and its components are essential in determining the effect of such parameters on yield (Singh *et al,* 1997). A detailed understanding of plant character correlation and heritability is important in any hybridization breeding work. This understanding enhances confidence in selection (Rao *et al*, 1997; Gupta and Ramanjam 1974; Nazi, 1999). Other statistical methods used in analysing yield component relationship and selections are genetic advance, (Kato 1997) path coefficient analysis, (Dewey and Lu, 1959). Phenotypic and genotypic coefficients of variation can be complex for inter character relationship where the use of correlations alone is

insufficient (Singh and Chaudhary1985, Ariyo *et al.*, 1987) in explaining the cause and effect of relationship. The development of cowpea varieties that would be tolerant to diverse environments and still give high yield is a major objective of cowpea breeding. Stability performance with respect to yield and yield components is achieved by genotype testing in diverse environments. The environments are characterized by soil types, soil fertility levels, moisture regimes, climate, topography, cropping systems pest and disease incidence etc. (Dashiell *et al.* 1994; Ariyo 1990a; Ntare and Aken'ova 1985). Measuring GXE interaction is important in determining an optimum breeding strategy for releasing genotypes with adaptation or stability to target environments by using different stability techniques. These include partitioning of variance components (simple analysis of variance) into genotype, environment and GXE interaction. Although significant levels of each of these components are tested, no insight is given as to the response of particular genotype to environment giving rise to these interaction (Powel *et al.*1986; Zobel et al.1988). The regression of individual yields on environmental index as a means of evaluating stability was proposed originally by Yates and Cochran (1938). It was indicated that an average over all genotype response to the varying environmental conditions could be obtained by plotting individual genotype values against the trial means. The method of Finlay and Wilkinson (1963), was similar to that of Yates and Cochran (1938) but striking difference was in the definition of the regression coefficient value (b), of the yield of an individual cultivar on the mean yield of all cultivars as a stability parameter. In this method, a genotype is considered stable if the mean yield is high and the slope is 1.0 and unstable where slope is greater than 1.0. This method was further improved upon by Eberhert and Russell (1966) which considered the regression coefficient (b) values as a response parameter and introduced the mean square for the

deviations from regression (S_i^2D) as a stability parameter. A stable genotype was one with a regression coefficient of 1.0 and with a deviation mean square near zero. This parameter has been extensively used by many workers (Breese, 1969, Freeman and Perkins, 1971; Ntare and Aken'ova, 1985; Ariyo 1995) though the validity had been subjected to various criticism (Easton and Clement; 1973, Byth et al., 1976, Powel et al., 1986) on the non-linearity of some responses. The AMMI model is commonly used because both the main effects and the interaction effects are considered important (Crossa *et al.* 1990; Yan and Hunt 2001). It is used to better understand GXE interactions and make more reliable recommendations about cultivars adaptation (Gauch and Zobel, 1996).

The objectives of this study therefore are to:

1. examine and classify the extent of variations among cowpea accessions using multivariate techniques
2. study GXE interaction in cowpea genotypes and determine the effect of the environments on the performance of each genotype.
3. determine the heritability and inter-character relationships between some characters in cowpea.
4. estimate the gene action and interaction and
5. investigate the reliability of early generation selection for yield and yield components.

CHAPTER TWO

2.0 LITERATURE REVIEW

2.1 The Taxonomy of Cowpea plant:

Cowpea belongs to the order *Fabales*, family *Fabaceae*, Subfamily *Faboideae*, tribe phaseoleae, and sub tribe phaseolinae and genus vigna, (Ng and Marechal, 1985). All cultivated groups of cowpea belong to the species unguiculata. The species unguiculata is divided into four cultigroups namely unquiculata, biflora, sesquipedalis and textilis (Ng and Padulosi, 1991; Padulosi, 1993). There are about 150 species of *vigna* (Verdcourt 1970; Marechal *et. al,* 1978).The classification and nomenclature of the wild taxa within *Vigna unquiculata,* however, is complicated and confusing. The cultivated specie is believed to have originated from the wild taxa indigenous to southern and eastern Africa. The center of origin and domestication had been based on botanical and cytological evidence, geographical distribution, cultural practices and historical records (Steel and Mehra, 1980;Ng 1995). Although, De Candole (1886) suggested that the origin of a cultivated plant is found where the wild relative grows but this has been disputed by Ng and Padulosi (1997) that a wild plant may have been growing else where. That the wild *Vigna unquiculata* occur diversely in Southern Africa in the region of Namibia, Botswana, Zambia, Mozambique is a suggestion that southern Africa is the center of origin (Padulosi and Ng, 1997). The process of evolution of *Vigna unguiculata* led to changes in growth habit from perennial to annual, cross breeding to inbreeding and consequently to the domestication after selection. The center of diversity of cultivated cowpea is found in West Africa in regions of Nigeria, Niger, Burkina Faso, Mali,

Cameroon, Togo and Benin Republic (Ng, 1995). *Vigna unguiculata* is diploid (2n = 22). It is an annual plant with wide or narrow lanceolate and sometimes hastate leaflets. The lateral leaflets are sometimes oblique and slightly lobed. The roots are small, adventitious and sometimes tuberous; the peduncle is intermediate in length (14 – 35cm). The plant height ranges from 60 – 200cm tall. The flowers are small with pale marvel, yellow or white petals (Fatokun *et al*,1993b).

2.2 Ecology and growth habit:

A cowpea plant is cultivated mainly in dry agro ecology, which includes derived, Guinea, Sudan and Sahel Savanna ecologies. In West and Central Africa including Nigeria, cultivation in humid agro ecology results in very low yield with poor seed quality. Moreover, cowpea is drought tolerant and hardy and thus, survives under dry soil conditions and still maintains normal growth habit. In Nigeria, cowpea is grown mainly in the Northern part where unimodal rainfall is prevalent thus allowing for one season production in a year. With the advent of irrigation schemes two seasons in a year under irrigation and rain fed condition production would enhance grain and fodder yield. But pest incidence militate against such rainfed cowpea production (Byth et al., 1987).

Growth habit of cowpea can be determinate or semi determinate with spreading stems providing cover for the soil and thus suppressing weeds and preventing soil erosion. Early maturing and late maturing growth types are known. The early maturing type grows and matures between 60 – 70 days while the late maturing type matures between 90 – 120 days. If early maturing erect or semi-erect types are grown as sole crops, it is expected that the yield would be as high as that of the cereals on a productivity per day basis (Singh and Sharma, 1996).

2.3 Production:

About 12.5 million hectare of land is cultivated to cowpea with a production of 4 million tonnes annually since 1997 (Singh *et al*, 1997). Cowpea is widely distributed throughout the tropics but Central and West Africa account for over 64% of the area of cultivation. Important cowpea growing countries include Mali, Burkina Faso, Senegal, Ghana, Cameroon, India, U.S.A, Sri Lanka, Indonesia, Brazil, Zambia, Malawi etc. (Singh and Sharma 1996) with the availability of new Varieties, cowpea cultivation is increasing in these countries (Zhang, 1991). The main cowpea producing countries are located in Africa, central and southern America as well as parts of Asia.

The main area of cowpea production extended from West and Central Africa to Cameroon through Senegal and sahelian zones (Fery 1990) all located in dry Savanna ecology. Nigeria is the largest cowpea producer in Africa with about 2.1 million tones. The Northern Nigeria (with dry savanna) is seen to produce 89% of this total output while the west zones struggle with remaining less than 20% production (Ng and Marechal, 1985).

2.4 Breeding methods:

Plant breeding aimed at developing high yielding varieties for different ecological zones is a necessity. About 68 countries have identified and released improved cowpea varieties; Brazil with a total of 18 varieties, Benin republic 28, Ghana 32, Sri Lanka 24, Botswana 9 and Nigeria 43 (Fatokun *et al*, 1997; Singh 2000). In comparative study of different breeding methods, the mean performance of F_3 progenies derived from single seed descent method was found better than those progenies developed through single plant selection for yield and yield components (Fasoulas,1981;Barone *et al*, 1992). Better still, broad sense

heritability estimate was higher in the population developed through the single seed descent. Yan and Hunt (2001); Gomathinayagam *et al*, (1998) showed that testing and selecting genotypes at given locations or environments decrease the GXE interaction and hence ensure stable performance of improved varieties over a wide range of environments. Vigna unquiculata is a single crop species but the requirements of each variety within the unquiculata genus are extremely diverse from region to region and thus make breeding programs more complex (Tian and Xu, 1993; Singh and Sharma, 1996). Varietals differences include, days to maturity, plant type (erect or creeping) seed coat colour, and seed type with emphasis on protein content and short cooking time (Tyagi and Chawla 1999). It is therefore, not possible to have a single variety suitable for all locations and conditions. As such, there is need to develop varieties within the vigna unguiculata with different attributes that of course will be resistant to major biotic and abiotic constraints (Singh and Sharma 1996 Dana and Karmakar 1990).

2.5 Character variation and path analysis in cowpea:

Character variability in cowpea is essentially partitioned into heritable and non-heritable components. This partitioning determines to a large extent the most effective breeding procedures. Character variability can be further classified as phenotypic or genotypic depending on genetic and or environment influence on the character.

A number of studies have been carried out on cowpea with the aim of improving the yield through character selection. Singh and Mehndiratta (1970), found high genetic coefficient of variation for number of seeds per pod, 100 seed weight and length of pod. Singh and Chaudhary (1996), obtained high genotypic and phenotypic variation for days to 50% flower, number of seed per pod, 100- seed weight and seed yield in cowpea. Redoma and

Mackill (1996) reported significant variation in seedling of vigna and noted gene interaction in cowpea character improvement.

Singh and Mehndirata (1970), reported that seeds per pod; 100-seed weight and number of pods per plant accounted for above 50 % variations in yield.

Seed yield was the most variable character with highest phenotypic and genotypic variations including pod length Ariyo (1995). On the contrary, Ajibade *et al,*(2000) reported leaf surface as most variable character followed by seed yield.

Response of correlated characters are sufficiently predicted only when genetic correlations and heritabilities are known. Correlation between traits examines the effect of one trait on another following selection. Selection could be successful and reliable if practiced on characters with high heritability and genetic variability. More importantly, such highly heritable characters must be correlated with yield. (Araujo and Coulman 2002). Correlation studies can be easy with fewer characters but as more characters are involved in correlations, the indirect associations between characters become more complex. In such a situation therefore, path- coefficient analysis becomes useful in identifying characters with direct and indirect associations with seed yield (Dewey and Lu, 1959; Ariyo 1995; Rao, *et al*, 1997).

Character association in cowpea (Ariyo 1995; Ajibade and Morakinyo, 2000) revealed number of peduncle per plant, number of branch per plant, and seeds per pod to positively associate with seed yield. However, pod length, and pods per peduncle showed negative indirect effect on seed yield Ariyo (1995). But in mungbean, (Niazi, et al., 1999) reported that pod length, weight of 100- seeds and pod diameter had negative indirect effect via plant height on yield, while number of seeds per pod gave direct influence on yield of mungbean.

2.6 Heritability estimates and genetic advance:

The effectiveness of selection for a trait depends on proportion of genetic and non-genetic causes in its expression. This is expressed as the heritability of the trait. Therefore, the heritability of a character influences the methods chosen for population improvement (Cristina and Hall, 1995). Genetics of pod yield and its components were studied by Rao *et. al.*(1997),who reported the broad and narrow sense heritabilities for pod weight to be 84% and 75% respectively. This indicated good index for effective selection. But Cristina and Hall, (1995) found 38% and 58% broad and narrow sense heritabilities respectively for these same traits in two crosses, TVX 309 x Prima and TVX-309 x CB- 46, of cowpea. Bhushana *et al.* (2000), estimated heterosis for several traits in 36 hybrids of cowpea and observed a midparent heterosis of 171. 5% for number of branches per plant; 11.5% for pod length and 20% for 100 seed weight. Sangwan and Lodhi (1998) reported that better parent heterosis ranged from 28.8% to 84% for yield / ha; 81.6% for pods per plant, and 20.4% for number of seeds per pod. Damarang (1994) reported heritability and genetic advance for number of pods per plant to be 94.4% and 39.2 respectively while 100 -seed weight recorded 83.3% heritability and 28.17% genetic advance. Ketata et al. (1976), reported that moderate genetic advance and high heritability estimate resulted in substantial progress in the improvement of wheat crop genotypes. Also, Ismail and Hall (1993) used estimates from heritability and genetic advance to develop cowpea hybrids with defensive mechanism against environmental stress. Ojo and Amanze (2001), predicted the yield of soybean through heritability and genetic advance and found pod weight per plant, days to maturity and branch number per plant to substantially contribute

to the yield of soybean. Singh and Chaudhary, (1996) reported high heritability and genetic advance for 100-seed weight and plant height.

2.7 Biodiversity:

Multivariate statistical analyses deal mainly with data that consist of sets of measurements on a number of individual objects. The measurements made on a single individual can be assembled into a column vector, which can be random vector with a probability law describing the populations. Characteristics of univariate distribution of essential interest are the mean as a measure of location and standard deviation, as a measure of variability. But in multivariate analysis, the essential interest lies in the dependence between different variables (Everett and Dunn, 1990). A univariate procedure involving the use of critical difference at 1% to separate characters means and hence discriminate among them was proposed by Weatherup (1980). In the procedure, days to 50% flowering had the most separations among the characters. This character also recorded the highest F- ratio and the least coefficient of variation, (CV). Ariyo and Aken'ova, (1986), and Hall (1980), also identified days to 50% as most discriminating character in okra, and wheat respectively. The use of multivariate analysis is complex, but it has been found to illustrate relative genetic diversity in germ plasma collection. Different statistical methods are used in analyzing covariance structures. These include Principal Component Analysis and Canonical correlations while Linkage Cluster Analysis shows pattern of relationship between genotypes and a hierarchical mutually exclusive grouping with reduced variances. The multivariate techniques resolve several phenotypic measurements into fewer, interpretable and more easily visualized dimensions and elucidate their patterns of variation. The Principal Component Analysis (PCA) explains the reduction of

multivariate data (character or genotypes) into units or components, which account for meaningful amount of variation in the germplasm or population. From this reduced components a few dimensional relationship can be plotted using two or more independent axes (Sneath and Sokal, 1973). The use of PCA poses a problems of operational ambiguity in deciding the number of axes to retain as, different investigators report different number of axes retained (Atchley and Bryant, 1975). Unlike the PCA, the Canonical Analysis separates and forms two sets of variates from which highly correlated variables are separated to form a new unit of within and between groups (Lawley and Maxwell, 1971). The Cluster Analysis which includes Single Linkage (SLCA) and average linkage (UPGMA) is used to decrease the number of individual units or characters by classifying or sorting such into groups with the objective of minimizing loss of information (Martins and Rhodes, 1972). These groups reveal an existing relationship. The choice of type of cluster depends on the similarity of the groups formed. As such, clustering can be hierarchical as in (SLCA) or non- hierarchical as in average cluster analysis (UPGM). The SLCA gives a hierarchical classification of homogenous multivariate characters and uses the coefficient of similarity to form a dendogram (Sneath and Sokal 1973). Hotelling (1933), first developed PCA and canonical.

These techniques have been extensively used by Rhodes and Martines, (1972); Akoroda, (1983); Ariyo and Odulaja, (1991); Ariyo (1993); Alika (1993); Tatineni *et al.*1996), to explain genetic diversity among crops (Yam, Okra, Maize, Wheat and cotton). Where the SLCA cannot interprete the plots from the principal components, the UPGMA becomes a better alternative.

2.8 Genetic Analysis:

2.8.1 Generation Mean Analysis (GMA): In genetic studies, one approach that determines the magnitude of gene effect is the generation mean technique of Mather and Jinks (1982) involving the scaling test of Cavalli (1952). This design provides detailed information on the gene interaction levels. The theory of GMA was developed for diploid organisms whose genes segregate independently and are homozygous in the parent lines. Given different generations of a cross of crop including the backcrosses, it is possible to evaluate the adequacy of a scale. The adequacy must satisfy two conditions which are, the additivity of gene effects and independence of heritable components from non- heritable ones (Singh and Chaudhary 1988). Better still, the test of adequacy of scales is important because estimation of additive and dominance components of variances are made assuming the absence of gene interaction. One of the assumptions of additive type of model, the simple scaling test of Mather, (1949) can be used .A few families (not more than 4 families) are used at a time. An improvement on this test was later devised by Cavalli (1952) using the joint scaling test which include any combination of families at the same time. The test uses weighted least square method to estimate for a three parameter model M, d and h, (Kearsey and Jinks 1985). The adequacy of these three-parameter models confirms the absence of any gene interaction. However, when the estimations are not significant implying non- adequacy, in any of the three parameters it is therefore advisable to refit the model (Singh and Chaudhary 1985; Mather and Jinks 1982). The Generation Mean Components have been used (Mather and Jinks, (1982); Kearsey and Jinks (1985); Carlos *et al.* (1995); Ram (1997); Khattak *et al.*(2002)), to evaluate the genetic component of interaction on crops (Peas, wheat, soybean, greengram and mungbean)

2.8.2 Early Generation Selection:

Variations occur in early generation than later generations. Hence, early generation selection becomes desirable in genotypes possessing all the desirable genes in either the homozygous or heterozygous condition. These desirable genes are often found in the F_2 generation with its frequency declining in subsequent generations (Sneep 1977). It was argued (Sneep 1976) that the chances of recovery of a plant with all the desired genetic traits for yield reduces with advancement in generations. In other words the percentage of homozygous genotype increases as generation increases. Therefore, selections at the early generation preferably at F_2 assumes that most desirable gene combinations can be identified even in the heterozygous and the proportion of plant with these combinations decreases rapidly with advancing generations. Furthermore, if these combinations are not selected in the earliest possible generation preferably at F_2, they will be lost (Sneep, 1977; Rasmusson, 1987).

Selection for yield and yield component in early generations has produced varying result. According to Abdelkader *et al.* (1984), Singh and Singh (1997), only plant height and kernel weight showed effective selection in the early generation while harvest index, grain yield and totals dry matter traits were ineffective when selected in the early generation of bread wheat. Also, Cristina and Hall (1995), reported effective early generation selection at F_2 for early days to flowering in cowpea.

Generally, it has been reported that early generation selection can be effective for simple-inherited traits such as days to flowering and maturity, number of pods per plant etc, but ineffective for more complex traits like yield (Depauw and Shebeski 1973; Singh and Singh, 1997). There are opposing views to early generation selection Mevetty and Evang (1980), Alexander *et al.* (1984), reported delaying selection unitl reaching near

homozygosity in the later generation (F_4) Falcinelli *et al*, (1983), reported effective selection of grain weight and plant height at F_3 and F_4 generations in bread wheat. In the analysis of response to early generation selection, the use of realized heritability estimates have been proved useful and reliable for both effectiveness of selection and comparison of different selection methods (Falconer 1981, Singh and Singh 1997).

2.9 Genotype x Environment (GxE) interaction and stability Analysis:

2.9.1 Analysis of variance (ANOVA) Method.

The Partitioning of variation using ANOVA describes the main effect in the source of variation based on the additive model (Kempthorne 1984).

Significant GXE interaction complicates the selection of superior genotype(s) across contrasting environments. An ANOVA test of GXE interaction may be non- significant even though other sources of variation in the environment are important. This includes the major criticism in the use of ANOVA method (Zobel *et al*. 1988; Snedecor and Cochran, 1980). Although the techniques provides no insight into the particular type of step in assessing the importance of GXE interaction in diverse environments, the significance is statistically tested. Measurement of GXE interaction is important, as this determine the optimum breeding strategy for releasing genotypes with adequate adaptation (Yan and Hunt 2001). The adaptability therefore can be used in the interpretation of results from mutilocational trials conducted over years (Gauch and Zobel 1996; Ariyo 1997; Yan and Hunt 2001). The possible impact of GxE interaction analysis on crop yield improvement can be used to identify the constraints to productivity and hence formulate strategies for breeding research.

2.9.2 Stability analysis:

Factors affecting genotype stability include temperature, water and soil nutrients, pest and disease incidences etc. All these give a holistic influence known as the environment. Therefore, genotype stability is affected by both the genetic and environmental factors. Cultivar stability performance is measured using GXE interaction. GXE interaction therefore, expresses the changes in the relative performance of genotypes across environments at different sites or at same site in different years. (Fox *et al.* 1997; Yan and Hunt, 2001; Gauch and Zobel, 1996). Since plant breeding research is considered as a systematic search for improved genotypes within a distribution of varied genotypes, it is therefore pertinent to say that an improvement in a genotype will have its maximum value in one particular environment and hence result in successful selection of such genotypes. Crop improvement activities would have been simplified if there were no genotype by environment interaction. If there were no interaction, the best genotype in one environment will be best genotype in all environments (Falconer and Mackey 1996). However, changes in relative performance of genotypes across environments make selection difficult by reducing the correlation between genotype and phenotype variations. A lot of stability techniques have been used (Ariyo 1987, 1981, Shukla 1972, Kang 1991,). Wricke, 1965 developed the ecovalent (Wi) concept, but Shukla (1972) developed unbiased estimator ((δ_i^2) approach though similar to Wricke's ecovalent Mean square. Huhn (1979) developed the non parametric statistics (S^3i). In reality, the ecovalence (Wi), Shukla's stability ((δ_i^2) ,Huhn's (Si) Statistics are similar in their effectiveness (Dashiel *et al*;1994; Annichiarico 1997). These stability parameters have been found to simultaneously combine high yield and stability of performance and thus make selection

more precise (Dashiell *et al*, 1994). However, Kang and Magari (1995) explained that the stability variance (δ_i^2) will be of limited practical use unless yield or any other character is integrated with it for simultaneous selection of high yielding and stable genotypes. The success of identifying high yielding genotypes from yield trial data depends on the effectiveness of the statistical analysis used for understanding patterns in the data, accurate yield estimates and selection of superior genotypes (Gauch and Furnas 1991).Apart from establishing high yielding genotypes, it is equally essential to combine high yield with stability of performance. Several workers have combined yield and stability (Kang and Pharm 1991; Lin *et al*, 1986; Ntare and Aken'ova 1985; Ariyo 1987; Kang and Miller, 1984). Precision in selection of high yielding genotype and stability of performance has been successfully carried out (Kang 1991). This method regarded genotypes with the lowest rank- sum as most desirable. Indeed, the method assigned equal weights to yield and the stability variance (δ_i^2) with the lowest are having a rank of 1. The yield and (δ_i^2) ranks for each genotype were summed up and the genotypes with the lowest genotype rank sum were regarded stable. This method has been criticized (Kang 1991, Kang and Pham 1991) as not taking into account the significant levels of the stability variances (δ_i^2).

The rank-sun method was improved upon by testing the significance of the (δ_i^2) using appropriate F test. In so doing, a modification of the rank-sum was assignment of a stability rating of O, for non- significant δ^2_1; 4, for significant δ^2_1 at 5% level of probability and 8 for significant δ^2_1 at 1% probability level. This rating is added to the yield rank of a genotype and selection is made, based on the sum, such that genotypes are

adjudged to be stable or unstable in accordance with the significant level of the δ^2_i (Kang 1991, Kang and Pharm 1991, Kang and Magari 1995).

