“GENETIC VARIABILITY AND PATH ANALYSIS FOR YIELD ATTRIBUTING TRAITS IN COWPEA (*Vigna unguiculata* (L.) Walp.)”

M.Sc. (Ag.) THESIS

by

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COLLEGE OF AGRICULTURE
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“GENETIC VARIABILITY AND PATH ANALYSIS FOR YIELD ATTRIBUTING TRAITS IN COWPEA (*Vigna unguiculata* (L.) Walp.)”

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CERTIFICATE – I

This is to certify that the thesis entitled **“Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)”** submitted in partial fulfillment of the requirement for the degree of **“Master of Science in Agriculture”** of the Indira Gandhi Krishi Vishwavidyalaya, Raipur, is a record of the bonafide research work carried out by **Ku. KIRAN TIGGA** under my guidance and supervision. The subject of the thesis has been approved by the Student's Advisory Committee and the Director of Instructions.

No part of the thesis has been submitted for any other degree or diploma (certificate awarded etc.) or has been published / published part has been fully acknowledged. All the assistance and help received during the course of the investigations have been duly acknowledged by her.

Chairman
Advisory Committee

Date:

THESIS APPROVED BY THE STUDENT’S ADVISORY COMMITTEE

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Member : Dr. R.N. Sharma ______________________

Member : Dr. N.K. Choubey ______________________

Member : Dr. R.R. Saxena ______________________

CERTIFICATE – II

This is to certify that the thesis entitled **"Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)"** submitted by **Ku. KIRAN TIGGA** to the Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) in partial fulfillment of the requirements for the degree of **M. Sc. (Ag.)** in the **Department of Plant Breeding and Genetics** has been approved by the external examiner and Student's Advisory Committee after an oral examination.

EXTERNAL EXAMINER

Date:

Major Advisor ____________________

Head of the Department ____________________

Dean/ Dean Faculty ____________________

Director of Instructions ____________________

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LIST OF ABBREVIATIONS

Abbreviations	**Description**
%	Per cent
&	And
°C	Degree Celsius
ANOVA	Analysis of variance
CD	Critical difference
Cm	Centimetre
CV	Coefficient of variation
et al.	and others/ co-workers
Fig.	Figure
g	Gram
i.e.	That is
Kg	Kilogram
ml	Milli litre
S. No.	Serial Number
SEm±	Standard error of mean
SEd	Standard error of difference
TSS	Total soluble solids
Wt	Weight
viz.	Namely
ha.	Hectare
rg.	Regression coefficient
h^2	Heritability
GA	Genetic advance
GCV	Genotypic coefficient of variation
PCV	Phenotypic coefficient of variation

CHAPTER-I

INTRODUCTION

Pulses occupy an important position in the agrarian economy of our country. They provide the cheapest and only economic source of protein which is vital and indispensable for both the human and bovine population. The cowpea (*Vigna unguiculata* (L.) Walp.) despite its name is more closely related to the beans than the peas; is an important food and fodder legume crop and an integral part of traditional cropping system in the semi-arid regions of the tropics and warm sub-tropics (Singh *et al.,* 2003), covering Asia, Africa, Southern Europe, Southern United States and Central and South America where it provides more than half the portion and some essential nutrients in human diets (Oluwatosoin, 1997).

Cowpea a warm-season annual and herbaceous legume being drought tolerant is well adapted to the drier regions of the tropics where other food legumes do not perform well. It grows well even in the soils with more than 85% sand and with less than 0.2% organic matter and low levels of phosphorus. They suitably fit in crop rotations and is also used as a green manure crop, restore soil fertility by fixing nitrogen and checking soil erosion.

Cowpea is of major importance to the livelihoods of millions of people in less developed countries of the tropics particularly in Asia and Africa. It is consumed in many forms like young leaves, green pods and green seeds are used as vegetables and dry seeds are used in various food preparations. Cowpea is considered nutritious with a protein content of about 23-25% and is a rich source of vitamins and minerals, making it extremely valuable where many Indian vegetarian people can not afford protein foods such as meat and fish.

The cowpea is a very old crop, probably native to Central Africa, although it has been grown in South-Eastern Asia for more than 2000 years. Major diversity in cowpea is found in Asia and Africa but the precise origin of cowpea has been a matter of speculation and discussion for many years. Based on the distribution of diverse wild cowpea, East and Southern Africa are considered as the primary region of diversity. Vavilov (1939) considered India as the main *Centre of Origin*. In India, it has been known since the Vedic times. Cowpea belongs to the family leguminosae/ fabaceae, sub-family faboideae, genus *Vigna* and species *unguiculata* with chromosome number 2n = 22 (Steele, 1976). The cowpea is one of several species of the widely cultivated genus *Vigna* has been subdivided in five sub species; three cultivated, *unguiculata*, *sesquipedalis* and *cylindrica* and two wild, *dekindtiana* and *mensenensis* (Verdcourt, 1970).

The name "cowpea" is probably of American origin from the fact that the plant was an important source of hay for cows in the United States and was first used in print in 1798. Cowpea has a number of common names, including southern pea, black-eyed pea, crowder pea and it is known internationally as lubia, niebe, coupe or frijole. Similarly in Africa cowpea is known by many names such as niebe, wake, ewa and kunde. Cowpea has been under cultivation in India from ancient times where it is known by many vernacular names like Lobia (Hindi), Barbati (Bengali), Urohi (Assami), Sonta (Garhwali), Chavati (Marathi), Alasande (Kannada) and Manpayar (Malayalam).

Based on the FAO data, the estimated worldwide area under cowpea is over 12.76 million ha, with over 7.56 million tonnes annual productions. India is the largest cowpea producer in Asia and together with Bangladesh, Indonesia, Myanmar, Nepal, Sri Lanka, Pakistan, Philippines, Thailand, and other far eastern countries, there may be over 1.5 million hectares under cowpea in Asia (FAO, 2007). In India peas has occupied an area of 0.314 million hectares, with a total production of 2.56 million tonnes in 2007-

08 (Anon., 2009 a), while in Chhattisgarh, during 2007-08 area and production of cowpea was 11574.00 hectares and 46257.20 M tonnes, respectively (Anon., 2009 b), The yield level of cowpea in Chhattisgarh is low, which is mainly due to the non-availability of desirable high yielding, disease and insect resistant varieties and poor management practices. Hence, the high yield potential and quality are the main targets for effective breeding programme in this crop.

In self–fertilizing crop like cowpea, the breeder aims at creating new variability by effecting crosses between carefully chosen parents and subsequent selection. Before embarking on any selection programme to develop high yielding types, it is imperative to have knowledge of the magnitude of variability and inter-relationship among different characters in the materials for the characters, which needs to improve. However, the prevalent crop varieties in the region are low yielding. Thus selection for high yielding lines is desirable. Recently a grain type variety "*Khalleshwari*" is released by Indira Gandhi Krishi Vishwavidyalaya, Raipur in 2006.

Yield, a complex and quantitatively inherited character is highly influenced by environmental fluctuations and determined by several component characters. There may not be individual gene but various minor genes may be responsible for yield. So selection for yield should take into account related characters as well. Hence, the knowledge of correlation between yield and its component characters and among the component characters is essential for yield improvement. Path coefficient analysis provides an effective means of partitioning the genotypic correlation coefficients into direct and indirect effects of the component characters on yield, Hence, correlation and path analysis aid in the selection of superior genotypes for more yields in cowpea from the breeding population and cluster analysis is commonly used for studying the genetic diversity of accessions (Perry and McIntosh, 1991).

Hence, a research programme entitled “Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)” was planned with the following objectives:-

1. To study the genetic variability among various genotypes of cowpea for yield and its component traits.
2. To work out the relationship of seed yield with its component in cowpea**.**
3. To estimate the direct and indirect contribution of various attributes on seed yield of cowpea.

CHAPTER-II

REVIEW OF LITERATURE

Cowpea is an important tropical legume with high protein and essential nutrients. It is grown for green pods as vegetable, seeds as pulse and foliage as fodder. The cowpea is highly nutritious. Its green or dried pods are almost as good as pea. It is an inexpensive source of protein, calcium and vitamin A. The crop also helps in maintaining the soil fertility through symbiotic nitrogen fixation. Considering the importance of cowpea in Indian agriculture, attempts have been made to improve the productivity of this crop in recent past.

The development of new variety in any crop species is mainly governed by the availability of genetic variability for the desired character. Genetic material is of greatest interest to the plant breeders as it plays a vital role in framing a successful breeding programme. Knowledge of association among the various characters and path coefficient are of paramount significance to a plant breeder for launching an effective and efficient selection programme.

The accumulation of knowledge and under standing does not proceed in a straight line. Each significant step forward usually becomes possible when different lines of informations are brought together to create a new and deeper perspective. The following account is therefore, intended to accumulate knowledge about the topics relevant to the present investigation in Cowpea. The previously published reports are reviewed in order to obtain a complete understanding of the subject under the following headings:

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation analysis

2.4 Path coefficient analysis
2.5 Divergence analysis

2.1 Genetic variability:

The knowledge on the nature and extent of genetic variability in any crop species plays an important role in framing a successful breeding programme. The genetic variability is the raw material of the plant breeding industry on which selection works to evolve superior genotypes, therefore, its thorough understanding is very important for efficient utilization in crop improvement. The extent of variability in a crop is of paramount importance in its improvement. There are two kinds of variability in crop plants, genetic and non-genetic. The genetic variability is the pre-requisite of any crop improvement programme. The non-genetic variability is the result of genetic and environmental interactions. The non-genetic or phenotypic component of variability is however, not of much use to breeders, since it cannot be perpetuated from generation to generation.

Vavilov (1951) advocated that wide range of variability provides better scope of selecting desirable genotype. The study of genetic variability was made for the first time by the great biologist Fisher (1918) and subsequently the estimates of genotypic and phenotypic variations were used to predict the expected genetic response. Subsequently a number of other workers have also discovered several techniques for the estimation of components of variance (Lush, 1940 and Robinson, 1966). The genetic variability has been studied by many scientists in a number of crop plants.

Some of the earlier reports of genetic variability in cowpea have been reviewed in the following paragraphs.

Trehan *et al*. (1970) observed highly significant differences for nine characters among forty varieties of cowpea. The estimates of genetic variance were high for number of branches, pods per plant and peduncle length and medium values for all other characters studied. High genetic coefficient of variation was obtained for number of branches, pods per plant, yield per plant and length of peduncle. Genetic advance in percentage of mean was highest for pods per plant. Selection and improvement for characters like length of peduncle, pods per plant and yield per plant can be based on this phenotypic performance.

Bapna and Joshi (1973) working on cowpea, observed high genotypic coefficient of variation for number of pods per plant, number of seeds per plant, hundred seed weight, number of days to flowering and maturity. The genetic advance was high for number of pods, seeds per pod and hundred seed weight.

Bliss *et al.* (1973) recorded medium to high heritability for seeds per pod, 50 seed weight and methionine content. The Genotypic Coefficient of Variation (GCV) was higher for 50 seed weight; seeds per pod, percent protein and methionine content and yield was having high positive correlation with 50 seed weight at both phenotypic and genotypic levels.

Vaid and Singh (1983) obtained high phenotypic and genotypic coefficient of variation for the characters like plant height, number of pods, pod length and pod yield per plant.

Yadav and Bhutani (1988) observed highly significant differences for days to 50% flowering, plant height, branches per plant, pods per cluster, length of pods, thickness of pods, seeds per pod, pods per plant, yield per plant. Dry matter content showed non significance difference among the genotypes studied. The estimates of genetic advance and heritability (broad sense) were high for yield and number of pods per plant.

Das *et al*. (1993) observed that the number of pods per plant, plant height, primary branches per plant, days to flower, pod length, pod weight, seeds per pod, 100 seed weight and pod yield per plant showed highly significant differences among the genotypes. Similarly Sreekumar *et al.* (1996) obtained high values of genotypic coefficient of variation and phenotypic coefficient of variation for pod length and number of seeds per pod.

Singh and Verma (1999) evaluated 600 cowpea germplasm and recorded high coefficient of variation for yield per plant, plant height, 100 seed weight and pods per peduncle.

Ewa Ubi *et al*. (2001) observed high variability for days to flowering, pod length and 100 seed weight. The highest GCV was observed for 100 seed weight.

Vidya *et al*. (2002) obtained wide range of variability for number of pods per plants, green pod yield per plant and pod characters indicating diversity among yard-long bean cultivars. Yield of vegetable pods per plant recorded highest genotypic and phenotypic coefficient of variation followed by number of pods per plants and pod weight. Similarly Singh *et al*. (2003) revealed that high value of genotypic and phenotypic coefficient of variation were recorded for plant height, number of primary branches per plant, number of peduncles per plant, number of pods per plants and green pod yield per plant.

Nigude *et al*. (2004a) observed that the genotypic and phenotypic coefficients of variation were higher for plant height, grain yield per plant and number of pods per plant. The magnitude of Phenotypic Coefficient of Variation (PCV) was higher than GCV for all the characters studied.

Resmi *et al*. (2004) obtained considerable genetic variability among 30 genotypes for yield and yield contributing traits. High PCV and GCV were recorded for pod yield per plant, pods per kg, inflorescence per plant and pod weight.

Narayanankutty *et al.* (2005) evaluated sixty-three accessions of vegetable cowpea for 12 quantitative characters including yield in a field experiment conducted in Kerala, India. High variability was observed for pod yield, pod weight, number of pods per plant, pod length, number of pickings and 100 seed weight.

2.2 Heritability and genetic advance:

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimate alone. However, it is not necessary that a character showing high heritability also exhibit high genetic advance (Johnson *et al*., 1955). Numerous experiments were conducted by breeders to determine relative importance of environmental and genetic variance. Lush (1940) defined the broad sense heritability as the ratio of genotypic variance to total variance. Different methods of estimating heritability have been given by Kaul (1967) and Reddy & Heyne (1968).

Johnson *et al*. (1955) stated that the broad sense heritability estimates may vary greatly depending upon the unit for which the variance is considered, further emphasized that the effectiveness with which selection of genotypes can be based on the phenotypic performance. The value of heritability depends on all the components of variance; a change in any one of these components will affect the estimates. The amount of progress reported through selection for obtaining the best individuals cannot be made on the basis of heritability alone. The genetic progress would enhance with an increase in heritability estimate. Hence, the heritability estimate could be best utilized in conjugation with genetic advance in predicting genetic gain. Burton (1952) has suggested that genotypic coefficient of variation together with heritability estimate would give the best picture expected for selection.

Literature available about heritability and genetic advance on cowpea is reviewed here:

Trehan *et al*. (1970) studied important yield contributing characters in cowpea and found medium values of estimates of heritability for all characters studied except days to flowering for which the estimates were low. Genetic advance was high for pod yield per plant, pod length and number of pods per plant.

Bapna and Joshi (1973) studied broad sense heritability in cowpea and observed high heritability estimates for number of pods per plants, seeds per pod, seed weight, number of days to flowering and maturity, genetic advance was high for number of pods per plant, seed yield per plant and 100-seed weight.

Veeraswamy *et al*. (1973) studied eight characters in cowpea and found high estimates of heritability coupled with high values of genetic advance for pod length, pod weight and number of pods per plant.

High genetic advance for number of pods per plant (Bordia *et al*., 1973; Tikka *et al*., 1977), pod yield per plant (Pandita *et al*., 1982), seed yield per plant (Vaid and Singh, 1983) was reported in cowpea.

Yap *et al*. (1977) observed high heritability estimates for only pod length in cowpea. Angadi *et al*. (1978) recorded high genetic advance for number of branches per plant, number of pods per plant, seed yield per plant and 100-seed weight.

Jana *et al*. (1982) reported that GCV was high for number of pods per plant, and vegetable pod yield per plant. Heritability, genetic advance along with phenotypic and genotypic variances were high for days to flower and 1000 grain weight.

Shobha (1994) reported high magnitude of heritability coupled with high genetic advance for vegetable pod yield and pod weight.

Sreekumar *et al.* (1996) obtained high values of heritability for pod length and number of seeds per pod along with high genetic advance, indicating additive gene action, whereas number of days to flower and number of days to first picking with low genetic advance.

Ram and Singh (1997) revealed pod length and green pod yield per plant as high heritability estimates combined with high genetic advance.

Rangaiah and Nehru (1998) observed high heritability for number of pods per plant, pod length, pod weight and seed weight in cowpea and high heritability coupled with high genetic advance for pod length and pod weight in cowpea.

Genetic advance was high for pod weight and yield per plant, which can be relied upon for the effective genetic improvement of cowpea (Shobha and Vahab, 1998).

Vardhan and Savithramma (1998) recorded high heritability for number of pods per plant and pod length.

Hazra *et al*. (1999) revealed that high value of phenotypic and genotypic coefficient of variation, heritability and genetic advance was observed for plant height and green pod yield per plant in cowpea.

Ewa Ubi *et al*. (2001) observed a very high heritability and genetic advance for 100 seed weight where as moderate heritability coupled with low genetic advance for days to 50 percent flowering.

Vidya *et al.* (2002) evaluated 50 genotypes of vegetable cowpea and observed high genotypic coefficient of variation, heritability in broad sense and genetic advance for yield of vegetable pods per plant, number of pods per plant, pod weight and pod length. High genetic advance were observed for plant height, peduncle length, number of primary branches per plant, number of peduncles per plant and green pod per plant (Pal *et al*., 2003).

Venkatesan *et al*. (2003b) reported high heritability coupled with high genetic advance for plant height, dry matter production, pods per plant and seed yield per plant indicating the importance of additive gene effects and pod length also exhibited high heritability.

Narayanankutty *et al.* (2003a) conducted genetic variability and divergence studies on thirty-seven genotypes of vegetable cowpea, which revealed significant differences for all the twelve characters studied. High phenotypic coefficient of variation and genotypic coefficient of variation were noticed for fruit yield, pods per plant and weight of pod. High heritability coupled with high genetic advance was also observed for the above characters, indicating additive gene action and emphasized the effectiveness of selection for the improvement of these traits.

Resmi *et al*. (2004) obtained high heritability coupled with high genetic advance for pod yield per plant, pods per kg, inflorescence per plant, pod weight and keeping quality of pods indicating scope of selection for improvement in these characters.

2.3 Correlation analysis:

Yield of plant is not a unitary character but depends on the development of various plant characters. Contribution of each character towards increase in yield varies from crop to crop. Some of them have substantial contribution while others have meager. Correlation helps in finding out the association between different characters and measure the strength of relationship between two variables.

The concept of correlation was represented by Galton (1888) and he suggested the need of coefficient of correlation to describe the degree of association between variables. Later the theory of correlation was developed by Pearson (1904). The concept of correlation was later on elaborated and discussed by Fisher (1918) and Wright (1921) for plant breeding programmes. Thereafter, Searle (1961) described the mathematical implications of correlation coefficient at phenotypic, genotypic and environmental levels.

A brief review of correlation of seed yield and its components in cowpea is summarized below:

Premsekar *et al*. (1964) observed that yield of pod weight was positively and significantly correlated with number of pods per plant, length of pod and number of seeds per pod in F_1 and F_2 derivatives of an interspecific cross between *Vigna sesquipedalis* x *Vigna sinensis*.

Trehan *et al*. (1970) worked out correlation coefficient and reported that seed yield per plant was significantly correlated with seeds per pod, length of peduncle and pods per plant can be used for indirect selection of pod yield per plant.

Bapna *et al.* (1973) studied the correlation between yield and agronomic characters in cowpea and reported that pods per plant, seeds per pod and seed size were main components of yield with high magnitude of positive and significant correlation

Bliss *et al.* (1973) reported positive correlation between yield and seed weight and also among seed yield, pods per plant and seeds per pod. Aryeetey and Laing (1973) observed that yield per plant was positively correlated with pods per plant but it was negatively correlated with pod length. Bordia *et al*. (1973) recorded that pods per plant, seeds per pod, 100 seed weight and pod length was positively correlated with green pod yield.

Lakshmi and Gaud (1977) and Tikka *et al*. (1977) noted significant and positive correlation among principle yield components namely pods per plant seeds per pod and seed size in cowpea.

Erskine and Khan (1978) observed positive correlation between seed yield and pods per plant; and negative correlations among seed yield, seeds per pod, seed weight and pod length.