The traditional analysis of genotype environment interaction has focused on the analysis of stability (Wricke, 1962, Eberhert and Russell, 1966; Shukla, 1972, Huhn 1979, Kang 1991) rather than adaptation. AMMI model was developed to address the shortcomings in the use of traditional ANOVA, stability parameters, and linear and non linear regression analysis and PCA. ANOVA failed to identify and separate the interaction components, the stability parameters only identified stable genotypes without specific location adaptation, the regression analysis accounted for only a small proportion of the interaction sum of square and the PCA could not identify and separate the genotype and environment main effects. The improvement upon all these stability parameters was enhanced via the development of AMMI model. The AMMI model sometimes called the bi -plot model was first described by Bradu and Gabriel (1978) and later by Kempthorn (1984), Zobel *et al.* (1988), and much later by Gauch (1993). Apart from giving an insight into the environmental factors underlying GXE interaction, (Zobel et al 1988, Mclaren and Chaudhary, 1994, Yan and Hunt, 2001). The Model integrates and subsumes several statistical models usually applied to yield data. Furthermore, the use of the AMMI bi -plot (kempthorn, 1984; Crossa *et al.* 1990; Haji and Hunt, 1991). A better result interpretation from AMMI have been complemented by correlation studies between significant principal components and underlying variables of the environments, genotypes and or agronomic characters. From the correlation between environmental PC scores and environmental measurements (temperature, latitude, Soil status), significant or non significant interactions can be observed in the genotypes and the environment (Mclaren and

Chaudhary, 1994). Yan and Hunt (2001), also reported plant height and maturity date as the major genotypic causes of GXE interaction in winter wheat. Various workers have used AMMI model to select for stable genotypes adaptable to specific location (Haji and hunt 1999; in wheat, Ariyo 1998 and Ariyo and Ayo-Vaughan 2000, in okra, Yan and Hunt 2001, in rye, Ntawuruhunga 2001 and Fox *et al.* 1997, in cassava).

CHAPTER THREE

3.0 MATERIALS AND METHODS

3.1 Experimental sites:

The experimental sites for this research work were chosen from two agro-ecological zones of Guinea savannah (Ogbomoso) and humid (derived) savannah Abeokuta. The location sites are the Teaching and Research Farm of Ladoke Akintola University of Technology (LAUTECH), Ogbomoso 04^0 234E 08 ° 15N and University of Agriculture (UNAAB), Teaching and Research Farm, Abeokuta 7^0 29N $3^0$30E The soil sample taken from a depth of 15cm at the LAUTCH Farm before planting had a pH of 6 .8 and classified as ultisol (USDA 1975). The UNAAB Farm soil with a pH of 6.2 and classified as ferric luvisol (USDA 1975). The rainfall, temperature and location

co- ordinates data of the two locations used are presented in Appendix 1.

3.2 Genetic diversity evaluation:

Thirty one cowpea genotypes from different eco-geographical areas in West African countries (Table 1) were sourced from the cowpea germplasm unit of International Institute of Tropical Agriculture (IITA), Ibadan. The experiment was carried out during the 2000 late rainy season at Teaching and Research Farm of UNAAB. Land preparation was by ploughing - harrowing to effectively turn and soften the soil and remove stumps. Three seeds each of the thirty-one genotypes were sown in single row plots arranged in a randomized complete block design with three replications. Each row was 4m long with

60cm inter row spacing and 40cm intra row spacing. Blocks were separated from one another by 1m spacing. Three plant stands were thinned to two stands after two weeks of planting giving a total of 22 plant stands per row plot. At planting a mixture of Galex and Gramozone (50 ml and 50ml mixture in 20 litres of water) was sprayed to control pre – emergent and post- emergent weeds. This was followed by manual weeding 6 weeks after planting (WAP). Insect pests were controlled using karate at 50ml per 20 litres of water.

3.2.1 Data Collection and Analysis:

From the 18 inner competitive plant stands per row plot, agronomic data were collected on twenty-seven characters on each of the thirty-one genotypes .The observations covered qualitative and quantitative characters. Some of the qualitative characters were determined visually (Feel / touch) while the quantitative characters were determined by measurement / by counting as presented in Table 2.

Table 1 **Origin/ Source of Cowpea Genotypes**

Number	Genotypes	Origin/ Source	Morphological Characteristics
1	LDPD	Kaduna North Western Nigeria	Erect
2	TVx-3236	Ogun State, South Western Nigeria	Erect
3	Danilla (Dan)	Kaduna North Western Nigeria	Erect
4	Owode	Ogun State, South Western Nigeria	Erect
5	Ife brown (IFB)	Oyo State South Western Nigeria	Erect
6	IT90k – 277-2	Oyo State South Western Nigeria	Erect
7	IT 95k – 1091-3	Oyo State South Western Nigeria	Erect
8	IT97k-508-2	Oyo State South Western Nigeria	Erect
9	IT95k—1090-12	Oyo State South Western Nigeria	Erect
10	IT 90k – 76	Oyo State South Western Nigeria	Erect
11	IT 97k-499-39	Oyo State South Western Nigeria	Erect
12	IT93k-686-2	Oyo State South Western Nigeria	Erect
13	IT97k- 1034-94	Oyo State South Western Nigeria	Erect
14	IT90k-59	Oyo State South Western Nigeria	Erect
15	AGRIB VI	Oyo State South Western Nigeria	Erect
16	KVX-745-119	Burkina-Faso (Northern)	Erect
17	KVX-745-11k	Burkina-Faso (Southern)	Erect
18	KVX-745-17k	Burkina-Faso Southern	Erect
19	KVX-414-22-72	Burkina-Faso(Eastern)	Erect
20	KVX-795-17P	Burkina-Faso North-West	Erect
21	IAR 48B	Kaduna, Zaria	Erect
22	Tvu 14912	Niger republic	Prostrate
23	Tvu 13096	Niger republic	Prostrate
24	Tvu10817	Cameroun South West Province	Semi-Erect
25	Tvu 10840	Cameroun, Eastern Province	Semi-Erect
26	Tvu 14345	Senegal	Erect
27	Tvu 14390	Senegal	Erect
28	Tvu13240	Benin republic	Erect
29	Tvu13241	Benin republic	Erect
30	Tvu12200	Ghana	Prostrate
31	Tvu 12201	Ghana	Prostrate

Table 2: Characters measured and methods of scoring / Measurement

S/No	Characters	Method of Measurement score	Rating scale qualitative character	Nature of character
1	Flower colour	Visual estimation	White =0. =1,purple = 1 yellow =3,	Qualitative
2	Stem pigmentation	Visual estimation	None=0,Node only= 1 All =2	Qualitative
3	Leaf shape	Visual estimation	Oblique=1, lanceolate=2has=3	Qualitative
4	Seed coat texture	Felt	Rough =1, smooth =2	Qualitative
5	Seed coat colour	Visual estimation	White=1, brown=2, milk =3 black=4, dark=5, red=6	Qualitative
6	Seed eye colour	Visual estimation	Black =0 brown=1, dark b =2 ,white =3	Qualitative
7	Greenness of leaf	Visual estimation	Green =1, dark green =2,	Qualitative
8	Leaf pubescence	Felt	Glaberoos = 1, medium =2	Qualitative
9	Fresh pod colour	Visual estimation	Green = 1, darkgreen =2,	Qualitative
10	Dry pod colour	Visual estimation	Brown=0, purple =1, purple + patches =2	Qualitative
11	Pod shape	Visual estimation	Straight =1, curved =2,	Qualitative
12	Days to 5% flower	Observed	-	Quantitative
13	Number of branch/ plant	Counted	-	Quantitative
14	Length of branch	Measured (cm)	-	Quantitative
15	Number of peduncle per plant	Counted	-	Quantitative
16	Number of pods per peduncle	Counted	-	Quantitative
17	Number of pods per plant	Counted	-	Quantitative
18	Pod length	Measured (cm)	-	Quantitative
19	Peduncle length	Measured (cm)	-	Quantitative
20	Days to 95% maturity	Observed	-	Quantitative
21	Height at flowering	Measured (cm)	From base to tip	Quantitative
22	Number of seeds per pod	Counted	-	Quantitative
23	100-seed weigh	Weighed (g)	-	Quantitative
24	Leaf width	Measured (cm)	-	Quantitative
25	Height at maturity	Measured (cm)	-	Quantitative
26	Pod width	Measured (cm)	-	Quantitative
27	Length of internode	Measured (cm)	-	Quantitative

Source: IITA Cowpea descriptor 1976.

The means were subjected to simple ANOVA and Covariance using the NTSYS Ver. 2.0 of Rohlf (2001). Following the ANOVA and covariance analysis of the means, the principal component (PC), Single linkage cluster and average cluster and canonical correlation analyses were performed with the NTSYS package at the Biometrics unit of the International Institute of Tropical Agriculture (11TA) Ibadan.

3.3 GXE interaction, and stability and adaptability studies:

Two locations comprising of Ogbomoso and Abeokuta two different agro-ecological zones were used. Guinea savannah agro-ecology (location 1), and humid savannah agro-ecology (location 2). The humid savannah of Abeokuta is actually a transition between humid and dry savannah. This study was carried out over a two- year period (1999-2001) with two planting seasons in each year to give a total of four planting seasons. In each season at each location, land preparation was done by ploughing and harrowing. A total of twenty genotypes selected from the thirty one accessions were planted out in a Randomized Complete Block design with three replications. Each plot size was 2.7 x 2.4m and spaced 60cm between plots and 45cm within plots. Three seeds were sown per hole and later thinned to two plants stands at 2WAP to give a total of 70 plant stands per plot. After seed sowing, a mixture of Galex; and Gramozone (50:50ml) was sprayed to control pre and post emergent weeds. This was later followed by manual weeding as at when due. Field pests were controlled using karate at 50ml to 20 litres of water.

3.3.1 Data collection and Analysis:

In each location for each planting season, agronomic and yield data were collected on each of the three inner competitive rows on plot basis as described by Gomez and Gomez (1984) and Wahua (2000); observations were made on the following characters:

Days to 50%flowering

Number of branches per plant

Number of peduncles per plant

Number of pod per peduncle

Length of peduncle

Length of pod

Days to 95% maturity

Number of seeds per pod

100-seed weight (g)

Seed yield (t/ha)

Seed yield was estimated from the weight of the threshed seeds. Plot means for each character and yield were subjected to analysis of variance using SAS 2000 package. Stability variance was calculated for the characters of each genotype as outlined by Shukla (1972) from the following equation:

$$\delta_i^2 = \frac{P}{(p-2)(q-1)} \sum_{j=1} \delta (X_{ij} - X_{i.} X_{.j} + x...)^2 \quad — \quad \frac{SSGXE}{(P-1)(P-2)(Q-1)}$$

Where:

Xij = Mean of genotypes in i^{th} and j^{th} environments.

X^{u}_{I} = Mean of genotypes in i^{th} environment

Xj = Mean of genotypes in j^{th} environment

X...= Overall mean of the genotypes in all environments

SS_{GXE} = Sum of square due to GXE interaction

P= Number of genotypes

q= Number of environments

Genotypes with significant δi^2 were adjudged unstable. This stability parameter is considered to be an efficient means for determining contribution of each genotype to GXE interaction (Kang 1988, Kang and Miller, 1994).

This stability variance was integrated with yield to obtain the modified rank sum value of each genotype. According to Kang (1991), Shukla's (1972) stability variance parameters (δi^2) were assigned a rating of 0 where δi^2 was not significant and 4 where δi^2 was significant at 5% level and 8 where δi^2 was significant at 1% level. This rating is added to the yield rank of a genotype, and selection is based on the sum.

Genotypes with the lowest sums are selected. The δi^2 statistics was calculated using Kang's (1991) basic programme. Yield data were also subjected to Additive Main effect ad Multiplicative Interaction (AMMI) analysis using the MATMODEL Version 2-0 (Gauch and Zobel 1996), the AMMI model linear equation is as follows:

$$Yger = \mu + {}_{g} + \beta_e + \Sigma_n \lambda_n Y_{gn} \delta_{en} + \ell_{ge} + E_{ger}$$

Where:

Yger = the yield of genotype (g) in environment e for replicate r,

μ = Grand mean.

g = Mean deviation of the genotype (g) (genotype mean minus grand mean).

β_e= Mean deviation of the environment mean e.

Σ_n = The singular value for IPCA axis n,

Y_{gn} = the genotype (g) eigenvector value for IPCA axis n,

δ_{en} = the environment e eigenvector value for IPCA axis n.

δ_{en} = the Residual and

E_{ger} = the error.

This AMMI model integrate and subsumes several statistical models usually applied to yield trial data including the additive (ANOVA), the multiplicative term known as the PCA and Finlay and Wilkinson regression models (Zobel et al., 1988). The expectation of the genotype x environment mean squares E(GxEMS) was calculated as a linear combination of two parameters following the methods of Mclaren and Chaudhary (1994). Thus,

$$[\ E(G \times EMS) = \delta^2_e + \delta^2_{p/r}\ ]$$

Where:

δ^2_e = Error/environmental variance

$\delta^2_{p/r}$ = Pooled error Mean square divided by number of replicates ;in each environment.

The bi-plot of the AMMI was obtained from the graphical ordination of mean grain yield and the first and second interaction principal component (IPCA I). This bi-plot illustrate the response of the genotypes to environment or location indices as well as their interactions which consequently results in adoption to specific agro-ecologies (Gauch, 1993). Genotypes and environments with large PCA scores positive or negative have high interaction, while genotypes and environments with small PCA scores (near zero) are considered to have small interactions with stable performance.

3.4 Character variation, correlation and heritability:

Yield and yield component data collected were subjected to analysis of variance and covariance using the method of Falconer (1989) and Singh and Chaudhary (1999). The mean squares obtained from the variance and covariance matrices were used to obtain the phenotypic, genotypic and environmental correlations as follows:

$$Rg = \frac{Cov\ gxy}{\sqrt{\delta^2 g \times \delta^2 gy}}$$

$$Rp = \frac{Cov\ Pxy}{\sqrt{\delta^2 px * \delta^2 py}}$$

Where:

Cov gxy is the genotypic covariance of characters x and y and

δ^2 gx and δ^2 gy = Genotypic variance of characters x and y.

Cov pxy is the phenotypic covariance of characters x and y and

δ^2 px and δ^2 py = phenotypic variance of characters x and y.

Environmental correlations were calculated as follows:

$$Rp = \delta Hx\ Hy\ r_A + e_x\ e_y\ r_E$$

Where:

Rp = Phenotypic correlation between two characters

H = broad sense heritability of the characters

r_A = genotypic correlation between two characters

$e = (1 - H)^{1/2}$

rE = environmental correlation between two characters.

A path analysis was carried out to determine the direct and indirect effects of some characters on yield using the procedure outlined by Dewey and Lu (1959).

3.5 Generation Mean Analysis:

This experiment was carried out in two phases. Phase I was conducted to produce the FI generation in a green house at IITA, Ibadan in 2000 and 2001 .The second phase was carried out at the Teaching and Research Farm of LAUTECH, Ogbomoso during the second planting season (August 2000), to produce F_2 and backcross generations. Two phenotypically contrasting genotypes were used as parents, Danilla and Ife- brown. Danilla is late maturing, white seeded, long branches and peduncles below the plant canopy. Ife-brown is early maturing brown seeded, short branches with peduncles carrying pods above the plant canopy. Crosses between Danilla (P_1) and Ife-brown parent (P_2), were made in March 2000, at a green house at IITA Ibadan. The parental plants were grown in 24 of 12 cm plastic pots. At the on set of flowering, ready to open staminate flowers of the male parents (P_1), were removed from the inflorescence at the early morning of the day. Simultaneously the female flowers of the female parent (P_2) that opened the same day were identified. The pollen grains of the P_1 were carefully dusted on the stigma of the female flower (P_2) to produce F_1. After maturity, the F_1 progeny seeds were harvested and replanted alongside with the parental genotypes. The same pollination procedure was used and the F_1 seeds crossed to P_1 and P_2 to produce backcross to better parent (Bc_1) and backcross to the other parent (Bc_2). The F_1 seeds were also planted out in the green house to raise the F_2 seeds. In the late planting season of August 2001, the parent lines, F_1 , F_2, Bc_1 and Bc_2 seeds were sown. Each of the P_1, P_2, F_1, Bc_1 and Bc_2

genotypes were planted out in a 4- single-row-plots of 6m long. The F_2 generation was planted out in 15 single row plots. All the families were arranged in a Randomized Complete Block design with three replications. The spacing was 60cm between rows and 45 cm within rows; field pests ware controlled using karate at 50ml per 20 litres of water. Weeding was done manually when necessary. The P_1, P_2,, F_1, Bc_1 and Bc_2 were each planted to a total of 60 plant stands. While the F_2 family gave a total of 225 plant stands. Data were collected from 60 plants for P_1, P_2, F_1, F_2, Bc_1 and Bc_2 but 210 plants were observed for the F_2 generation.

3.5.1 Data Collection and Analysis:

Data from each family were collected on days to 50% flowering, number of branch per plant, number of peduncles per plant, length of peduncle number of pods per plant, number of seeds per pod, 100-seed weight and days to 95% maturity. The means of the generations were used to estimate mid- parent mean (M), additive (d) and dominance (h) gene effects following the joint- scaling test of Marther and Jinks, (1982); Cavalli, (1952), using weighted least squares.

3.6 Response to early-generation selection studies:

Two crosses of true breeding cowpea genotypes were generated by using Ife- brown as a common parent in crosses involving Danilla and IAR48w. The phenotypes of the three parents are different. Ife –brown has brown seed coat, Danilla and IAR 48w have white

seeds. The crosses were made in a green house at IITA using same pollination procedure as earlier described (experiment 3.5). The Ife-brown x Danilla (F_1) and Ife-brown x IAR 48w (F_1) were grown to produce the F_2 in the early planting season of March 2001. In the 2001 late planting season, the F_2 seeds from each cross were planted in a 6mx3m plot with three replications. Three seeds were sown per hole and later thinned to two plant stands. The spacing was 60cm between rows and 45cm within rows to give 14 plant stands per row and a total of 140 plant stands per plot. Ife-brown was planted to one plot to serve as a check. The seeds of the F_2 from each of the two crosses were grown to generate the F_3. The F_3 seeds were planted out in the early planting season of 2002, using Randomized Complete Block design with three replications. Each plot was with 60 cm inter and 45cm intra -row spacing. The total plant stands per plot was 140. In the early season of 2003, a total of 120 plants seeded as F_4 plants from the F_3 progeny. Plot size and seeding rate were the same as the previous seasons.

3.6.1 Data collection and analysis:

From the three inner competitive rows of each plot in each generation. Observations were made on the following:

Days to 50% flowering,

Number of branches per plant,

Number of peduncles per plant,

Number of pods per plant,

Number of pods per peduncle,

Length of peduncle,

Length of pod,

100-seed weight,

Number of seeds per pod,

Days to 95% maturity and

Seed yield (g/plant).

Data on each trait in each generation were collected using a divergent (high and low value select ion) approach. In this approach twenty plant stands, were selected in each plot from each generation. Performance of each generation was determined by selecting from the 20 plants (10 best highest performing plants and 10 least performing plants). The traits are scored as high and low for each generation. Simple ANOVA was used to calculate the percentage high to low values for the selected traits in each family.

Two systems of response to selection were developed

1. Selection in F_2 plant with response to F_3
2. Selection in F_3 plant with response to F_4.

From the data, a realized heritability estimate was calculated for each trait in each generation following the method of Sneep (1997) and Falconer (1981). Realized habitability (RH) was calculated as:

$$RH = [(H_{t+1} - L_{t+1})/_{TH+1} \Big/ [(H_t - L_t)/_{TH})$$

Where;

H=mean value of the selected high group for a trait

L=Mean value of the selected low group for a trait.

T= The generation in which selection occurred

TH= The subsequent generation in which the response was measured.

CHAPTER FOUR

4.0 RESULTS

4.1 Means, ranges and analysis of variance:

From the data collected, the following results were obtained:

The means, ranges, mean squares and coefficient of variation of twenty-seven characters measured for the thirty-one cowpea genotypes are presented in Table 3. There were significant differences among the characters except for greenness of leaf, days to 95% maturity, 100-seed weight, pod width and fresh pod colour. The coefficient of variation (CV) values ranged from 10.42% for days to maturity to 178.17% for flower colour. Very high CV was observed for coloration in the stem, flower, fresh pod and seed coat. But the quantitative characters showed very low to moderate variability. Heights at flower and maturity, however, recorded above average variability of 70.82% and 56.08% respectively. 100-seed weight had 20.25%, number of seeds per pod had 27.14, seed coat texture had 34.69% and seed coat colour gave 71. 77%.

4.2 Principal Component Analysis (PCA):

The eigen values, total and cumulative variations of six principal component axes are presented in Table 4. Only five of the 27 principal components had eigen values greater than 2.00. The first three component axes had eigen values 4.73, 3.10 and 2.78 respectively and altogether accounted for 40.78% of the total variation and each succeeding component accounted for progressively smaller variations. The first five principal components jointly explained about 57.28% of total variations and are therefore seen as important in describing the 31 genotypes.

Table 3: Means, Range, Mean Square (MS) and Coefficient of Variation (cv) of Characters from 31 Cowpea Genotypes.

Serial no	Character	Mean	Range	MS	CV%
1	Flower Colour	1.54	0.00-4.00	42.19**	178.17
2	Stem Pigmentation	0.71	0.00-2.00	1.01*	97.18
3	Leaf Shape	2.36	1.00-3.00	4.27*	30.12
4	Seed Coat Texture	1.23	1.00-2.00	2.39*	34.69
5	Seed Coat Colour	2.16	1.00-6.00	8.57**	71.77
6	Seed Eye Colour	1.87	0.00-3.00	2.11**	45.24
7	Greenness of Leaf	1.22	1.00-2.00	0.97*	34.69
8	Leaf Pubescence	1.23	1.00-2.00	1.07*	34.72
9	Pod Shape	1.42	1.00-2.00	0.98*	35.31
10	Days to 50% Flower	47.87	37.50-63.42	29.25*	14.31
11	Number of Branch	4.74	3.00-9.00	48.39**	30.29
12	Length of Branch (cm)	117.23	22.00-245.00	49.41**	61.71
13	Number of Peduncle/Plant	1.66	0.00-2.80	1.33*	41.03
14	Number of Pods/ Plant	25.88	9.00-97.00	114.37**	53.97
15	Pod Length (cm)	12.55	8.00-19.00	6.48*	19.61
16	Length of Peduncle	23.87	7.00 -36.00	9.61**	31.01
17	Days to 95% Maturity	67.71	56.00 -84.00	0.22	10.42
18	Height at Flower (cm)	84.36	29.00 -225.00	278.09**	70.82
19	Number of Seeds/Pod	10.34	6.00 -16.00	6.01*	27.14
20	100-Seed weight	15.32	11.00 -22.00	2.31*	20.25
21	Leaf Width	6.69	3.40 -10.00	1.93*	21.56
22	Height at Maturity (cm)	99.52	26.60 – 43.00	201.77**	56.08
23	Pod Width	0.57	033-0.70	0.83*	18.95
24	Internodes Length (cm)	5.55	3.00-9.20	7.21**	27.79
25	Fresh Pod Colour	1.42	1.00-2.00	16.22*	35.35
26	Dry Pod Colour	0.71	0.00-5.00	3.19*	96.46

*, ** = Significant F- test at $P \leq 0.05, 0.01$ respectively.

Recheck table for correction.

Table 4. **Eigen value, percentage total variation of the first six component axes of the ordination of the 31 cowpea genotypes**

Principal Component	Eigen Value	Variation accounted for (%)	Cumulative Percentage (%)
1	4.73	18.17	18.17
2	3.10	11.93	30.10
3	2.78	10.68	40.78
4	2.28	8.62	49.39
5	2.05	7.89	57.28
6	1.64	6.33	63.62

The scores of the major characters describing the first three principal axes are presented in Table 5. The first axis was mainly loaded by plant heights at both flowering and maturity. Only quantitative characters of mainly pre- harvest vegetative growth phase are located on axis one. The second principal component was found to be loaded by pod and seed characteristics particularly number of seeds per pod. The third principal component comprised mainly of days to flowering and maturity. The major characters in the three axes are height at flower and maturity (0.35,0.34); number of seeds per pod (0.42), fresh and dry pod colour (0.36,0.34) and leaf width (o.31).

The configuration of the thirty –one cowpea genotypes along the first three principal component axes are illustrated in Figs 1,2 and 3. The ordination showed genotype Tvu 14345 (22),Tvu 14390 (25),Tvu 13096 (26) and Tvu 12201 (28) from Niger Republic, Cameroun, Senegal, and Benin Republic respectively to be most distinct from the other genotypes in Fig 1. KVX-745-119 (26) and Tvu 1221(30), from Burkina-Faso and Ghana respectively, were however most distinct genotype in Figs 2 and 3.

4.3 Cluster Analysis:

The dendogram drawn from the Single Linkage Cluster (SLCA) Analysis is shown in Fig 4. All the accessions were distinct from each other at 100% level of similarity while at 84.0% level, all the accessions had formed a single cluster. LDPD (accession 1) from Nigeria was different from the others above 97% level of similarity.IT90K-1091-3 (accession 7),and IT90K-508-2 (accession 8),were most similar to each other. At 97% level of similarity, accessions 7,8,15,21 and 27 fom Nigeria and Senegal had joined together. While at 84% similarity level, accessions 13 and 30 from Niger and Ghana had joined the 29 accessions to form a single cluster. On the contrary, the average cluster

analysis (UPGMA), (fig 5) revealed all the accessions to have formed an average cluster at 80% level of similarity while at 89.9%level, 29 accessions had joined to form an average cluster even as the remaining 3 accessions from Nigeria, Senegal and Ghana had also formed an average cluster. These two average clusters joined at 80% similarity level.

Table 5 Eigen Vector of major traits of the first principal components used in ordination

Axis1		Axis 2		Axis 3	
Character	Score	Character	Score	Character	Score
No. of branches/plant	0.25	Seed Coat colour	0.30	Leaf Pubescence	-0.33
No.of peduncles/Plant	0.25	Number Seed/pod	0.42	Days to 50% flower	- 0.48
Length of Peduncle	0.26	Pod width	– 0.26	Length of branch	- 0.28
Height at flowering	0.35	Fresh pod colour	0.36	Days to maturity	- 0.47
Height of maturity	0.34	Dry pod colour	0.34	Leaf width	0.31

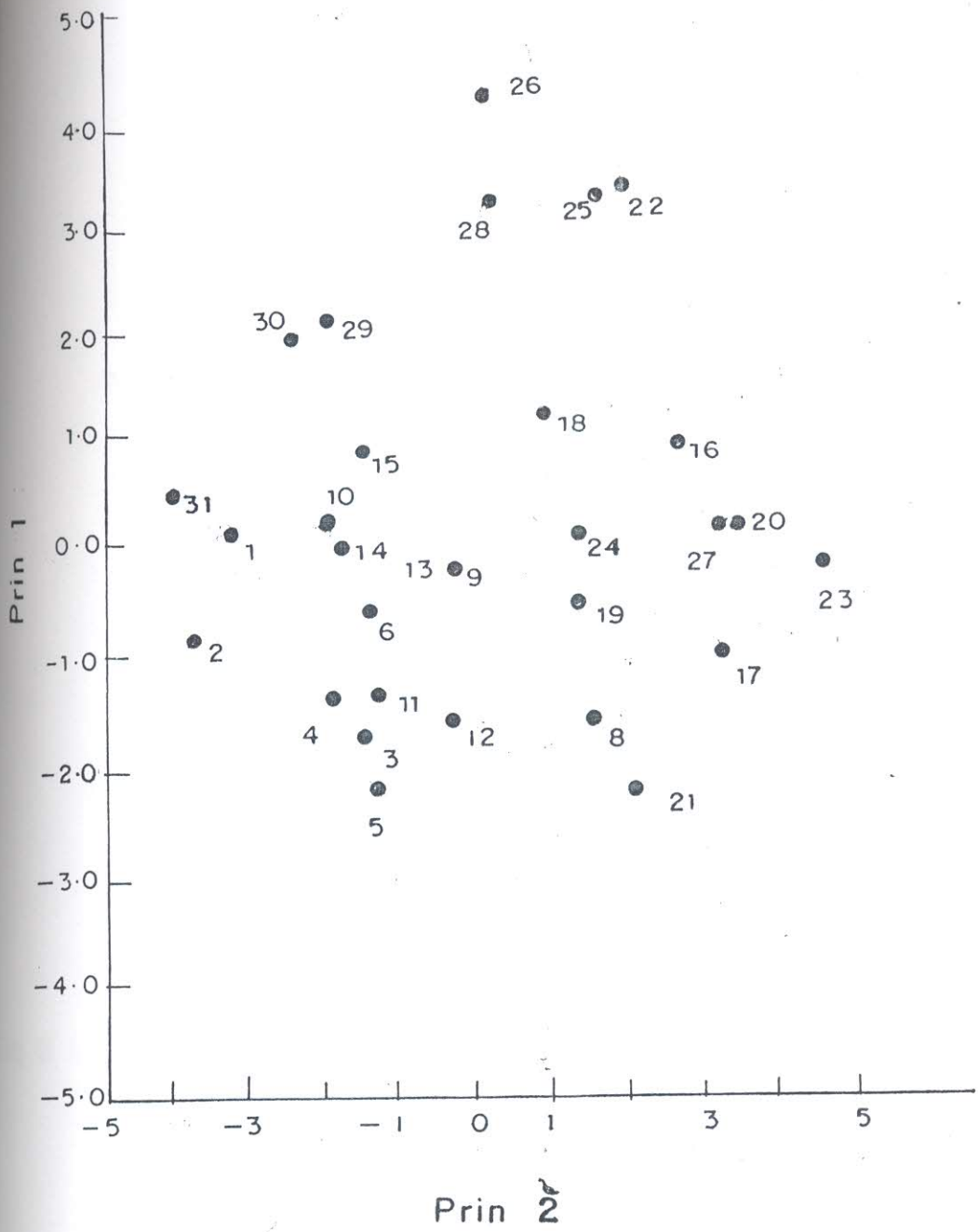

Fig. 1 ; Configuration of the 31 cowpea genotypes under Principal Component Axes 1 and 2 .

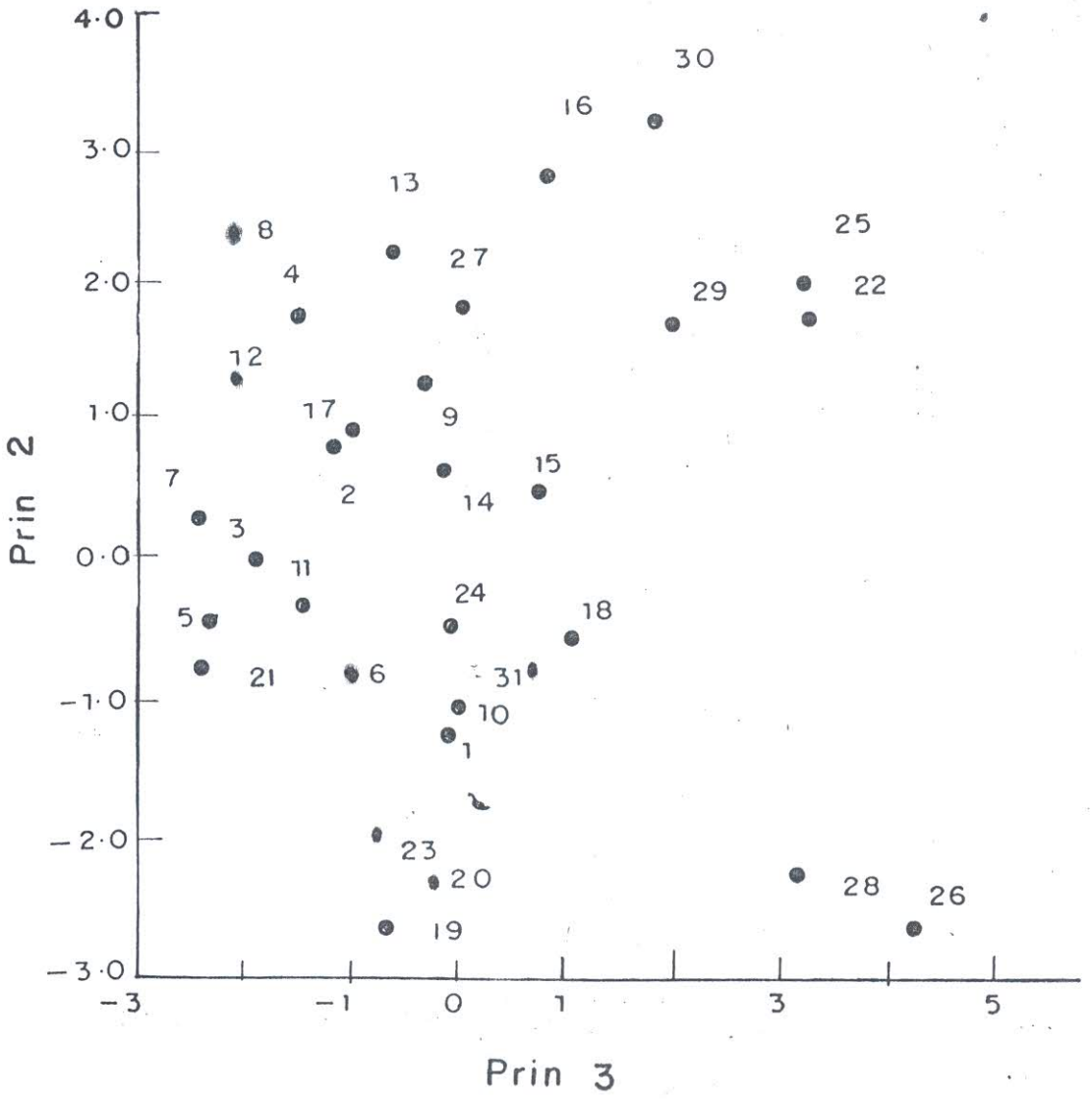

Fig.2 : Configuration of the 31 cowpea genotypes under principal Component Axis 2 and 3

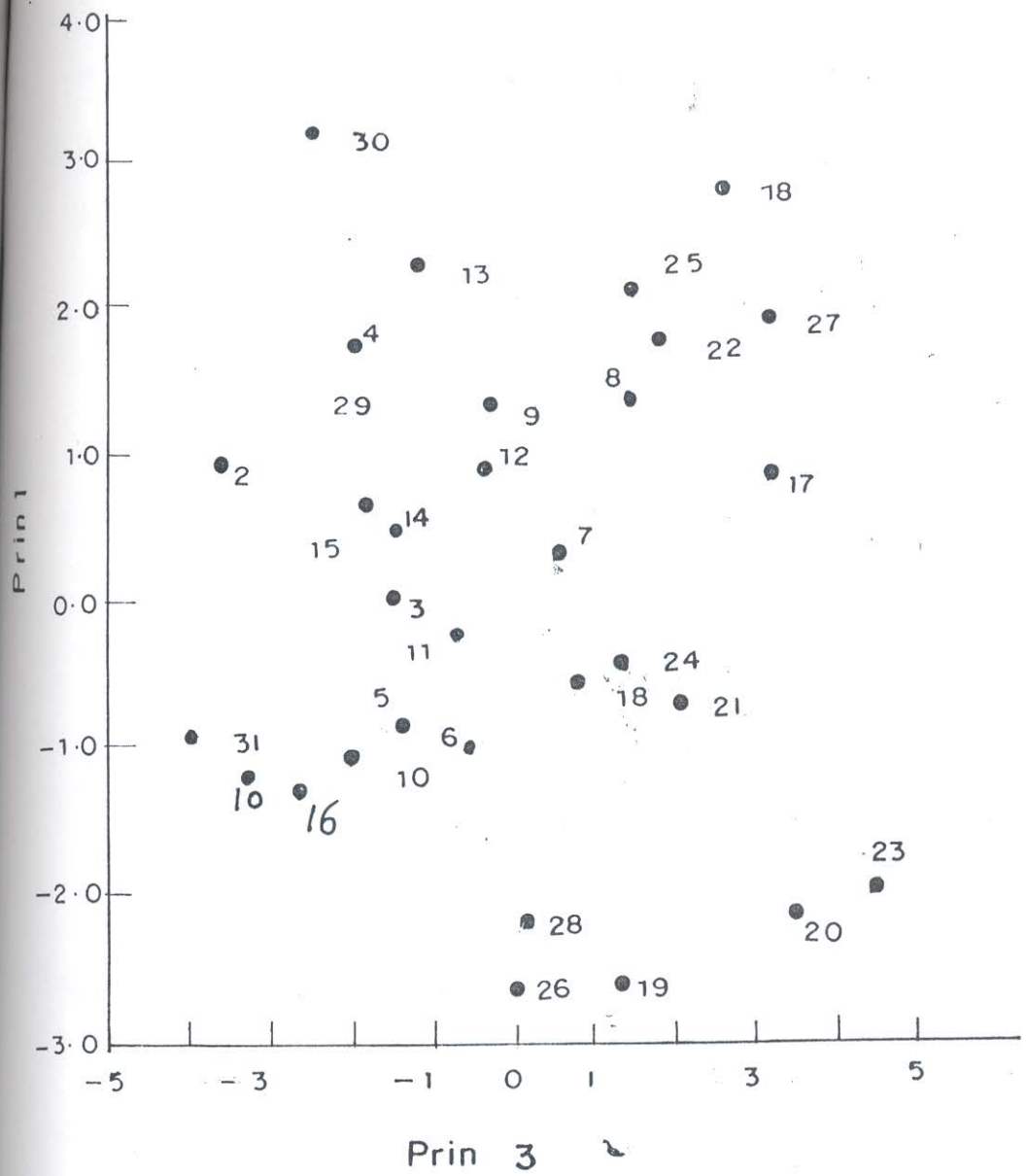

Fig.3: Configuration of the 31 cowpea genotypes under principal Component Axis 1 and 3

The accessions were sorted into six distinct clusters by FASTCLUS procedure of SAS 2.0 (Table 6). Clusters 1, 11, 1V and V contained three, two, five and one accessions respectively. While clusters III and VI contained twelve and eight accessions respectively. Accessions in group I exhibited the longest branches. This was followed by accessions in Group II and VI. The shortest branch was recorded for accessions in group III. The accessions in clusters I, III, IV and V had 4 branches while accessions in clusters 11 and 1V produced on the average, six branches each. The pod and peduncle number were highest for accessions in group 1 followed by accessions in group III. Accessions in group II were earliest to flower and maturity followed by accessions in cluster I. Accessions in group VI recorded the highest number of days to maturity.

4.4 Canonical Analysis:

The eigen values, variances, and the correlations between original variables and the canonical variables are presented in Table 7. The first three canonical variables had eigen values greater than 2.0 and accounted for 28.37, 20.4 and 11.19% of the total variances respectively. The first four variables captured about 69.32% of the total variation. Seed coat (0.54) was the most important character in the first canonical axis. Branching traits were most important in the second axis while branch length and flowering date were most important in describing the variations in the fourth and fifth canonical axes.

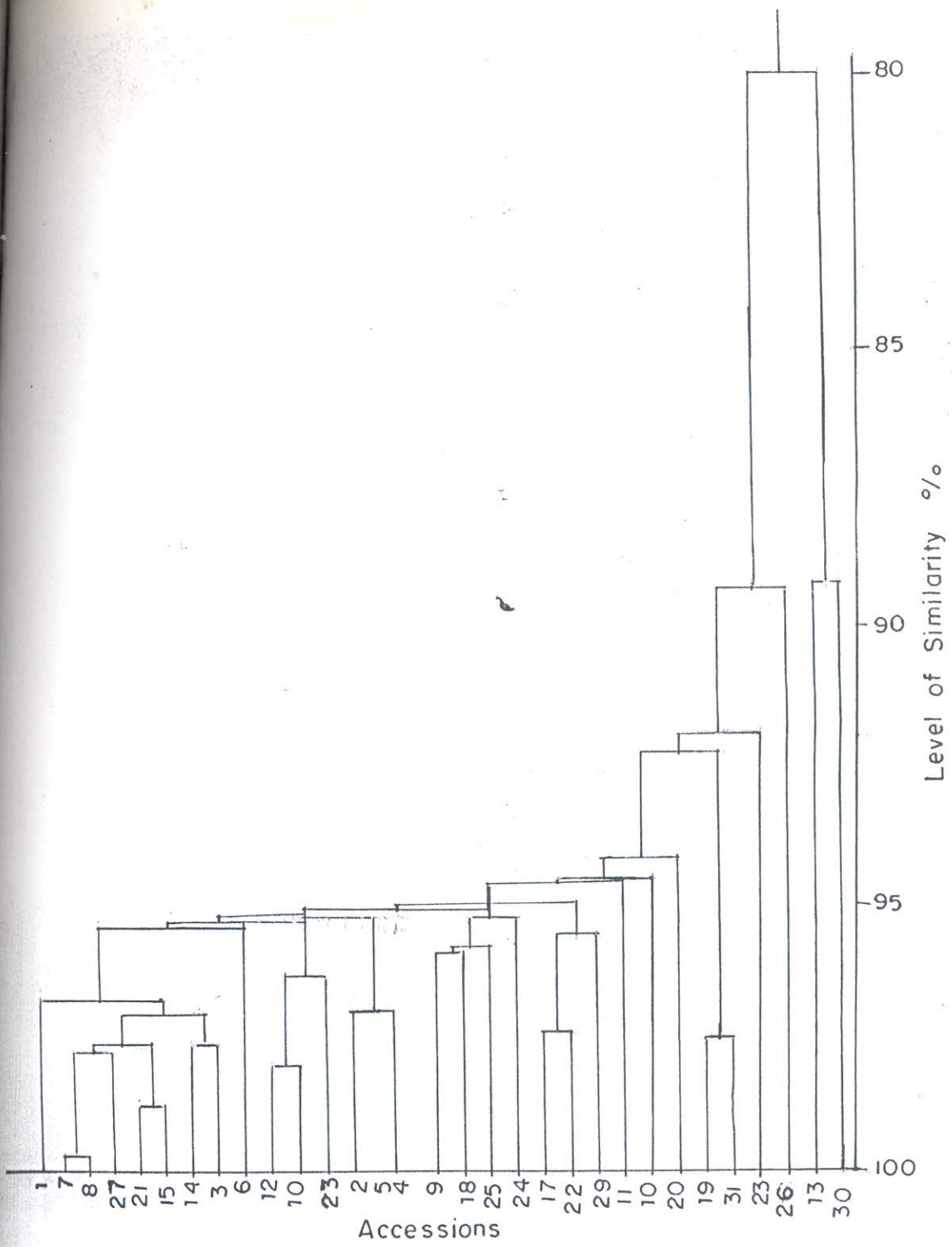

Fig.4 : Dendrogram from the single Linkage Cluster Analysis (SLCA) of the 31 cowpea genotypes .

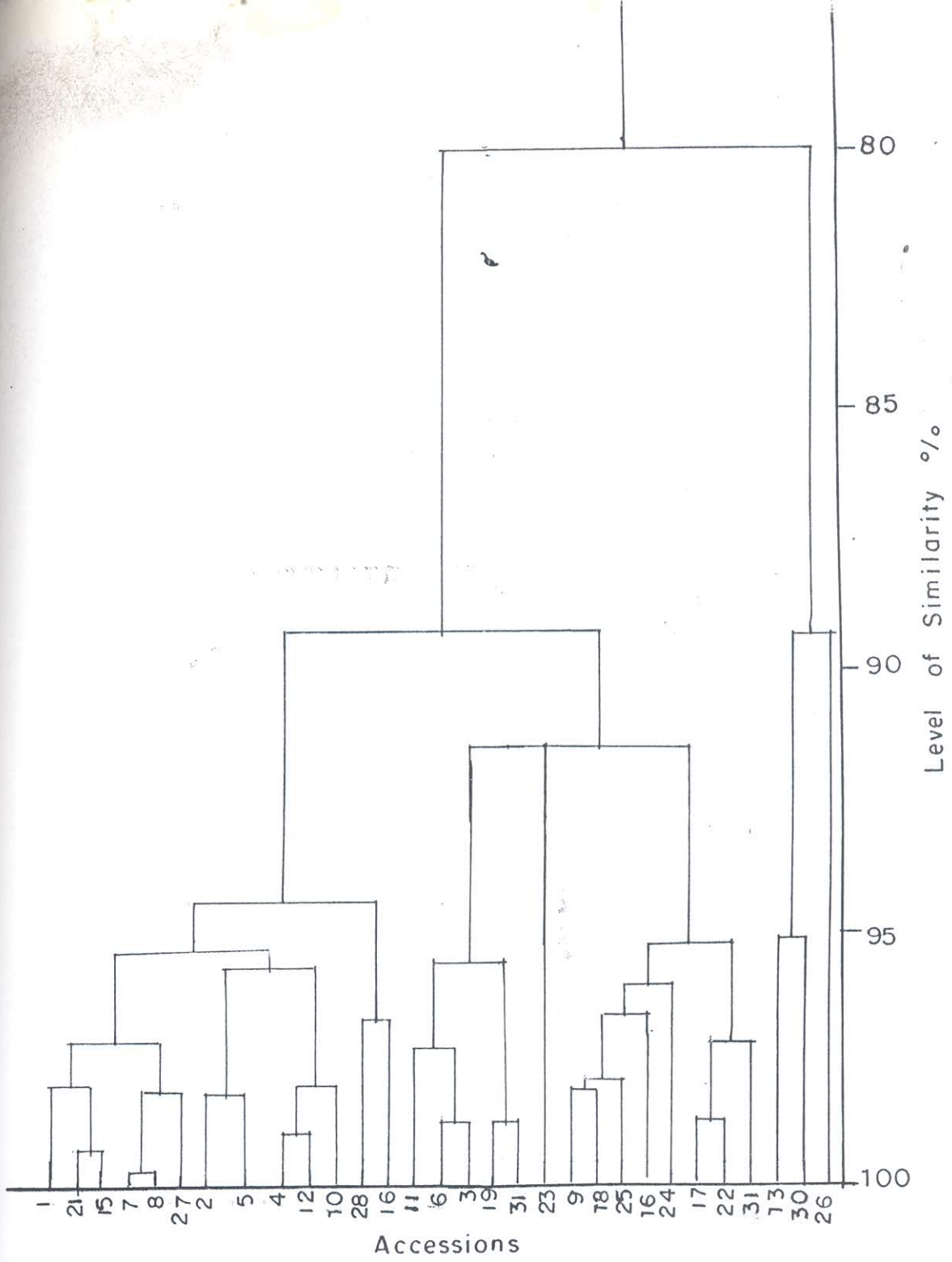

Fig.5 : Average Cluster Analysis (UPGMA) of the 31 cowpea genotypes

Table6: Mean, coefficient of variation (CV) and the components (in brackets) of six clusters with major characteristic patterns of 31 cowpea genotypes by FASTCLUS procedure.