The results of correlation and path analysis in cowpea carried out by Hanchipal *et al.* (1979) revealed that seed yield per plant was positively correlated with plant height, number of branches, number of pods and dry pod yield per plant in winter sown cowpea, while it was positively correlated with number of seeds per pod and dry pods per plant in summer sown cowpea. They also recorded that 100 seed weight was negatively correlated with number of pods per plant and number of branches per plant in both the seasons.

Pandey and Tiwari (1981) worked out correlation of morpho-physiological and sink parameters in cowpea and reported that green pod yield and seed yield were positively and significantly correlated with pods per plant and 100 seed weight.

Jana *et al.* (1983) reported that pod yield was positively and significantly associated with number of pods per plant. Number of pods per plant was also positively and significantly associated with number of primary branches. The number of primary branches was negatively correlated with days to flower and pod length but positively associated with green pod yield per plant.

Obisesan (1985) studied association among yield components in 14 genotypes of cowpea and reported that number of pods per plant, 100 seed weight and number of seeds per pod were positively related to yield.

Choulawar and Borikar (1987) noted that pod yield per plant was positively and significantly correlated with plant height, pod length and 100 seed weight.

Patil *et al*. (1989) observed that yield was highly correlated with pods per plant, 100 seed weight, clusters per plant, pod length and days to 50% flowering in cowpea.

Tewari and Gautam (1989) revealed that high and positive correlations were found between green pod yield and primary branches per plant, pods per cluster, clusters per plant, 100 seed weight and seeds per pod in cowpea.

Altnbas and Sepetoglu (1993) revealed that seed yield per plant was significantly and positively correlated with number of pods per plant, number of seeds per pod and number of branches per plant whereas thousand seed weight was negatively and significantly associated with number of pods per plant and seeds per pod.

The positive association of pod yield with number of pods per plant, pod weight and pod length was reported by Shobha (1994).

Biradar *et al*. (1996) observed that seed yield was positively correlated with component traits except plant height in F_2 generation. Among them pod weight per plant, pod length, seeds per pod, clusters per plant and pods per plant showed consistent positive association with seed yield.

Golsangi *et al*. (1996) also observed that seed yield was positively and significantly correlated with number of pods per plant, length of pod, pod yield per plant and number of seeds per pod in cowpea.

Ram and Singh (1996) evaluated 34 genotypes and revealed that green pod yield per plant has strong positive correlation with plant height, pod length, pod diameter. It has also positive association with peduncle length and days to flower. The yield trait pod length had significantly positive association with plant height, pod diameter, and total soluble solids. The number of branches had strong positive correlation with pods per plant.

Sreekumar *et al*. (1996) found green pod yield was found positively correlated with number of fruiting points per plant, number of pods per plant, pod length, and number of seeds per pod.

Naidu *et al*. (1996) recorded significant and positive correlation with seed yield, pods per plant, pod length, seeds per pod and seed weight in determinate and indeterminate population of cowpea.

Chattopadhyay *et al*. (1997) studied genotypic and phenotypic correlation of green pod yield with various component characters in 20 genotypes of vegetable cowpea grown in two seasons reported that pod length, green pod weight, dry pod weight, seeds per pod and 100 seed weight had positive and significant association with green pod yield.

Sharma and Mishra (1997) recorded high positive correlation of seed yield with pods per peduncle. Oluwatosin (1997) noted that yield was negatively correlated with protein content in 15 genotypes of cowpea grown at three locations,

Rangaiah and Nehru (1998) found high correlation coefficients for number of pods per plant, pod length and pod weight in cowpea.

Vardhan and Savithramma (1998) reported that positive association of pod yield with number of pods per plant, pod weight and pod length.

Singh *et al*. (1998) studied the correlation in cowpea and revealed that in general, genotypic correlation coefficients were higher than their corresponding phenotypic once. Seed yield per plant was positively and significantly associated with clusters per plant, pods per plant and total biomass per plant.

Vardhan and Savithramma (1998) noted significant and positive correlation of green pod yield per plant with pod length, pod width, fresh pods per plant, biomass and harvest index in cowpea.

The genotypic and phenotypic correlation studies by Nakawuka and Adipala (1999) revealed that branches per plant, pods per plant and seeds per pod had significant positive association with grain yield.

Singh and Verma (2002) evaluated 600 cowpea germplasm and found that seed yield was positively correlated with 100-seed weight and pod length. Pod length and plant height were positively correlated with 100-seed weight and also found that a negative correlation between 100-seed weight and number of pods per peduncle, number of days to 50% flowering and number of days to 50% maturity.

Vidya and Oommen (2002) studied 10 quantitative traits in 50 genotypes of yard long bean and reported pod yield per plant was highly significant and positive correlation with number of pods per plant, number of pods per inflorescence, pod weight, length of harvesting period, pod girth and pod weight at genotypic level.

Narayanankutty *et al*. (2003b) observed in 37 divergent vegetable cowpea germplasm that the number of pods per plant, number of pickings, average weight of pods and pod length were positively and significantly correlated with yield per plant both at phenotypic and genotypic levels. Days to first picking showed significant negative correlation with number of pickings, yield per plant and pods per plant.

Neema and Palaniswami (2003) studied character association in F_2 population of 28 cross combination and found that the characters like plant height, pod yield and pod length had significant positive association with grain yield at both genotypic and phenotypic levels. Pod yield showed significant positive correlation with number of pods, pod length and no of grains per pod.

Venkatesan *et al*. (2003a) reported that branches per plant, clusters per plant, pods per cluster, pods per plant and pod yield had positive direct correlation with total yield at both genotypic and phenotypic level. Number of clusters per plant showed positive association with number of branches per plant, number of pods per cluster and number of pods per plant. Number of pods per plant and number of clusters per plant might be regarded as the most yield component.

Yadav *et al*. (2003) recorded green pod yield per plant was positive and significant association with plant height, pods per cluster, pod length, pods per plant, seeds per pod and pod dry matter.

Nigude *et al*. (2004a) proved that grain yield per plant was significantly and positively associated with all the characters except pod length and test weight at both levels in cowpeas.

Peksen and Artik (2004) reported that pod length and 100 seed weight showed positive and significant correlation with seed yield per plant.

Anbumalarmathi *et al.* (2005) studied that single plant yield had positive and significant association with clusters per plant, pods per plant, pod length, seeds per pod and 100-seed weight as indices for improving yield in cowpea.

Kumawat and Raje (2005b) observed that correlation analysis of seed yield has significant positive correlation with branches per plant, clusters per plant, pods per plant, biological yield per plant and harvest index in cowpea.

Lovely and Radhadevi (2006) carried out association studies in 50 genotypes of yard-long bean and observed that pod yield per plant had strong positive correlation with pods per cluster, pods per plant, pod weight, pod length, pod breadth and seeds per pod.

Biradar *et al.* (2007) revealed that analysis of covariance indicated that the trait of interest yield is positively and significantly associated with its contributing morphological characters. Highest yield was realized through pod number and indirectly by branch number in cowpea.

Alege and Mustapha (2007) investigated that positive correlations were obtained between leaf number and stem diameter, leaf number and number of seeds per pod, number of branches and plant height and negative correlation existed between number of pods per plant and number of seeds per pod.

2.4 Path coefficient analysis

Path coefficient analysis is a plant breeder's technique used to study the partitioning of the correlation coefficient into the components of direct and indirect effects (Li, 1956). Path coefficient analysis is used as an effective tool in finding out the direct and indirect attributes of different contributing characters towards yield. Each component possesses a large direct effect on yield and its important indirect effect result via different yield components (Fonseca and Patterson, 1968).

Seed yield is the product of interaction of many component characters. The study of association between various yield attributes with yield provides a basis for further breeding programmes. However, correlation study does not reveal the direct and indirect contribution of individual character towards seed yield. In such situation, the path analysis provides an effective measure to find out the direct and indirect contribution of an individuals attribute towards the seed yield.

Singh and Mehandiratta (1970) determined the direct and indirect effects of different correlation characters on grain yield. They reported that the pods per plant, number of grains per pod and 100 seed weight had direct positive effect on yield. The indirect contribution of pods per plant was negative via grains per pod and 100 seed weight.

Lian (1975) recorded direct effects of pods per plant, pod length, seeds per pod and 100 seed weight on yield in long bean. Wien and Littleton (1976) observed days to pod maturity had direct effect on yield; whereas 100 seed weight and grain weight contributes indirectly towards cowpea.

Chopra and Singh (1977) conducted path analysis and recorded that leaf numbers, plant height, branch number; branch length and stem girth contributes directly towards yield in cowpea.

Hanchipal *et al.* (1979) carried out correlation and path analysis in cowpea. The results revealed that direct influence of number of branches per plant on seed yield, whereas seeds per pod contributed indirectly via number of branches in cowpea.

Murthy (1982) performed path analysis considering seed yield as dependent variable in F_2 populations of cowpea and reported that pods per plant was major contributor to yield, followed by pod length, seeds per pod and test weight. He further suggested that a selection index based on these characters would be more effective rather than selection for yield alone.

A path coefficient analysis of pod yield made by Jana *et al.* (1983) revealed that number of pods per plant exhibited the highest magnitude of direct effect towards pod yield. The maximum indirect effect came from number of primary branches via number of pods per plant, whereas in negative direction maximum indirect effect exerted by days to flower via the same character.

Padhey *et al*. (1984) suggested that pod length, pods per plant, seeds per pod and test weight were main components of seed yield in cowpea. Chikkadyavaiah (1985) reported that direct effects of plant spread, pods per plant and seeds per pod on seed yield in cowpea. Natarajrathnam *et al*. (1986) recorded the maximum direct contribution of pod weight per plant on seed yield in cowpea.

Patil *et al*. (1989) studied path coefficient analysis and indicated that pods per plant, 100 grain weight and seeds per pod had the greatest positive direct effect on pod yield.

Based on path coefficient analysis, Patnaik and Roquib (1990) suggested that direct selection for days to maturity, days to 50% flowering and number of seeds per pod can lead improvement in yield of cowpea.

Golsangi *et al*. (1992) studied the components affecting the seed yield in cowpea through path coefficient analysis and reported that pods per plant were the most important yield component followed by seeds per pod.

Sawant (1994) recorded pods per plant exhibited the highest effect on seed yield followed by seeds per pod, days to 50% flowering, plant height and pod length. Ariyo (1995) reported that seed yield in cowpea was affected by weight of 100 seeds, seeds per pod, branches per plant and pods per peduncle.

Golsangi *et al*. (1996) reported that pods per cluster and pod length had exhibited direct positive effect on seed yield under normal spacing, whereas pod yield alone showed direct positive effect on seed yield under wide spacing.

Ram and Singh (1996) evaluated 34 genotypes and path coefficient analysis exhibited economically positive direct effect for pods per plant on pod yield but it was suppressed out by negative indirect effects via other variables especially pod length and number of branches. The direct effects of peduncle length, protein percentage and days to maturity on pod yield were also positive. Plant height and days to flowering had positive correlation with pod yield but their direct effects were negative indicating that dwarf plant type with early flowering is desirable for higher yield.

Chattopadhyay *et al*. (1997) determined the components of green pod yield in 20 genotypes of cowpea and reported that green pod weight, dry pod weight, pod number and seeds per pod were most important components, having high magnitude of direct positive effect on green pod yield in cowpea. Rangaiah and Nehru (1998) observed high direct effect for pod weight and number of pods per plant in cowpea.

Singh *et al*. (1998) studied the yield factors on 45 exotic and indigenous genotypes of cowpea and reported that pods per plant and total biomass per plant were most important components; hence selection based on these traits would be useful for improvement in grain yield of cowpea.

Path coefficient analysis carried out by Nakawuka and Adipala (1999) revealed that number of branches per plant, number of pods per plant and number of seeds per pod were the major direct contributors for yield in cowpea.

Vidya and Oommen (2002) recorded that maximum direct effect on pod yield was shown by number of pods per plant followed by pod weight and number of pods per inflorescence. Number of pods per plant also exerted positive indirect effect through length of harvesting period and number of pods per inflorescence while pod weight showed positive indirect effect via pod length and pod girth and negative indirect effect via number of pods per plant.

Kumari *et al.* (2003) reported path analysis of the number of clusters, pods and seeds per plant, and 100-seed weight showed the greatest positive direct effects on seed yield, whereas the number of days to maturity and flowering exhibited the greatest negative direct effects on seed yield per plant.

Narayanankutty *et al*. (2003b) observed that number of pods per plant, followed by average weight of pods and number of pickings, had the greatest positive direct effects on pod yield. The direct effects of pod length and days to first picking were low mainly due to high indirect effects via average weight of pods and number of pickings.

Subbaiah *et al*. (2003) revealed that the number of pods per plant had strong positive direct effect as well as indirect effects through various traits on green pod yield. The other traits namely number of branches per plant, pod length, pod weight, and number of seeds per pod also had strong positive influence on green pod yield.

Venkatesan *et al*. (2003a) evaluated 20 genotypes of diverse origin and path analysis showed positive direct effect on number of pods per plant, pod length, clusters per plant, seeds per pod and hundred seed weight on yield.

Yadav *et al*. (2003) recorded dry matter in pod, pods per plant, seeds per pod and plant height are main components of green pod yield per plant in path analysis studies.

Peksen and Artik (2004) revealed that pod length had highest direct positive effect on seed yield per plant followed by 100 seed weight and number of pods per plant. On the other hand seed yield per plant was directly and negatively affected by pod length and number of branches per plant.

Anbumalarmathi *et al.* (2005) studied that pods per plant, seeds per pod and 100-seed weight had high direct effect on single plant yield. Clusters per plant showed high indirect effect through pods per plant on grain yield.

Kumawat and Raje (2005b) observed that path analysis indicated the high positive direct effect of clusters per plant, biological yield per plant and harvest index on seed yield per plant.

Lovely and Radhadevi (2006) carried association studies in 50 genotypes of yard-long bean and the maximum positive direct effect on pod yield was observed for pods per plant followed by pod weight, pods per cluster, pod length, seeds per pod, main stem length and pod breadth.

2.5 Divergence analysis:

Among several statistical methods developed for measuring the divergence between populations, multivariate analysis or D^2 statistics has been effectively used for quantitative estimate of genetic variability. In this context, Mahalonobis's D^2 statistics is an effective tool in quantifying the degree of divergence at genetic level and it also provides a quantitative measure of association between geographic and genetic diversity based on genotype distance (Mahalonobis, 1936). He introduced the idea of statistical field in which each point represented the centre of density cluster belonging to a particular normal population specified by (i) the means of the characters and (ii) the measure of covariances at the particular point in the field. The advantage with D^2 statistics is that it enables us to obtain an indication of the distances in the p-dimensional shape in which samples are most distinct as also to obtain an estimate of the extent to which the sets in multiple measurements differ.

A brief review of divergence analysis in cowpea based on D^2 statistic is summarized below.

Dharmalingam and Kadambavanasundaram (1989) observed that wide genetic diversity was present among the 13 clusters formed. The genotypes CO-2 and G-5 in cowpea belonging to the two most divergent clusters were recommended as suitable for inclusion in heterosis breeding programmes.

Thiagarajan and Natarajan (1989) revealed that on the basis of multivariate analysis the number of pods per plant, number of seeds per pod and seed yield per plant made a large contribution to the genetic divergence. There was no parallelism between geographic and genetic diversity.

Hazra *et al*. (1993) grouped cowpea genotypes belonging to three cultigroups (*unguiculata, bioflora* and *sesquipedalis*) into four clusters using D^2 statistics. Maximum inter cluster distance between cluster I and IV and minimum between III and IV was observed. The clustering pattern revealed that genetic diversity was not related to geographical diversity. The characters like plant height/vine length, pod length, pod weight, 100 seed weight and pod yield per plant will offer good scope for rational selection because of their important contribution towards genetic divergence of cowpea. They also concluded that genotypes of same cultigroup did not necessary clustered together which might have arisen due to presence of number of intermediate types.

Hazra *et al.* (1996) used genetic divergence technique for choosing parents for hybridization with a view for improving vegetable cowpea involving three cultigroups viz *unguiculata, bioflora* and *sesquipedalis*. Impact of environment on the composition of clusters was evident. Genotypes stable in their grouping in both the environments were considered as good breeding material. Crosses involving the genotypes of *bioflora* and *sesquipedalis* were likely to produce recombinants with desirable characters of both cultigroup because of very high order to divergence between the genotypes of these cultigroups.

Rewale *et al*. (1996) grouped the genotypes into 19 clusters, of which 11 had only one genotype each. There was no relationship between geographical origin and genetic diversity.

Anbuselvam *et al*. (2000) observed that analysis of variance revealed significant variability among genotypes for all traits studied. The highest inter cluster distance

(924.80) was observed between clusters II and IV, indicating high genetic divergence between genotypes belonging to these clusters.

Awopetu and Aliyu (2000) studied genetic diversity within 25 cowpea accessions originating from different ecological areas. The results showed dissimilar biotypes that can be tentatively categorized into early, intermediate and late flowering and eventual pod-maturity groups for further selection. It was observed that geographical distribution as well as previous improvement status or genetic background of the materials basically affected the genotypic relationships among and within the groups and subgroups respectively.

Ushakumari *et al*. (2000) employed D^2 analysis in fifty genotypes of cowpea and grouped all into 13 clusters. IT-86-F-310-6 gave the highest values for number of branches, pod length, and seeds per pod, while IT-87-D-272 gave the highest values for plant height, clusters per plant, pods per cluster, and single plant yield. The highest contributions towards divergence were recorded for plant height (22.69%), seeds per pod (17.63%), number of branches (16.82%), number of pods per cluster (15.27%) and pod length (13.47%).

Borah and Khan (2001) evaluated 60 cowpea cultivars for genetic diversity. The grouping of cultivars into 10 clusters indicated high genetic divergence among the cultivars. The clustering pattern showed that geographic diversity was not an index of genetic diversity. Based on intercluster distance and cluster means for 13 characters (plant height, number of branches and leaves, leaflet length and width, stem thickness, days to 50% flowering, dry matter and green fodder yields, dry weight of leaves and stems, leaf/stem ratio, and crude protein content), clusters I, II, IX, and X were the most genetically diverse. Dry matter yield, green fodder yield and plant height recorded the highest contribution to total genetic divergence, suggesting that these traits are good criteria for the selection of parents for hybridization programmes.

Narayanankutty *et al.* (2003a) conducted genetic variability and divergence studies on thirty-seven genotypes of vegetable cowpea. The thirty-seven genotypes were grouped into eleven clusters using D^2 statistics. In general, the intercluster distances were higher than intracluster distances. The maximum intercluster distance was between clusters VIII and X, followed by clusters VI and X and clusters VIII and IX, respectively. The intracluster distance was maximum in cluster VII.

Neema and Palaniswami (2003) employed D^2 to cluster eight parents and twenty eight hybrids at two locations to asses the relation between the genetic divergence and heterotic expression. Six clusters were made for each location which differs in constitution. The hybrids produced by selection of parents based on D^2 clustering showed high heterotic effect.

Venkatesan *et al*. (2004) grouped the cowpea population into six clusters, of which clusters II and III had the maximum number of genotypes. Analysis collaborated the absence of parallelism between geographic origin and genetic diversity. Intracluster distance was maximum in cluster V and minimum in cluster II. The intercluster distance was maximum between II and VI. Clusters per plant, pods per cluster, pods per plant and seed yield per plant had the maximum contribution towards total divergence.

Nigude *et al*. (2004b) studied the nature of magnitude of genetic diversity in a set of 45 cowpea genotypes from indigenous and exotic sources. The genotypes were grouped into five clusters using Mahalanobis D^2 statistics. Cluster-I was the largest with 28 genotypes followed by cluster-II with 11 genotypes and cluster-III with 4 genotypes. The clusters IV and V were monogenotypic. The maximum inter-cluster distance was observed between clusters III and V followed by distance between clusters II and III.

Clusters I and III exhibited the minimum inter-cluster distance. The number of branches per plant, test weight, biomass (dry weight) at harvesting and number of pods per plant had contributed considerably towards divergence.

Kumari *et al.* (2004) grouped fifty genotypes of cowpea into four clusters on the basis of D^2 values. Maximum numbers of genotypes (45) were included in cluster I, while cluster II and III had two genotypes each, and cluster IV had only one genotype. The cluster pattern of genotypes revealed that the genetic diversity was not always related with geographical diversity. Genotypes in cluster IV recorded high mean values for number of clusters, number of pods, 100-seed weight, seed yield per plant, dry weight per seedling, vigour index and in vitro protein digestibility, with low values for pod length and tannin content. Genotypes in cluster I showed maximum mean values for standard germination and shoot length. Divergent parents from cluster I, cluster III and cluster IV may be used in hybridization programmes to get transgressive segregants for high seed yield and quality traits in cowpea.

Kumawat and Raje (2005a) evaluated fifty genotypes of cowpea for yield and its components and grouped the genotypes into 6 clusters. Average intra-cluster distance ranged from 0.00 (cluster IV) to 5.622 in (cluster II). Seed yield per plant had the highest contribution towards the total genetic divergence followed by seeds per pod, days to 50% flowering, plant height and reproductive period.

Madheshia and Pandey (2005) reported that sixty-five genotypes were grouped into 24 clusters. Significant differences were observed for each character under study. The maximum intra cluster distance was observed in cluster VIII, whereas inter cluster distance between clusters XVII and XXII. The days to first flower and number of pods per plant contributed towards maximum divergence. Based on cluster mean and cluster distance desirable and promising genotypes were also identified.

Magloire (2005) at Bloemfontein worked out genetic divergence of 20 genotypes the results showed a relatively high level of dissimilarity among the accessions for most of the morphological traits analyzed, especially for accessions from different countries. This indicates better possibilities for genetic improvement of the crop through selection and cross breeding.

Mandavi (2005) carried out divergence study on 20 collected germplasm reported presence of appreciable amount of genetic diversity for green pod yield and its components and observed non interallelism among the genotypes and place of collection, showing lot of scope for selection for green pod yield and reported that D^2 value recorded for different characters for varying genotypes in cowpea revealed the presence of appreciable genetic diversity in the genotypes included in the investigation and geographical distribution had no relation to genetic diversity.

Narayanankutty *et al.* (2005) evaluated sixty-three accessions of vegetable cowpea for 12 quantitative characters including yield. High variability was observed for pod yield, pod weight, number of pods per plant, pod length, number of pickings and 100 seed weight. The genotypes were grouped into 8 clusters with variable number of genotypes. Clustering pattern indicated no association between geographical distribution of accessions and genetic divergence. The characters like pod weight, pod yield, number of pods per plant and pod length had the highest contribution to genetic divergence.

Lesly *et al*. (2006) applied D^2 statistics in 169 cowpea genotypes and grouped it all into 46 clusters. Significant differences were observed for all the characters under study. The inter cluster distance was maximum between cluster 11 and 42 followed by 34 and 42. The number of pods per plant contributed maximum divergence which was followed by harvest index and days to flower termination. They further suggested based on cluster distance and *perse* performance of genotypes, selection can be made to get intercrosses to recover good recombinants and desirable segeregants.

Pandey (2007) grouped forty-four cowpea genotypes into nine clusters. Cluster III had minimum days to first flower opening in addition to maximum number of pods per plant and primary branches. Cluster II, V, VII had maximum yield per plant, 100 seed weight, pod length and number of seeds per pod respectively. Cluster II had minimum days to maturity whereas VII had maximum days to maturity. He further suggested that genotypes from high and low cluster mean were most promising for hybridization programme.

Suganthi *et al.* (2007) carried out D^2 statistics among thirty genotypes which were grouped into eleven clusters. Maximum inter cluster distance was found between cluster I and XI, indicating that genotypes of these clusters were more divergent. The diversity among the genotypes measured by inter cluster distance was adequate for improvement of cowpea by hybridization and selection.

Valarmathi *et al*. (2007) evaluated sixty genotypes of *Vigna unguiculata* var. *unguiculata* and 9 genotypes of *Vigna unguiculata* var. *sesquipedalis*. All the accessions were grouped into 12 clusters. Both the varieties were grouped in distinctly different clusters. Days to maturity contributed maximum to the genetic divergence followed by 100 seed weight, number of branches per plant and number of seeds per pod.

CHAPTER-III

MATERIALS AND METHODS

This chapter deals with a concise description of the materials used and the methodologies adopted during the course of investigation. The present investigation "**Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)**" was conducted during *kharif* 2008 at Instructional cum Research Farm and molecular biology laboratory of the Department of Plant Breeding and Genetics, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, Chhattisgarh, India.

The details of materials used and the methodologies applied in the investigation are described below:

3.1 Location and climate:

Raipur is situated in the central part of Chhattisgarh at $21^0$16'' N latitude and $81^0$36'' E longitude with an altitude of 289.56 meters above mean sea level. The climatic condition of Raipur is hot and sub-humid type. The average (50 years) annual rainfall ranges in between 1200 to1400 mm and mostly received from the mid of June to end of September (above 85%), with occasional light showers during winter and summer seasons. May is the hottest and December is the coolest months. The average maximum and minimum temperatures are 43.0°C and 9.3°C in month of May and December 2008, respectively. The atmospheric humidity is high from June to September.

Agro-climatic conditions play an important role for seed yield in cowpea. Weekly average meteorological data i.e. maximum and minimum temperature, rainfall, relative humidity, wind velocity and sunshine hours during crop period (*kharif* 2008), as recorded at Meteorological Observatory, Indira Gandhi Krishi Vishwavidyalaya, Raipur (C.G.) are presented in appendix and depicted in fig 3.1.

The weather during crop period in general was favourable to cowpea. The maximum temperature varied from 28.9°C to 33°C in standard meteorological week no. 31 and 29 with mean value of 31.1°C. Similarly, minimum temperature ranged in between 13.0°C to 25.1°C in standard meteorological week no. 48 and 34 with mean value of 21.8°C; however it started going down from standard meteorological week no. 42 particularly in the month of October and November where crop was at harvest. Sufficient rains were received (589.2mm) in 28 rainy days. There were no rains after October 8th, 2008; sunshine hours were relatively less especially in July and August but from September onwards sufficient sunshine was available to the crop. Other meteorological parameters were normal to the crop.

3.2 Experimental details:

The experimental material for the present investigation comprised of 22 genotypes of cowpea including indigenous as well as exotic origin and elite breeding lines. The material for the study was received from Dept. of Plant Breeding and Genetics, College of Agriculture, Raipur. Twenty two genotypes used in the present study are listed in Table 3.1 and field view of experiment in Plate I.

Table 3.1: List of genotypes/ entries along with source

S. No.	Code	Genotype	Source
1	CP-13	CPD-103	Durgapura, Rajsthan
2	CP-14	VCP-04-001	Vamban, Tamilnadu
3	CP-15	VCP-04-003	Vamban, Tamilnadu
4	CP-16	ACM-05-2	Madurai, Tamilnadu
5	CP-17	ACM-05-7	Madurai, Tamilnadu
6	CP-18	CPD-91	Durgapura, Rajsthan
7	CP-19	GC-502	S.K. Nagar, Gujrat
8	CP-20	HC-08-02	Hissar, Haryana
9	CP-21	KBC-1-M	Bangalore, Karnataka
10	CP-22	CPD-83	Durgapura, Rajsthan
11	CP-23	GC-601	S.K. Nagar, Gujrat
12	CP-24	RC-101 (C)	Durgapura, Rajsthan
13	CP-25	GC-3 (C)	S.K. Nagar, Gujrat
14	CP-26	Subhra	-
15	DCP-2	DCP-2	IARI, New Delhi
16	DCP-6	DCP-6	IARI, New Delhi
17	VBN-1 (LC)	VBN-1 (LC)	Vamban, Tamilnadu
18	TCM-138-1	TCM-138-1	Trombay, Mumbai
19	TCM-148-1	TCM-148-1	Trombay, Mumbai
20	V-130	V-130	IARI, New Delhi
21	V-240	V-240	IARI, New Delhi
22	Khalleshwari (LC)	Khalleshwari(LC)	IGKV, Raipur (C.G.)

The sowing of material was done on 14th July, 2008, as per the experimental details described below. All prophylactic measures were adopted to grow a healthy crop.

Season : *kharif* 2008
Design : Complete Randomized Block Design (CRBD)
Replication : Three
Genotypes : 22
Date of Sowing : July 14th 2008
Plot size : 4 m x 1.8 m
Number of rows/ plot : 6
Spacing : 30 cm x 10 cm
Fertilizer dose : 20: 50: 20 kg N:P_2O_5:K_2O per ha.

3.3 Observations recorded:

Observations were recorded on competitive and randomly chosen five plants from each genotype and from each replication. Phenological observations like flowering and maturity recorded on plot basis. Average of the data from the sampled plants in respect of different quantitative characters was used for various statistical analyses.

3.3.1 Days to 50 per cent flowering:

Days to 50 per cent flowering was recorded in terms of number of days taken to 50 per cent flowering from the date of sowing in individual plots.

3.3.2 Days to maturity:

Days to maturity was recorded in terms of number of days taken from the date of sowing to the physiological maturity on plot basis.

3.3.3 Plant population per plot:

The total number of plants were counted and recorded on plot basis at the time of maturity.

3.3.4 Plant height:

Plant height was measured in centimeters at the time of maturity from the ground level to the tip of the main stem of the plant and averaged.

3.3.5 Number of branches per plant:

The number of branches was counted emerging from the plant base at the time of maturity and averaged.

3.3.6 Number of clusters per plant:

The number of pod bearing clusters per plant on each of the randomly selected five plants was counted at harvest and averaged.

3.3.7 Number of pods per plant:

The number of pods per plant on each selected five plants were counted from first picking to last picking and averaged.

3.3.8 Pod length:

The length of randomly selected five pods was measured in centimeter and averaged.

3.3.9 Number of seeds per pod:

Number of seeds was counted from randomly selected five pods of each plant and averaged.

3.3.10 Seed yield per plant:

The weight of total seeds per plant was recorded in grams for the individual selected five plants after sun drying with the help of electronic balance and averaged.

3.3.11 100-seed weight:

Well developed and sun dried 100 seeds were counted and weighed in grams from each genotype.

3.3.12 Seed yield per plot:

The weight of total seeds produce from each plot was recorded in grams for estimation of yield performance of the genotype and for further statistical analysis five plants seed yield was added to each respective plot.

Quality characters/ seed parameters:

Quality parameters were worked out by using the method suggested by Williams *et al.* (1983).

3.3.13 Seed volume:

Weight of 50 seeds was recorded and then these 50 seeds were transferred to a 50 ml measuring cylinder and 25 ml deminerialised water pipetted in. Seed volume (ml/seed) was calculated as follows:

$$\text{Seed volume} = \frac{(\text{Total volume} - 25)}{50}$$

3.3.14 Seed density:

Seed density was recorded as g / ml and calculated from seed weight and volume by using following formula:

Seed weight

$$\text{Seed density} = \frac{\qquad}{\text{Seed volume}}$$

3.3.15 Hydration capacity per seed (g):

Fifty seeds were weighed and transferred to a 125 ml Erlenmeyer flask and 100 ml water was added. The flask was tightly stoppered and left for overnight at room temperature (22^{o}C). Next day water was drained out from the flask and super fluous water was also removed with absorbent paper and the swollen seeds reweighed. Hydration capacity per seed was recorded as:

$$\text{Hydration capacity/ seed (g)} = \frac{\text{Weight after soaking - weight before soaking}}{50}$$

3.3.16 Hydration index:

Hydration index was estimated as:

$$\text{Hydration index} = \frac{\text{Hydration capacity per seed}}{\text{Original seed weight (g)}}$$

3.3.17 . Swelling capacity per seed (ml):

After reweighing the soaked seeds, they were transferred into a 100 ml measuring cylinder and 50 ml water was added into it. Swelling capacity per seed was recorded as:

Volume after soaking - volume before soaking

$$\text{Swelling capacity/ seed (ml)} = \frac{}{50}$$

3.3.18 Swelling index:

Swelling index was estimated as:

$$\text{Swelling index} = \frac{\text{Swelling capacity per seed}}{\text{Seed volume (ml)}}$$

3.3.19 Seed coat colour, size and shape:

Seed colour, size and shape were observed after the harvesting and threshing of pods.

3.4 Statistical analysis:

The data was finally subjected to various analyses as per the objectives.

3.4.1 Analysis of variance:

The data based on mean values were taken for analysis of variance as suggested by Panse and Sukhatme (1978), which is based on the following linear model

$$Yij = \mu + ti + bj + eij$$

Where,

i = number of treatments (1, 2, 3….. n)

j = number of replications (3)

Yij = value of i^{th} treatment in j^{th} block

μ = general mean

ti = effect of ith treatment

bj = effect of jth block

eij = random error with restrictions that eij ~ N (0, σ^2) has normal distribution.

Table 3.2: The skeleton of ANOVA (analysis of variance)

Source of variation	Degree of freedom	Sum of squares	Mean sum of square	F ratio	Expected mean sum of square
Replications	r-1	SS_r	Mr	Mr/ Me	-
Genotypes	t-1	SS_t	Mt	Mt/ Me	$\sigma^2_e + \sigma^2_g$
Error	(r-1)(t-1)	SS_e	Me	-	σ^2_e
Total	rt-1				

Where,

r = Number of replications

t = Number of treatments

σ^2_e = Expected error mean sum of square

σ^2_g = Expected genotype mean sum of square

The significance of difference among treatment means was tested by F test at 5% level of significance. If significant F value was found, critical difference was calculated to test the significance of difference between any two treatment mean as follows:

a. Critical difference (CD):

CD = SEd X t value at 5 % at error degree of freedom

$$SEd = \sqrt{\frac{2\ EMS}{r}}$$

Where,

SEd = Standard error of difference between two treatment means

EMS = Error mean sum of square

r = Number of replications

b. Standard error of mean

$$SEm = \sqrt{\frac{EMS}{R}}$$

c. Coefficient of variation (CV) (%)

Coefficient of variation is a standard deviation expressed as percentage of mean and calculated as

$$CV\ (\%) = \frac{SD}{\overline{X}} \times 100$$

Where,

SD = Standard deviation

$\overline{X}$ = Mean of character

3.4.2 Estimation of variability parameters:

3.4.2.1 Range

The range of the distribution was expressed by the limit of the smallest and the largest value of each observation.

3.4.2.2 Mean

The mean was calculated by summing up all the observations and then dividing by the total number of observations, as given below;

$$\overline{X} = \frac{\Sigma Xi}{N}$$

Where,

ΣXi = Sum of all observations

N = Total number of observations

3.4.2.3 Estimation of variance and Coefficient of variation:

The phenotypic and genotypic components of variance were computed according to formulae given by Lush (1940). However, genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in percentage were calculated according to following formula;

$$\sigma^2 g = \frac{Mt - Me}{r}$$

Where,

$\sigma^2 g$ = Genotypic variance,

Mt = Treatment mean sum of square,

Me = Error mean sum of square ($\sigma^2 e$)

a. Phenotypic coefficient of variation (PCV)

$$\sigma^2 p = \sigma^2 g + \sigma^2 e$$

$$\text{PCV} = \frac{\sigma p}{\bar{X}} \times 100 \qquad \{\sigma p = \sqrt{\sigma^2 p}\}$$

Where,

$\sigma^2 p$ & σp = Phenotypic variance and its standard deviation,

$\sigma^2 g$ & σg = Genotypic variance and its standard deviation,

$\sigma^2 e$ = Environmental variance,

$\bar{X}$ = General mean.

b. Genotypic coefficient of variation (GCV)

$$\text{GCV} = \frac{\sigma g}{\bar{X}} \times 100 \qquad \{\sigma g = \sqrt{\sigma^2 g}\}$$

3.4.2.4 Heritability (h^2_{bs}) (in per cent):

Heritability estimates (Broad sense) for green pod yield and its components was calculated based on the ratio of genotypic variance to the phenotypic variance and was expressed in percentage (Hanson *et al.*, 1956)

$$\sigma^2_g$$

$$h^2\,({}_{bs})\,(\%) = \frac{\rule{3em}{0.4pt}}{\sigma^2_p} \times 100$$

Where,

$h^2\,({}_{bs})$ = Heritability in broad sense

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

The broad sense heritability estimates were classified as low, moderate and high as follows:

0 - 50 % = Low

51 - 70% = Moderate, and

> 70% = High

3.4.2.5 Genetic advance as percent of mean:

Genetic advance was estimated by using the method suggested by Johnson *et al.* (1955) and the formula is:

$$GA = k.\, h^2.\sigma p$$

Where,

GA = Genetic advance,

k = Selection differential (at 5%, k= 2.06),

h^2 = Heritability estimate,

σp = Phenotypic standard deviation.

GA was reported as percentage of mean and it was calculated as follows:

Genetic advance

$$\text{Genetic advance as percentage of mean} = \frac{\qquad}{\bar{X}} \times 100$$

The GA was categorized as,

>50% = High,

30 - 50% = Moderate, and

< 30% = Low.

3.4.3 Correlation coefficient:

Correlation coefficients were calculated for all possible combinations among all the twelve characters at phenotypic and genotypic levels as per the formula given by Searle (1961).

The significance of correlation coefficients was tested against Fisher's table value for (n-2) degree of freedom at 5 per cent and 1 per cent level of significance, where n is the number of genotypes.

i. Phenotypic correlation between characters x and y

$$r\ xy(p) = \frac{\text{Cov } xy\ (p)}{\sqrt{(\text{Var } x(p))\ (\text{Var } y(p))}}$$

ii. Genotypic correlation between characters x and y

$$r\ xy(g) = \frac{\text{Cov } xy\ (g)}{\sqrt{(\text{Var } x(g))\ (\text{Var } y(g))}}$$

iii. Environmental correlation between characters x and y

$$r\ xy(e) = \frac{\mathrm{Cov}\ xy\ (e)}{\sqrt{(\mathrm{Var}\ x(e))\ (\mathrm{Var}\ y(e))}}$$

Where,

Cov xy(p), Cov xy(g), Cov xy(e)	= phenotypic, genotypic & environmental co-variances between characters x and y, respectively.
Var x(p), Var x(g), Var x(e)	= phenotypic, genotypic & environmental variance of character x, respectively.
Var y(p), Var y(g), Var y(e)	= phenotypic, genotypic & environmental variance for character y, respectively.

3.4.4 Path coefficient analysis

The path analysis was originally developed by Wright (1921) and elaborated by Dewey and Lu (1959). Path coefficient analysis splits the genotypic correlation coefficients into the measures of direct and indirect effects. It measures the direct and indirect contribution of independent variables to dependent variable.

The results of path coefficient analysis were interpreted as per following scale suggested by Lenka and Mishra (1973). Table 3.3

Table 3.3: Scale of path coefficient analysis

Value of direct / indirect effects	**Rate / scale**
0.00-0.09	Negligible
0.01-0.19	Low
0.20-0.29	Moderate
0.30-0.99	High
>1.00	Very high

Path coefficients were estimated using simultaneous equations. The equation shows a basic relationship between correlation coefficient and path coefficient. These equations were solved by presenting them in matrix notations.

$$A = B.C$$

The solution for the vector 'C' may be obtained by multiplying both sides by inverse of B matrix i.e. B^{-1} thus,

$$B^{-1} A = C$$

After calculation of the values of path coefficients i.e. 'C' vector, it is possible to obtain the path value for residual (R). Residual effect was calculated using formula referred from Singh and Chaudhary (1985).

$$R = \sqrt{1- \Sigma d_i \ X \ r_{ij}}$$

Where,

d_i = Direct effect of ith character.

r_{ij} = Correlation coefficient of ith character with jth character.

Direct and indirect effects of different character on seed yield were calculated at genotypic level.

Path coefficients were obtained by simultaneous equations, which express basic relationship between correlation and path coefficient.

$$r_1y = P_{1y} + P_{2y}\, r_{12} + P_{3y}\, r_{13} + \ldots\ldots p\ (n-1)y\ r_1(n-1)$$

$$r_2y = P_{2y} + P_{1y}\, r_{21} + P_{3y}\, r_{23} + \ldots\ldots p\ (n-1)y\ r_2(n-1)$$

$$r_3y = P_{3y} + P_{2y}\, r_{32} + P_{1y}\, r_{31} + \ldots\ldots p\ (n-1)y\ r_3(n-1)$$

↓

Similarly for (n-1)

$$r\ (n-1)_y = P\ (n-1)y + P(n-2)_y\ r\ (n-1)\ (n-2)\ldots\ldots\ldots\ldots,$$

$$P\ \{n-(n-1)\ y\ r(n-1)\ \{n-(n-1)\}$$

Where,

y = the dependent variable

r = Genotypic or phenotypic correlation coefficients between a pair of characters

n = Total number of characters

3.4.5 Divergence analysis

The genetic divergence among the genotypes was carried out using Mahalonobis' D^2 statistic (Rao, 1952). It measures group distance based on multiple characters. With x_1, x_2, x_3,………..x_p as the multiple measurements available on each individual and d1, d2, …...dp as $\bar{x}_1^1-\bar{x}_1^2$, $\bar{x}_2^1-\bar{x}_2^2$, ….$\bar{x}_p^1-\bar{x}_p^2$, respectively being the difference in the means of two populations (Singh and Chaudhary, 1985), Mahalanobis'(1936) D^2-statistics is defined as follows-

$$ {}_pD^2 = b_1d_1+b_2d_2+\ldots\ldots\ldots+b_pd_p $$

Where,

b_i values are to be estimated such that the ratio of variance between the populations to the variance within the populations is maximized. In terms of variance and covariance, the D^2 value is obtained as follows:

$$ {}_pD^2 = W^{ij}\,(\bar{x}_i^1-\bar{x}_i^2)\,(\bar{x}_j^1-\bar{x}_j^2) $$

Where,

W^{ij} is the inverse of estimated variance covariance matrix.