Character	Clusters						Grand Mean
	1	11	111	1V	V	Vl	
			1,2,3,9,10,12	4,5,6,11,13	22	7,8,16,17	
	18,26,28	20,23	14,15,25,29,30,31			19,21,24,27	
Length of Branch	217.61(27.0)	173(34)	57(10.3)	135.6(43.4)	84(7.0)	148.5(39.2)	13.85(43.3)
Number of Branch	4(35)	6(23)	4(34)	4(35)	4(35)	6(22)	4.7(4.5)
Days to 50% flower	44(15.6)	42(16.3)	47.4(14.5)	45(15)	53(13.1)	52.6(13.0)	40.3(14.6)
Pod length	12.3(.20.0)	12.5(19)	12.7(19.4)	14.2(17.3)	16(15.4)	11(22)	13.1(18.9)
Weight at Maturity	74(75.4)	261(21.4)	69.7(80.0)	66.6(83.4)	186(30.0)	112(49.8)	128(56.7)
No. of peduncles/plt	2.1(30.1)	2(28.3)	1.9(35.7)	1.8(37)	2(34)	0.8(85)	1.8(41.7)
No. pods/plant	48.7(39.8)	29(66.7)	47.3(41)	23.8(81)	35(55)	21.5(90)	34(62.3)
Height at flowering	4.57(1101)	222(23.1)	56.5(90.8)	59(87.0)	180(28.5)	110.1(46.7)	112.2(62.9)
Internode length	5.9(26.1)	3.8(40.5)	5.0(25.7)	3.6(42.8)	7.1(21.6)	5.1(30.2)	5.2(29.6)
Days to 95% maturity	65.7(10.7)	62(11.3)	67(10.5)	65.2(10.8)	68(10.4)	72.3(9.7)	66.7(10.6)

Table 7 **Eigen values, total variance, cumulative Variance and Correlation between original and Canonical variables in 27 characters measured on 31 cowpea genotypes**

Canonical Variables	Eigen Value	Total Variance	% Cumm.	Correlation of Canonical Variable With				
1	4.71	28.32	28.37	Seed coat texture(0.6)	Seed coat colour (0.54)	Greenness of leaf (0.46)	Length of branch (0.48)	Number of seeds per pod (0.51)
2	3.12	20.41	48.78	Seed eye colour (0.39)	Number of branch (0.43)	Length of branch (0.61)	Pod length (–0.31)	Length of peduncle (– 0.29)
3	2.07	11.19	58.97	Seed coat colour (-0.55)	Seed eye colour (0.45)	Number of branch (0.36)	Number of peduncles/plant (- 0.39)	Number of pods/plant (– 0.55)
4	1.62	10.35	69.32	Leaf Pubescence (0.34)	Length of branch (0.42)	Height of flower (– 0.37)	Number of seeds (0.28)	Height at maturity (– 0.37)
5	1.03	9.02	78.34	Days to 50% flower (0.39)	Pod length (–0.41)	Days to maturity (0.33)	Internode length (0.25)	Leaf width (0.27)

4.5 Discriminant Analysis:

The first two discriminant variables accounted for 57.53% of the total variation (Table 8). The remaining three eigen values were low and had a total variation of 37.87%. The first discriminant function with 36.31% variation was negatively correlated with 100-seed weight (-0.32) but positively correlated with pod width (0.30), stem pigmentation (0.40) and flower colour (0.44).The second function is largely correlated with seed coat colour and number of branches per plant while the third discriminant function related much with seed eye colour and number of peduncles per plant. No character was particularly prominent in the fourth canonical function but canonical variable five correlated largely with fresh pod colour. The plot of the centroids of the 31 accessions along the first and second canonical vectors are represented in fig. 6. The two axes captured 48.78% of the total variations among the accessions. AGRIB VI (accession 15) and KVx -795-17p (accession 20) each from Nigeria and Burkina Faso North West were the most separated.However, some of the accessions were not separated. For example, accessions 25,29,30 and 31 from Burkina Faso, Cameroun and Ghana were not separated. The canonical correlations analysis and the discriminant analysis identified similar characters to be important although few discrepancies were found in that while canonical function was negatively correlated with pod length. Discriminant analysis was positively correlated with pod length. Also, peduncle length was negatively correlated with third canonical function and positively correlated with third discriminant function.

Table 8 Eigen value total variance; cumulative variance and pooled within- group correlations between discriminant variables and the canonical discriminant functions.

Discriminant Canonical	Eigen Value	Total Variance Cumulative %		Pooled within-group correlation with				
1	19.23	36.31	36.31	100 seed weight (– 0.32)	Dry pod colour (.0.27)	Stem pigmentation (0.40)	Flower colour (0.44)	Pod width (0.30)
2	12.19	21.22	57.53	Seed coat colour (0.84)	Leaf pubescence (0.38)	Number of branch (0.89)	Number of pods peduncle (0.50)	Pod length (0.54)
3	9.73	17.03	74.56	Seed coat texture (0.21)	Seed eye colour (0.67)	Days to 50% flower (0.48)	Length of branch/plant (0.56)	Number of peduncles/ plant (0.81)
4	5.32	11.79	86.35	Leaf shape (0.19)	Greenness of leaf (0.35)	Pod shape (0.14)	Days to maturity (0.23)	Height at flowering (– 0.24)
5	2.17	9.05	95.40	Seed coat colour (-0.28)	Pod shape (– 0.36)	Leaf width (0.14)	Pod width (0.26)	Fresh pod colour (0.98)

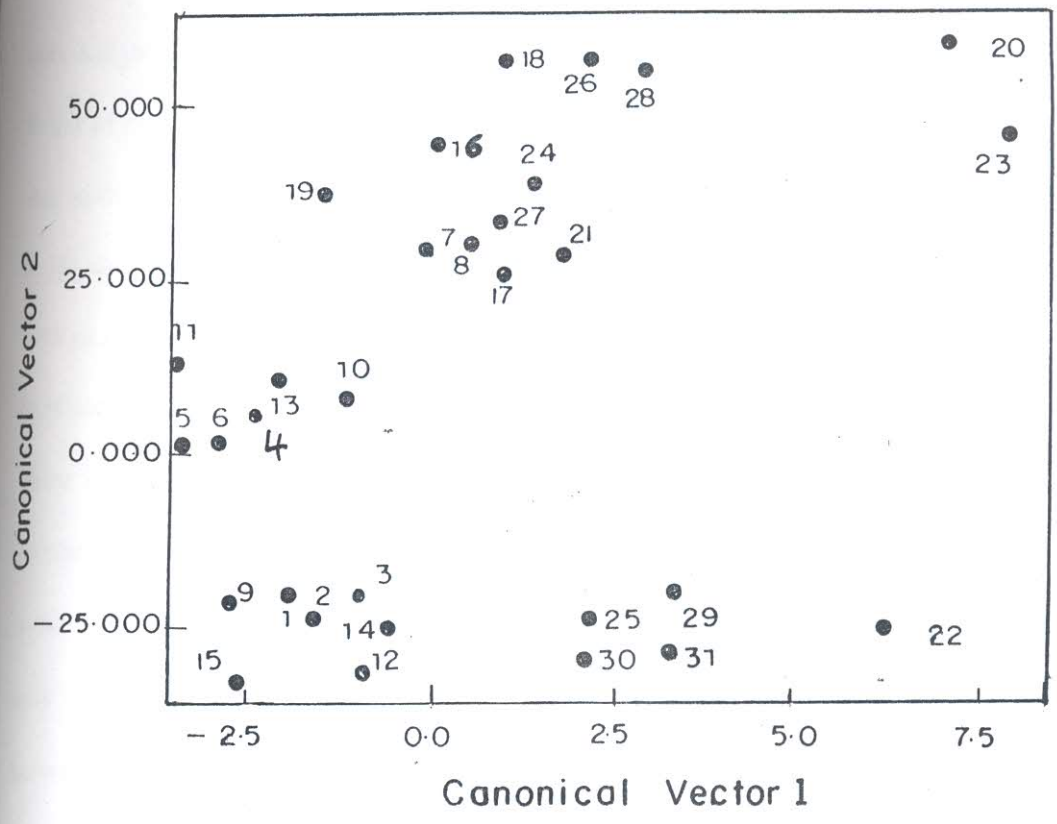

Fig. 6 ; Ordination of the centroids of the 31 cowpea genotypes on discriminant canonical vectors 1 and 2

4.6 Character Correlation Studies:

The phenotypic correlation coefficients between eleven cowpea characters and seed yield in two locations are presented in Table 9. Days to flower significantly and positively correlated with branch number(0.44;0.34), peduncle length (0.55;0.57), pod-length (0.56;0.39), days to maturity (0.60;0.64) and seed number(0.49;0.41). In the two locations it correlated positively with seed yield (0.31) in the first location but negatively with 100-seed weight in the second location. Branch number was significantly correlated with length of peduncle (0.42; 0.49), maturity date (0.49; 0.32), seed number (0.37; 0.41) and seed yield (0.35, 0.36) in the two locations. whereas, the correlation with branch length (0.38) and pod length (0.38) was significant only in the second location. While peduncle number positively correlated with only days to maturity (0.31; 0.32) in both locations. It correlated (0.41) with number of pods per plant and seed yield only in the first location There was low and negative correlation (-0.41) between 100-seed weight and peduncle number. Whereas, number of pods per peduncle was positively correlated with seed yield in the locations, but the correlation with number of pods per plant (0.34),was significant only in the first location . Also, peduncle length showed significant positive correlation between branch length, maturity date, seed number and seed yield in the two locations. But the correlation with seed weight (-0.44) was negative only in the second location . Similarly, pod number only correlated positively with seed yield (0.84; 0.67) in both locations ; but had correlation with maturity date (0.33), in the first location. Branch length showed significant positive correlation with number of seeds per pod (0.53, 0.50) in both locations but had correlation with maturity dates (0.35) and seed yield (0.44) only in the first location 1only. But pod length showed negative correlation with seed weight (-0.46) in the first location and the correlation with seed yield (0.39) was positive

only in the first location also. Maturity date was positively correlated with seed number (0.50; 0.35) and seed yield (0.50; 0.36).Number of seeds per pod recorded positive and significant correlation (0.66;0.63) with seed yield in the two locations.

Table 9: Phenotypic Correlation Coefficient among twelve cowpea characters in two seasons

Character	Loc.	No. Of Branch/ Plant	No. of Peduncle/ Plant	No. of Pods/ Plant	Length of Peduncle.	No. of Pod/ Plant	Length Of Branch	Pod Length	Days to 95% Maturity	No. of seeds/ Pods	100 seed weight (g)	Seed yield Plant (g)
Days to 50% flower	1	0.44*	0.14	-0.15	0.55**	0.15	0.23	0.56**	0.60**	0.49**	-0.21	0.31*
	2	0.34*	0.18	0.08	0.57**	-0.16	0.29	0.39*	0.64**	0.41*	-0.36*	0.24
Number of branch/plant	1	-	0.2	0.19	0.42*	028	0.28	0.03	0.49**	0.37*	-0.23	0.35*
	2	-	0.17	0.24	0.49**	0.05	0.38*	0.38*	0.32*	0.41*	-0.28	0.36*
Number of peduncles/	1	-	-	0.03	0.21	0.43	0.21	-0.04	0.31*	0.23	-0.10	0.41*
Plant	2	-	-	0.21	0.32	0.23	-0.04	-0.10	0.32*	0.13	-0.41*	0.27
Number of	1	-	-	-	0.12	0.34*	0.12	0.06	0.15	0.21	0.06	0.36*
pods/peduncles	2	-	-	-	0.25	0.24	0.10	0.11	0.22	0.22	0.21	0.32*
Length of Peduncles	1	-	-	-	-	0.17	0.48**	0.16	0.61**	0.63**	-0.20	0.40*
	2	-	-	-	-	0.13	0.38*	0.24	0.55**	0.54**	-0.44*	0.52**
Number of	1	-	-	-	-	-	0.22	0.19	0.33*	0.23	-0.08	0.84**
	2	-	-	-	-	-	-0.09	-0.24	0.11	0.06	-0.07	0.67**
Pods/plants												
Length of branches	1	-	-	-	-	-	-	0.29	0.35*	0.53*	-0.22	0.44**
	2	-	-	-	-	-	-	0.42*	0.11	0.50**	-0.29	0.28
Pod length	1	-	-	-	-	-	-	-	0.19	0.43**	-0.46**	0.39*
	2	-	-	-	-	-	-	-	0.22	0.32*	0.17	0.09
Days to 95% maturity	1	-	-	-	-	-	-	-	-	0.50**	-0.22	0.50**
	2	-	-	-	-	-	-	-	-	0.35*	0.41	0.36*
Number of seeds/pods	1	-	-	-	-	-	-	-	-	-	-0.14	0.66*
	2	-	-	-	-	-	-	-	-	-	-0.29	0.63*
100 seed weight (g)	1	-	-	-	-	-	-	-	-	-	-	-0.09
	2	-	-	-	--	-	-	-	-	-	-	-0.21

1 *,* = Significant at 05 and 01% probability respectively = Location 1; 2 = Location 2

Genotypic correlation coefficients among the characters are presented in Table 10. Days to flower showed significant positive genotypic correlation with all the characters in both locations except with number of pods per peduncle (0.33) that was significant only in the second location .Branch number correlated positively with pod number per peduncle (0.31; 0.47), length of peduncle (0.82; 0.71),number of seeds per pod (0.61;0.64), length of branches (0.41; 0.21) and seed yield (0.36; 0.54) in both locations. But its correlation with pod length (-0.33; -0.61)was negative in both locations. Number of peduncles per plant recorded positive correlation with number of pods per peduncle (0.51; 0.71), length of peduncle per plant (0.52;0.53), number of seeds per pod (0.55;0.38),and seed yield (0.49;0.43) but had negative correlation with 100-seed weight (-0.44;-0.81) all in both locations. However, its correlation with pod length (-0.33) was negative in the first location. Pod number per peduncle had positive and significant correlation with branch length (0.56, 0.89) but negative correlation with seed yield (-0.74, -0. 85) in both locations. Correlation with pod length (0.82) and 100- seed weight (0.58), were positive and significant only in the first location. Meanwhile, its correlation with peduncle length (0.53), was positive and significant only in the second location. Similarly, Length of peduncle had positive correlation with number of pods per plant (0.33;0.39), length of branch (0.60;0.57) days to maturity (0.71;0.72), number of seeds per pod (0.79;0.85) and seed yield (0.51;0.88) but its correlation with 100-seed weight (-0.26; -0.66) was negative all in both locations. Pod numbers per peduncle recorded positive and significant genotypic correlation with pod length (0.25;0.39) and seed yield (0.84;-0.62) in both locations, although its correlation in the second location was negative while its correlation with maturity date (0.59) was positive and significant only in the first location. All the characters were significant and positively correlated with branch length, except its

correlation with seed weight (-0.52) that was negative but significant in the second location and its correlation with seed yield (-0.48) that was negative in the first location. Pod length correlated positively with seed number (0.63;0.63) in both locations, while its correlation with seed yield (0.70;-0.33) was positive in the first location and negative in the second location respectively. Also, its correlation with days to maturity (0.44) was positive in location 2,while its correlation with 100-seed weight was negative (-0.48) in the second location.

Number of seed per pod correlated negatively with seed weight (-0.31, -0.79), but its correlation with seed yield (0.85; 0.88) was positive and significant in the locations. But the correlation of seed weight with seed yield was negative (-0.69) in the second location. The environmental correlation coefficients among the characters are presented in Table 11. Days to flower correlated positively with most of the characters in the locations; its correlations with branch length (-0.93; -0.47) was negative in both locations and negative with peduncle number per plant (-0.41) in the second location. However, its correlation with number of pods per peduncle (0.33), was positive in location 2. Its association with seed yield (0.98) was positive in the first location.

Environmental correlation of branch number with the characters were significant and positive in both locations except its correlations with number of peduncle per plant (0.66) and number of pods per plant (0.53), that were positive only in location 1. Number of peduncles per plant correlated significantly with pods per peduncles (0.47; 0.81), length of peduncle (0.57; 0.70), pod length (0.49; 0.41), days to maturity (0.82; 0.30) and seed number (0.58; 0.67) in both locations; but its correlation with pod number (0.59), was significant only in location 1. Its correlation with seed yield (0.65), was significant only in location 2. Pods per peduncle, recorded significant and positive correlation with pods per

plant (0.43; 0.57), seed number (0.39; 0.52) 100-seed weight (0.92;0.79) and seed yield (0.33; 0.86) in both locations. Whereas, its correlation with length of peduncle (-0.72) and days to maturity (-0.62) were negative but significant only in the second location. Length of peduncle correlated positively and significantly with number of pods per plant (0.86; 0.42), length of branch (0.67;0.66), days to maturity (0.76; 0.82), 100-seed weight (0.92;0.79), and seed yield (0.75; 0.26) in the locations. But its correlation with pod length (0.57) was positive only in the second location, and significant with number of seed per pod (0.36) only in the first location.

Number of pods per plant showed significant environmental correlation with length of branch (0.32) in the second location its correlation with 100-seed weight (0.47) was significant in the first location. Branch length correlated significantly with all the characters in the locations, its correlation with 100- seed weight (-0.52) was negative in the second location. Pod length correlated positively with number of seed per pod (0.75; 0.92) and seed yield (0.96 ;0.62) in the locations. But its correlation with maturity date (0.61) and 100-seed (0.78) were positive in the second location. Days to maturity correlated positively with seed number (0.60; 0.39) in both locations; but its correlation with 100-seed weight (0.43) was positive in the second location, and positive in the first location for seed yield (0.76). Number of seed per pod recorded negative correlation with 100-seed weight (-0.31;-0.79) in the locations.

Table 10: Genotypic correlation coefficient among twelve cowpea characters in two location

Character	Location	No/brch /Plt	No. of pdncl /plt	No. of pods/ pdncl	Lgth of pdncl	No. of pods/plt	Lgth of brch	Pod length	Days to 95% mat.	No. of seeds /pod	100-seed wt (g)
Days to 50% flower	1	0.84**	0.50**	0.23	0.91**	0.40**	0.75**	0.39*	0.78**	0.76**	0.34*
	2	0.59**	0.31*	0.33*	0.74*	-0.38*	0.40*	0.51**	0.90**	0.79**	0.53**
No/branch/Plant	1	-	0.56**	0.31*	0.82**	0.59**	0.41*	-0.33*	0.77**	0.61**	-0.39*
	2	-	0.21	0.47*	0.71**	0.65**	0.74**	-0.51*	0.59**	0.64**	-0.58**
No. of pdncls /plt	1	-	-	0.51**	0.52**	0.36*	0.23	-0.33*	0.76**	0.55**	-0.44**
	2	-	-	0.74	0.53**	0.22	0.15	-0.35	0.20	0.38*	-0.81**
No. of pods /pdncl	1	-	-	-	0.13	-0.09	0.56*	0.82*	-0.09	0.19	0.58**
	2	-	-	-	0.53**	0.75**	0.89**	0.17	-0.07	0.66**	-0.47**
Lgth of pdncl	1	-	-	-	-	0.33*	0.60**	0.27	0.71**	0.79**	-0.26*
	2	-	-	-	-	0.39*	0.57**	0.44*	0.72**	0.85**	-0.66**
No. of pods /plt	1	-	-	-	-	-	0.18	0.25*	0.59**	0.42*	-0.18
	2	-	-	-	-	-	-0.21	0.39*	0.08	0.13	-0.05
Lgth of branch	1	-	-	-	-	-	-	0.44*	0.41*	0.65**	0.31*
	2	-	-	-	-	-	-	0.54*	0.34*	0.77**	-0.52**
Pod lgth	1	-	-	-	-	-	-	-	0.21	0.63**	0.06
	2	-	-	-	-	-	-	-	0.44*	0.63**	-0.48**
Days to 95% maturity	1	-	-	-	-	-	-	-	-	0.57**	-0.25
	2	-	-	-	-	-	-	-	-	0.81**	-0.42**
No. of seeds /pod	1	-	-	-	-	-	-	-	-	-	-0.31*
	2	-	-	-	-	-	-	-	-	-	-0.79**
100-seed wt (g)	1	-	-	-	-	-	-	-	-	-	-
	2	-	-	-	-	-	-	-	-	-	-

Table 11. Environmental; correlation coefficient among twelve characters of cowpea in two locations

Character	Loc	No of brch	No of ped/plant	No of pods/ped	Lgth of ped	No of pods/plt	Lgth of brnch	Pod length	Days to mat.	No of seeds/pod	100-seed wt. (g)	Seed yield (g/plt)
Days to 50% flower	1	0.87**	0.66**	0.51**	0.45**	0.95**	-0.93**	0.54**	0.93**	0.94**	0.42*	0.98**
	2	0.79**	-0.41*	0.33*	0.82**	0.90**	-0.47**	0.60**	1.06**	1.09**	0.67**	0.02
No. of Bra/ Plant	1	-	0.66**	0.36*	0.25*	0.53**	0.56**	0.93**	0.76**	0.86**	0.55**	0.37*
	2	-	0.26	0.35*	0.86**	0.16	1.00**	0.81**	0.79**	0.84**	0.87**	0.76**
No. of ped/ plant	1	-	-	0.47*	0.57**	0.59**	0.13	0.49**	0.82**	0.58**	0.75**	0.22
	2	-	-	0.81**	0.70**	0.08	0.22	0.41*	0.30*	0.67**	0.25	0.65**
No of Pod/ Ped	1	-	-	-	0.05	0.43*	0.22	0.63**	0.61	0.39*	0.41*	0.33*
	2	-	-	-	-0.72**	0.57**	0.02	0.24	-0.62**	0.52**	0.32*	0.86**
Length of ped	1	-	-	-	-	0.86**	0.67*	0.33	0.76**	0.36*	0.92**	0.75**
	2	-	-	-	-	0.42*	0.66*	0.57**	0.82**	0.80	0.79**	0.26*
No of Pod/ Plant	1	-	-	-	-	-	0.24	0.29	0.50**	0.98	0.47**	0.14
	2	-	-	-	-	-	0.32*	0.9	0.01	0.12	0.05	0.12
Length / of Branch	1	-	-	-	-	-	-	0.53**	0.44*	0.71**	0.32*	0.45**
	2	-	-	-	-	-	-	0.63**	0.48**	0.91**	0.69**	0.48**
Pod /Length	1	-	-	-	-	-	-	-	0.23	0.75**	0.12	0.96**
	2	-	-	-	-	-	-	-	0.61**	0.92**	0.78**	0.62**
Days to 95% Mat	1	-	-	-	-	-	-	-	-	0.60**	0.21	0.76**
	2	-	-	-	-	-	-	-	-	0.39**	0.43*	1.21
No of Seeds/ Pod	1	-	-	-	-	-	-	-	-	-	-0.31*	-1.02
	2	-	-	-	-	-	-	-	-	-	-0.79*	-1.13
100-Seed Weight(g)	1	-	-	-	-	-	-	-	-	-	-	0.23
	2	-	-	-	-	-	-	-	-	-	-	0.24

*, ** = Significant at 05, 01 probability levels. 1 = Location 1; 2 =Location 2

4.6.1 Direct and indirect effects of characters on seed yield :

The direct and indirect effects of some cowpea characters on seed yield as well as the residual factors in the two locations are presented in Table 12. In the first location, number of peduncles per plant (5.44), number of pods per plant (2.83) and number of branch per plant (2.01) recorded the highest direct effects on seed yield. Number of peduncles per plant which had the largest direct effect also had a large indirect effect through reduction in weight of 100-seeds (-3.01) in the first location. Number of branch with large direct effect on seed yield also had high indirect effect through reduction in days to maturity (-1.65) and weight of 100-seeds (-0.93) in the first location. The large direct effect of number of pods per plant in the first location was masked by the large negative indirect effect of number of peduncles per plant (-3.41) and days to maturity (-2. 08) resulting eventually in non significant genotypic correlation coefficient between number of pods per plant and seed yield. The non-causal factor (residual), in the first location was (10.66).

In the second location, number of pods per plant had the highest direct effect (2.57) with large indirect effect through reduction in length of branch (-1.21) and number of seeds per pod (-1.13). Number of branch again recorded large positive direct effect (2.32) but this was masked through reduction in length of branch (-0.84). Number of seeds per pod recorded the smallest direct effect with number of peduncles per plant recording high indirect effect in the second location. In all, the non-causal correlation (residual) in the second location was (-6.15).