CHAPTER-IV

RESULTS AND DISCUSSION

The results and the salient findings of the present investigation **"Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)"** conducted during *kharif* season of 2008, are presented in this chapter under appropriate heads. Observations on growth and yield attributing traits and seed characters were recorded, analyzed statistically and results are illustrated through appropriate tables, figures and appendices. The genetic information has been obtained through analysis of genetic variability, heritability, genetic advance, association, existing among characters at genotypic and phenotypic levels, path and divergence analyses. Examination of the data reveals several points of interest, which are discussed along with the interpretation of the results keeping in view the findings of other scientists. At the outset, it may be pointed out that, in the present study seed yield and 100-seed weight showed considerable association with the yield attributing traits of the crop. The results obtained from present investigation are presented and discussed under the following heads:-

4.1 Analysis of variance
4.2 Estimates of genetic variability, heritability and genetic advance
4.3 Estimation of correlation coefficients
4.4 Path coefficient analysis
4.5 Divergence analysis

4.1 Analysis of variance

Analysis of variance worked out for seed yield and its component characters along with quality characters, indicated that the mean sum of squares due to genotypes were highly significant for the characters *viz*., days to 50 per cent flowering, days to maturity, plant population per plot, plant height, pod length, number of seeds per pod, 100-seed weight, seed yield per plant, seed yield per plot, seed volume, seed density, hydration capacity, hydration index, swelling capacity and swelling index. Number of branches per plant, number of pods per plant and number of clusters per plant showed non-significant difference among the genotypes studied (Table 4.1). The high magnitude of variability among the genotypes for seed yield and attributing traits indicated that enough scope is there, for the improvement of various traits in selection.

Similar results for pod length were found by Trehan *et al.* (1970), Yadav and Bhutani (1988), Das *et al.* (1993), Ewa Ubi *et al.* (2001), Vidya *et al.* (2002), Narayanankutty *et al.* (2005); for days to 50% flowering by Yadav and Bhutani (1988), Das *et al.* (1993), Ewa Ubi *et al.* (2001); for plant height by Yadav and Bhutani (1988), Das *et al.* (1993); for number of seeds per pod by Yadav and Bhutani (1988), Das *et al.* (1993); for seed yield per plant by Yadav and Bhutani (1988); for 100 seed weight by Das *et al.* (1993), Narayanankutty *et al.* (2005).

4.2 Estimates of genetic variability, heritability and genetic advance

The genetic variability was estimated and is presented in Table 4.2, 4.3 and 4.4 for twenty-two diverse genotypes and discussed here character wise.

4.2.1 Mean and Range

The mean performance and range of variation for 22 genotypes for seed yield and its component characters are presented in Table 4.4 and are described here:

1. Days to 50% flowering:

The days to 50 per cent flowering ranged from 41.33 (CPD-103) to 76.33 (V-130) days with a mean of 56.18 days.

2. Days to maturity:

The mean for days to maturity was 74.24 days and it ranged from 55.67 (GC-502) to 104.00 (Khalleshwari) days. Some genotypes viz. CPD-103, RC-101 (C), GC-601, KBC-1-M, VCP-04-001, ACM-05-2, VCP-04-003, CPD-83, Subhra, CPD-91, HC-08-02, GC-3 and ACM-05-7 exhibited early maturity.

3. Plant population per plot:

The plant population per plot ranged from 37.33 (HC-08-02) to 185.67 (KBC-1-M) with the general mean of 130.65 plants.

4. Plant height:

The plant height for genotypes ranged from 56.87 cm (HC-08-02) to 176.93 cm (V-240) with the general mean of 124.47 cm.

5. Number of branches per plant:

The number of branches per plant was recorded in between 2.93 (GC-502) to 4.47 (DCP-6) with a mean of 3.69 branches per plant.

6. Number of clusters per plant:

The number of clusters per plant was observed between 5.13 (V-240) to 7.47 (Subhra) with a mean of 6.19 clusters per plant.

7. Number of pods per plant:

The mean for number of pods per plant was 11.16 and ranged from 8.53 (GC-502 and CPD-83) to 22.10 pods in variety Subhra.

8. Pod length:

The length of pod for genotypes ranged from 10.73 cm (DCP-2) to 19.47 cm (VCP-04-001) with the general mean of 13.45 cm.

9. Number of seeds per pod:

The number of seeds per pod ranged from 10.00 (CPD-83) to 15.87 (KBC-1-M) with the general mean of 12.08 seeds.

10. Seed yield per plant:

The seed yield per plant ranged from 1.186 g (KBC-1-M) to 6.934 g (ACM-05-2) with an overall mean of 3.90 g.

11. 100-seed weight:

The 100-seed weight ranged from 6.27 g (ACM-05-7) to 16.33 g (CPD-83) with an overall mean of 9.66 g. Among the genotypes, DCP-2, Khalleshwari, GC-601, CPD-91, CPD-103, GC-502 and RC-101 (C) exhibited the higher test weight above 10 g/ 100 seeds.

12. Seed yield per plot:

The mean for seed yield per plot was 323.90 g and it ranged from 58.80 g (Khalleshwari) to 803.3 g (GC-502).

13. Seed volume:

The seed volume was observed between 0.040 ml (Subhra) to 0.143 ml (DCP-2) with a mean of 0.100 ml.

14. Seed density:

The seed density was observed in between 0.804 g/ml (TCM-138-1) to 1.444 g/ml (Subhra) with a mean of 1.06 g/ml.

15. Hydration capacity per seed (g):

The hydration capacity for genotypes ranged from 0.061 g (ACM-05-7) to 0.142 g (Khalleshwari) with the general mean of 0.100 g.

16. Hydration index:

The hydration index for genotypes ranged from 0.604 (KBC-1-M) to 1.524 (Khalleshwari) with the general mean of 1.02.

17. Swelling capacity per seed (ml):

The swelling capacity was observed between 0.041ml (V-130) to 0.142 ml (Khalleshwari) with a mean of 0.100 ml.

18. Swelling index:

The swelling index in was observed between 0.339 (V-130) to 2.557 (Subhra) with a mean of 1.07.

4.2.2 Estimation of genotypic and phenotypic coefficients of variation (PCV and GCV)

The estimation of genotypic and phenotypic components of variation is of primary importance to get an idea of relative extent of heritable and non heritable variation. Thus, the components of variation such as genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were computed. The phenotypic coefficients of variation were marginally higher than the corresponding genotypic coefficient of variation, demonstrating the influence of environment in the expression of the character under study.

The estimated genotypic and phenotypic variation helped in getting a clear understanding of the variability present among the various genotypes (Table 4.4).

Among the different yield attributing traits, seed yield per plot had the highest magnitude of PCV (78.275) and GCV (75.702). The high magnitude of PCV and GCV (above 20%) was also observed for seed yield per plant (46.755 and 34.094) followed by swelling index (39.756 and 38.971), swelling capacity (30.340 and 30.058), plant population per plot (32.220 and 21.660), days to maturity (27.639 and 27.588), plant height (27.942 and 23.090), seed volume (26.610 and 26.502), hydration index (26.120 and 23.721), days to 50% flowering, hydration capacity (21.752 and 21.723) and 100 seed weight (21.214 and 21.145). The high PCV than GCV obtained for the traits, seed yield per plot and seed yield per plant indicate that sufficient variability is present in the studied population for exploitation in the heterosis programme. However the large difference between PCV and GCV obtained for the two traits reveal that the environment plays a vital role in the expression of these traits. Among the quality trait, hydration index exhibiting high PCV than GCV reveal that such traits can be genetically improved through the studied material. The remaining traits showing high heritability was found little difference between their PCV and GCV values.

Similar results for high GCV for number of pods per plant was found by Trehan *et al.* (1970), Bapna and Joshi (1973), Vaid and Singh (1983), Vidya *et al.* (2002), Singh *et al.* (2003), Nigude *et al.* (2004a); for seed yield per plant by Trehan *et al.* (1970), Nigude *et al.* (2004a); number of seeds per plant by Bapna and Joshi (1973); for 100 seed weight by Bapna and Joshi (1973); for days to 50% flowering by Bapna and Joshi (1973); for days to maturity by Bapna and Joshi (1973); but it was not in favour with the findings of Das *et al.* (1993), Sreekumar *et al.* (1996) for number of seeds per pod and pod length.

Similar results for high GCV and PCV for plant height were reported by Vaid and Singh (1983), Singh *et al.* (2003), Nigude *et al.* (2004a).

In present study, moderate (10-20%) to low (<10%) phenotypic and genotypic coefficient of variation were observed for number of seeds per pod (16.591 and 12.966), pod length (16.290 and 14.289), seed density (14.580 and 14.173) and number of branches per plant (17.128 and 7.619). High phenotypic coefficient of variation for number of pods per plant (38.357) and moderate genotypic coefficient of variation (16.320) for the traits were observed which was favoured by the findings of Jana *et al.* (1982). Williams *et al.* (1983) and Waldia *et al.* (1991, 1995) had reported high magnitude of genetic variation for seed volume, seed density, swelling capacity, swelling index and hydration index.

4.2.3 Heritability and genetic advance as per cent of mean

Heritability and genetic advance are the important parameters for selecting genotypes that permits greater effectiveness of selection by separating out environmental influence from the total variability. Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will exhibit high genetic advance (Johnson *et al.,* 1955). Estimates of heritability also give some idea about the gene action involved in the expression of various polygenic traits.

Heritability estimates provides the assessment of amount of transmissible genetic variability to total variability, happens to be the most important basic factor that determines the genetic improvement or response to selection. However, the degree of improvement attained through selection is not only dependent on heritability but also on the amount of genetic variation present in the breeding population and the extent of selection pressure applied by the breeder. The parameter, genetic advance (GA) as per cent of mean is more reliable index for understanding the effectiveness of selection in improving the traits because its estimates is derived by involvement of heritability, phenotypic standard deviation and intensity of selection. Thus, heritability and genetic advance as per cent of mean in combination provides clear picture regarding the effectiveness of selection for improving the plant characters.

Heritability and genetic advance as per cent of mean were estimated for 22 genotypes. The results of which are presented in Table 4.4.

High magnitude of heritability (>70%) was obtained for most of the characters. The highest heritability was recorded for days to 50 per cent flowering (99.89%) followed by hydration capacity (99.74%), days to maturity (99.63%), 100-seed weight (99.34%), seed volume (99.19%), swelling capacity (98.15%), swelling index (96.09%), seed yield per plot (93.54%), seed density (94.02%), hydration index (82.48%) and pod length (76.94%). Moderate (50-70%) heritability was recorded for plant height (68.29%), number of seeds per pod (61.07%) and seed yield per plant (53.17%). However, number of branches per plant (19.79%) and number of pods per plant (18.10%) were exhibited low (<50%) heritability.

The present findings are similar for number of seeds per pod by Bliss *et al.* (1973), Bapna and Joshi (1973) and Sreekumar *et al.* (1996); for days to 50% flowering by Bapna and Joshi (1973) and Jana *et al.* (1982); for days to maturity by Bapna and Joshi (1973); for pod length by Veeraswamy *et al.* (1973), Yap *et al.* (1977), Sreekumar *et al.* (1996), Ram and Singh (1997), Rangaiah and Nehru (1998), Vardhan and Savithramma (1998) and Vidya *et*

***al.* (2002); for 100 seed weight by Ewa Ubi *et al.* (2001); for seed yield per plant by Venkatesan *et al.* (2003).**

But not the accordance to Trehan *et al.* (1970) and Ewa Ubi *et al.* (2001) for days to 50% flowering; Bapna and Joshi (1973), Veeraswamy *et al.* (1973), Rangaiah and Nehru (1998), Vardhan and Savithramma (1998), Vidya *et al.* (2002) and Venkatesan *et al.* (2003) for number of pods per plant; Hazra *et al.* (1999) and Venkatesan *et al.* (2003) for plant height.

These characters representing high values of heritability and genetic advance emerge as ideal traits for improvement through selection due to high variability and transmissibility. Thus, the characters mentioned above are likely to show very high response to selection practiced in breeding population.

The highest genetic advance as percentage of mean was found in seed yield per plot (148.798%) followed by swelling index (77.482%), swelling capacity per seed (60.411%), days to 50% flowering (55.854%), seed volume (53.564%) and seed yield per plant (50.739%). Moderate magnitude of genetic advance was obtained for days to 50% flowering (46.845%), followed by hydration capacity per seed (44.002%), hydration index (43.700%), 100 seed weight (42.743%) and plant height (38.929%). Whereas, low magnitude of genetic advance was obtain for plant population per plot (29.714%) followed by seed density (27.836%), pod length (25.494%), number of seeds per pod (20.952%), number of pods per plant (14.156%) number of branches per plant (7.04%).

High heritability coupled with high genetic advance was noted for days to maturity, seed volume, swelling capacity, swelling index and seed yield per plot suggesting the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters.

High heritability coupled with moderate to low genetic advance was found in the characters days to flowering, pod length, 100-seed weight, seed density, hydration capacity and hydration index.

Moderate heritability coupled with high to moderate genetic advance was found for the characters plant height and seed yield per plant. While moderate heritability coupled with low genetic advance was found in number of seeds per pod only. Characters showing high to low heritability estimates coupled with medium to low genetic advance as percentage of mean indicates greater contribution of dominance and epistasis variance in the expression of characters.

The characters plant population per plot, number of branches and number of pods per plant showed low heritability coupled with low genetic advance. The characters showing low heritability coupled with low genetic advance are worthless in the breeding programme due to low transfer genetic materials from one generation to other Table (4.5).

Similar results were found for seed yield per plant by Bapna and Joshi (1973), Vaid and Singh (1983) and Venkatesan *et al.* (2003). But not the accordance to Trehan *et al.* (1970), Rangaiah and Nehru (1998) and Vidya *et al.* (2002) for pod length; Trehan *et al.* (1970), Bapna and Joshi (1973), Veeraswamy *et al.* (1973), Bordia *et al.* (1973), Tikka *et al.* (1977), Angadi *et al.* (1978), Vidya *et al.* (2002) and Venkatesan *et al.* (2003) for number of pods per plant; Bapna and Joshi (1973) and Ewa Ubi *et al.* (2001) for 100-seed weight; Angadi *et al.* (1978) for number of branches per plant; Jana *et al.* (1982), Sreekumar *et al.* (1996) and Ewa Ubi *et al.* (2001) for days to 50% flowering; Pal *et al.* (2003) and Venkatesan *et al.* (2003) for plant height.

4.3 Estimation of correlation coefficients

4.3.1 Correlation of attributing characters with seed yield

To estimate the association between two characters, correlation coefficient at phenotypic, genotypic and environmental levels were worked out in all possible combinations amongst yield components (Table 4.6).

The results showed that genotypic correlations were higher than their corresponding phenotypic correlations. Hence the correlation at genotypic levels are discussed in general but interrelationship at phenotypic level has also been considered at certain points, wherever these were found necessary for explaining the present findings.

Association studies revealed significant positive correlation of pods per plant with seed yield per plant suggesting significance of this character during selection for higher seed yield in cowpea. Other characters like days to 50% flowering, days to maturity and seeds per pod had non-significant positive association with seed yield per plant indicating that these characters can also be used for indirect selection for seed yield in cowpea. Positive relationship of flowering and maturity indicates the possibilities of combining early maturity with high seed yield in this crop.

In the present study, seed yield per plant exhibited a significant positive correlation with number of pods per plant (0.457), similar results have also been reported by Trehan *et al.* (1970), Biradar *et al.* (1993), Erskine and Khan (1978), Sreekumar *et al.* (1996), Naidu *et al.* (1996), Rangaiah and Nehru (1998), Reshmi (1998), Vardhan and Savithramma (1998), Singh *et al.* (1998), Patil *et al*. (1989), Jana *et al*. (1983), Hanchipal *et al.* (1979). Narayanankutty *et al.* (2003), Kumawat and Raje (2006), Singh and Verma (2002), Vidya and Oommen (2002) and Anbumalarmathi *et al.* (2005). This trait can be used for indirect selection of seed yield per plant. Seeds per pod had non-significant but positive correlation with seed yield, hence it should also be given due weightage in selection scheme. Trehan *et al.* (1970), Bapna *et al.* (1973), Bordia *et al.* (1973), Lakshmi and Gaud (1977), Tikka *et al.* (1977), Obisesan (1985), Altnbas and Sepetoglu (1993), Biradar *et al.* (1996), Golsngi *et al.* (1996), Naidu *et al.* (1996), Vidya and Oommen (2002) have also found positive relationship of this trait with seed yield in cowpea.

4.3.2 Association among the traits influencing seed yield

Phenological characters like flowering (0.559) and maturity (0.516) being positively correlated had significant positive association with plant height. This clearly indicates that taller types might be delayed in flowering and maturity, which is also evidenced by their mean values. The results further showed positive association of these two traits with number of branches per plant which also had positive association with plant height. This reveals the possibilities of developing early maturing cowpea varieties with high yield but due weightage should be given to higher number of branches as it had shown positive relationship with plant height. Persual of mean performance and range of variation for branch number it vary from 2.93 to 4.47 branches per plant but there are certain genotypes like Subhra which had plant height of 90.73 cm and also had higher number of branches per plant (4.13). Other genotypes like HC- 08-02 and ACM-05-7 had good combination of dwarfing genes and moderate number of branches, which showed that there are possibilities of combining desirable genes for plant height, higher number of branches, early maturity and high grain yield in cowpea by applying conventional and /or mutation breeding. Jana *et al.* (1983) have reported that the numbers of branches were negatively correlated with days to 50% flowering in this crop.

Number of branches per plant (0.474) exhibited significant positive correlation with pods per plants at phenotypic level, however due to higher environmental effect it was non-significant at genotypic level. This showed that these traits (branch and pods per plant) undoubtedly are important yield contributors but also very much influenced by environmental factors. Hence proper agronomy and favorable environments are required for proper expression of these traits. The path analysis discussed later clearly indicates that these two traits had shown their substantial contribution towards seed yield. It is further revealed that number of pods per plant had shown its indirect effect on seed yield, through number of branches per plant. This trait had shown its positive association with seeds per pod. Thus it is clear that selection for higher number of branches, pods per plant and seeds per pod will be rewarding for yield improvement in cowpea. Similar results were reported by Jana *et al.* (1983), Ram and Singh (1996), Nakawuka and Adipala (1999), Peksen and Artik (2004) and Biradar *et al.* (2007).

Days to maturity exhibited significant negative association with pod length (-0.485) indicating that delayed in flowering will also reduce the pod size. Similarly, number of pods per plant also had significant negative association with pod length (-0.498) indicating that increase in number of pods will not support to the longer pod size/length. Similar findings have also been reported by Bliss *et al.* (1973), Erskine and Khan (1978) and Neema and Palaniswamy (2003).

Number of pods per plant further exhibited significant negative (-0.842) correlation coefficient with 100-seed weight. This clearly indicates that for improving grain yield plant breeders should go for higher number of pods but with due care in respect to pod length and seed size as they had shown negative relationship with this character. In accordance to above findings Bliss *et al.* (1973), Erskine and Khan (1978), Hanchipal *et al.* (1979), Singh and Verma (2002), Neema and Palaniswamy (2003) and Alege and Mustapha (2007) have also supported negative association of number of pods per plant with pod length and 100-seed weight.

Genotypic correlation revealed that pod length had significant positive correlation with number of seeds per pod (0.775) indicating that the increase in pod size with higher number of seeds per pod would be helpful in increasing the harvest index and ultimately seed yield. But its non-significant negative association with 100-seed weight gave an indication that increase in seed size may adversely affect the total number of seeds per plant. Hence, plant breeders should be attentive while exercising selection for these traits. Lovely and Radhadevi (2006) have also expressed the similar opinion.

Days to maturity exhibited significant negative association with pod length indicating that delayed in flowering will also reduce the pod size. Similarly number of pods per plant also had significant negative association with pod length indicating that increase in number of pods will not support to the longer pod size/length.

The number of branches showed highly significant positive correlation with seeds per pod (0.515) and pods per plant (0.474) at genotypic and phenotypic level respectively. However, its highly significant environmental correlation clearly gave an indication of environmental influence on these traits. Hence, care should be taken while exercising selection. Similar results were reported by Lakshmi and Gaud (1977) and Tikka *et al.* (1977).

At genotypic level, number of pods per plant showed highly significant negative correlation with 100-seed weight (-0.842) and pod length (-0.498), indicating that plant breeders should make careful attempts for combining higher number of pods with long pods having bold seeds. However, more number of crosses should be attempted for combining these desirable traits together. Similar results were also obtained by Singh and Verma (2002).

The present findings do not give the real picture of association of seed yield with its attributing traits. This might be due to nature of this crop, being non determinate type and fodder type. It is generally cultivated for green fodder because it has very good regenerating capacity. Cultivation of cowpea as legume is very common in arid regions of India but it is also being tried in high rainfall areas like Chhattisgarh particularly at Raipur. More over the results gave an indication that higher number of pods with longer size and more number of seeds are the important characters to be considered for higher seed yield. Other characters like maturity, plant height, number of branches per plant and seed size which had shown their indirect involvement in increasing the number of pods and seeds per pod and ultimately to the seed yield seem to be important and due weightage should be given to these traits while excersing selection for higher seed yield.

4.3.3 Association among quality/ seed characters

To provide better understanding in improving seed quality through selection, association among seed size and seed characters were estimated in all possible combinations at genotypic (G), phenotypic (P) and environmental (E) levels and are presented in Table 4.7. In the present study seed size exhibited a highly significant positive association with seed volume (0.818), hydration capacity (0.959) and swelling capacity per seed (0.592) at genotypic level. Such studies are not reported in this crop but very well reported in chickpea and field pea, which is also, consumed as whole seed.

Phenotypic correlation study reveals that seed size has highly significant positive correlation with seed volume (0.811) and swelling capacity per seed (0.588). This indicates that if the selection of the genotype is to be done for the swelling capacity per seed, then one can prefer large seed. Ghosh and Panda (2006) also reported positive correlation between seed size, swelling capacity, swelling index and seed volume in chickpea and field pea.

Hydration capacity per seed had significant positive correlation with swelling index (0.454) at genotypic level. Seed density had highly significant positive correlation with swelling index (0.712 and 0.700) at genotypic and phenotypic levels respectively. Environment effect also had significant role on this as evidenced by its significant positive association (0.649).

Similarly, seed density showed significant positive correlation with hydration capacity (0.467) at genotypic level suggesting that increase in the mass per unit volume increases its capacity to absorb more water. Seed volume showed significant negative correlation with swelling index (-0.531, -0.532) at genotypic and phenotypic levels respectively and highly significant negative correlation with swelling index (-0.781) at environmental level. Seed volume also had highly significant negative correlation with hydration index (-0.589, -0.585) and seed density (-0.533, -0.520) at genotypic and phenotypic levels respectively. Similarly, environmental correlation reveals that the seed volume had highly significant negative correlation with seed density (-0.697) and swelling capacity (-0.525).

Swelling capacity had significant positive correlation with swelling index (0.461, 0.467) at genotypic and phenotypic level and highly significant positive correlation with swelling index (0.785) at environmental level too. Hydration index showed highly significant positive correlation with swelling index (0.694, 0.680) at genotypic and phenotypic levels respectively.

Similarly, Ghosh and Panda (2006) also reported positive interrelationship between seed size, swelling capacity, hydration capacity, swelling index in chickpea and field pea and Williams *et al.* (1983) and Waldia *et al.* (1995) reported significant positive correlation of seed volume with hydration capacity, swelling capacity and among themselves. Similarly, Wang *et al.* (2003) found a positive correlation between seed weight and hydration capacity in Gram.

4.3.4 Simple correlation of seed characters

Results presented in Table 4.8 reveals that seed volume had highly significant positive correlation with 100-seed weight (0.8105) but highly significant negative correlation with hydration index (-0.5844) and significant negative correlation with swelling index (-0.5324) and seed density (-0.5207).The above findings suggested that the large seeds have more seed volume but the hydration and swelling capacity per unit volume gets decreased.

Swelling capacity per seed being highly significant positive correlation with 100 seed weight (0.5875) and significant positive correlation with swelling index (0.4673) suggesting that the large seeds absorb more water with increase in their size, swelling index had highly significant positive correlation with seed density (0.6983) and hydration index (0.6794).

Williams *et al.* (1983) and Waldia *et al.* (1995) reported the positive and significant correlation of seed mass with seed volume, hydration capacity, and swelling capacity and among themselves in Gram.

Cowpea or Lobia is commonly cooked as whole seed rather than split pulse; hence larger seeds with high hydration and swelling capacity are desired. In these study seed volume and swelling capacity had shown positive association with 100-seed weight indicating that increase in seed size there will be corresponding increase in seed volume and swelling capacity also similarly, the results further reveal that increase in seed density will also help in increasing swelling index which had positive association with hydration index and swelling capacity. Hence, preference for medium bold seeds should give in the selection scheme.

4.4 Path coefficient analysis

4.4.1 Direct effect of attributes on seed yield

Association among the variable give an idea of its direction but could not quantify its direct or indirect contribution towards seed yield. But path analysis which is further partitioning of genotypic correlation, explains this. The results of present study presented in Table 4.9 reveals the genotypic path of various attributes on seed yield, depict that in present study days to maturity had the highest direct effect (16.044) on seed yield. Though it had non-significant positive association with seed yield yet had high heritability with moderate genetic advance. Hence, this character seems to be important contributor of seed yield and must be considered in selection for high seed yield. Other important character having considerable direct effect was number of pods per plant (1.421) which had shown high heritability and moderate genetic advance and also had significant positive association with seed yield. This is an important yield attributing trait. Number of branches showed high direct effect (1.982) on seed yield followed by pod length (1.332). Seeds per pod showed high direct effect (0.654) on seed yield. Similar results were reported by Nakawuka and Adipala (1999), Padhey *et al.* (1984), Yadav *et al.* (2003) and Venkatesan *et al.* (2003a). These characters had major direct contribution for yield in cowpea.

On the other hand, the highest negative direct effect on seed yield was exhibited by days to 50% flowering (-16.854) which would be nullified by its via effect through days to maturity (15.746) followed by 100-seed weight (-0.329) and plant height (-0.207) although these characters shown non-significant negative correlation with seed yield. For these traits the positive indirect effect exerted via other traits should be considered. These findings are not in favour of that reported by Jana *et al.* (1983).

4.4.2 Seed size (100-seed weight) is dependent

The results presented in Table 4.10 shows genotypic path of various quantitative attributes to seed size. Highly significant negative association of 100-seed weight (seed size) was observed with number of pods per plant with negative direct effect (-0.704). Seeds per pod showed high negative direct effect (-0.891) but was having non significant correlation with 100 seed weight. This reveals that the above traits are worthless to consider it in the selection criteria.

Pod length had high positive direct effect (0.866) showing non significant positive correlation with 100 seed weight due to high indirect effect exerted by days to 50% flowering. The character plant height (0.024) is showing low positive direct effect on 100 seed weight. Similar results were found by Subbaiah *et al.* (2003), for character pod length had strong positive direct effect. Lian (1973), Venkatesan *et al.* (2003a), Yadav *et al.* (2003) and Murthy (1982); for pod length high positive direct effect followed by plant height, 100 seed weight, Venkatesan *et al.* (2003a), Yadav *et al.* (2003).

Days to 50% flowering showed very high positive direct effect (6.372) but was having non significant negative correlation with 100-seed weight due to low indirect effect of seeds per pod (0.133) and plant height (0.014) and very high negative indirect effect through pod length (-0.328), number of branches per plant (-1.058) and days to maturity (-5.000).

Days to maturity showed very high negative direct effect (-5.095) on 100 seed weight followed by number of branches per plant (-1.335).The character days to 50% flowering was however positive indirect effect by days to 50% flowering. Number of pods per plant (-0.704) had high negatively direct effect on 100 seed weight with non significant positive correlation. Similar results were also reported by Kumari *et al*. (2003), for days to 50% flowering for highly negative direct effects on seed yield per plant.

Number of branches per plant also had very high negative direct effect (-1.335) on 100 seed weight but with non significant positive correlation due to highly positive indirect effect through days to maturity (5.051) phenotypic. The other characters, pod length (0.226) and plant height (0.018) showed positive direct effect on number of branches per plant, while negative indirect effect of days to maturity (-3.302), seeds per pod (-0.459) and number of pods per plant (-0.140) were also observed. The present findings are in accordance to Subbaiah *et al.* (2003) for pod length, number of branches per plant.

Number of pods per plant had high negative direct effect (-0.704) due to very high indirect effect of days to maturity (-1.034) and high indirect effect of pod length (-0.432), number of branches per plant (-0.265) which leads to highly significant negative correlation with 100 seed weight.

4.4.3 Quality/seed characters

Rapid improvement on seed quality can be presumed only if selection should be performed in right direction for quality parameters. Thus, the rate of improvement is expected to be rapid if differential emphasis should be based on the degree of direct and indirect influences of quality parameters. Hence, it is important to measure the direct and indirect contribution of different quality parameters on seed size.

Path coefficient analysis as presented in Table 4.11 revealed that seed volume had the highest positive direct effect (0.9225) on seed size or 100 seed weight followed by seed density (0.3122), swelling capacity per seed (0.1737), hydration index (0.1389) and hydration capacity (0.0806) whereas, low negative direct effect was observed by swelling index (-0.1108).Similar results were also reported by Singh and Mehandiratta (1970).

Seed volume having significant positive correlation with seed size had high positive direct effect towards. Swelling capacity per seed also had positive direct effect (0.1737) and was having highly significant positive correlation with 100-seed weight. It also exhibited high indirect effect via seed volume, suggesting that the seed characters like seed volume, seed density and swelling capacity are the important parameters in contact to seed weight and seed characters in cowpea. It can be concluded from the present findings of association and path analysis that number of pods, pod length with higher number of seeds per pod, plant height, number of branches per plant, days to maturity and 100 seed weight are important contributors to wards seed yield in cowpea. Plant breeders working on yield improvement in cowpea should pay proper attention which excersing selection for these traits. Among the seed characters seed volume, seed density, swelling capacity and hydration index are the important characters related to seed size in cowpea.

4.5 Divergence analysis

The parental diversity in optimum magnitude is required to obtain superior genotypes in the segregating generations. Furthermore, the evaluation of data obtained by any germplasm collections represents many duplicate accessions. These object, although desirable genetically, create a difficult task in recognition from data tables. Such duplicate accessions which differ from each other in one or two characters significantly pose a difficult situation for resolving distinct types. Thus, for characterizations of germplasm for genetic diversity, the genetic divergence analysis is very useful as it provides classification of material into different homogenous groups.

The existence of genetic divergence among the 22 cowpea genotypes was examined by employing Mahalanobis's D^2 statistics. The clustering pattern of 22 genotypes on the basis of D^2 analysis has been presented in Table 4.12. The entries were grouped into IV distinct clusters. The highest number of genotypes appeared in cluster I, which possessed 10 genotypes, *viz*, CPD-103, VCP-04-001, ACM-05-2, CPD-91, GC-502, KBC-1-M, CPD-83, GC-601, RC-101 (C) and GC-3 (C). The second highest number of entries was found in cluster III which comprised of 8 genotypes *viz.,* DCP-2, DCP-6, VBN-1 (C), TCM-138-1, TCM-148-1, V-130, V-240 and Khalleshwari (LC). Cluster II comprised of three genotypes, namely, VCP-04-003, ACM-05-7 and HC-08-02. Genotype Subhra a standard variety of cowpea independently belong to cluster IV. Clustering of genotypes clearly indicate their genetic diversity and their was no geographical diversity. Similar results were also reported by Nigude *et al.* (2004b) for cluster I had largest genotype followed by cluster III and cluster II.

4.5.1 Intra and inter cluster distances

The estimates of intra and inter cluster distances represented by D^2 values are presented in Table 4.13 and depicted in Fig. 4.1. The maximum intra-cluster distance (3.377) was obtained for cluster I followed by (2.795) cluster III and (2.014) cluster II.

The lowest intra cluster D^2 value was shown by cluster IV (0.000) which had only one genotype belonging to the cluster. The highest inter cluster D^2 values were observed between cluster I and cluster IV (8.045) followed by cluster III and IV (7.925), cluster II and cluster IV (7.086) and cluster II and cluster III (4.864). The lowest inter cluster was found between cluster I and cluster III (3.548) followed by cluster I and cluster II (4.151).

The hybrids between genotypes of different clusters will express high heterosis and throw more useful segregants. The most suitable clusters would be cluster I & cluster IV as highest inter cluster distance is observed between these two clusters. Similar results found by Kumawat and Raje (2005a) that intra cluster distance ranged for Cluster IV (0.000) to Cluster I (3.377).

4.5.2 Cluster means

The intra-cluster group means for 17 characters presented in Table 4.14 revealed marked difference between the 4 clusters in respect of cluster means for different characters.

The cluster mean for days to 50 per cent flowering was highest for cluster III (72.54 days) followed by cluster IV (48.67 days) and cluster II (47.89 days). The lowest cluster mean showed by cluster I (46.33 days).

In case of character, days to maturity, the highest cluster mean was obtained for cluster III (100.62 days) followed by cluster II (60.67 days) and cluster IV (60.67 days) while cluster I (58.57 days) showed the lowest cluster mean value.

The highest cluster mean for plant population was observed for cluster III (141.00) followed by cluster I (136.30) and cluster IV (117.67). The lowest cluster mean was observed for cluster II (88.56).

The highest cluster mean value for plant height was observed for cluster III (143.56) followed by cluster I (123.15) and cluster IV (90.73). The lowest cluster mean value was showed by cluster II (89.20).

Cluster IV (4.13) showed the highest cluster mean value for number of branches per plant followed by cluster III (3.92) and cluster I (3.56). The lowest mean was observed for cluster II (3.36).

Cluster IV (22.10) showed the highest cluster mean value for pods per plant followed by cluster II (12.01) and cluster III (11.57). The cluster I (9.49) showed the lowest cluster mean value.

Cluster I (14.88) showed the highest cluster mean for pod length followed by cluster IV (13.10) and cluster III (12.27). Cluster II (11.93) showed the lowest cluster mean value.

The highest cluster mean value for character number of seeds per pod was observed for cluster IV (13.93) followed by cluster I (12.58) and cluster II (11.51). The lowest cluster mean value was showed by cluster III (11.43).

The highest cluster mean value for character cluster per plant was observed for cluster IV (7.47) followed by cluster II (6.22) and cluster I (6.16). The lowest cluster mean value was observed for cluster III (6.05).

Cluster I (0.11) and Cluster III (0.11) showed the highest cluster mean value for seed volume followed by cluster II (0.06). Cluster IV (0.04) showed lowest cluster mean value for these traits.

Cluster IV (1.44) showed the highest cluster mean value for seed density followed by cluster II (1.06) and cluster III (1.05), cluster I (1.03) showed lowest cluster mean value.

The highest cluster mean value for character hydration capacity was observed for cluster I (0.13) followed by cluster III (0.11) and cluster IV (0.08). The lowest cluster mean value was shown by cluster II (0.07).

The highest cluster mean value for character hydration index was observed for cluster IV (1.45) followed by cluster II (1.15) and cluster III (1.00). The lowest cluster mean value was showed by cluster I (0.94).

The highest cluster mean value for character swelling capacity was observed for cluster III (0.11) followed by cluster I (0.10) & cluster IV (0.10). The lowest cluster mean value was showed by cluster II (0.05).

The highest cluster mean value for character swelling index was observed for cluster IV (2.56) followed by cluster III (1.80) and cluster I (0.99). The lowest cluster mean value was showed by cluster II (0.89).

The highest cluster mean value for character 100-seed weight was observed is cluster I (10.62) followed by cluster III (9.75) and cluster II (7.21). The lowest cluster mean value was observed for cluster IV (6.83).

Cluster IV (5.35) showed the highest cluster mean for seed yield per plant followed by cluster III (4.13) and cluster I (3.79). Cluster II (3.22) showed lowest cluster mean value. Similar results were reported by Kumari *et al.* (2004) for cluster IV had high mean value for number of cluster per plant, pod per plant, seed yield per plant. Pandey (2007) reported that the cluster I had minimum days to maturity whereas III had maximum days to maturity.

The per cent contribution of 17 characters towards total genetic divergence (Table 4.15) showed that days to 50 per cent flowering (53.68%) exhibited highest per cent contribution towards total genetic divergence, followed by hydration index (15.58%), 100-seed weight (13.42%), swelling capacity (11.69%), seed volume (2.60%), swelling index (1.73%), seed density (0.87%) and seed yield per plant (0.43%). Similar to this results Thiagarajan and Natrajan (1989) and Kumawat and Raje (2005) reported maximum contributing days to 50% flowering towards genetic divergence.

Variation for seed shape, size and seed coat colour in 22 genotypes:

Maximum variation for this character was observed. Seed coat colour observed were among 22 genotypes had a greater variability in seed colour *viz.,* cream, light brown, brown, dark brown with cream spot, cream with brown patches around eye and white with grey patches around eye, whereas in seed size only one showed very large seeds, nine showed large seeds, nine moderate seeds and rest three were small seeded. In seed shape smooth and wrinkled shape seed surface was observed (Table 4.16) (Plate II, III and IV).

Variation for seed size:

Total 22 genotypes were categorized as small, medium, large and extra large seeds and accordingly number of genotypes was noted as order (Table 4.16).

Variation for seed coat colour:

Total 22 genotypes were categorized as cream, cream with brown patches around eye, dark brown with cream spot, brown, light brown, creamish white and white with grey patches around eye and accordingly number of genotypes were noted as order (Table: 4.17).

Table 4.16: Variation for seed size

Sr. No.	Category	Frequency of genotypes	Name of genotypes
1.	Small	3	ACM-05-7, HC-08-02 and Subhra
2.	Medium	11	VCP-04-001, VCP-04-003, ACM-05-2, KBC-1-M, GC-3(C), DCP-6, VBN-1(LC), TCM-138-1, TCM-148-1, V-130 and V-240
3.	Large	7	CPD-103, CPD-91, GC-502, GC-601, RC-101(C), DCP-2 and Khalleshwari (LC)
4.	Extra large	1	CPD-83

Table 4.17: Variation for seed coat colour

Sr. No.	Seed colour	Frequency of genotypes	Name of genotypes
1.	Cream	7	CPD-103, ACM-05-7, HC-08-02, DCP-6, TCM-138-1, V-240 and Khalleshwari (LC)
2.	Cream with brown patches around eye	8	VCP-04-003, CPD-91, CPD-83, GC-601, GC-3 (C), Subhra, VBN-1(LC) and V-130
3.	Dark brown with cream spot	1	VCP-04-001
4.	Brown	3	ACM-05-2, GC-502 and DCP-2
5.	Light brown	1	KBC-1-M
6.	Creamish white	1	RC-101(C)
7.	White with grey patches around eye	1	TCM-148-1

Variation for seed shape:

Total 22 genotypes were categorized as smooth and wrinkled seed shape and accordingly number of genotypes was noted as order (Table 4.18).

Table 4.18: Variation for seed shape

Sr. No.	**Seed shape**	**Frequency of genotypes**	**Name of genotypes**
1.	Smooth	16	CPD-103, VCP-04-001, ACM-05-2, ACM-05-7, CPD-91, GC-502, HC-08-02, KBC-1-M, GC-601, RC-101(C), Subhra, DCP-2, DCP-6, VBN-1(LC), TCM-148-1 and V-240
2.	Wrinkled	6	VCP-04-003, CPD-3, GC-3(C), TCM-138-1, V-130 and Khalleshwari (LC)

CHAPTER-V

SUMMARY, CONCLUSIONS AND SUGGESTIONS FOR FUTURE RESEARCH WORK

The present investigation entitled **"Genetic variability and path analysis for yield attributing traits in cowpea (*Vigna unguiculata* (L.) Walp.)"** was carried out at Instructional cum Research Farm and Laboratory of the Department of Plant Breeding and Genetics, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, (C.G.) during *kharif* 2008.