Table 12: Direct and Indirect Effects of Some Characters on Seed Yield in Cowpea

Character	Loc	Days to flwr	No of branch	No of pdcls/ plt	No of pods/ pdcls	Lgth of pdncls	No of pods/ plt	Lgth of brch	Pod lgth	Days to 95% mat	No of seeds / pod	100 seed wt	Geno. Corr.
Dys to flwr	1	**0.97**	0.39	0.13	0.48	1.17	0.52	0.83	0.37	0.74	0.43	1.34	0.66**
	2	**1.31**	0.22	0.15	0.51	0.93	0.71	0.99	1.23	0.95	0.38	0.86	0.63**
No of brch/plt	1	1.43	**2.01**	0.14	0.67	0.84	0.29	1.37	0.92	-1.65	0.58	-0.93	0.36*
	2	0.81	**2.32**	0.60	0.12	0.03	0.43	-0.84	2.17	0.03	0.34	0.46	0.54**
No of pdcls/plt	1	0.16	3.16	**5.44**	1.27	0.55	3.17	0.19	0.13	1.29	0.31	-3.01	0.49**
	2	0.77	0.58	**1.03**	0.49	2.04	0.22	1.25	1.05	0.94	0.66	1.12	0.43*
No of pods/pdcl	1	0.42	0.32	2.15	**0.82**	2.76	1.22	0.05	1.17	1.41	0.07	0.97	0.35*
	2	0.63	0.75	0.93	**1.05**	4.13	2.40	0.18	1.40	1.22	0.18	1.22	0.85**
Lgth of pdcl	1	1.38	0.22	1.16	0.81	**1.31**	0.57	0.07	0.09	0.30	1.82	1.13	0.61**
	2	0.15	0.08	2.70	0.93	**1.79**	1.31	0.16	0.55	0.14	1.17	0.03	0.88**
No of pods/plt	1	0.77	0.51	-3.41	1.31	0.29	**2.83**	0.82	0.41	2.08	4.20	0.29	-0.84**
	2	0.18	1.22	0.82	1.16	0.11	**2.57**	-1.21	0.85	1.21	-1.13	0.87	0.14
Lgth of brch	1	0.41	0.76	2.44	0.81	0.08	0.53	**0.86**	0.28	1.48	0.19	0.38	0.48**
	2	0.13	0.19	1.21	0.53	1.16	0.08	**0.66**	1.24	3.22	1.01	0.52	0.37*
Pod lgth	1	0.37	0.43	0.53	0.22	0.81	0.44	0.38	**1.48**	0.35	0.39	0.52	0.70**
	2	0.41	0.17	0.09	1.31	1.21	0.07	0.03	**0.93**	0.11	1.21	0.31	0.33*
Days to 95% mat	1	1.22	2.01	0.13	0.16	1.27	1.18	0.48	0.87	**0.63**	0.48	0.27	0.62**
	2	3.19	1.28	3.10	0.73	0.43	0.33	1.01	0.12	**0.44**	0.51	0.91	0.77**
No of seeds/pod	1	1.22	0.24	0.41	0.81	0.57	2.27	1.01	1.12	2.53	**0.56**	1.13	0.85**
	2	0.81	1.03	1.26	1.01	0.18	1.06	0.17	0.75	0.71	**0.07**	0.89	0.88**
100 seed wt	1	0.41	0.53	0.50	0.82	0.23	0.13	0.31	0.18	0.33	0.28	**1.76**	0.18
	2	0.53	1.00	0.41	1.23	1.04	0.50	1.44	0.53	1.27	0.31	**0.28**	0.69**

*** = Significant at 05; .01 probability level 1=Ogbomoso location 2=Abeokuta location Total residual location 1= -10.66, Total residual location 2= -6.15

4.7 Genotype x Environment Interaction:

4.7.1 Stability Analysis

The Mean values of the characters studied across the twenty varieties are presented in Table 13. Genotypes varied significantly for all the characters. Branch length and seed yield showed widest variations across the genotypes. The results of joint regression analysis for the twenty genotypes in respect of their characters evaluated are presented in Table 14. The genotypes were significantly different from each other in respect of all the characters. The effect of the environment was significant for all characters. GXE interaction has been partitioned into linear (heterogeneity) and non-linear components. The heterogeneity component was significant for all the characters except for branch number. The deviation mean square was not significant for number of peduncles and number of pods plant while the other characters recorded significant deviation from linearity.

Table 13: **Mean of twelve agronomic and yield characters of the twenty cowpea genotypes across four environments.**

Genotype	Days to 50% flwr	No Brnch /plt	No Pedcl/ plt	No.of pods/ Pedcl	Lgth of pedcl	No of Pods /plt	Lgth of Branch	Pod length	Days to 95% mat	No seeds / pod	100-seed wt (g)
Danilla	43.92	2.67	15.92	2.17	22.75	18.17	37.08	10.25	77.08	7.42	13.67
İT97k-499-39	41.53	3.33	13.58	2.17	23.17	26.25	45.9	13.17	62.00	10.00	12.17
IT90k-76	42.75	3.13	12.83	2.08	27.50	21.83	25.33	12.17	64.50	8.83	15.33
IT95k-1091-3	40.75	3.33	12.83	2.17	32.17	22.83	69.25	14.57	63.91	10.67	14.92
TVx-3236	46.33	2.75	15.33	2.25	26.83	26.08	55.25	12.42	68.50	9.75	12.42
IT92k-686-2	41.50	3.83	12.25	1.92	21.17	21.25	29.25	13.67	69.97	8.58	15.59
IAR-48B	46.00	3.50	11.58	2.00	26.58	23.00	52.85	12.67	71.00	7.33	16.33
LDPD	42.08	3.42	11.58	2.17	29.58	24.57	50.42	11.94	63.92	10.00	10.17
Owode	45.66	3.33	19.42	2.25	31.75	26.17	51.92	13.08	67.58	9.83	16.92
IT95K1090-12	44.68	2.75	13.00	2.08	28.83	23.67	101.50	14.33	66.67	10.33	14.17
IT90k-277-2	46.08	3.08	13.17	2.08	30.10	21.42	72.42	12.33	69.67	10.50	14.25
IFB_{stop}	42.00	3.75	17.42	2.33	29.83	23.58	47.83	12.42	66.92	9.75	13.25
IAR 48W	48.33	3.84	13.58	2.28	33.58	20.21	43.38	16.81	75.63	8.42	14.51
IT90k-508-2	43.33	4.00	12.17	2.00	27.92	2o.00	73.75	14.17	68.33	10.42	10.51
IT90k-59	40.92	3.21	15.172	1.91	21.08	27.75	86.92	13.78	67.58	9.33	11.76
AGRIB VI	42.25	2.92	11.12	2.42	22.33	26.00	74.12	15.92	63.50d	9.08	13.17
IT90k-1034-94	43.50	3.08	11.54	1.92	19.75	23.00	78.42	17.33	65.75	10.33	13.33
IT97k-113-6	42.32	2.50	11.83	2.42	23.67	24.83	28.67	16.08	67.50	10.33	10.75
Medino.I	32.33	1.33	9.92	2.00	3.50	14.92	6.25	9.25	50.20	4.58	23.17
Medino II	34.50	0.42	11.33	1.58	3.42	18.17	5.83	9.92	49.67	5.08	19.41
CV (%)	7.86	34.01	27.21	25.73	18.51	30.99	50.27	14.69	5.26	14.81	15.06
L.S.D(%)	0.19	0.10	0.08	0.07	0.22	0.28	0.54	0.14	0.19	0.12	0.15

Table 14: Joint Regression analysis of characters for twenty cow pea genotypes across four Environments

Source of Variation	Df	Days to 50% flwr	No.of Brch /plt	No.of Pedcles/ plant	No. of pods/ pdcle	Length of peduncle	No.Pod /Plant	Length of Brnch	Pod length	Day to 95% maturity	No. seed Per pod	100-sd wt	Seed yield (g/plt)
Eviron	3	161..5**	13.28**	78.39*	12.38**	510.18**	130.65**	93.55**	87.36**	360.44	69.40*	81..29**	30.19**
Gen	19	159.79**	10.57**	67.12*	8.52**	415.01**	117.23**	706.82**	69.16**	299.81**	63.29**	75.08**	263.81**
Het.	19	48.23*	4.13	31.43*	3.41*	378..36**	93.25**	620.42**	51.82**	25.73 **	51..22**	63.19**	220.17**
Dev	38	95.83**	9.75*	4.82	1.33	49.20*	80.57**	101.65**	12.17	76.16*	10.01*	18.21*	66.03
Pooled error	160	10.73	2.55	1.72	0.93	7.51	23.41	44.28	3.01	18.28	1.29	2.35	21.41

*, * * Significant , $P < 0.05, 0.01$ respectively.

Regression coefficient, b for the twelve characters are shown in Table15. For days to flower, IT97k-499-39,IT95k-1091-31 and Owode recorded regression coefficient equal to 1.0. IT90K-76, TVx 3236, IAR 48B, IT90K-1090-12, Ife-brown, AGRIBVI and IT90K-1034-34 had regression coefficients significantly less than 1.0. The other genotypes genotypes recorded regression coefficients significantly higher than 1.0 for number of branches per plant while only IT90K-76 and IT90K-59 recorded regression coefficients equal to 1.0 IT90K-686-2, IAR 48B, IT90K-1090-12, IT90K-277-2, AGRIBVI, Medino 1 and Medino II had regression coefficients less than 1.0. Equal number of genotypes recorded regression coefficients significantly greater than and less than 1.0 for number of pods per plant as the remaining eight genotypes recorded regression coefficients equal to 1.0. Only IT90K-1090-3, TVx 3236, IAR48B, IT90K-1090-12 and IT90K-59 recorded regression coefficients equal to 1.0 for length of branch, other genotypes had regression coefficients greater than or less than 1.0. For pod length, only IT97K-4999-39 and Medino II recorded regression coefficient less than 1.0 while the remaining genotypes had regression coefficient either greater than or equal to 1.0. For days to maturity, IT90K-1091-3, LDPD, IT90K-508-2, IT90K-59 and IT97K-113-6 had regression coefficients significantly less than 1.0 as IT97K-499-39, IT97K-686-2, Owode, IT90K-1090-12 and IT90K-1034-94 had coefficients equal to 1.0. The remaining ten genotypes recorded regression coefficients significantly greater than 1.0. However, only AGRIB VI and Medino II had regression coefficients less than 1.0 with the other genotypes recording either greater than 1.0 or equal to 1.0 regression coefficients for number of seeds per pod. Similarly only IT90K-508-2 and IT90K-1034-94 had regression coefficient less than 1.0 for weight of 100 seeds. The remaining genotypes had regression coefficients greater than or equal to 1.0. The deviation mean square for the characters measured is presented in

Table 15: Regression coefficient (b) for eleven characters of 20 cowpea genotypes across 4 environments

Genotype	Day to50%	No of branch	No of peduncles	No of pods/ peduncle	Length of peduncle	No of pod/ plt	Length of branch	Pod length	Day to 95% maturity	No of seeds /pod	100 seed weight
Danilla	1.65	1.55	1.11	1.31	0.86	0.49	1.71	1.36	1.69	0.93	1.27
	±0.71[b]	±0.21[b]	±0.22[a]	±0.51[b]	±0.29[a]	±0.18[c]	±0.82[b]	±1.30[b]	±0.38[b]	±0.21[a]	±0.90[a]
IT97k-499-39	1.23	1.70	1.08	0.94	1.22	1.71	1.82	0.38	1.08	1.51	1.60
	±0.20[a]	±0.79[b]	±0.29[a]	±0.42[a]	±0.33[a]	±0.17[b]	±1.10[b]	±0.45[c]	±1.11[a]	±0.33[b]	±0.98[b]
IT90k-76	0.56	0.85	1.60	0.68	1.17	0.27	1.32	1.68	1.54	0.63	1.11
	±0.69[c]	±0.51[a]	±0.57[b]	±0.51[c]	±0.53[a]	±0.61[c]	±0.51[b]	±1.21[b]	±0.58[b]	±0.13[a]	±0.88[a]
IT95k-1091-3	0.81	1.22	1.10	1.31	0.81	0.80	1.05	0.71	0.36	1.34	0.81
	±0.39[a]	±0.77[b]	±0.50[a]	±0.32[b]	±0.38[a]	±0.42[a]	±0.51[a]	±0.49[a]	±.031[c]	±0.72[b]	±1.20[a]
TVx-3236	0.73	1.41	1.29	1.21	0.46	0.51	0.76	0.58	1.42	1.30	1.60
	±0.31[c]	±0.21[b]	±0.58[b]	±0.73[a]	±0.78[c]	±0.83[c]	±0.51[a]	±0.63[a]	±0.66[b]	±0.22[b]	±0.70[b]
IT92k-686-2	1.30	1.08	1.32	1.36	0.69	0.43	0.53	1.21	1.11	1.39	1.73
	±0.81[b]	±0.91[c]	±0.89[b]	±0.55[b]	±0.28[a]	±0.19[c]	±0.07[c]	±0.91[a]	±0.72[a]	±0.80[b]	±0.92[b]
IAR-48B	0.97	0.41	0.83	1.70	1.28	0.83	1.08	1.66	1.63	1.58	1.41
	±0.33[c]	±0.33[c]	±0.39[a]	±0.41[b]	±0.38[a]	±0.88[a]	±0.19[a]	±0.73[b]	±0.91[b]	±1.01[b]	±0.82[b]
LDPD	1.31	1.79	0.41	1.47	1.22	1.58	1.58	1.91	0.33d	1.01	0.91
	±0.80[b]	±0.30[b]	±0.32[c]	±0.41[b]	±0.31[a]	±0.88[b]	±0.92[b]	±1.03[b]	±0.21[c]	±0.70[a]	±0.75[a]
Owode	0.83	1.63	0.53	0.92	1.08	1.72	1.70	1.00	0.90	0.88	1.41
	±0.21[a]	±0.52[b]	±0.72[c]	±2.1[a]	±0.31[a]	±0.76[b]	±0.38[b]	±0.78[a]	±0.83[a]	±0.53[a]	±0.87[b]
1090-12	0.42	1.06	0.72	1.34	0.41	0.82	0.99	1.41	0.62	1.60	1.03
	±0.40[c]	±1.03[c]	±0.23[a]	±0.41[b]	±0.23[c]	±0.73[a]	±0.67[a]	±0.51[b]	±0.51[a]	±0.80[b]	±0.62[a]
IT90k-277-2	1.60	0.48	1.56	1.18	1.50	0.60	0.43	1.73	1.41	1.22	1.60
	±0.41[b]	±0.13[c]	±0.81[b]	±0.43[b]	±0.96[b]	±0.39[a]	±0.05[c]	±0.48[b]	±1.20[b]	±0.29[a]	±0.31[b]
Ife-brown	0.63	1.58	0.28	0.93	1.63	1.70	1.31	1.34	1.29	1.73	0.81
	±0.21[c]	±0.23[b]	±0.01[a]	±0.41[a]	±1.20[b]	±0.18[b]	±0.51[b]	±0.82[b]	±0.31[b]	±0.41[b]	±0.31[a]
IAR48w	1.70	1.61	1.80	0.87	1.60	1.61	0.43	1.67	1.53	1.81	0.70
	±0.18[b]	±0.81[b]	±0.52[b]	±0.82[a]	±1.23[b]	±0.76[b]	±0.92[c]	±1.22[b]	±1.07[b]	±0.49[b]	±1.21[a]
IT90k-508-2	1.81	1.73	0.99	1.39	0.18	0.91	0.50	1.03	0.51	1.90	0.52
	±0.70[b]	±0.92[b]	±0.41[a]	±0.21[b]	±0.01[c]	±0.18[b]	±0.79[c]	±0.41[b]	±0.46[c]	±0.31[b]	±0.63[c]
IT90k-59	1.66	0.85	0.43	0.81	0.62	1.22	0.81	1.61	0.41	0.96	1.76
	±1.29[b]	±1.21[a]	±0.82[c]	±0.31[a]	±0.51[a]	±0.33[a]	±0.50[a]	±0.88[b]	±0.53[c]	±0.91[a]	±0.71[b]
AGRIB VI	0.53	0.49	1.70	0.86	0.54	0.80	1.33	0.63	1.51	0.35	0.63
	±0.11[c]	±0.08[c]	±0.39[b]	±0.51[a]	±0.63[c]	±0.41[a]	±0.58[a]	±0.60[a]	±0.87[b]	±0.05[c]	±0.77[a]
IT90k-1034-94	0.93	1.77	1.63	0.93	1.31	0.41	1.51	0.88	0.91	1.50	0.51
	±0.32[c]	±0.67[b]	±0.73[b]	±1.21[a]	±0.65[b]	±0.05[c]	±0.71[b]	±0.420[a]	±0.51[a]	±0.41[b]	±1.21[c]
IT97k-113-6	1.50	1.32	0.41	1.61	0.51	0.43	1.44	1.70	0.16	1.27	1.85
	±0.33[b]	±1.20[b]	±0.31[c]	±0.17[b]	±0.90[c]	±0.61[c]	±1.41[b]	±0.22[b]	±0.21[c]	±0.48[a]	±0.41[b]
Medino I	1.73	0.22	1.36	0.51	0.43	1.51	0.40	1.41	1.64	0.98	1.76
	±1.12[b]	±2.13[c]	±0.81[b]	±0.32[c]	±0.18[c]	±0.73[b]	±1.20[c]	±0.89[b]	±0.21[b]	±0.21[a]	±0.20[b]
MedinoII	1.50	0.13	1.01	0.63	0.81	1.03	0.21	0.28	1.59	0.31	1.91
	±0.53[b]	±1.23[c]	±0.38[a]	±0.32[c]	±0.31[a]	±0.42[a]	±0.46[c]	±0.17[c]	±0.43[b]	±0.21[c]	±0.39[b]

a= regression coefficient equal to 1.0, b= regression coefficient greater than 1.0 c= regression coefficient significant Less than 1.0

Table 16.The deviation mean square for days to flower was significant for the genotypes except Danilla, TVx 3236, IT92K-686-2, Owode, IT90K-508-2, IT90K-59 and AGIBVI showing that these were not stable with respect to days to flower. Only IT90K-1031-94, Medino I and II were significant for number of branches per plant. Similarly only IT96K-277-2 and IT90K-508-2 had significant deviation mean square with respect to number of peduncles per plant. Similarly only IT95K-1091-3 and IT90K-59 recorded significant deviation mean square for number of pods per peduncle. The deviation mean square was equally significant with respect to length of peduncle for Danilla, IT92K-686-2, LDPD, Owode and IT97K-113-9. Only Medino I and II however had significant deviation mean square with respect to number of pods per plant. All the genotypes recorded significant deviation mean square for length of branch. But only Medino I and II had significant deviation mean square for pod length. Similarly, only IT95K-1091-3, IAR 48W and Medino I recorded significant deviation mean square for days to maturity. Also IT90K-1090-12 had significant deviation mean square for number of seeds per pod. IAR-48B, IAR-48W and Medino I had significant deviation mean square for weight of 100-seeds.

Unbiased estimator (δi^2) for the characters are shown in Table 17. For days to flower, δi^2 identified IT92K-686-2, IT97K-499-39, IT90K-76, IT95K-1091-3, LDPD, IT90K-1090-12, IT90K-1034-94 and Medino II to have significant δi^2. Where only IT90K-59,IT90K1031-94,MedinoIand Medino II had significant δi^2 for number of branches per plant. With respect to number of pods per plant, only IAR-48B, Medino I and MedinoII had significant δi^2. Days to maturity and number of seeds per pod recorded significant δi^2

for IT95K-1091-3, IT96K-277-2, IAR48W and AGRIBVI. All the genotypes recorded significant δi^2 for length of branch.

Ecovalence mean squares (WMS) for the characters are presented in Table 18. IT95K-1091-3, LDPD, Owode, IT90K-508-2, Medino I and II recorded significant WMS for number of branch per plant whereas, only TVx-3236, IT90K-1090-12, IT95K-277-2, Medino I and II had significant WMS with respect to number of peduncles per plant. Similarly only IAR-48B and IT90K-59 had significant WMS for number of pods per peduncle. TVx-3236, IT90K-1090-12, IT90K-59, IT97K-113-6 and Medino II recorded significant WMS for number of pods per plant. Length of branches recorded significant WMS for all the genotypes except IT95K-1091-3. But only Danilla, IAR-48W, AGRIBVI, and IT97K-113-6 had significant WMS with respect to length of pod. A number of genotypes had significant WMS for days to maturity while only IT90K-76, IAR-48B, IT90K-508-2 and Medino II recorded significant WMS for number of seeds per pod.

Table 16: Deviation Mean square (S^2di) for twelve characters of 20 cowpea genotypes across 4 environments.

Geno	Days to 50%	No of branch / plant	No of peduncles / plant	No of pod / peduncle	Length of peduncle	No of pod/ plant	Length of branch	Pod length	Day to 95% maturity	No of seeds/pod	100 seed weight
Danilla	1.3	0.31	0.53	1.17	2.81^c	0.81	38.10^c	1.16	1.93	0.93	1.01
IT97k-499-39	3.10^c	0.22	1.22	1.18	0.40	1.19^c	12.22^c	1.31	1.17	1.01	1.23
IT90k-76	2.5^c	1.41	0.11	0.88	1.71	0.11	29.21^c	0.81	0.20^c	0.93	1.91
IT95k-1091-3	4.10^c	0.62	0.31	3.01^c	0.81	0.44	10.23^c	1.51	4.10^c	1.08	0.71
TVx-3236	1.21	0.04	0.48	0.81	1.19	0.31	5.41^c	1.27	1.53	0.92	1.41
IT92k-686-2	0.63	0.31	0.33	1.22	2.01^c	0.77	9.77^c	1.22	1.27	1.88	0.79
IAR-48B	12.41	1.29	0.19	0.93	1.22	0.54	48.17^c	0.01	0.91	0.31	3.71^c
LDPD	3.41^c	1.83^c	0.08	1.48	3.17^c	0.81	32.19^c	1.27	1.21^c	1.76	4.01
Owode	1.73	0.71	0.37	0.21^c	4.22^c	0.17	10.13^c	1.28^c	1.93^c	0.53	1.11
IT96 K-1090 –12	8.61^c	0.14	1.88	0.45	0.71	0.41	41.22^c	0.59^c	0.87	2.19^c	0.93
IT96k-277-2	5.34^c	0.32	3.17^c	0.31	0.61	1.48	10.19^c	1.28	1.21	0.67	1.08
Ife-brown	3.21^c	0.41	0.18	0.22	0.19	1.27	4.27^c	1.79	1.01	1.81	1.03
IAR48w	2.73	0.00	1.44	0.53	0.19	0.36	37.22^c	2.01	2.09^c	0.35	2.81^c
IT90k-508-2	0.38	0.51	5.20^c	3.95^c	4.01^c	0.39	13.19^c	1.35	1.57	0.26	0.36
IT90k-59	1.41	0.21	0.21	5.41^c	1.53	0.87	61.22^c	1.51	1.26	0.83	0.81
AGRIB VI	1.69	0.13	0.37	1.29	0.17	0.43	41.79^c	1.05^c	1.71^c	1.16	1.17
IT90k-1034-94	2.10^c	4.21^c	0.11	0.33	1.01^c	0.23	18.29^c	1.49^c	0.08	1.01	1.10
IT97k-113-6	19.20^c	0.13	1.92	0.17^c	2.00^c	1.28	37.63^c	1.70	1.77	0.93	0.97^c
Medino I	11.22^c	3.21^c	1.04	1.21	0.18^c	2.71^c	31.27^c	2.81^c	3.19^c	0.67	2.73^c
Medino II	13.43^c	5.22^c	0.93	1.88	1.83^c	3.10^c	50.18^c	4.10^c	1.76	1.83^c	4.19^c

C = Deviation Mean square (S^2di) significantly greater than 0 = unstable

Table 17: Unbiased estimator (σi^2) for each of the 12 characters of cowpea genotypes across 4 environment