The experimental material comprising 22 genotypes of cowpea was grown in Randomized Complete Block Design (RCBD) with three replications and observations on five competitive plants were recorded for days to 50% flowering, days to maturity, plant population per plot, plant height, number of branches per plant, pods per plant, pod length, seeds per pod, clusters per plant, 100 seed weight, seed yield per plant and seed yield per plot and seed characters *viz.,* seed volume per seed (ml), seed density, hydration capacity per seed, hydration index, swelling capacity per seed, swelling index, seed colour, seed size and seed shape were recorded for estimation of genetic variability, heritability and genetic advance, correlation analysis, path coefficient analysis and genetic divergence.

Analysis of variance worked out for seed yield and its component characters along with quality characters, indicated that the mean sum of squares due to genotypes were highly significant for all the characters except number of branches per plant, number of pods and number of clusters per plant.

Among the different yield attributing traits seed yield per plot had the highest magnitude of PCV and GCV. The high magnitude of PCV and GCV (above 20%) was also observed for seed yield per plant followed by swelling index, swelling capacity, plant population per plot, days to maturity, plant height, seed volume, hydration index, days to 50% flowering, hydration capacity and 100 seed weight; whereas moderate (10-20%) to low (<10%) genotypic and phenotypic coefficient of variation were observed for number of seeds per pod, pod length, seed density and number of branches per plant.

Most the characters studied showed high broad sense heritability. Among them having high heritability estimates were days to 50% flowering, hydration capacity, days to maturity, 100 seed weight, seed volume, swelling capacity, swelling index, seed density, seed yield per plot, hydration index and pod length. It was moderate for plant height, number of seeds per pod and seed yield per plant and low for number of branches and number of pods per plant. The seed yield per plot showed the highest genetic advance as percentage of mean followed by swelling index, swelling capacity, days to maturity, seed volume and seed yield per plant. The characters which showed moderate genetic advance as percentage of mean were days to 50% flowering, hydration capacity, hydration index, 100 seed weight and plant height. Whereas, plant population per plot, seed density, pod length, number of seeds per pod, number of pods per plant and number of branches per plant showed low genetic advance.

High heritability coupled with high genetic advance was noted for days to maturity, seed volume, swelling capacity, swelling index and seed yield per plot; high heritability coupled with moderate to low genetic advance was found for days to flowering, pod length, 10 seed weight, seed density, hydration capacity and hydration index; moderate heritability coupled with high to moderate genetic advance was found for plant height and seed yield per plant; while moderate heritability coupled with low genetic advance was found for number of seeds per pod only; the characters like plant population per plot, number of branches and number of pods per plant showed low heritability coupled with low genetic advance.

Correlation coefficient analysis revealed that seed yield per plant exhibited a significant positive correlation with number of pods per plant; considering genotypic correlation, the character days to 50% flowering had a highly significant positive correlation with days to maturity, number of branches per plant and plant height, at phenotypic level. Days to 50% flowering showed highly significant positive correlation with days to maturity and significant positive correlation with plant height. Number of pods per plant showed significant positive correlation with seed yield per plant.

Genotypic correlation reveals that pod length had highly significant positive correlation with seeds per pod was also found highly significantly positively correlated with seeds per pod. The plant height showed highly significant positive correlation with number of branches per plant but other traits were non-significantly correlated with plant height at genotypic level. Days to maturity showed highly significant positive correlation with number of branches per plant and plant height at genotypic level while at phenotypic level days to maturity showed significant positive correlation with plant height only. The number of branches showed highly significant positive correlation with seeds per pod at genotypic level. Similarly number of branches showed positive correlation with number of pods per plant, whereas environmental correlation revealed highly significant positive correlation of number of branches with number of pods per plant. Seed size exhibited a highly significant positive association with seed volume, hydration capacity and swelling capacity per seed at genotypic level.

Phenotypic correlation study reveals that seed size has highly significant positive correlation with seed volume and swelling capacity per seed. Hydration capacity per seed had significant positive correlation with swelling index at genotypic level. Seed density had highly significant positive correlation with swelling index at both levels of correlation. Similarly, the seed density showed significant positive correlation with hydration capacity at genotypic level, swelling capacity had significant positive correlation with swelling index at genotypic and phenotypic level and highly significant positive correlation with swelling index at environmental level. Hydration index showed highly significant positive correlation with swelling index at genotypic and phenotypic level.

Simple correlation study of seed characters revealed that seed volume had highly significant positive correlation with 100 seed weight, whereas swelling capacity per seed being highly significant positive correlation with 100 seed weight and significant positive correlation with swelling index; swelling index had highly significant positive correlation with seed density and hydration index.

Path coefficient analysis revealed that days to maturity had the highest direct effect on seed yield. Other important characters having considerable high direct effects were number of pods per plant, number of branches, pod length and seeds per pod. In case of Seed size (100 seed weight), days to 50% flowering showed very high positive direct effects and pod length had high positive direct effect; for quality (seed) characters path coefficient analysis revealed that seed volume had the highest positive direct effect on seed size followed by seed density, swelling capacity per seed, hydration index and hydration capacity. Seed volume had high positive direct effect and was showing highly significant positive correlation with 100 seed weight; swelling capacity per seed also had positive direct effect.

Genetic divergence of 22 genotypes was estimated and classified into four clusters. Clusters I had the maximum genotypes (10) followed by clusters III (8), clusters II (3) and clusters IV had only one genotype. The maximum intra-cluster distance was obtained for cluster I (3.377) followed by cluster III (2.795). The highest inter cluster distance observed was in between cluster I and cluster IV (8.045) followed by cluster III and IV (7.925), cluster II and cluster IV (7.086) and cluster II and cluster III

(4.864). The lowest inter cluster was found between cluster I and cluster III (3.548) followed by cluster I and cluster II (4.151).

The cluster mean for days to 50 per cent flowering and maturity was highest in cluster III (72.54 and 100.62 days). Plant height for cluster III (143.56), number of branches per plant for cluster IV (4.13), pods per plant for cluster IV (22.10), pod length for cluster I (14.88), number of seeds per pod for cluster IV (13.93), clusters per plant for cluster IV (7.47), seed volume for cluster I (0.11) and cluster III (0.11), seed density for cluster IV (1.44), hydration capacity for cluster I (0.13), hydration index for cluster IV (1.45), swelling capacity for cluster III (0.11), swelling index for cluster IV (2.56), 100-seed weight by cluster I (10.62) and seed yield per plant for cluster IV (5.35).

Conclusions:

Based on the results the following conclusions are drawn from the present investigation.

1. The high magnitudes of variability among the genotypes for seed yield and attributing traits indicated that enough scope is there, for the improvement of various traits in selection.
2. The high PCV than GCV obtained for the traits, seed yield per plot and seed yield per plant indicate that sufficient variability is present in the studied population for exploitation in the heterosis programme.
3. Among the quality trait, hydration index exhibiting high PCV than GCV reveal that such traits can be genetically improved through the studied material.
4. High heritability coupled with high genetic advance was noted for days to maturity, seed volume, swelling capacity, swelling index and seed yield per plot suggesting the predominance of additive gene action in the expression of these characters which could be utilized through selection for the genetic improvement of these characters.

5. Characters showing high to low heritability estimates coupled with medium to low genetic advance as percentage of mean indicates greater contribution of dominance and epistasis variance in the expression of characters.
6. The characters showing low heritability coupled with low genetic advance are worthless in the breeding programme due to low transfer genetic materials from one generation to other
7. In present correlation studies seed volume, hydration capacity and swelling capacity had significant positive association with 100 seed weight. Hence, improvement of 100 seed weight per plant can be achieved by improving these characters.
8. Path coefficient analysis revealed that emphasis should be based on seed volume and swelling capacity for the genetic improvement of 100 seed weight.
9. Considerable amount of genetic divergence was present among 36 genotypes. Intercrossing of genotypes from different clusters showing superior mean performance may help in obtaining higher yield.

Suggestions for future research work:

Based on the results obtained from the present investigation, the following future line of work is suggested.

1. In order to confirm the findings the experiment should be conducted over years and locations.
2. The experiment should be conducted in all three seasons, over the years and at various locations to find out the stable genotypes across the seasons.
3. Future studies on relationship of seed size with protein content can be made in this crop.
4. There is need to screen the genotypes against biotic (disease and insect pests) and abiotic stresses (drought tolerant/resistant).
5. Genetic variability observed and evaluated under this study should fully be utilized for genetic improvement of cowpea.

6. Diverse parents belonging to different cluster should be involved in the hybridization programme, best on their merit of characters. Beside this more number of germplasm should also be incorporated in hybridization programme.
7. Bigger seeds have positive contribution towards seed yield. However, there is need to quantify the optimum seed size and future studies can be taken on this aspect.
8. The selection criteria may be benefited by using more number of traits including quality traits.

“GENETIC VARIABILITY AND PATH ANALYSIS FOR YIELD ATTRIBUTING TRAITS IN COWPEA (*Vigna unguiculata* (L.) Walp.)”

by

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ABSTRACT

The present investigation was conducted during *kharif* 2008 at Instructional cum Research Farm and Laboratory of the Department of Plant Breeding and Genetics, College of Agriculture, Indira Gandhi Krishi Vishwavidyalaya, Raipur, (C.G.). The experimental material comprising 22 genotypes of cowpea was conducted in Randomized Complete Block Design (RCBD) with three replications for estimation of genetic variability, heritability and genetic advance, correlation analysis, path coefficient analysis and genetic divergence.

Analysis of variance revealed significant differences among the genotypes for all the characters studied except for number of branches per plant, number of pods per plant and number of clusters per plant. The highest magnitude of genotypic and phenotypic variation was observed for seed yield per plot, seed yield per plant, swelling index, swelling capacity, plant population per plot, days to maturity, plant height, seed volume, hydration index, days to 50% flowering, hydration capacity and 100 seed weight. High heritability coupled with high genetic advance was observed for days to maturity, seed volume, swelling capacity, swelling index and seed yield per plot indicating that heritability is due to additive gene action and selection based on these characters may be effective.

Correlation coefficient analysis revealed that seed volume, hydration capacity and swelling capacity had significant positive association with 100 seed weight. Hence, improvement of 100 seed weight per plant can be achieved by improving these characters.

Path coefficient analysis revealed that seed volume and swelling capacity had positive direct and significant correlation with 100 seed weight while number of pods per plant had negative direct effect and also negative significant correlation with 100 seed weight. Therefore, emphasis should be given to seed volume and swelling capacity for the genetic improvement of 100 seed weight.

Divergence analysis revealed that considerable amount of genetic divergence was present in the material under study. Based on Mahalanobis’s D^2 statistic, genotypes

grouped into four non-overlapping clusters showed genetic diversity rather geographical diversity. Intercrossing of genotypes from different clusters showing superior mean performance may help in obtaining higher yields. Genotypes belonging to cluster I may produce better heterosis and segregants with the genotypes of cluster III and IV.

The present investigation revealed that selection for the characters such as seed yield per plant, biological yield, number of capsules per plant, days to maturity and number of primary branches per plant is important to evolve high yielding genotypes of cowpea. Development of dual type cowpea can also be taken up as one of the breeding objective.

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APPENDIX - I

WEEKLY METEOROLOGICAL DATA: JULY-NOVEMBER (*kharif* 2008)

Week no.	Date	Max. Temp. (°C)	Min. Temp. (°C)	Rain-fall (mm)	Rainy days	Relative Humidity (%)		Vapour Pressure (mm)		Wind velocity (Kmph)	Evapo-ration (mm)	Sun Shine (hours)
						I	II	I	II			
27	Jul 02-08	31.8	24.7	22.2	2	86	64	21.9	21.2	12.4	6.0	2.8
28	15-Sep	31.7	24.9	30.4	2	88	64	22.4	21.9	10.6	5.9	4.2
29	16-22	33.0	24.7	58.0	1	89	61	23.0	22.0	6.9	5.1	3.4
30	23-29	31.1	24.6	12.4	2	94	75	23.0	22.8	7.9	3.4	1.8
31	30-05	28.9	24.9	39.5	2	93	81	23.2	23.1	8.0	2.3	1.5
	Average	**31.3**	**24.8**	**32.5**	**1.8**	**90**	**69**	**22.7**	**22.2**	**9.2**	**4.5**	**2.7**
32	Aug 06-12	30.0	25.0	71.9	4	92	71	23.0	23.3	9.3	3.6	1.8
33	13-19	30.5	24.7	50.8	3	92	74	23.1	23.4	8.2	3.7	3.1
34	20-26	30.8	25.1	35.8	2	91	70	22.8	22.4	5.9	4.1	3.1
35	27-02	30.2	24.4	43.4	2	93	80	23.4	23.0	6.1	4.0	3.9
	Average	**30.4**	**24.8**	**50.5**	**2.75**	**92**	**73.75**	**23.1**	**23.0**	**7.4**	**3.9**	**3.0**
36	Sep 03-09	31.9	23.9	22.2	2	92	72	22.6	21.9	3.8	3.7	5.6
37	16-Oct	31.0	24.6	24.6	3	92	69	23.0	22.9	6.7	3.9	5.8
38	17-23	30.5	23.9	165.4	2	93	75	22.2	21.7	8.8	3.4	4.2
39	24-30	31.8	23.2	0.0	0	89	59	21.2	19.9	5.2	5.2	8.8
	Average	**31.3**	**23.9**	**53.1**	**1.75**	**91.5**	**68.75**	**22.3**	**21.6**	**6.1**	**4.1**	**6.1**
40	Oct 01-07	32.2	23.7	12.6	1	94	67	22.9	22.5	2.6	3.6	7.1
41	14-Aug	32.9	22.1	0.0	0	92	47	20.5	17.0	2.4	7.4	3.9
42	15-21	32.0	19.8	0.0	0	88	39	17.5	13.5	2.7	8.5	4.4
43	22-28	30.6	17.4	0.0	0	85	36	14.6	11.6	3.7	4.6	7.7
44	29-04	31.8	15.4	0.0	0	91	28	13.8	9.7	2.5	4.1	7.7
	Average	**31.9**	**19.7**	**2.5**	**0.2**	**90**	**43.4**	**17.9**	**14.9**	**2.8**	**5.6**	**6.2**
45	Nov 05-11	31.1	16.2	0.0	0	89	37	14.4	11.9	1.8	3.4	7.2
46	18-Dec	29.1	17.5	0.0	0	89	47	15.2	14.0	4.1	3.7	5.1
47	19-25	30.9	16.7	0.0	0	90	41	14.6	13.2	3.0	7.7	3.8
48	26-02	30.5	13.0	0.0	0	86	37	10.8	11.0	1.7	3.4	8.3
	Average	**30.4**	**15.9**	**0.0**	**0**	**88.5**	**40.5**	**13.8**	**12.5**	**2.7**	**4.6**	**6.1**
	Mean/total	**31.1**	**21.8**	**589.2**	**28**	**90.4**	**58.8**	**20.0**	**18.8**	**5.7**	**4.6**	**4.8**

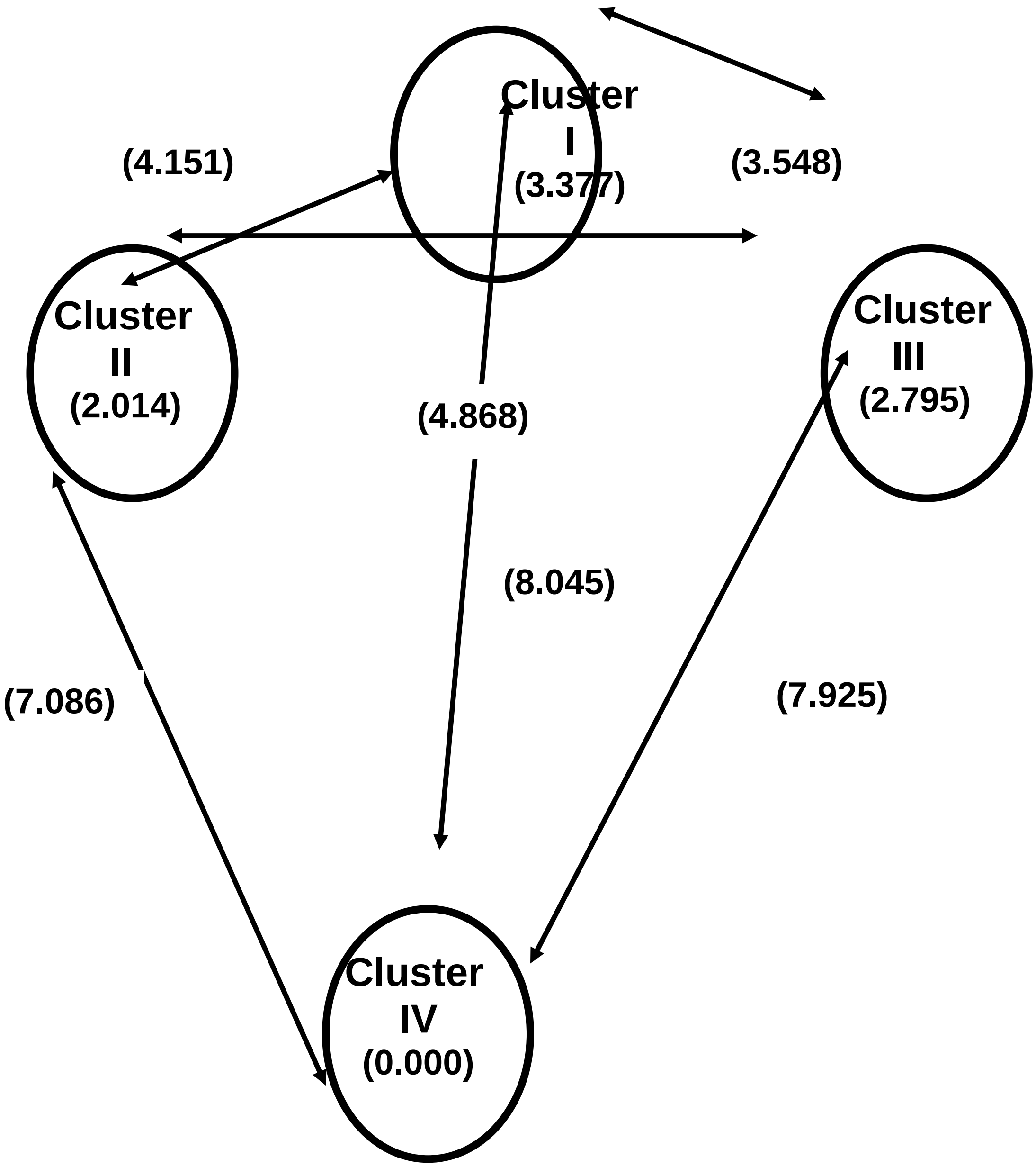

Fig 4.1: Diagrammatic presentation of intra and inter cluster distances in cowpea

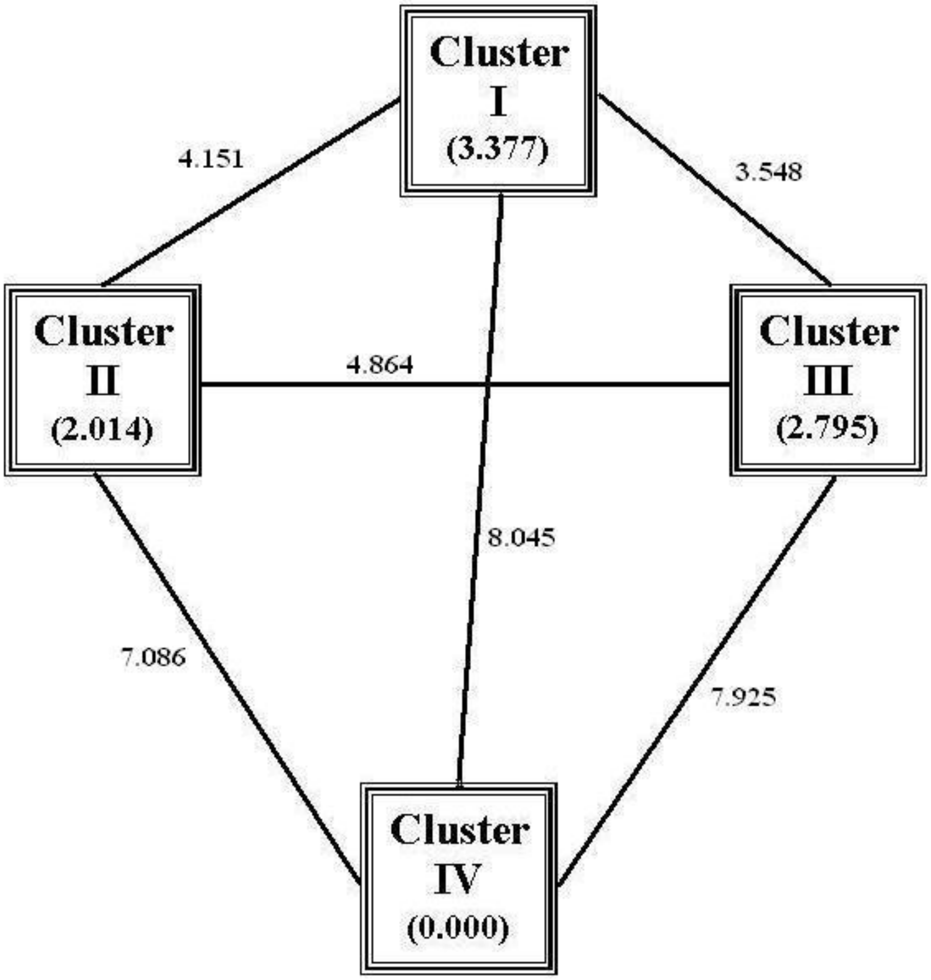

Fig 4.1 Diagrammatic presentation of intra and inter cluster values for D^2 analysis

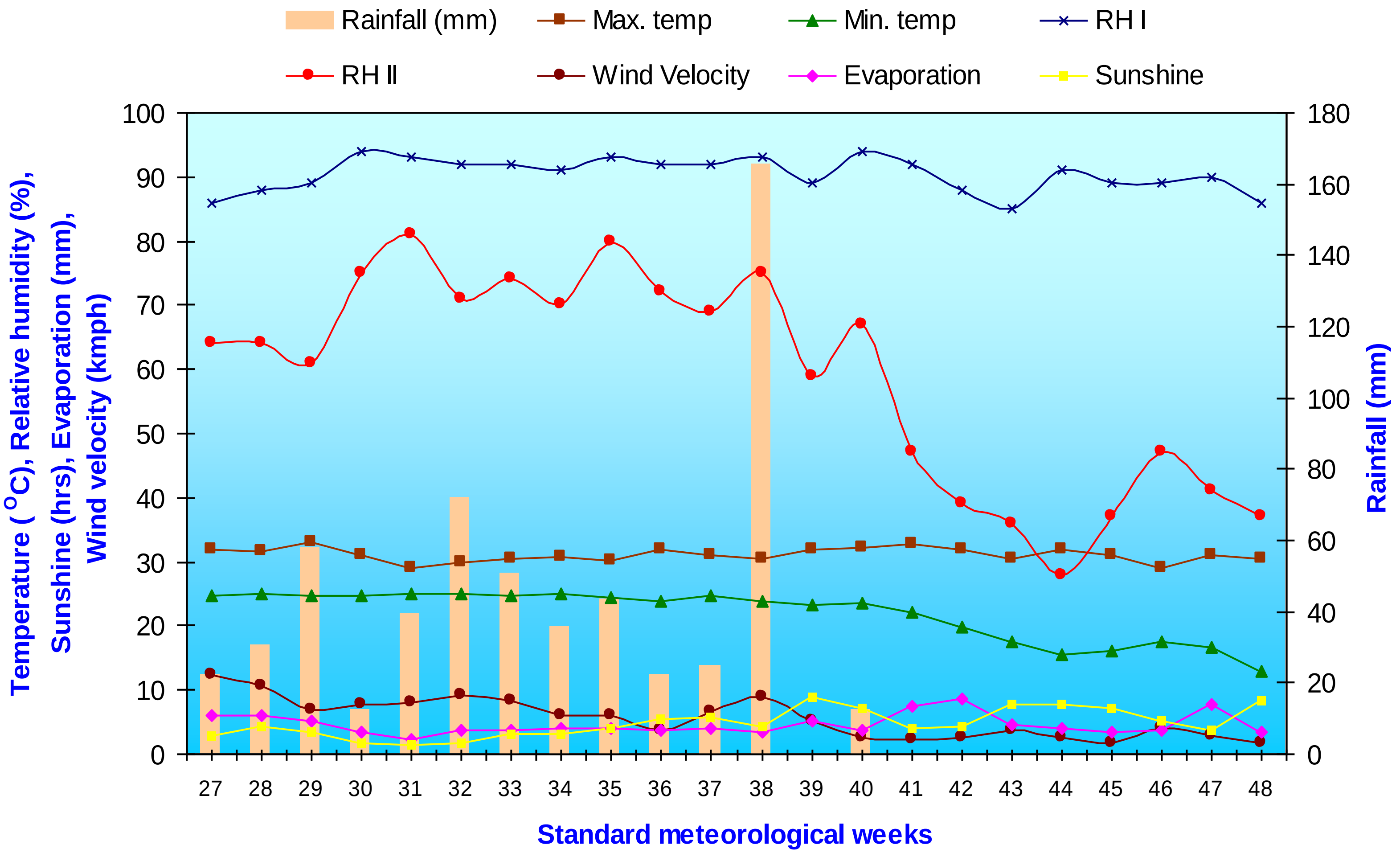

Fig. 3.1: Weekly meteorological data during crop growth period of cowpea (*kharif* 2008)

TABLE 4.1: ANALYSIS OF VARIANCE FOR DIFFERENT CHARACTERS

Sr. No.	**Observations / Characters**	Mean sum of square		
		Replication df 02	**Genotypes df 21**	**Error df 42**
1	Days to flowering	3.591**	505.579**	0.178
2	Days to maturity	**4.061**	**1260.101****	**1.569**
3	**Plant population/plot**	**1297.015**	**3365.285****	**975.475**
4	**Plant height**	**456.335**	**2861.623****	**383.564**
5	**No. of branches**	**0.628**	**0.558**	**0.321**
6	**No. of pods/plant**	**6.045**	**24.974**	**15.016**
7	Pod length	0.900	12.188**	1.107
8	**No. of seeds/pod**	**5.001**	**8.923****	**1.564**
9	**No. of clusters/plant**	**1.946**	**1.252**	**1.748**
10	100 seed weight	0.007	12.553**	0.028
11	**Seed yield/plant**	**1.327**	**6.864****	**1.558**
12	**Seed yield/plot**	**8615.666**	**184533.348****	**4155.582**
13	Seed volume	0.000028**	0.002000**	0.000005
14	Seed density	**0.0020**	**0.0684****	**0.0014**
15	**Hydration capacity**	**0.0000026**	**0.0013994****	**0.0000012**
16	Hydration index	0.0010	0.1871**	0.0124
17	**Swelling capacity**	**0.000018**	**0.002672****	**0.000017**
18	**Swelling index**	**0.0014**	**0.5336****	**0.0071**

* Significant at 5% probability level

** Significant at 1% probability level

Table 4.2: MEAN PERFORMANCE OF 22 COWPEA GENOTYPES

GENOTYPE	DF	DM	PPP	PH	BR	PP	PL	SP	CP
CPD-103	41.33	56.33	156.00	121.60	3.23	9.40	12.73	10.87	5.27
VCP-04-001	51.67	58.67	120.67	156.07	4.27	9.73	19.47	15.73	6.27
VCP-04-003	45.67	59.33	108.67	116.93	3.27	11.87	12.27	10.27	6.20
ACM-05-2	49.33	59.00	101.67	118.47	3.53	10.80	15.67	14.27	6.20
ACM-05-7	50.67	61.67	119.67	93.80	3.53	12.93	11.27	12.47	6.60
CPD-91	43.33	61.00	156.00	140.13	3.13	9.73	12.73	10.43	5.80
GC-502	43.67	55.67	139.33	87.80	2.93	8.53	15.17	12.53	6.80
HC-08-02	47.33	61.00	37.33	56.87	3.27	11.23	12.27	11.80	5.87
KBC-1-M	51.67	58.33	185.67	168.40	4.20	10.07	16.73	15.87	6.13
CPD-83	45.67	60.33	114.33	130.07	3.73	8.53	14.70	10.00	6.33
GC-601	44.67	58.00	101.33	105.53	3.60	9.67	14.60	11.20	5.60
RC-101 (C)	42.67	56.67	115.00	76.47	3.53	9.13	12.77	11.20	6.13
GC-3 (C)	49.33	61.67	173.00	127.00	3.47	9.33	14.23	13.73	7.07
Subhra	48.67	60.67	117.67	90.73	4.13	22.10	13.10	13.93	7.47
DCP-2	72.33	100.33	124.33	124.93	3.87	10.27	10.73	11.53	5.20
DCP-6	70.67	99.67	116.67	162.13	4.47	13.87	12.43	11.87	6.80
VBN-1 (LC)	71.67	98.67	163.67	150.73	4.07	11.73	12.03	10.87	5.87
TCM-138-1	72.33	99.67	141.33	126.13	3.87	14.03	12.47	10.47	7.27
TCM-148-1	71.67	100.00	117.33	113.27	3.33	10.40	11.43	10.60	6.47
V-130	76.33	101.67	171.33	142.53	4.30	11.80	11.93	10.53	5.47
V-240	72.67	101.00	176.67	176.93	3.40	10.37	13.57	12.73	5.13
Khalleshwari(LC)	72.67	104.00	116.67	151.80	4.07	10.07	13.60	12.87	6.20

DF = Days to 50% flowering.
DM = Days to maturity.
PPP = Plant population per plot.
PH = Plant height.
BR = Number of branches per plant.
PP = Pods per plant.
PL = Pod length.
SP = Seeds per pod.
CP = Clusters per plant.

Table 4.3: MEAN PERFORMANCE OF 22 COWPEA GENOTYPES

GENOTYPE	SW	SYPN	SYP	SV	SD	HC	HI	SC	SI
CPD-103	10.30	3.152	460.0	0.127	0.928	0.075	0.657	0.077	0.605
VCP-04-001	9.87	5.318	593.3	0.103	0.968	0.131	1.316	0.138	1.344
VCP-04-003	8.47	3.060	313.3	0.077	0.884	0.090	1.313	0.066	0.854
ACM-05-2	9.70	6.934	700.0	0.103	1.023	0.100	0.956	0.098	0.955
ACM-05-7	6.27	4.315	510.0	0.059	1.030	0.061	1.005	0.043	0.736
CPD-91	10.63	4.342	668.0	0.090	1.167	0.097	0.921	0.101	1.120
GC-502	10.27	6.563	803.3	0.102	0.941	0.112	1.165	0.118	1.157
HC-08-02	6.90	2.282	76.7	0.049	1.260	0.070	1.129	0.053	1.084
KBC-1-M	9.17	1.186	220.0	0.103	1.113	0.094	0.604	0.078	0.755
CPD-83	16.33	1.484	169.3	0.141	1.101	0.120	0.774	0.139	0.987
GC-601	11.13	3.158	310.0	0.121	0.942	0.100	0.877	0.099	0.818
RC-101 (C)	10.33	2.236	260.0	0.100	1.027	0.103	1.006	0.099	0.993
GC-3 (C)	8.43	3.494	602.0	0.083	1.138	0.091	0.962	0.097	1.172
Subhra	6.83	5.354	623.3	0.040	1.444	0.084	1.451	0.102	2.557
DCP-2	11.63	4.863	127.2	0.143	1.065	0.135	0.890	0.139	0.977
DCP-6	9.53	5.698	127.7	0.104	1.078	0.103	0.916	0.097	0.931
VBN-1 (LC)	9.13	3.633	120.9	0.097	1.106	0.112	1.043	0.124	1.274
TCM-138-1	9.00	3.475	60.3	0.103	0.804	0.104	1.253	0.097	0.943
TCM-148-1	8.50	4.777	70.7	0.089	1.048	0.101	1.082	0.112	1.254
V-130	9.53	2.720	61.9	0.120	0.825	0.061	0.613	0.041	0.339
V-240	9.37	3.650	189.2	0.084	1.300	0.101	0.927	0.117	1.401
Khalleshwari(LC)	11.27	4.121	58.8	0.102	1.062	0.142	1.524	0.142	1.392

SV = Seed volume.
SD = Seed density.
HC = Hydration capacity.
HI = Hydration index.
SC = Swelling capacity.
SI = Swelling index.
100 SW = 100 seed weight.
SYP = Seed yield per plant.

TABLE 4.4: GENETIC PARAMETERS OF VARIATION FOR SEED YIELD AND ITS COMPONENTS

Characters	**Mean ($\bar{X}$)**	**Range**		**PCV (%)**	**GCV (%)**	**$h^{2}_{(bs)}$ (%)**	**GA (%)**
		Min.	**Max.**				
Days to 50% flowering	56.18	41.33	76.33	23.115	23.103	99.89	46.845
Days to maturity	74.24	55.67	104	27.639	27.588	99.627	55.854
Plant population/plot	130.65	37.33	185.67	32.220	21.603	44.953	29.714
Plant height	124.47	56.87	176.93	27.942	23.090	68.290	38.929
No. of branches	3.69	2.93	4.47	17.128	7.619	19.787	7.049
No. of pods/plant	11.16	8.53	22.1	38.357	16.319	18.103	14.156
Pod length	13.45	10.73	19.47	16.290	14.288	76.938	25.494
No. of seeds/pod	12.08	10	15.87	16.591	12.966	61.074	20.952
No. of clusters/plant	6.19	5.13	7.47	NS	NS	NS	NS
100 seed weight	9.66	6.27	16.33	21.214	21.145	99.344	42.743
Seed yield/plant	3.90	1.186	6.934	46.755	34.094	53.174	50.739
Seed yield/plot	323.90	58.8	803.3	78.274	75.702	93.535	148.798
Seed volume	0.10	0.04	0.143	26.609	26.502	99.189	53.564
Seed density	1.06	0.804	1.444	14.580	14.137	94.017	27.836
Hydration capacity	0.10	0.061	0.142	21.752	21.723	99.738	44.002
Hydration index	1.02	0.604	1.524	26.120	23.721	82.476	43.700
Swelling capacity	0.10	0.041	0.142	30.340	30.058	98.146	60.411
Swelling index	1.07	0.339	2.557	39.756	38.971	96.087	77.482

Table 4.5: Summary of the traits influencing high heritability and high genetic advance

Characters	h^2 b	Genetic advance per cent
Days to 50% flowering	H	M
Days to maturity	H	H
Plant population per plot	L	L
Plant height (cm)	M	M
Number of branches per plant	L	L
Number of pods per plant	L	L
Pod length	H	L
Seeds per pod	M	L
Clusters per plant	-	-
100 seed weight	H	M
Seed yield per plant	M	H
Seed yield per plot	H	H
Seed volume	H	H
Seed density	H	L
Hydration capacity	H	M
Hydration index	H	M
Swelling capacity	H	H
Swelling index	H	H

L = Low **M = Moderate** **H = High**

TABLE 4.4: GENETIC PARAMETERS OF VARIATION FOR SEED YIELD AND ITS COMPONENTS

Characters	Mean ($\bar{X}$)	Range		PCV (%)	GCV (%)	h^2 (bs) (%)	GA (%)
		Min.	Max.				
Days to 50% flowering	56.18	41.33	76.33	23.115	23.103	99.89	46.845
Days to maturity	74.24	55.67	104	27.639	27.588	99.627	55.854
Plant population/plot	130.65	37.33	185.67	32.220	21.603	44.953	29.714
Plant height	124.47	56.87	176.93	27.942	23.090	68.290	38.929
No. of branches	3.69	2.93	4.47	17.128	7.619	19.787	7.049
No. of pods/plant	11.16	8.53	22.1	38.357	16.319	18.103	14.156
Pod length	13.45	10.73	19.47	16.290	14.288	76.938	25.494
No. of seeds/pod	12.08	10	15.87	16.591	12.966	61.074	20.952
No. of clusters/plant	6.19	5.13	7.47	NS	NS	NS	NS
100 seed weight	9.66	6.27	16.33	21.214	21.145	99.344	42.743
Seed yield/plant	3.90	1.186	6.934	46.755	34.094	53.174	50.739
Seed yield/plot	323.90	58.8	803.3	78.274	75.702	93.535	148.798
Seed volume	0.10	0.04	0.143	26.609	26.502	99.189	53.564
Seed density	1.06	0.804	1.444	14.580	14.137	94.017	27.836
Hydration capacity	0.10	0.061	0.142	21.752	21.723	99.738	44.002
Hydration index	1.02	0.604	1.524	26.120	23.721	82.476	43.700
Swelling capacity	0.10	0.041	0.142	30.340	30.058	98.146	60.411
Swelling index	1.07	0.339	2.557	39.756	38.971	96.087	77.482

NS= Non significant

TABLE 4.7: PHENOTYPIC (P), GENOTYPIC (G) AND ENVIRONMENTAL (E) CORRELATION COEFFICIENTS AMONG DIFFERENT YIELD COMPONENTS IN COWPEA

CHARACTERS		SV	SD	HC	HI	SC	SI	100SW
		1	**2**	**3**	**4**	**5**	**6**	**7**
1	**P**	1.000	-0.520*	0.060	-0.585**	0.390	-0.532*	0.811**
	G	1.000	-0.533*	0.301	-0.589**	0.400	-0.531*	0.818**
	E	1.000	-0.697**	0.070	-0.100	-0.525*	-0.781**	-0.169
2	**P**		1.000	0.075	0.164	0.188	0.700**	-0.186
	G		1.000	0.467*	0.178	0.186	0.712**	-0.202
	E		1.000	-0.010	-0.066	0.347	0.649**	0.118
3	**P**			1.000	0.002	0.168	0.040	0.187
	G			1.000	0.013	1.139	0.454*	0.959**
	E			1.000	-0.004	-0.286	-0.203	0.196
4	**P**				1.000	0.253	0.680**	-0.381
	G				1.000	0.254	0.694**	-0.385
	E				1.000	0.134	0.116	0.153
5	**P**					1.000	0.467*	0.588**
	G					1.000	0.461*	0.592**
	E					1.000	0.785**	0.248
6	**P**						1.000	-0.205
	G						1.000	-0.215
	E						1.000	0.273
7	**P**							1.000
	G							1.000
	E							1.000

***Significant at 5% level @ n-2 df (0.423)**
****Significant at 1% level @ n-2 df (0.537)**

Table 4.5: Summary of the traits influencing high heritability and high genetic advance

Characters	h^2 b	Genetic advance per cent
Days to 50% flowering	H	M
Days to maturity	H	H
Plant population per plot	L	L
Plant height (cm)	M	M
Number of branches per plant	L	L
Number of pods per plant	L	L
Pod length	H	L
Seeds per pod	M	L
Clusters per plant	-	-
100 seed weight	H	M
Seed yield per plant	M	H
Seed yield per plot	H	H
Seed volume	H	H
Seed density	H	L
Hydration capacity	H	M
Hydration index	H	M
Swelling capacity	H	H
Swelling index	H	H

L = Low **M = Moderate** **H = High**

TABLE 4.6: PHENOTYPIC (P), GENOTYPIC (G) AND ENVIRONMENTAL (E) CORRELATION COEFFICIENTS AMONG DIFFERENT YIELD COMPONENTS IN COWPEA