Geno	Day to 50%	No of branch	No of peduncle /plant	No of pods/ peduncle	Lgth of peduncle	No of pods/ plant	Lgth of branch	Lgth of pod	Days to maturity	No of seeds	100 seed weight
Danilla	0.66	1.17	2.23	2.81	8.72*	2.22	11.22*	0.31	2.22	1.04	1.11
IT97k-499-39	10.67*	2.05	1.22	5.1*	3.21*	1.11	4.17*	1.17	3.17	3.21	0.81
IT90k-76	5.88*	2.35	2.91	3.22	1.17	3.01	6.21*	1.33	2.17	3.27	0.31
IT951-1091-3	6.51*	1.22	1.28	6.17*	1.23	3.22	6.93*	0.81	10.25*	4.59*	1.39
TVX-3236	0.41	1.71	1.31	3.22	1.77	1.21	10.01*	0.54	0.71	4.01	1.41
IT92k-686-2	3.31*	2.18	2.17	2.01	2.01	3.08	5.08*	3.48	3.22	3.33	1.22
IAR-48B	2.29	0.92	4.19*	1.17	1.23	6.77*	7.27*	2.22	1.22	2.06	5.69*
LDPD	10.32*	3.22	3.27	3.21	2.73	2.44	5.22*	3.01s	0.91	3.31	2.17
Owode	0.22	1.01	1.81	1.22	1.23	3.27	8.19*	8.23*	0.66	3.49	1.22
IT96k-1090-12	5.38*	3.41	3.23	0.79	0.91	1.38	10.73*	9.10*	3.01	1.21	12.70
IT96k-2772-2	0.57	0.77	1.11	0.66	0.45	3.71	4.17*	3.41	10.44*	10.71*	0.73
Ife-brown	0.41	2.21	2.21	0.71	2.39	0.24	11.29*	0.63	3.11	10.71	0.73
IAR48w	0.86	3.17	0.77*	1.72	4.23*	1.27	5.22*	0.01	10.27*	5.40	3.66*
IT90k-508-2	0.41	3.22	3.21	3.18	0.04	3.01	6.71*	3.17	1.31	1.13	4.10
IT90k-59	2.22	8.11*	2.17	1.01	2.06	1.21	8.19*	4.00	3.22	4.21	0.42
AGRIBVI	2.00	3.22	0.61	2.27	2.51	0.77	1.21	2.03	5.17*	3.41*	0.13
IT90k-1034-94	6.17*	6.10*	0.31	2.71	1.09	2.06	6.71*	5.22*	0.99	1.21	1.00
IT97k-113-6	11.13	0.13	1.22	1.22	1.16	0.09	11.51*	10.31*	1.28	0.77	0.57
Medino1	1.22	10.21*	1.51	5.08*	8.01*	3.27*	1.41*	1.31	0.51	0.08	4.94*
Medino II	3.79*	5.08*	2.19	6.41*	11.13*	10.31*	13.01*	2.04	0.92	1.19	1.20

Table 18: Ecovalent mean square (WMS) for each of the 12 Characters

Genotype	Days 50%	No of branch/ plant	No of peduncles / plant	No of pods/ peduncle	Length of peduncle	No of pods / plant	Length of branch	Length of pod	Days to maturity	No of seeds	100-seed weight(g)
Danilla	0.31	0.41	3.17	6.17	6.19[b]	0.31	34.31[b]	10.08[b]	3.21	8.18	3.16
IT97-499-39	0.41	0.31	0.21	0.96	0.77	1.41	1.76[b]	2.11	5.41[b]	3.27	1.33
IT90k-76	4.65[b]	0.51	0.43	0.41	0.63	3.01	10.03[b]	1.20	0.73	5.71[b]	4.21[b]
IT95k-1091-3	0.40	4.31[b]	1.31	1.93	0.61	0.69	0.13	0.28	4.12[b]	0.53	2.17
TVx-3236	0.82	0.46	3.22[b]	2.08	3.17	30.73[b]	13.09[b]	2.17	4.51[b]	0.98	1.83
IT92k-686-2	7.66[b]	0.18	0.51	1.24	1.93	0.90	11.00[b]	0.13	8.21[b]	1.63	2.17
IAR-48B	3.71[b]	0.41	1.38	5.16[b]	2.51	0.17	0.42	0.19	6.01[b]	3.81[b]	1.93
LDPD	6.22[b]	4.22[b]	0.18	2.13	0.13	2.19	12.21[b]	1.02	0.13	2.27	3.23
Owode	0.71	6.19[b]	0.37	1.27	11.07[b]	1.01	13.1[b]	0.63	1.21	1.51	0.67
IT96K-1090-12	0.16	1.73	4.13[b]	0.41	1.15	3.08[b]	4.17[b]	2.19	1.66	1.21	0.91
IT96k-277-2	6.91[b]	1.31	6.21[b]	0.22	0.41	1.18	13.01[b]	0.34	0.71[b]	2.93	3.20
Ife-brown	0.40	1.19	1.21	0.51	1.31	0.05	8.88[b]	0.35	0.50	0.31	3.10
IAR-48w	0.21	2.17	2.38	0.24	5.41[b]	0.18	6.21[b]	4.53[b]	12.21	1.56	4.01
IT9k508-2	0.17	1.99[b]	1.66	0.81	0.21	2.17	12.01[b]	6.12	5.30[b]	12.06[b]	10.11[b]
IT90k-59	81.19[b]	1.81	0.49	4.28[b]	0.44	4.21[b]	10.21[b]	0.65	0.19	3.61	5.31[b]
AGRIBVI	10.22[b]	0.91	0.50	1.93	1.63	6.71	4.60[b]	6.16[b]	6.48[b]	0.39	2 16
IT90k-1034-94	4.13[b]	2.13	0.11	0.63	0.32	2.01	5.81[b]	1.71	6.11[b]	2.99	0.94
IT97k-113-6	6.50[b]	0.03	1.21	3.17	2.19	6.13[b]	6.31[b]	4.19[b]	4.21[b]	1.28	6.07[b]
Medino I	15.39[b]	7.28[b]	3.01[b]	0.18	4.11[b]	1.41	10.69[b]	0.48	2.16	4.81	4.09[b]
MedinoII	10 22[b]	3.21[b]	1.22[b]	3.09	3.53[b]	4.06[b]	3.01[b]	1.08	4.17[b]	5.01[b]	5.27[b]

b= Ecovalence Variance significantly greater than 0 = unstable.

4.8 Simultaneous Selection for Yield and Stability Performance:

The mean yield, regression coefficient (b), deviation mean square (S^2di), unbiased estimator (δi^2) and ecovalence mean square (WMS) for the twenty genotypes are presented in Table 19. The mean yield ranged from 29.13g/plant (IT97K-499-39) to 10.74g/plant for Medino II. IT97K-499-39, produced the highest mean yield while Medino I and II produced the lowest mean yield and recorded regression coefficients equal to 1.0. While Danilla, IT95K-1091-3 and IT90K-1034-94 with above average and less than average mean yields, had regression coefficients greater than 1.0. Fewer genotypes (IT95K-1090-12, IT90K-508-2 and Medino I and II) which had above average and below average mean yields, were identified as unstable by only the deviation mean square. But the deviation mean square and the unbiased estimator, were both significant for IT95K-1091-3, Medino I and II, with above average and below average mean yields respectively, and therefore unstable. Also, IAR-48B, IAR-48W, IT90K-1034-94, Medino I and II, with their respective below average mean yields were considered unstable with the Ecovalence mean square. Using the modified rank sum method of Kang (1991), the results of simultaneous selection for high yield and stability performance is given in Table 20. The method selected IT97K-499-39 and IT97K-113-6 as highest yielding genotypes. Most of the genotypes having above average mean yield with non-significant δi^2 were selected. The linear regression analysis according to Finlay and Wilkinson (1963) is presented in Table21. The linear regression accounted for 85% of the treatment sum of squares, leaving 15% in the residual. The genotype, environment and GXE accounted for 53.79%, 5.13% and 15.19% respectively of the GXE interaction sun of squares while the residual accounted for 28%. The genotype, environment, joint, genotype regressions and

residual were all significant. The environmental regression was however not significant. The residual regressions contained more than the amount accounted for by the genotype regressions in the GxE sum of squares. It in fact accounted for more than the joint and genotype regressions combined. It is therefore possible that some of the variations were still confounded within the residual.

Table 19: Mean Yield (g/plant), regression coefficient (b) Finlay and Wilkinson deviation Mean Square (S^2di) and unbiased estimator (δi^2) (Shukla 1972) and Ecovalence Mean Square (Wms) (Kang and miller 1984) For 20 cowpea genotypes.

Genotype	Mean yield (g /plt.)	Regression coefficient b± se	Deviation Mean Square (S^2 di)	Unbiased estimator (δi^2)	Ecovalence Mean Square
Danilla	19.71	1.55 ± 0.14^{b}	0.87	1.742	1.67
IT97k-499-39	29.13	1.2 ± 0.05^{a}	0.66	1.59	2.14
IT90k-76	20.81	0.79 ± 0.93^{a}	0.95	1.74	1.68
IT95k-1091-3	20.42	2.35 ± 0.19^{b}	2.47^{e}	15.80^{a}	0.63
TVX	23.93	1.07 ± 0.24^{a}	0.61	0.48	2.26
IT92k-686-2	22.18	0.41 ± 0.32^{c}	1.36	4.28^{a}	0.51
IAR48B	16.51	1.92 ± 0.37^{b}	1.25	3.17	9.51^{c}
LDPD	24.81	1.01 ± 0.16^{a}	0.12	0.19	0.44
Owode	24.43	1.19 ± 0.44^{a}	1.07	2.85	2.51
IT7k-1090-12	21.75	0.44 ± 0.17^{c}	1.18	3.21	1.63
IT96k-277-2	19.35	1.18±0.24a	0.26	0.09	0.72
IFB	24.00	1.14 ± 0.16^{a}	0.72	2.01	0.75
IAR 48W	18.83	-0.09 ± 0.01^{c}	0.93	2.82	9.82^{c}
IT90k-508-2	20.66	2.39 ± 0.16^{b}	3.20^{e}	2.20	9.03^{c}
IT90k-59	23.25	1.63 ± 0.43^{b}	1.47	3.05	2.01
AGIBVI	22.17	0.57 ± 0.21^{a}	0.62	0.75	3.01
IT90k-1034-34	19.00	1.67 ± 0.33^{b}	0.78^{e}	11.02^{a}	13.73^{c}
IT97k-113-6	26.50	2.41 ± 0.19^{b}	0.69	1.83	0.93
Medino I	17.26	-0.17 ± 0.08^{c}	1.60^{e}	11.01^{a}	7.63^{c}
Medino II	10.72	-0.19 ± 0.09^{c}	1.91^{e}	10.47^{a}	15.72^{c}
Mean	22.01				

b = Regression coefficient (b) significantly greater than 1

a = Stability parameter significantly greater than 0.

e = Deviation Mean square (s^2 di) significantly greater than 0.

c = Ecovalence Mean square significantly greater than 0.

Table 20: Mean Yield (g/plant), Yield rank (Y), 50% to selections stability parameter Stability rating (Z) and selected genotypes (S) (Kang 1991).

Genotype	Mean Yield (kg/plt.)	Rank (Y)	Selected genotypes (S)	Unbiased estimator (δi^2)	Stability rating (Z)	Rank sum (Y+Z)	Selected genotypes (50%) (S)
Danilla	19.71	14	---	4.22*	4	18	-----
IT97k-499-39	29.13	1	S	3.50	0	1	S
IT90k-76	20.81	10	S	9.41**	8	18	---
IT95k-1091-3	20.42	11	S	1.72	0	11	----
TVX	23.93	6	S	3.17	0	6	S
IT92k-686-2	22.18	9	S	3.28	0	9	S
IAR 48B	16.51	17	---	12.51**	8	23	---
LDPD	24.81	3	S	5.71*	4	7	S
Owode	24.43	4	S	6.74	4	8	S
IT97k-1090-12	21.75	11	S	8.13	8	19	---
IT96k-277-2	19.35	15	---	7.25*	4	19	----
IFB	24.00	5	S	3.11	0	5	S
IAR 48W	18.83	16	----	3.33*	4	20	---
IT90k-508-2	20.66	13	S	2.17	0	13	----
IT90k-59	23.25	7	S	3.21	0	7	s
AGIBVI	22.17	8	S	2.06	0	8	s
IT90k-103-1	19.00	20	---	0.13*	4	24	---
IT97k-113-6	26.50	2	S	0.93	0	2	s
Medino I	17.26	18	---	0.81	0	18	----
Medino II	10.74	19	---	1.38	0	19	---

*, ** =Significant at 5% and 1% levels of probability

4 sig. at 5%; 8 = sig. at 1%

Table 21: Regression Analysis yield of 20 cowpea genotypes following Finlay and Wilkinson (1966)

Source	Df	Sum of square	Mean square
Treatment	49	242828.26	3073.77
Genotype (G)	19	19783.409	10412.36***
Environment (E)	3	762.3407	2540.44***
GXE	57	36777.08	645.22**
Joint Regression	1	379.42	379.42**
Genotype Regr.	18	7211.49	400.63**
Envi. Regression	2	1713.0	85.65^{ns}
Residual	36	29015.46	805.98**
Error	152	12048.94	79.26
Total	239	254877.21	1066.43

*, **, *** = Significant at 0.05, 0.01 and 0.001 levels of probability respectively.

n s = not significant.

The AMMI analysis is shown in Table 22. The genotype, environment and the GXE interaction were significant and accounted for 8.91%, 7.12% and 15.19% respectively of the treatment SS. The first and second interaction PCA axes were significant and captured 68. 25 % and 27.95% respectively, of the total variation in the GXE interaction SS. Furthermore the IPCA 1 and IPCA 2 captured 36.84% and 33.33% of the interaction degree of freedom. The Mean square of the first interaction PCA (IPCA1) is about double that of the residual whose mean square was indeed not significant.

The AMMI model therefore explains the structural variations in the GXE interaction better than the linear regressions (LR) which was loaded with unexplained component within the data. IT97K-499-39 (G2), TVx3236 (G5), LDPD (G8), Owode (G9),AGRIB VI (G16) and IT97KK-113-6 (G18) recorded very low and positive PCA scores closest to zero and therefore considered stable. IT97K499-39 (G2), Owode (G19), Ife-brown (G12) and IT97K-113-6 (G18) are adaptable to Ogbomoso environment, while IT97K499-3 (G2), TVx-3236 (G5) and IT97K113-6 (G18) will perform well in Abeokuta location.

The mean yields of the twenty genotypes grown in four location -season environments and the first PCA scores are presented in Table 23. About 55% of the genotypes (11 genotypes) produced above average mean yields. The AMMMI – 1 biplot is illustrated in figure 7.The abscissa shows the main effects while the ordinates show the first PCA axis The AMMI-1biplot accounts for 98.5% of the treatment sum of squares leaving an insignificant 1.5% in the residual.

Table 22: AMMI Analysis of variance of 20 cowpea genotypes yield in four environments

Source	Df	Sum of squares	Mean square
Treatment	79	242828.26	3073.77
Total	239	254877.21	1666.43
Genotype (G)	19	19783.48	1041.236***
Environment E	3	7621.34	2540.46***
GXE	57	36777.08	645.22**
IPCA 1	21	25099.11	1480.91***
IPCA 2	19	10281.43	541.13*
Residual	17	1341.14	78.89
Error	152	12048.94	79.26

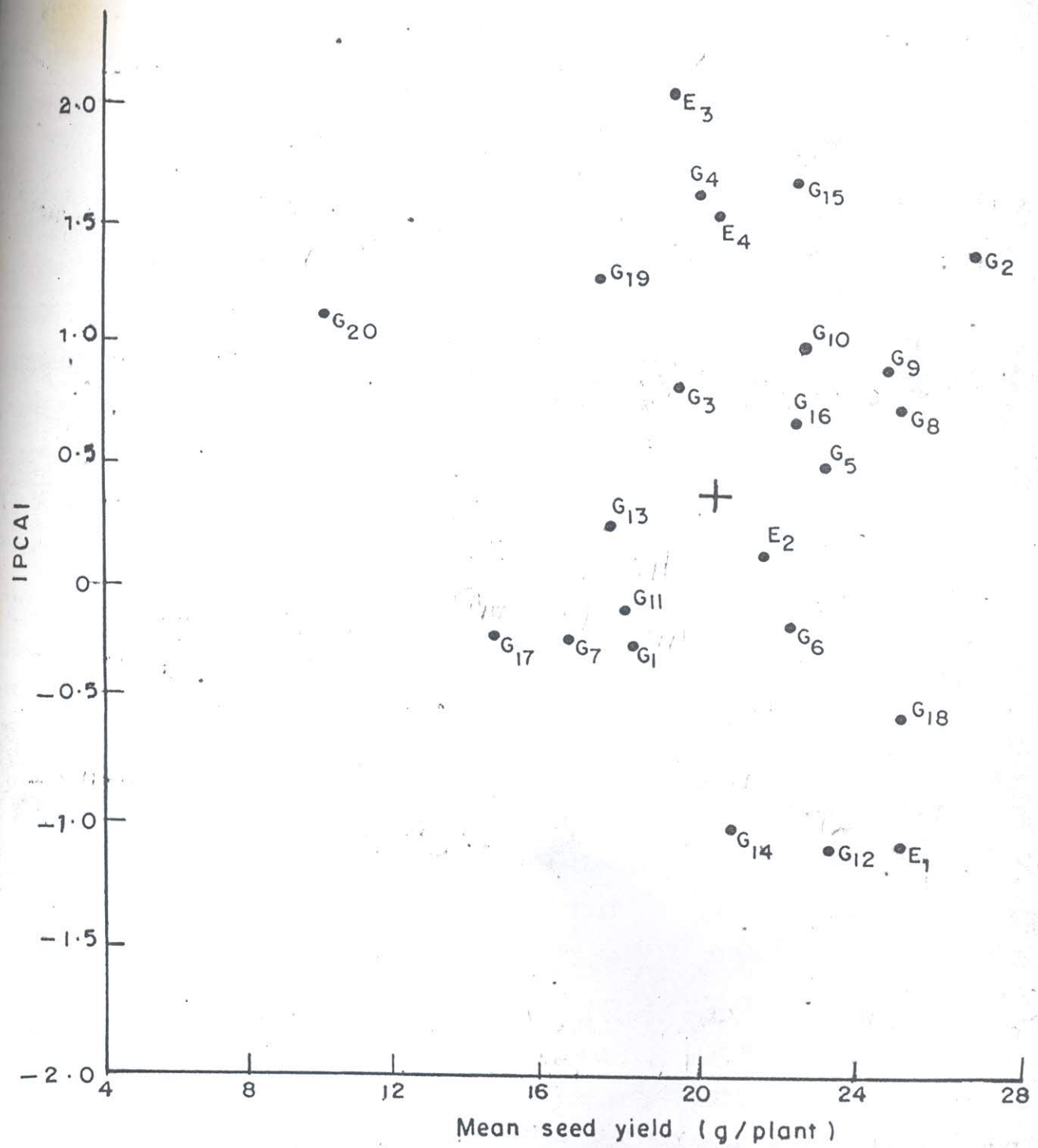

Fig. 7 :– Biplot of the AMMI model For 20 cowpea yield trial grown in Four environments

Table 23: Mean yield (g/plant) and first PCA from AMMI analysis of 20 cowpea Genotypes grown in four environments (E).

Genotypes	Location I		Location II		Mean	IPCA score
	Ogbomoso (E 1)	Ogbomoso (E2)	Abeokuta (E3)	Abeokuta (E4)		
Danilla	23.81	19.70	18.71	16.75	19.69	-0.41
IT97k-499-39	34.83	29.70	27.88	25.81	29.17	0.83
IT90k-76	20.41	18.21	25.50	15.63	19.43	0.32
IT95k-1091-3	17.51	28.01	22.71	15.06	20.42	-1.18
TVX	23.53	18.66	27.93	24.00	23.93	0.19
IT92k-686-2	23.51	18.72	27.53	23.72	22.18	0.64
IAR 48 B	23.41	20.51	10.80	9.76	16.51	-0.42
LDPD	28.51	16.15	28.03	18.25	24.81	0.15
Owode	28.41	28.41	25.31	15.23	24.43	0.39
1090-12	19.11	16.53	28.73	121.56	21.75	0.55
IT96k-277-2	25.26	17.10	21.26	15.46	19.65	-0.14
IFB	28.17	26.37	22.16	20.22	24.00	-1.28
IAR48W	16.00	19.01	23.00	17.01	21.83	-0.10
IT90k-508-2	12.96	16.55	22.01	28.81	19.66	-1.19
IT90k-59	17.51	17.35	31.25	26.06	23.25	1.23
AGIBVI	23.57	18.81	29.86	20.17	22.17	0.24
IT90k-1034-34	27.14	18.93	10.26	8.40	15.00	-0.26
IT97k-113-6	33.41	26.69	29.63	20.40	25.50	-0.86
Medino I	15.71	15.01	21.89	17.40	17.26	0.85
Medino II	9.10	7.10	10.01	15.45	10.74	0.66
Mean	24.62	22.31	19.01	20.38	4.70	
IPCA	-1.22	-0.20	1.54	1.09		

Table. 24 Seed yield of the top 10 genotypes as estimated by AMMI model.

OGBOMOSO ES	MAIN EFFECT	INTERACTION	FINAL YIELD
IT97K-499-39	32.21	-1.01	21.20
TVX-3236	26.67	-0.23	26.34
LDPD	27.85	-0.18	27.67
Owode	27.45	-0.48	26.99
IT90K-1090-12	124.39	-0.67	23.72
IT96K-277-2	22.69	0.17	22.86
Ife – brown	27.04	1.56	28.60
IT90K- 508- 2	23.20	1.45	24.65
AGRIB VI	25.21	-0.29	24.92
IT95K-1091-3	23.56	1.44	25.00
OGBOMOSO LS			
IT97K-499-39	29.90	-0.17	28.73
TVX-3236	24.26	-0.04	24.22
LDPD	25.54	-0.03	25.51
Owode	25.17	-0.08	25.09
IT90K-1090-12	22.08	-0.11	21.97
IT96K-277-2	20.38	0.03	20.41
Ife – brown	24.73	0.26	24.99
IT90K- 508- 2	20.89	0.24	21.13
AGRIBVI	22.90	-0.05	22.85
IT95K-1091-3	21.25	0.24	21.49
ABEOKUTA ES			
IT97K-499-39	26.60	1.28	27.88
TVX-326	20.96	0.29	21.25
LDPD	21.24	0.23	21.47
Owode	21.86	0.60	22.46
IT90K-1090-12	18.78	0.85	19.63
IT96K-277-2	17.08	-0.22	16.86
Ife – brown	21.43	-1.97	19.46
IT90K- 508- 2	17.59	1.83	19.42
AGRIB VI	19.60	0.37	19.47
IT95K-1091-3	17.95	-1.82	16.13
ABEOKUTA LS			
IT97K-499-39	127.97	0.91	28.88
TVX-3236	22.33	0.21	22.54
LDPD	23.61	0.16	23.77
Owode	23.21	0.43	23.64
IT90K-1090-12	20.15	0.60	20.75
IT96K-277-2	18.45	-0.15	18.30
Ife – brown	22.80	-1.40	21.40
IT90K- 508- 2	18 96	-1.30	17.66
AGRIB VI	20.97	0.26	21.13
IT95K-1091-3	19.32	-1.29	18.03

ES = Early season
LS = Late season

Table 25 Correlation coefficients between genotypes PC 1 and PC 2 scores and agronomic and yield character

Character	Correlation coefficient PC 1	PC 2
Days to 50% flower	0.65*	0.41
Number of branch / plant	0.63**	0.51*
Number of peduncle / plant	0.19	0.08
Number of pods / peduncle	0.38	0.21
Number of pods per plant	0.71**	0.83**
Length of branch	0.47	0.61*
Pod length	-0.69*	0.60
Days to 95% maturity	0.48	0.54
Number seed / pod	0.60*	0.63*
100-Seed weight	-0.18	-0.58
Seed yield g/plant	0.89**	0.91**

*, ** = Significant at P < 0.05 and 0.01 respectively.

4.9 Generation mean analysis:

Means along with their respective standard errors for the eight characters studied in the cross IFBx Danilla is presented in Table (26). The mean of the F1 with respect to days to flower tended towards the mean of the smaller parent IFB (F2). The mean values recorded for the characters in F2 and Backcross one (BC_1) were larger and closer to the mean values of the P_1 except for number of branch per plant, that recorded lower but closer mean values to the P_2 . The mean values of BC_1 for days to 50% flower, number of peduncles per plant, number of pods per plant and seed number were higher than what were obtained in the two parents. Whereas, all the characters in BC_2 recorded mean values ranging from the P_1 to P_2 as none was higher than the P_1 means.

Each family variance for the nine characters studied are presented in Table 27. The variances of the F2 generation for the characters were higher than the variances of the other families. Days to flower recorded the highest variance (10.34) followed by length of peduncle (9.74) number of pods per plant (7.41) and number of peduncles per plant (5.31). In all, the F1 family recorded the lowest variance for all the characters in the four generation families.

Table 26: Means and standard errors, of eight cowpea characters in a cross Danilla xIFB.

Character	P_1(Danilla)	P_2(IFB)	F_1	F_2	BC_1	BC_2
Days to 50% flwr	50.33± 0.20	36.67± 0.14	39.00± 0.08	52.33± 0.31	53.0± 0.26	43.67± 0.26
No of Brch/plt	4.43± 0.11	2.33± 0.09	2.10± 0.08	2.92± 0.17	2.42± 0.20	3.47± 0.13
No of peduncle	18.23± 0.20	11.22±0.14	14.42± 0.13	18.76± 0.35	19.25± 0.15	16.33± 0.21
Lgth of peduncle	28.66±0.19	42.00± 0.12	31.71±0.15	37.33±0.40	30.24±0.17	40.00±0.20
No of pods/plt	46.00±0.23	57.64±0.25	44.64±0.22	52.33±0.58	48.30±0.26	57.25±0.32
No of seeds /pod	9.00± 0.12	10.43±0.09	9.72±0.08s	11.00±0.69	13.02±0.16	10.74±0.15
Dys to 95% Mat	82.37± 0.17	65.00±0.16	68.53±0.14	73.00±0.45	82.11±0.21	77.68±0.20
100-seed wt(g)	12.16±0.16	9.7±0.13	8.43±0.10	12.95±0.38	11.22±0.27	11.27±0.13

Table 27: Within family variance of a cross Danilla x Ife brown

Character	P_1	P_2	F_1	F_2	Bc_1	Bc_2
Days to 50% flower	1.25	5.31	0.82	10.34	7.79	5.91
Number of branch /plant	0.48	0.49	0.83	1.06	0.55	0.96
Number of peduncle/plant	1.25	2.49	2.05	5.31	3.68	2.63
Length of peduncle	2.94	2.05	2.87	9.74	4.51	2.54
Number of pods/plant	3.74	3.31	5.91	7.41	4.19	6.13
Number of seeds/plant	0.47	0.82	0.94	0.64	1.63	1.76
Days to 95% maturity	1.63	8.20	2.49	0.64	1.65	2.62
100-seed weight	0.86	0.94	1.25	1.74	1.89	1.43
Number of plants	60	60	120	240	100	100

Results of Joint scaling test are presented in Table 28. The additive and dominance gene effects controlled the variation in the traits. Additive gene effects (D) were larger for days to flower as well as for length of peduncle. The model was extended to a six- parameter model including three interaction terms (i), (j) and (l) of Jinks and Jones (1958); Hayman (1958) (Table 29). Additive (d) dominance, (h) additive x additive (i), additive x dominance (j) and dominance x dominance (l) effects were each calculated. Length of peduncle and number of seeds per pod showed a satisfactory fit with five-parameter model (M) (d), (h), (j), (l) by dropping i which had very little genetic effect. Similarly, number of branches per plant showed best fit with (M), (d), (h), (i) and (j) by dropping, (l). Opposite signs with (i) and (l) indicated duplicate gene action. This applied to days to flower, length of reduncle, number of pods per plant and number of seeds per pod. Only days to maturity indicated negative sign with (h), (i), (j), and (l) effects. The remaining characters displayed same signs with i and l indicating complementary gene action. The interactive gene effects of additive x dominance (j) components also manifested for all the characters studied. Meanwhile, the two other gene interaction components (i) and (l) were very low for number of branches per plant.

The estimates of the components of genetic variance, D, H and F, degree of dominance $(H/D)^{1/2}$, broad and narrow sense heritability estimates are presented in Table 30. The adequacy of additive–dominance model was further tested by partitioning the variations to show type of allelic or non-allelic relationship. Both the Additive (D) and dominance (H) components were greater than zero and therefore found significant for all the characters studied. H was higher for all the traits except length of peduncle where D was greater than H. Positive degree of dominance (F), of individual gene interaction were recorded for days to flower, number of pods per plant, number of peduncles per plant and 100-seed

weight. It is also of note that the degree of dominance may not be unidirectional as revealed in the negative F ratios for number of branch and seed per pod and days to maturity. It therefore suggested dominance towards the smaller parent (Ife brown). Heritability in the narrow sense ranged from 10.49% for 100-seed weight to 67.12% for length of peduncle.

Table 28 Joint scaling test using weighted least square means with three parameter Model M, D, H of Mather and Jinks (1985), Singh and Chaudhary (985).

Character	M	D	H	X^2
Days to 50% flower	52.03±0.16	10.33±0.41	3.07±0.83	103.43
Number of branch/plant	2.92± 0.08	-0.75± 0.32	4.49± 0.71	17.24
Number of peduncle/plant	18.75± 0.14	2.92± 0.32	-4.12± 0.89	52.17
Length peduncle	35.39±0.22	-9.76± 0.12	-4.96± 2.14	10.11
Number of pod/plant	52.33± 0.41	-8.55± 0.41	-5.08± 0.91	19.51
Number of seed /plant	14.00± 0.09	0.29± 0.24	-2.83± 0.04	1.25
Days to 95% maturity	73.00± 0.19	4.45± 0.27	-7.27± 1.31	148.22
100-seed weight	13.93± 0.08	-1.11± 0.21	2.71± 0.41	65.71

Table 29: Genetic Component estimates of six Generation means fitted to a six parameter model of Hayman (1958), Jinks and Jones (1958) in a cross Danilla x Ife-brown

Character	M	D	h	i	j	L
Days to 50% flower	52.03 ± 0.16	10.33** ± 0.41	3.07** ± 0.83	1.97** ± 1.04	-12.63** ± 0.72	-16.23 ± 1.95
Number of branch / plant	2.92 ± 0.08	-0.75** ± 0.32	4.49** ± 0.71	0.70 ± 0.71	1.05** ± 0.32	0.78 ± 1.32
Number of peduncles /plant	18.75 ± 0.14	2.92** ± 0.32	-4.12** ± 0.89	-3.84* ± 0.87	6.43** ± 0.87	-9.02* ± 1.45
Length of peduncle	35.33 ± 0.22	-9.76** ± 0.12	-4.46** ± -2.11	0.84 ± 1.26	-16.43** ± 0.46	-5.66 ± 1.62
Number of pods / plant	52.33 ± 0.44	-8.95** ± 0.41	-5.08** ± 0.91	1.78 ± 1.08	-14.45** ± 0.75	-18.60 * ± 2.17
Number of seeds /pod	14.00 ± 0.09	0.29 ± 0.24	-2.83* ± 0.04	0.41 ± 1.01	3.51** ± 0.52	-6.07* ± 0.89
Days to 95% maturity	73.00 ± 0.19	4.45** ± 0.27	-7.27* ± 1.31	-2.09* ± 0.93	-21.85** ± 0.48	-27.01* ± 2.99
100- seed weight	13.95 ± 0.08	-1.11* ± 0.21	2.71** ± 0.41	-1.76** ± 0.63	4.29* ± 1.31	-7.33* ± 1.11

Table 30 Estimates of additive (D) and dominance (H),direction of dominance (F), degree of dominance (H/D), broad and narrow sense heritability (Hb; Hn) for eight characters in a Cross Danilla x Ife-brown Cowpea.

	Days to 50% flwr	Number of branch/plant	Number of peduncles/plt	Length of peduncle	No of pods/plt	No of seed/pod	Dys to 95% mat	100 sd wt
D	13.96	1.22	8.62	24.86	5.00	1.86	-5.98	0.32
H	42.41	4.32	17.97	16.48	30.63	11.35	13.36	41.59
F	1.88	-0.41	1.05	1.97	1.94	-0.13	-0.97	0.47
$H/D^{½}$	1.74	1.88	1.44	0.84	2.48	2.47	1.50	11.40
Hb	89.16	72.43	82.00	89.34	76.60	87.29	67.31	63.30
Hn	35.56	25.84	40.05	67.12	18.72	21.48	31.77	10.49

4.10 Early Generation Selection:

The means of the characters with high performance and those with low performance expressed in percentage are presented in Table 31. The character increase derived from the F_3 were generally higher than those derived from F_2 and F_4 generations except for number of branches and number of peduncles per plant. Similarly observations were made in the IFB x IARW (Table32). The percentage of characters with high performance to characters with low performance was highest for the characters in the F3 generation.

Table 31: Means of selected family groups of F_2, F_3 and F_4 for high and low Characters expressed in a cross IFB x Dan of cowpea.

Cross A IFBX Dan. Character	Family	High (H)	Low (L)	(H-L/H)%
Number of Days to 50% flower	F_2	35.23	30.51	16.67
	F_3	43.16	33.06	30.30
	F_4	40.22	34.13	15.00
Number of branch/ plant	F_2	6.30	3.20	50.00
	F_3	4.22	3.32	35.00
	F_4	3.13	2.10	33.00
Number of peduncle/ plant	F_2	15.21	8.20	46.67
	F_3	14.05	10.22	41.57
	F_4	12.32	7.06	28.63
Number of pods/ peduncle	F_2	3.20	2.06	33.33
	F_3	3.21	1.16	66.33
	F_4	3.27	2.23	33.33
Length of peduncle (CM)	F_2	51.76	26.04	49.96
	F_3	45.50	42.46	68.13
	F_4	43.00	39.24	38.13
Number of pods/ plant	F_2	23.21	39.42	39.63
	F_3	35.42	19.07	45.71
	F_4	20.17	16.51	20.00
Length of pod (CM)	F_2	13.53	6.41	52.59
	F_3	10.82	13.33	75.00
	F_4	9.60	7.05	27.08
Days to 95% maturity	F_2	82.12	68.40	16.69
	F_3	71.75	56.22	21.13
	F_4	70.13	66.61	7.04
Number of seeds/ pod	F_2	10.30	7.63	26.21
	F_3	14.05	9.20	34.29
	F_4	13.63	10.16	25.73
100-seed weight	F_2	13.06	10.22	53.08
	F_3	18.62	8.36	56.94
	F_4	17.13	8.41	52.56
Seed yield (g /plant)	F_2	29.20	22.40	24.14
	F_3	35.13	27.35	30.57
	F_4	30.60	25.06	20.00

Table 32: Means of selected family groups of F_2, F_3 and F_4 for high and low characters expression in a cross IFB x IAR 48W.

IFE Brown character X IAR 48 W		High	Low	Percentage high to low group
Days to 50% flower	F_2	40.4	32.0	20.01
	F_3	43.2	30.7	30.23
	F_4	41.2	33.1	20.13
Number of branch/ plant	F_2	5.0	2.0	60.00
	F_3	4.4	2.0	51.00
	F_4	3.7	2.1	43.24
Number of peduncles	F_2	10.4	5.7	45.19
	F_3	8.1	4.0	50.39
	F_4	10.7	7.2	32.71
Number of pods/ peduncle	F_2	2.2	1.0	50.10
	F_3	2.6	1.2	53.85
	F_4	2.1	1.0	47.62
Length of peduncle	F_2	33.1	25.2	24.24
	F_3	30.4	17.4	43.33
	F_4	28.6	24.7	13.64
Number of pods / plant	F_2	32.4	23.2	28.12
	F_3	31.3	20.0	35.48
	F_4	25.4	18.2	28.80
Length of pods (cm)	F_2	14.7	9.6	35.01
	F_3	10.1	6.1	40.00
	F_4	10.4	7.1	30.00
Days to 95% maturity	F_2	70.2	61.2	21.86
	F_3	65.7	50.3	23.08
	F_4	64.3	50.1	19.88
Number of seeds/ pod	F_2	16.1	12.1	25.00
	F_3	14.2	10.0	38.57
	F_4	10.6	7.2	28.10
100-seed weight (g)	F_2	12.2	8.2	33.33
	F_3	14.1	7.1	50.00
	F_4	10.7	6.8	40.00
Seed yield g/ plot	F_2	18.2	22.2	22.00
	F_3	21.7	11.5	28.31
	F_4	15.3	15.2	26.11

Realized heritability (Rh) derived from selection in F2 and response in F3 (Table 33) were moderate to high in both crosses (Ife-brown x Danilla; Ife-brown x IARW) for all the characters except for length of peduncle and 100-seed weight and seed yield.

The genetic advance (GA) for the characters in Ife-brown x Danilla and Ife-brown x IARW are presented in Table 34. The genetic advance was moderately high for the characters selected in F_3.

Although very low GA values were recorded for the characters selected in F_3 the differences were not remarkable. Inter-family correlation coefficient values for yield and the yield characters in the two crosses are presented in Table 35, number of branches, number of peduncles, number of pods per peduncle, pods per plant, length of pod and number of seeds per pod showed significant correlation with seed yield in F2 – F3 family in the two crosses. 100-seed weight was significantly correlated with seed yield but the correlation was in the opposite direction in the cross IFB x Dan. Similarly, length of pod recorded a negative but significant correlation with seed yield in the IFB x IARW.

Table 33: Family Realized heritability (%) for yield and yield characters in two crosses of cowpea (IFB xDAN; IFB x IARW)

Character	Family response	IFBxDanilla	IFBxIAR48W
Days to 50% flower	$F_2 - F_3$	37.1	50.1
	$F_3 - F_4$	30.0	45.7
No. of branch / plant	$F_2 - F_3$	68.2	54.3
	$F_3 - F_4$	40.1	49.7
No. of peduncle / plant	$F_2 - F_3$	41.4	40.2
	$F_3 - F_4$	50.6	55.3
No. of pods / peduncle	$F_2 - F_3$	64.2	68.2
	$F_3 - F_4$	50.2	50.1
Length of peduncle	$F_2 - F_3$	34.1	31.4
	$F_3 - F_4$	30.7	27.0
No. of pods / plant	$F_2 - F_3$	73.4	78.3
	$F_3 - F_4$	41.0	53.0
Length of pod	$F_2 - F_3$	50.2	48.4
	$F_3 - F_4$	43.7	29.2
Days to 95% maturity	$F_2 - F_3$	54.7	70.4
	$F_3 - F_4$	50.2	59.6
No. of seeds / pod	$F_2 - F_3$	50.9	60.0
	$F_3 - F_4$	40.2	47.9
100-seed weight	$F_2 - F_3$	30.5	31.5
	$F_3 - F_4$	36.0	39.2
Seed yield g / plot	$F_2 - F_3$	51.2	30.4
	$F_3 - F_4$	30.1	28.8

Table 34: Genetic advance (in percentage) for yield and yield characters in two crosses of cowpea for the selected families.

Character	Family Response	IFBxDanilla	IFBxIAR48W
Days to 50% flower	$F_2 - F_3$	41.3	36.2
	$F_3 - F_4$	40.4	30.5
Number of branch/ plant	$F_2 - F_3$	58.2	47.2
	$F_3 - F_4$	50.6	41.8
Number of peduncles / plant	$F_2 - F_3$	39.2	44.1
	$F_3 - F_4$	22.4	32.0
Number of pods/ peduncle	$F_2 - F_3$	53.0	38.1
	$F_3 - F_4$	41.2	40.2
Length of peduncle	$F_2 - F_3$	40.2	38.6
	$F_3 - F_4$	40.1	50.1
Number of pods / plant	$F_2 - F_3$	62.1	54.3
	$F_3 - F_4$	45.2	40.1
Length of pods (cm)	$F_2 - F_3$	30.7	27.2
	$F_3 - F_4$	31.2	30.1
Days to 95% maturity	$F_2 - F_3$	45.3	60.2
	$F_3 - F_4$	40.2	41.4
No. of seeds / pod	$F_2 - F_3$	64.1	54.9
	$F_3 - F_4$	52.2	40.0
100-seed weight (g)	$F_2 - F_3$	58.2	48.7
	$F_3 - F_4$	41.3	53.2
Seed yield g / plot	$F_2 - F_3$	50.4	40.2
	$F_3 - F_4$	42.1	36.7

Table 35: Inter-family correlation coefficients for yield and yield characters in the generations of two crosses of cowpea (Ife-brown x Danilla; Ife-brown x IARW).

Character	Family	Ife-brown X Danilla	Ife- brown X IARW
		Response	
Days to 50% flower	$F_2 - F_3$	0.27	0.41*
	$F_3 - F_4$	0.20	0.32
Number of branch/ plant	$F_2 - F_3$	0.76**	0.61**
	$F_3 - F_4$	0.51*	0.54**
Number of peduncles	$F_2 - F_3$	0.46*	0.23
	$F_3 - F_4$	0.14	0.17
Number of pods/peduncle	$F_2 - F_3$	0.40*	-0.51**
	$F_3 - F_4$	0.22	0.44**
Length of peduncle	$F_2 - F_3$	-0.19	0.26
	$F_3 - F_4$	-0.22	0. 12
Number of pods / plant	$F_2 - F_3$	0.73**	0.60**
	$F_3 - F_4$	0.34	0.50*
Length of pods (cm)	$F_2 - F_3$	0.51**	-0.40**
	$F_3 - F_4$	0.31	-0.49**
Days to 95% maturity	$F_2 - F_3$	0.24	-0.38*
	$F_3 - F_4$	0.41*	0.18
Number of seeds/ pod	$F_2 - F_3$	0.66**	0.50*
	$F_3 - F_4$	0.41*	0.60**
100-seed weight (g)	$F_2 - F_3$	-0.31	-0.41*
	$F_3 - F_4$	-0.17	0.22

*, **=Significant at 0.05, and 0.01 respectively.

CHAPTER FIVE

5.0 DISCUSSION

The significant wide variations between characters measured on the cowpea genotypes indicated genetic diversity for varietal improvement of cowpea. Branch length, number of pods per plant, height at flower, days to maturity, and days to flower, with relatively high variations indicated high prospect for selection in cowpea yield improvement. The genotypes with short branches and short stems (LDPD, Ife-Brown, IT97k-508-2 and AGRIB VI) could serve as parents when breeding for reduced plant canopy; and that seed yield could be improved using Danilla, AGRIB VI, Tvx-3236, IT97k-499-39, Owode and KVX-745-17k genotypes with higher seeds and pod numbers per plant as parents. That most of the genotypes flowered and matured at different periods, indicated that they were of different genetic background. The variation observed in stem, flower, dry pod, seed colour, height at flower, branch length, pod and seed number was indicative of genetic diversity. The identification by PCA of length of branch and peduncle, number of seeds per pod, seed coat texture and dry pod colour, height at flower and maturity and even length of peduncle as major components of variations among the accessions indicated the reliability in the use of these characters in distinguishing among cowpea varieties. It is worthy of note that length of branches automatically result in increased leaf number and hence increased photosynthetic apparatus which consequently increase accumulation of photosynthate leading to increased yield. Shalini *et al.* (2003), identified branch number, leaf length and node number as most variable characters in accessions of herb plant. Furthermore, selecting for these vegetative characters can also be very useful in breeding for reduced crop canopy or form. In addition to the characters identified by PCA, Canonical correlation analysis further included days to flower and maturity, number of

pods per peduncle, seed eye colour and leaf greenness as best variables that discriminated the cowpea genotypes. The identification of maturity period would enhance breeding for earliness in cowpea. The Principal component and Canonical correlation analyses identified the use of number of seed per pod, seed coat colour, height at flower and maturity, length of branch and fresh pod colour as criteria for classifying cowpea accessions. It is worthy of note that if pods are bone on branches, it follows that branching trait which determine seed number and consequently seed yield will be most reliable characters to be selected. Pod and seed characteristics may also be considered as criteria for classification where seed and pod colour attraction is the priority. According to Gower and Ross (1969), Sneath and Sokal, (1973), PCA resolves total variation into linear and independent smaller units which accounts for maximal variability in a data. Grain yield, fodder yield and maturity period are considered the ultimate variables in varietal development but seed quality characters including coat texture and colour must be equally considered particularly in Nigeria. Discriminant analysis highlighted seed weight, seed coat colour and texture and leaf shape as most important. Seed coat texture and colour influence choice of a given cowpea variety. Cowpea with smooth coat takes longer time to germinate and even cook as the coat is less permeable to water Singh *et al*, (1997). Therefore, cowpea breeding programme must consider seed quality characters in addition to seed quantity characters before successful yield improvement programme is carried out. The importance of quantitative and qualitative characters to yield has been identified by many workers (Rao, *et al.* 1997, Ariyo, 1993, Shalini *et al,* 2003).

PCA, discriminant and Canonical techniques are therefore identified to produce complementary result in that, while PCA and Canonical techniques considered both quantitative and qualitative characters as most important variables, Discriminant

technique identified seed quality characters as most important in cowpea grouping. Therefore Discriminant analysis and any of the PCA or Canonical analysis would be appropriate in describing the variation in cowpea accessions. Ariyo (1993) also reported some similarities between PCA, Canonical and Factor analyses in characters of okro. Nair *et al.*(1998), also reported similar techniques in multivariate analysis of sugarcane. Accession clustering grouped accessions from same origin together while others from different origins also clustered together. This implied that geographical diversity is not a measure of genotypic diversity in cowpea. That accessions within the same eco-geographic background recorded similar characteristics with accessions from other clusters clearly supported that geographical diversity is not a measure of genetic diversity in cowpea. It therefore explains that character evaluation, based on eco-geographic location of accessions, is not a true index of genetic diversity. This finding is at variance with an earlier study of Ariyo and Odulaja, (1991), who found correlation between genetic diversity and eco-geographical background. But the earlier work of Ariyo (1987), Gupta *et al.* (1991), and Rabbani *et al.* (1998), supports the finding that geographic diversity is not a measure of genetic diversity.

The genotypes revealed varied performance in yield and yield components for the seasons- location environments. The genetic make up of the genotypes allowed these genotypes to respond differently to the rainfall, relative humidity, solar radiation, etc. The intensity of sunshine was more pronounced in the late season that cowpea yield was lower in the late seasons for some genotypes. This may be attributed to the fact that water supply needed for continuos plant metabolic activities was not available. This therefore exposed the crops to moisture stress which did not allow vigorous crop growth and formation of seeds in the pods. However some genotypes still produced above average

mean yield despite the low rainfall. Cowpea and its grains have recorded variability in character estimates (Leleji 1975, Ariyo 1995, Niazi *et al.* 1999), Dhaliwal *et al*, 2002). Selection for higher yielding genotypes would be more rewarding and reliable if indirect selection for yield, and yield characters are considered. Characters which are phenotypically correlated but not genotypically correlated will not produce repeatable estimates of inter-character associations. Therefore any selection based on such a relationship will result in little or no genetic gain (Ariyo 1995, Cristina and Hall 1995).

Phenotypic correlation incorporates both genotypic and environmental correlations. It was observed that genotypic correlations were in most cases higher than the corresponding phenotypic correlations for most correlating character pairs. The difference in magnitude and direction as well as greater number of significant character relationships for genotypic correlation relative to phenotypic correlation confirmed the influence of environment indices on genetic character expression. Also, the non significant genotypic correlation between any two characters relative to its phenotypic counterpart is indicative of appreciable environmental effect and that selection of such characters will result in no meaningful effort in breeding programme. However, genotypic relationship is of paramount importance in plant breeding. The significant genotypic correlation between days to flower and branch number, number of peduncles per plant, length of branch, days to maturity and grain yield indicate their relative importance in any cowpea improvement programme. The significant genotypic correlation between days to flower with number of branch per plant and pod number per plant in the locations, indicate that branch and pod numbers could be increased with increased flowering period. Cristina and Hall,(1995) reported significant genotypic and phenotypic associations between days to flower, node of first floral bud and isotope discrimination for earliness in cowpea. However the

negative correlation between days to flower and pods per plant in the Abeokuta location is indicative of some compensatory relationship between the characters. Also the significant positive genotypic correlation of branch number with pod number, branch length, days to maturity and seed number implied that the more the branches, the more the pods formed on the branches, hence more seeds. Ordinarily, increase in branch number, as well as peduncle number, result in more pod formation on the peduncles, and consequently, more seed yield. However, the negative but significant correlation between branch number and seed weight; and branch length and seed weight indicated that selection for increase in length of branch might result in reduction in seed weight. That seed number correlated significantly but negatively with seed weight explains the fact that the more seeds are formed in the pods, the lighter the weight of such seeds. Ordinarily, a reduction in weight may result in reduction in size; and even allow more seeds to fill the pods. The negative effect however, have been absorbed by the increase in seed number, to still result in higher seed yield as evident in the significant positive correlation of seed number with seed yield. Kharednam and Niknejad (1974); Ariyo, *et al.* (1987), reported negative but significant correlation between seed number and seed weight in cowpea. Hybridization efforts therefore, should be focused at producing heavier seeds from lesser plant stands and lesser pod number than lighter seeds from greater and more plant stands with longer branch carrying pods. Cost of producing heavier seeds is lesser than cost of producing lighter seeds in terms of farm inputs (field area, planting stock, cultural practices etc.). Significant environmental and phenotypic correlation between seed yield and number of branch, number of pods, lengths of branch and length of peduncle in the two locations, and its correlation with duration of flowering and maturity in Ogbomoso location, implied that seed yield improvement based on the phenotypic performance of these characters will

not be effective and reliable. The negative environmental correlation of seed yields with seed number in both locations implied that pod filling can be impaired by sub-optimal environmental condition. The observed differences in environmental correlations with the characters studied exposed the existence of different environmental influence on character performance in each of the Ogbomoso and Abeokuta agroecology.

Inter-character correlation measures mutual association with no regard to cause and effect relationships, (Ariyo 1995). The direct and indirect effect of character is better explained by the path analysis (Dewey and Lu 1959, Niazi *et al,*1997). That branching trait and pod number are very important traits in cowpea yield explains the fact that branch number automatically result in increased pod number. That number of peduncles per plant had the largest direct effect on seed yield in spite of its low correlation with yield revealed the defect of selecting on the basis of inter- character correlations alone. Days to flowering had a large but negative direct effect on seed yield in the late planting season of Ogbomoso. A similar result was obtained by Ariyo *et al.* (1987), on Okra. This is probably because increase in days to flowering resulted in continuous abortion of flowers in the seasons of heavy rainfall. However, planting was carried out much earlier and this allowed sufficient flowering before on-set of heavy rains during the early planting season of Ogbomoso. This enhanced pod formation which eventually resulted to high yeild in the Ogbomoso early season. Therefore,genotypes can be sown immediately before or after heavy rains in the planting seasons so as to prevent flower abortions accompanied by heavy rainfall. Number of pods per peduncle and seed weight recorded large negative direct effect with low genotypic correlations on seed yield in the locations. This is a strong indication that these characters were under high environmental influence and therefore, caution should be taken in the selection of these characters as efforts to improve

yield via these characters may be diminished by unfavourable environmental factors. Board *et al.* (1997), recorded high negative direct effect of seed number and weight in soybean. The inconsistency observed on the direct and indirect effects of some characters on cowpea seed yield in both locations exposed the locational environmental influence on inter character associations. .The residual effect determines how best the causal factors account for the dependent factor which is the yield (Ariyo *et a*l, 1987). From its estimates therefore, it implied that the causal factors adequately accounted for the yield estimates. On the basis of path and correlations analyses, it is established that seed yield in cowpea is affected by number of pods per plant, branch number, length of pod and branch length. For hybridization and selection purposes, emphasis should be placed on those characters with high heritability in order to produce repeatable results.

The use of simultaneous selection parameters for high yield and stability in genotype x environment interaction (GxE) studies is of paramount importance as quality of selection is enhanced. Some genotype would have been dropped ordinarily based on one stability parameter alone. The use of only regression parameter to determine the stability of genotypes is often criticized as it assumes a strong linear response to environments. This of course, may not always hold as there were deviations from linearity which could not be explained by the error terms Therefore, phenotypic expression of a particular trait in a given environment is dependent on the mean performance, linear response to environment and stability of performance (Breese, 1969, Delacy *et al.* 1996, Ariyo, 1990).

The significant variance due to heterogeneity for all the characters except branch number implied that character variation among the genotypes are better predicted based on linear response to environmental changes. That seed yield and some of the other characters showed some amount of significant additive and non-additive response, indicated that

variation in seed yield of cowpea was under both environmental and genetic influence. Annicchiarico (1997), reported both additive and non additive influence on the yield of maize.That IT97K-499-39,IT90K-76,TVx-3236, LDPD,Owode and AGRIBVI produced above average yield and adapted to all environments by the stability parameters, is a pointer to the fact that these genotypes can still produce high yield even under high moisture stress. Although IT95K-1091-3 was high yielding it was considered unstable by the deviation mean square and unbiased estimator. IAR48B and IAR48W which were classified stable by the stability parameters had below average yield and therefore undesirable. From practical point of view therefore, use of regression coefficient in addition to any other stability parameter would show clearly the performance of genotypes. Therefore it is advised that regression coefficient and any other stability parameter be jointly used to select stable genotypes with consistent performance. This agrees with the work of Annicchiarico (1997), in the use of Unbiased estimator and Deviation mean square to select for stable genotypes.

On the basis of modified rank sum method, however, nine genotypes were adjudged stable at 50% selection level. This was against the thirteen genotypes adjudged stable by the yield rank and rank- sum methods. This explains the discriminatory abilities in the use of Rank Sum method. Kang (1995), identified eight out of fifteen varieties of maize as stable using the modified rank- sum method. That nine genotypes were identified stable in addition to having high yield is an indication of broader adaptation of these genotypes. On the other hand IT95k-1091-3, IT97k-1090-12-and IT90k-508-2, which were selected using yield rank can be test planted in specific environments to determine the environment most suitable for high yield and stable performance.

In the genotype x environment interaction study, the significant proportion of total variation due to GXE interaction implied that selection for cowpea grain yield based on the additive model alone could be misleading. This is because the specific components accounting for the GXE interaction could not be revealed, hence genotypes response to varying environments becomes unpredictable.

Unlike the linear regression analysis, the AMMI model explained the structural variations in the GXE interaction better than the LR. The main effect treatments were portioned into genotype, environments and GXE interaction. The percentage contribution of the environment to the total sum of squares showed that the locations represented a fair contrasting environment for GXE analysis in cowpea. Fox *et al.* (1997), Gauch, (1992) noted the usefulness of AMMI in superior genotypes selection even in multi locational field trials. Successful selection of genotypes with high yields, and structural display of the relationship between such genotypes and the given environment is enhanced using AMMI bi-plot (Crossa *et al.* 1990, Cooper *et al*, 1996). AMMI model identified IT92K-686-2 and IT90K-1090-12 in addition to TVx-3236, Owode, LDPD and AGRIB VI as having above average yield and low IPCA interaction and therefore most suitable for cultivation across the planting seasons, in Abeokuta.. When a genotype and environment have same sign on the PCA axis, their interaction is positive. But, if different their interaction is negative (Ariyo 1998). While Ife-brown and IT97K-113-6, would be suitable for cultivation in Ogbomoso specific environment.

The above average yield performance of IT97K-499-39, TVx-3236, LDPD, Owode and AGRIB VI in each of the second planting seasons, even under reduced rainfall testify to the fact that cowpea yield is not affected by low soil moisture content and that cowpea can be drought tolerant (Padulosi *et al*, 1995).

Correlation between PC scores and yield characters were significant across seasons. This indicated that the scores could adequately represent the genotype main effects. The PC2 scores had a near perfect correlation with yield than PC1 scores even though there was no remarkable difference. This is in agreement with the finding of Yan and Hunt, (2001), that PC 2 scores appeared better correlated with yield than PC1 scores with a significant difference. The evidence of equal importance of PC1 and PC 2 scores is manifested in the significant positive correlation between PC1 and 2 scores respectively with branch number and number of pods per plant. This implied that branch and pod number contributed immensely to GXE interaction among the genotypes. LDPD, IT97K-499-39, TVx-3236 and Owode which produced average branch and pod number still yielded far above average in the two locations Ogbomoso and Abeokuta. The negative and non significant correlation between PC scores and seed weight implied that weight of seeds is not important in seed yield determination. Therefore, breeding for higher seed number is more important than for higher seed weight in improving seed yield of the genotypes studied especially for IT95k-1091-3 and IAR- 48B with highest and lowest seed number s respectively.

The genes controlling the traits in smaller parent (IFB) were dominant over the larger parents for most of the traits studied. IFB flowered and matured earlier than Danilla. This implied that the use of IFB as a parent in selection for earliness can be successful. Earliness in maturity without increased yield is not a worth while effort. Therefore the effect of reduced branch number is nullified as dominant and epistatic gene effect was feasible in the mean values of F_2 and backcrosses for pod and seed number with heavier seed weight.

The mean values of the F_1, F_2 and backcrosses for seed number indicated transgressive segregation towards over dominance resulting in production of higher seed number from the progenies. Therefore selecting for more seed number even in the early generation of F_2 will be an added advantage over reduced branch number so as to effectively increase seed yield via seed number. This finding is at variance with the work of Drabo et al (1984), Leleji, (1974) who reported non transgressive segregation for seed number and size in cowpea. The high genetic variance of the F_2 populations for all the characters implied that selection for these traits especially in the early generation can be reliable and successful. Understanding the genetic determination of traits helps the breeder in formulating breeding techniques for combining desirable characters, dispersed in two or more genotypes into one (Singh and Chaudhary 1996). According to Tefera (1995), comparison of varieties released from direct selection of germplasm and hybridization indicated that recombinant inbred varieties yielded 9% higher than the former. Therefore, knowledge on the gene action in quantitative traits is important for enhancing cowpea yield especially for environment sensitive varieties.

According to Mather and Jinks (1982), Singh *et al.* (1984), gene interaction is considered complementary when i and l estimates have same sign and duplicate when the signs are opposite. This is true in the complementary gene actions for number of branch per plant, number of peduncles per plant, days to maturity and 100- seed weight.The effect of these complementary gene actions on these traits is such that yield improvement via peduncle number alone will not be successful until the other complementary traits are incorporated. The complementary effect of these traits will produce new recombinants capable of improving yield. This finding is in line with the work of Kearsey and Pooni (1996), Tefera and Peat (1997a), on Tef species and discovered complementary gene action

controlling culms length, panicle weight and spikelet per panicle. However, this finding is at variance with the earlier work of Singh et al (1997), in a cross of two inbred lines of pea where there was no complementary gene action in number of branch per plant and days to maturity. The duplicate nature of epistasis in the inheritance of days to flower, length of peduncle and number of seeds per pod, indicate the difficulty in exploiting these traits for cowpea improvement in the early generation. That H component was not zero (O) confirms that the traits were not dominant at all loci, but epistatic except peduncle length which exhibited partial dominance (D was higher than H). Moreover, that D values were less than H values indicated the presence of non-allelic relationship. Some of the dominant traits were ambidirectional in their respective effects. The direction of dominance for branch number, seed numbers and days to maturity were negative and towards the smaller parent (Ife-brown). According to Singh et al. (1987), negative F value indicate gene interaction towards smaller parent. Therefore, in breeding for increased branch number, seed number with reduced days to maturity, Ife-brown would serve as a reliable parent stock. Khattak, *et al.* (2002), reported partial dominance for plant height at first flower and first pod maturity for mungbean and that degree of dominance was towards the larger parent. Prior to this time, Singh, *et al.* (1987), had reported only partial dominance for days to flower, number of seeds and 100-seed weight in peas with dominance towards larger parent for days to flower and plant height. Successful crop manipulation requires identification of loci at which gene interaction occurs especially with respect to quantitative traits. (Mather 1949). The lowest additive genetic variation (0.32%) for 100-seed weight indicated non-genetic influence on the weight of cowpea seed; while length of peduncle was greatly under additive genetic control. The reliability in selection of these characters in development of inbred lines was manifest in the high

broad sense heritability estimates, which ranged from 63.30% for 100-seed weight to 89.34% for length of peduncles. Practically, the duplicate epistatic gene effect on flowering period length of peduncle and number of seeds per pod reveals the difficulty in improvement of these traits especially at the early generation selection of F_2 and BC_2. Therefore, to achieve success in breeding for reduced flowering date for example, high genetic variance and i interaction effects must be fixed. Tefera (2002) reported duplicate epistasis for days to heading, primary panicle branches and gain yield per plant in Tef crop. That *vigna unguiculata* is a diploid species, is the likely reason for duplicate gene interaction. Gene interaction was dominant and towards the smaller parent (Ife-brown) in the cross Danilla x Ife-brown for length of peduncle. Therefore, the long peducles recorded in the F_2 and Bc_2 would make early generation selection for this trait a worthwhile effort in improvement of seed quality via peduncle length. It is assumed that the longer the peduncle length, the lower the pest and disease incidence on the pods borne on the peduncle and consequently, the more the yield especially in humid areas where fungal disease incidence is high. Cowpea breeding programmes have released a lot of varieties originating from a lot of crosses for different desirable traits. But the specific cross of Danilla X Ife-brown is not yet exploited in achieving earliness with reduced crop canopy as well as improved yield.

On the early generation selection, persistence of the wide variations between selected high and low groups of the F_3 derived from F_2 indicated the expression of genetic variability in the early generation. This suggests that performance of branch number, lengths of pod and peduncle are better measured and selected for in the F_2 with respect to F_3 populations. Selection of pod and seed number and yield traits can be effectively made at an earlier generation of F_2 before proceeding to F_3 generation. This implied

effectiveness in direct and indirect selection for yield via pod and seed number in F_2 population. Flowering period, peduncle number and seed weight performed maximally at the later generation of F_4. Seed yield can be improved through indirect selection for these yield components at later generation of F_4.

The realized heritability (Rh), derived from selection in F_3 and response in F_4 were generally high for all traits. These high estimates, are actually expected because at the F_3 generation, variability is reduced and crops tended towards more stable inbred genotypes. Falcinelli *et al.* (1983), reported breeding towards homozygosity in cross pollinating crops from later generations. However, where environmental variation is reduced due to use of special designs, rh estimates becomes reliable for selection among F_2 plants. Fasoula, (1981), Mitchell *et al.* (1982), reported the use of honeycomb design to reduce environmental variation with special crops as check cultivars. The consequence of this special design was high rh in F2. Indirect selection based upon one or more of yield components is more effective than direct selection for seed yield itself (Smith 1976, Alexander *et al,* 1984). This is in consonance with the high Rh with response to all the traits except for maturity date and seed yield. Highest Rh with response in F_3 and selection in F_4, for branch number and maturity date demonstrated that selection can be effective and reliable with these two traits but less effective with flowering date, seed weight and direct selection for yield. Even though branch number recorded high mean value in F_2 high Rh and moderate mean value at the $F_3$was enough to assure for reliable indirect selection at the later generation (F3)

Estimates of genetic advance (GA) and Rh of a character can be very informative, and reliable in genetic breeding studies. This is because unbiased estimates can lead to substantial progress in improvement of crop genotypes (Ketata *et al*,1976). The moderate

Abstract

to high GA obtained for branch number, pods per peduncle, pods per plant, length of peduncle, days to maturity and seed number per pod in later generations suggested that environmental effects were very minimal on the performance of these traits.

In cowpea, moderate GA for days from flower to maturity is predictive and encouraging still (Falcinelli *et al*,1983). However, high estimates for GA and Rh are better realised only if most of the genetic effects are additive. This is because according to Ketata, *et al*.(1976), non-additive effects may reduce the amount of genotypic superiority available for future breeding programme.

That Rh and GA were on the high side in their respective character connotes the complementary use of the two estimates in best describing trait genetic performance in variable environments. Better still, the reliability of these selection indices foretells the use of direct and indirect trait selection in early and especially late generations for substantial yield improvement. The significant correlation coefficients of yield in F_3 and F_4 family generations with numbers of branch, peduncle, pods, seed number, and seed yield respectively, supported that seed yield improvement can be achieved via improved performance of these traits. The more the branch, the more, the pod number and hence increase in seed yield via increased seed number. More seeds resulted in lesser weight of seeds and hence the negative influence of seed weight on yield. Singh, and Singh (1997), reported significant correlation of kernels per spike; plant height and Grain yield in wheat. That these traits recorded high Rh in addition to significant positive correlation coefficient, have actually complemented the use of Rh and GA though, few discrepancies existed in individual trait selection. This fallout not withstanding, the use of these three selection indices have been complementary and informative in enhancing genetic and breeding work.

5.2 CONCLUSION AND RECOMMENDATION

The use of multivariate statistical technique is important in the classification of broad based accessions within a germplasm collection. In cowpea, the use of PCA or Canonical and Discriminant techniques resulted in the identification of both qualitative and quantitative characters that best described the variation within the accessions. PCA or Canonical correlation techniques complimented Discriminant analysis in that crop morphology and seed quality characters were best described using PCA or Canonical techniques while Discriminant technique best grouped accession variations based on the qualitative characters. The use of cluster analysis revealed correlation between genetic diversity and eco-geographic background. It revealed at a glance character performance based on accession groups. These variations within and between genotypes would be of practical value if the inter-character associations are known therefore, the various character performance are better determined under environmental and genetic influence. The characters were quite variable and exhibited higher genotypic correlation relative to the phenotypic correlation this indicated environmental influence to some extent. The inter-character relationship would serve as a guide in formulating hybridization procedure to be employed for genotype selection. The path analysis revealed some character to have direct or indirect effect on yield.

Heritability estimates were fairly high for most of the characters in Ogbomoso planting environment location this assumed lesser environmental effect on the performance of the genotypes. G x E interaction provided an opportunity to understand the performance of cowpea genotypes over the planting environments. The regression coefficient, S^2di, δi^2 and WMS stability parameters were discriminatory in identifying stable genotypes with

respect to the characters. Regression coefficient (b) and any of S^2di, WMS and δi^2 could be jointly used to select stable genotypes with consistent performance. S^2di and WMS identified fewer genotypes to be stable while δi^2 identified more genotypes to be stable. However, the integration of modified rank sum enhanced the quality of selection of high yielding and stable genotypes. Better still, from practical point of view, a combination of character stability variances with AMMI analysis, justified the selection of genotypes with average and or above average yield for specific and wide environment adaptation.

Cowpea traits are under additive- dominant gene effects. The additive gene effect for some traits would enhance pure line breeding. Days to flower, length of peduncle, number of pods per plant and number of seeds per pod are controlled by duplicate epistatic gene action and therefore would not ensure easy and successful hybridization effort in a meaningful cowpea improvement programme. Effective character selection at the earlier generation of F_2 than at the later generation of F_3 would enhance yield improvement. Character selection at later generations reduces variability as genotypes tend towards more stable inbred lines. The Genetic advance and realized heritability estimates are equally reliable and effective in selecting genotypes for effective breeding programme. Genetic advance and heritability estimate can be considered to achieve confidence in selection procedure leading to successful breeding research work.

RECOMMENDATION

Based on the findings of this study, the following recommendations are made:

1. Multivariate statistical techniques are appropriate for the classification of diversity among cowpea germplasm. Principal component and Canonical

techniques compliment the use of Discriminant analysis in exposing the diversity of cowpea genotypes based on qualitative and quantitative characters. Cluster analysis is particularly useful in grouping genotypes along side with their desirable traits expressed. This is desirable in choosing parents for hybridization.

2. The following characters should be included in the measurement of variability within cowpea germplasm: seed coat and texture, number of branch and length of branch, number of peduncles per plant, height at flowering and maturity date of flowering and maturity and number of seeds per pod. Depending on the focus of research, other characters may be included.

3. LDPD, Ife-brown and AGRIB VI could serve as sources of genes for reduced plant canopy and reduced days to maturity.

4. Seed yield could be increased by breeding for varieties with increase in branch number and length. This will eventually result in increased pod number and hence seed yield.

5. In the development and release of cowpea for cultivation, GxE analyses identified the following genotypes with stability of performance and average yield: IT97K-499-39, TVx-3236, LDPD Owode and AGRIB VI for wide and specific cultivation and even where the moisture status is unpredictable. Ife-brown and IT97K-113-6 for Ogbomoso and IT96K-686-2 and IT90K-1090-12 for Abeokuta specific environments respectively.

6. Cowpea cultivation under minor drought environment can still produce appreciable yield.

7. Additive-Dominant gene effects was adequate in explaining gene effects for cowpea traits. Additive gene effects for these traits were higher than the dominant gene effects. 8. There's possibility therefore in breeding for pure-line varieties and hybrids if breeding for increased seed weight is the objective. But where breeding for reduced days to maturity with more branches and increased peduncle length and more seeds are the objective, Ife-brown becomes a better parent stock especially in humid environment. There may be difficulty in improving cowpea performance via flowering date, number of pods per plant and number of seeds per pod as these traits are controlled by duplicate epistatic gene action.

8. Branch number, number of peduncle per plant days to maturity and 100-seed weight were controlled by complementary gene action. Therefore continous hybridization would lead to outstanding result.

9. Branch number, number of pods per plant and number of seeds per pod are better measured and selected for in the early generation of F_2.

10. Timing of character selection should ensure that yield traits are selected for at early generation of F2 as genetic variability is reduced and genotype performance tend towards stable inbred lines at later generations.

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Appendix 1: Mean monthly temperature, rainfall relative humidity for the study months (1999-2001) in Abeokuta location

Months	1999			2000			2001		
	Mean temp (°c)	Relative Humidity (%)	Rainf-all (mn)	Mean temp (°c)	Relative Humidity (%)	Rainfall (mn)	Mean temp (°c)	Relative Humidity(%)	Rainfall (mn)
January	26.0	71.2	2.1	27.0	75.0	92.5	25.6	73.7	2.6
February	26.0	54.2	8.1	27.8	67.1	94.7	26.2	53.4	8.6
March	25.3	68.1	78.2	26.1	70.5	97.2	26.8	68.2	80.0
April	28.3	95.3	91.3	29.2	78.2	94.7	25.6	72.0	105.0
May	27.8	82.4	100.8	28.1	82.0	103.3	25.0	75.9	110.3
June	27.2	84.0	110.5	26.4	88.7	14.2	24.2	81.1	105.9
July	25.6	83.3	115.0	25.7	88.3	147.2	23.8	82.8	115.5
August	25.4	75.2	90.8	25.1	60.7	92.6	26.5	70.1	99.62
September	25.4	70.2	93.00	26.12	60.0	86.0	20.6	79.7	100.11
October	25.9	57.0	18.00	26.7	85.1	30.1	21.6	74.0	34.5
November	27.3	61.1	3.51	28.4	50.4	3.7	21.4	70.3	5.4

Mean monthly temperature, rainfall relative humidity for the study months (1999-2001) in Ogbomoso location

Months	1999			2000			2001		
	Mean temp (°c)	Relative Humidity (%)	Rainfall (mn)	Mean temp (°c)	Relative Humidity (%)	Rainfall (mn)	Mean temp (°c)	Relative Humidity (%)	Rainfall (mn)
January	310	68.1	1.6	30.0	67.6	2.0	28.0	69.0	2.3
February	31.4	68.0	2.0	30.2	66.1	2.1	30.2	68.3	1.7
March	28.1	69.6	61.2	28.8	69.1	56.7	26.5	70.1	2.7
April	26.4	71.3	92.8	27.5	70.2	90.8	30.0	67.2	87.5
May	27.8	73.1	100.2	27.0	85.1	105.7	28.3	70.1	110.2
June	27.0	81.4	103.5	26.8	90.2	100.2	27.0	69.0	104.3
July	25.9	78.1	101.2	26.0	88.1	99.0	27.4	67.3	100.2
August	28.9	67.1	86.2	30.6	65.0	65.8	30.1	71.0	79.3
September	27.8	66.2	60.7	31.0	65.8	58.2	28.0	67.3	71.6
October	271	60.3	20.5	32.0	85.0	18.2	27.2	61.2	31.4
November	28.2	55.1	3.4	31.7	67.5	1.7	26.0	61.2	3.0