CHARACTERS			DF	DM	PH	BR	PP	PL	SP	100SW	SYP
			1	2	3	4	5	6	7	8	9
DF	**1**	**P**	1.000	0.979**	0.463*	0.348	0.105	-0.328	-0.119	-0.049	0.093
		G	1.000	0.981**	0.559**	0.793**	0.257	-0.378	-0.149	-0.049	0.128
		E	1.000	-0.032	0.076	-0.145	-0.164	0.207	-0.095	-0.055	0.003
DM	**2**	**P**		1.000	0.430*	0.286	0.085	-0.422	-0.237	0.017	0.082
		G		1.000	0.516**	0.648**	0.203	-0.485*	-0.308	0.018	0.116
		E		1.000	0.133	-0.033	-0.027	0.059	0.087	-0.243	-0.066
PH	**3**	**P**			1.000	0.382	0.022	0.251	0.175	0.244	-0.049
		G			1.000	0.736**	-0.400	0.297	0.247	0.296	-0.008
		E			1.000	0.222	0.320	0.133	0.044	-0.005	-0.114
BR	**4**	**P**				1.000	0.474*	0.120	0.196	0.036	0.056
		G				1.000	0.198	0.261	0.515**	0.060	-0.185
		E				1.000	0.538**	0.041	0.031	0.131	0.190
PP	**5**	**P**					1.000	-0.123	0.167	-0.356	0.123
		G					1.000	-0.498*	0.042	-0.842**	0.457*
		E					1.000	0.144	0.271	0.011	-0.030
PL	**6**	**P**						1.000	0.625**	0.219	0.071
		G						1.000	0.775**	0.242	0.111
		E						1.000	0.314	0.180	-0.001
SP	**7**	**P**							1.000	-0.242	0.139
		G							1.000	-0.311	0.388
		E							1.000	0.008	-0.194
100 SW	**8**	**P**								1.000	-0.155
		G								1.000	-0.233
		E								1.000	0.253

***Significant at 5% level @ n-2 df (0.423)**, ****Significant at 1% level @ n-2 df (0.537)**

DF = Days to 50% flowering.
DM = Days to maturity.
PH = Plant height.
BR = Number of branches per plant.
PP = Pods per plant.
PL = Pod length.
SP = Seeds per pod.
100 SW= 100 seed weight.
SYP= Seed yield per plant

TABLE 4.7: PHENOTYPIC (P), GENOTYPIC (G) AND ENVIRONMENTAL (E) CORRELATION COEFFICIENTS AMONG DIFFERENT YIELD COMPONENTS IN COWPEA (QUALITATIVE CHARACTERS)

CHARACTERS			**SV**	**SD**	**HC**	**HI**	**SC**	**SI**	**100SW**
			1	**2**	**3**	**4**	**5**	**6**	**7**
SV	**1**	**P**	1.000	-0.520*	0.060	-0.585**	0.390	-0.532*	0.811**
		G	1.000	-0.533*	0.301	-0.589**	0.400	-0.531*	0.818**
		E	1.000	-0.697**	0.070	-0.100	-0.525*	-0.781**	-0.169
SD	**2**	**P**		1.000	0.075	0.164	0.188	0.700**	-0.186
		G		1.000	0.467*	0.178	0.186	0.712**	-0.202
		E		1.000	-0.010	-0.066	0.347	0.649**	0.118
HC	**3**	**P**			1.000	0.002	0.168	0.040	0.187
		G			1.000	0.013	1.139	0.454*	0.959**
		E			1.000	-0.004	-0.286	-0.203	0.196
HI	**4**	**P**				1.000	0.253	0.680**	-0.381
		G				1.000	0.254	0.694**	-0.385
		E				1.000	0.134	0.116	0.153
SC	**5**	**P**					1.000	0.467*	0.588**
		G					1.000	0.461*	0.592**
		E					1.000	0.785**	0.248
SI	**6**	**P**						1.000	-0.205
		G						1.000	-0.215
		E						1.000	0.273

***Significant at 5% level @ n-2 df (0.423)**, ****Significant at 1% level @ n-2 df (0.537)**

SV = Seed volume.
SD = Seed density.
HC = Hydration capacity.
HI = Hydration index.
SC = Swelling capacity.
SI = Swelling index.
100 SW = 100 seed weight.

TABLE 4.8: ASSOCIATION OF SEED CHARACTERS TRAITS WITH SEED SIZE

Characters		Seed volume	Seed density	Hydration capacity	Hydration index	Swelling capacity	Swelling index	100 seed weight
		1	**2**	**3**	**4**	**5**	**6**	**7**
Seed volume	**1**	1.0000	-0.5207*	0.0644	-0.5844**	0.3889	-0.5324*	0.8105**
Seed density	**2**		1.0000	0.0646	0.1631	0.1881	0.6983**	-0.1850
Hydration capacity	**3**			1.0000	-0.0004	0.1606	0.0369	0.1839
Hydration index	**4**				1.0000	0.2531	0.6794**	-0.3806
Swelling capacity	**5**					1.0000	0.4673*	0.5875**
Swelling index	**6**						1.0000	-0.2054
100 seed weight	**7**							1.0000

****Significant at 1% level @ n-2 df (0.537)**
***Significant at 5% level @ n-2 df (0.423)**

TABLE 4.11: PATH ANALYSIS: 100 SEED WEIGHT IS DEPENDENT

Characters		**Seed volume**	**Seed density**	**Hydration capacity**	**Hydration index**	**Swelling capacity**	**Swelling index**	**‘r’**
		1	**2**	**3**	**4**	**5**	**6**	**7**
Seed volume	**1**	**0.9225**	-0.1626	0.0052	-0.0812	0.0676	0.0590	0.8105**
Seed density	**2**	-0.4803	**0.3122**	0.0052	0.0227	0.0327	-0.0774	-0.1850
Hydration capacity	**3**	0.0594	0.0202	**0.0806**	-0.0001	0.0279	-0.0041	0.1839
Hydration index	**4**	-0.5391	0.0509	0.0000	**0.1389**	0.0440	-0.0753	-0.3806
Swelling capacity	**5**	0.3588	0.0587	0.0129	0.0352	**0.1737**	-0.0518	0.5875**
Swelling index	**6**	-0.4912	0.2180	0.0030	0.0944	0.0812	**-0.1108**	-0.2054

Diagonal values are direct effects
Residual = 0.2233
‘r’: Correlation of 100 seed weight with yield components.

TABLE 4.9: PATH ANALYSIS: SEED YIELD PER PLANT IS DEPENDENT (GENOTYPIC PATH)

CHARACTERS		**Days to 50% flowering**	**Days To maturity**	**Plant height**	**Number of branches**	**Number of pods per plant**	**Pod length**	**Seeds Per pod**	**100 seed weight**	**'r'**
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**
Days to 50% flowering	**1**	**-16.854**	15.746	-0.116	1.571	0.366	-0.504	-0.098	0.016	0.128
Days to maturity	**2**	-16.541	**16.044**	-0.107	1.284	0.288	-0.646	-0.201	-0.006	0.116
Plant height	**3**	-9.422	8.271	**-0.207**	1.458	-0.568	0.396	0.161	-0.098	-0.008
Number of branches	**4**	-13.360	10.398	-0.152	**1.982**	0.282	0.348	0.336	-0.020	-0.185
Number of pods per plant	**5**	-4.337	3.256	0.083	0.393	**1.421**	-0.664	0.027	0.277	0.457*
Pod length	**6**	6.377	-7.774	-0.061	0.518	-0.708	**1.332**	0.507	-0.080	0.111
Seeds per pod	**7**	2.518	-4.946	-0.051	1.020	0.059	1.033	**0.654**	0.103	0.388
100 seed weight	**8**	0.820	0.296	-0.061	0.118	-1.196	0.323	-0.203	**-0.329**	-0.233

Diagonal values are direct effects
Residual = 0.3290
'r': Genotypic correlation of seed yield per plant with yield components

TABLE 4.10: PATH ANALYSIS: 100 SEED WEIGHT IS DEPENDENT (GENOTYPIC PATH)

CHARACTERS		**Days to 50% flowering**	**Days To maturity**	**Plant height**	**Number of branches**	**Number of pods per plant**	**Pod length**	**Seeds Per pod**	**‘r’**
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**
Days to 50% flowering	**1**	**6.372**	-5.000	0.014	-1.058	-0.181	-0.328	0.133	-0.049
Days to maturity	**2**	6.254	**-5.095**	0.012	-0.865	-0.143	-0.420	0.275	0.018
Plant height	**3**	3.562	-2.627	**0.024**	-0.982	0.281	0.257	-0.220	0.296
Number of branches	**4**	5.051	-3.302	0.018	**-1.335**	-0.140	0.226	-0.459	0.060
Number of pods per plant	**5**	1.640	-1.034	-0.010	-0.265	**-0.704**	-0.432	-0.037	-0.842**
Pod length	**6**	-2.411	2.469	0.007	-0.349	0.351	**0.866**	-0.691	0.242
Seeds per pod	**7**	-0.952	1.571	0.006	-0.687	-0.029	0.672	**-0.891**	-0.311

Diagonal values are direct effects
Residual = 0.2782
‘r’: Genotypic correlation of 100 seed weight with yield components

TABLE 4.12: GENOTYPES OF COWPEA INCLUDED IN DIFFERENT CLUSTERS

Cluster Number	Number of Genotypes included	Name of genotypes
I	10	CPD-103, VCP-04-001, ACM-05-2, CPD-91, GC-502, KBC-1-M, CPD-83, GC-601, RC-101 (C), GC-3 (C).
II	3	VCP-04-003, ACM-05-7, HC-08-02
III	8	DCP-2, DCP-6, VBN-1 (LC), TCM-138-1, TCM-148-1, V-130, V-240, Khalleshwari (LC)
IV	1	Subhra

TABLE 4.13: INTRA (BOLD AND DIAGONAL) AND INTER CLUSTER DISTANCE VALUES IN COWPEA

Cluster number	I	II	III	IV
I	**3.377**			
II	4.151	**2.014**		
III	3.548	4.864	**2.795**	
IV	8.045	7.086	7.925	**0.000**

TABLE 4.14: MEAN PERFORMANCE OF DIFFERENT CLUSTERS FOR SEED YIELD AND ITS COMPONENT TRAITS ALONGWITH QUALITY CHARACTERS

Clusters	DF	DM	PPP	PH	BR	PP	PL	SP	CP	SV	SD	HC	HI	SC	SI	100 SW	SYP
I	46.33	58.57	136.30	123.15	3.56	9.49	14.88	12.58	6.16	0.11	1.03	0.13	0.94	0.10	0.99	10.62	3.79
II	47.89	60.67	88.56	89.20	3.36	12.01	11.93	11.51	6.22	0.06	1.06	0.07	1.15	0.05	0.89	7.21	3.22
III	72.54	100.62	141.00	143.56	3.92	11.57	12.27	11.43	6.05	0.11	1.05	0.11	1.00	0.11	1.8	9.75	4.12
IV	48.67	60.67	117.67	90.73	4.13	22.10	13.10	13.93	7.47	0.04	1.44	0.08	1.45	0.10	2.56	6.83	5.35

DF = Days to 50% flowering.
DM = Days to maturity.
PPP = Plant population per plot.
PH = Plant height.
BR = Number of branches per plant.
PP = Pods per plant.
PL = Pod length.
SP = Seeds per pod.
CP = Clusters per plant.
SV = Seed volume.
SD = Seed density.
HC = Hydration capacity.
HI = Hydration index.
SC = Swelling capacity.
SI = Swelling index.
100 SW = 100-seed weight.
SYP = Seed yield per plant.

TABLE 4.15: CONTRIBUTION OF EACH CHARACTER TO DIVERGENCE

Characters	DF	DM	PP	PH	BR	PP	PL	SP	CP	SV	SD	HC	HI	SC	SI	100 SW	SYP	TOTAL
	1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	**15**	**16**	**17**	
Number of times appearing first in ranking	124	0	0	0	0	0	0	0	0	6	2	0	36	27	4	31	1	231
Per cent contribution	53.68	0	0	0	0	0	0	0	0	2.60	0.87	0	15.58	11.69	1.73	13.42	0.43	100

DF = Days to 50% flowering.
PH = Plant height.
PL = Pod length.
SV = Seed volume.
HI = Hydration index.
100 SW = 100-seed weight.

DM = Days to maturity.
BR = Number of branches per plant.
SP = Seeds per pod.
SD = Seed density.
SC = Swelling capacity.
SYP = Seed yield per plant.

PPP = Plant population per plot.
PP = Pods per plant.
CP = Clusters per plant.
HC = Hydration capacity.
SI = Swelling index.

TABLE 4.12: GENOTYPES OF COWPEA INCLUDED IN DIFFERENT CLUSTERS

Cluster Number	Number of Genotypes included	Name of genotypes
I	10	CPD-103, VCP-04-001, ACM-05-2, CPD-91, GC-502, KBC-1-M, CPD-83, GC-601, RC-101 (C), GC-3 (C).
II	3	VCP-04-003, ACM-05-7, HC-08-02
III	8	DCP-2, DCP-6, VBN-1 (LC), TCM-138-1, TCM-148-1, V-130, V-240, Khalleshwari (LC)
IV	1	Subhra

TABLE 4.13: INTRA (BOLD AND DIAGONAL) AND INTER CLUSTER DISTANCE VALUES IN COWPEA

Cluster number	I	II	III	IV
I	**3.377**			
II	4.151	**2.014**		
III	3.548	4.864	**2.795**	
IV	8.045	7.086	7.925	**0.000**

TABLE 4.14: MEAN PERFORMANCE OF DIFFERENT CLUSTERS FOR SEED YIELD AND ITS COMPONENT TRAITS ALONGWITH QUALITY CHARACTERS

Clusters	DF	DM	PPP	PH	BR	PP	PL	SP	CP	SV	SD	HC	HI	SC	SI	100 SW	SYP
I	46.33	58.57	136.30	123.15	3.56	9.49	14.88	12.58	6.16	0.11	1.03	0.13	0.94	0.10	0.99	10.62	3.79
II	47.89	60.67	88.56	89.20	3.36	12.01	11.93	11.51	6.22	0.06	1.06	0.07	1.15	0.05	0.89	7.21	3.22
III	72.54	100.62	141.00	143.56	3.92	11.57	12.27	11.43	6.05	0.11	1.05	0.11	1.00	0.11	1.8	9.75	4.12
IV	48.67	60.67	117.67	90.73	4.13	22.10	13.10	13.93	7.47	0.04	1.44	0.08	1.45	0.10	2.56	6.83	5.35

DF = Days to 50% flowering.
DM = Days to maturity.
PPP = Plant population per plot.
PH = Plant height.
BR = Number of branches per plant.
PP = Pods per plant.
PL = Pod length.
SP = Seeds per pod.
CP = Clusters per plant.
SV = Seed volume.
SD = Seed density.
HC = Hydration capacity.
HI = Hydration index.
SC = Swelling capacity.
SI = Swelling index.
100 SW = 100-seed weight.
SYP = Seed yield per plant.

TABLE 4.15: CONTRIBUTION OF EACH CHARACTER TO DIVERGENCE

Characters	DF	DM	PP	PH	BR	PP	PL	SP	CP	SV	SD	HC	HI	SC	SI	100 SW	SYP	TOTAL
	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	
Number of times appearing first in ranking	124	0	0	0	0	0	0	0	0	6	2	0	36	27	4	31	1	231
Per cent contribution	53.68	0	0	0	0	0	0	0	0	2.60	0.87	0	15.58	11.69	1.73	13.42	0.43	100

DF = Days to 50% flowering.
PH = Plant height.
PL = Pod length.
SV = Seed volume.
HI = Hydration index.
100 SW = 100-seed weight.

DM = Days to maturity.
BR = Number of branches per plant.
SP = Seeds per pod.
SD = Seed density.
SC = Swelling capacity.
SYP = Seed yield per plant.

PPP = Plant population per plot.
PP = Pods per plant.
CP = Clusters per plant.
HC = Hydration capacity.
SI = Swelling index.

TABLE 4.16: VARIABILITY IN SEED COLOUR, SIZE AND SHAPE IN COWPEA GENOTYPES

Sr. No.	Code	Genotype	Seed colour	Seed size	Seed shape
1.	CP-13	CPD-103	Cream	Large	Smooth
2.	CP-14	VCP-04-001	Dark brown with cream spot	Large	Smooth
3.	CP-15	VCP-04-003	Cream with brown patches around eye	Moderate	Wrinkled
4.	CP-16	ACM-05-2	Brown	Large	Smooth
5.	CP-17	ACM-05-7	Cream	Small	Smooth
6.	CP-18	CPD-91	Cream with brown patches around eye	Large	Smooth
7.	CP-19	GC-502	Brown	Large	Smooth
8.	CP-20	HC-08-02	Cream	Small	Smooth
9.	CP-21	KBC-1-M	Light brown	Moderate	Smooth
10.	CP-22	CPD-83	Cream with brown patches around eye	Extra large	Wrinkled
11.	CP-23	GC-601	Cream with brown patches around eye	Large	Smooth
12.	CP-24	RC-101 (C)	White	Large	Smooth
13.	CP-25	GC-3 (C)	Cream with brown patches around eye	Moderate	Wrinkled
14.	CP-26	Subhra	Cream with brown patches around eye	Small	Smooth
15.	DCP-2	DCP-2	Brown	Large	Smooth
16.	DCP-6	DCP-6	Cream	Moderate	Smooth
17.	VBN-1 (LC)	VBN-1 (LC)	Cream with brown patches around eye	Moderate	Smooth
18.	TCM-138-1	TCM-138-1	Cream	Moderate	Wrinkled
19.	TCM-148-1	TCM-148-1	White with grey patches around eye	Moderate	Smooth
20.	V-130	V-130	Cream with brown patches around eye	Moderate	Wrinkled
21.	V-240	V-240	Cream	Moderate	Smooth
22.	Khalleshwari (LC)	Khalleshwari(LC)	Cream	Large	Wrinkled

Table 4.2: MEAN PERFORMANCE OF 22 COWPEA GENOTYPES

GENOTYPE	DF	DM	PPP	PH	BR	PP	PL	SP	CP
CPD-103	41.33	56.33	156.00	121.60	3.23	9.40	12.73	10.87	5.27
VCP-04-001	51.67	58.67	120.67	156.07	4.27	9.73	19.47	15.73	6.27
VCP-04-003	45.67	59.33	108.67	116.93	3.27	11.87	12.27	10.27	6.20
ACM-05-2	49.33	59.00	101.67	118.47	3.53	10.80	15.67	14.27	6.20
ACM-05-7	50.67	61.67	119.67	93.80	3.53	12.93	11.27	12.47	6.60
CPD-91	43.33	61.00	156.00	140.13	3.13	9.73	12.73	10.43	5.80
GC-502	43.67	55.67	139.33	87.80	2.93	8.53	15.17	12.53	6.80
HC-08-02	47.33	61.00	37.33	56.87	3.27	11.23	12.27	11.80	5.87
KBC-1-M	51.67	58.33	185.67	168.40	4.20	10.07	16.73	15.87	6.13
CPD-83	45.67	60.33	114.33	130.07	3.73	8.53	14.70	10.00	6.33
GC-601	44.67	58.00	101.33	105.53	3.60	9.67	14.60	11.20	5.60
RC-101 (C)	42.67	56.67	115.00	76.47	3.53	9.13	12.77	11.20	6.13
GC-3 (C)	49.33	61.67	173.00	127.00	3.47	9.33	14.23	13.73	7.07
Subhra	48.67	60.67	117.67	90.73	4.13	22.10	13.10	13.93	7.47
DCP-2	72.33	100.33	124.33	124.93	3.87	10.27	10.73	11.53	5.20
DCP-6	70.67	99.67	116.67	162.13	4.47	13.87	12.43	11.87	6.80
VBN-1 (LC)	71.67	98.67	163.67	150.73	4.07	11.73	12.03	10.87	5.87
TCM-138-1	72.33	99.67	141.33	126.13	3.87	14.03	12.47	10.47	7.27
TCM-148-1	71.67	100.00	117.33	113.27	3.33	10.40	11.43	10.60	6.47
V-130	76.33	101.67	171.33	142.53	4.30	11.80	11.93	10.53	5.47
V-240	72.67	101.00	176.67	176.93	3.40	10.37	13.57	12.73	5.13
Khalleshwari(LC)	72.67	104.00	116.67	151.80	4.07	10.07	13.60	12.87	6.20

DF = Days to 50% flowering.
DM = Days to maturity.
PPP = Plant population per plot.
PH = Plant height.
BR = Number of branches per plant.
PP = Pods per plant.
PL = Pod length.
SP = Seeds per pod.
CP = Clusters per plant.

Table 4.3: MEAN PERFORMANCE OF 22 COWPEA GENOTYPES

GENOTYPE	SW	SYPN	SYP	SV	SD	HC	HI	SC	SI
CPD-103	10.30	3.152	460.0	0.127	0.928	0.075	0.657	0.077	0.605
VCP-04-001	9.87	5.318	593.3	0.103	0.968	0.131	1.316	0.138	1.344
VCP-04-003	8.47	3.060	313.3	0.077	0.884	0.090	1.313	0.066	0.854
ACM-05-2	9.70	6.934	700.0	0.103	1.023	0.100	0.956	0.098	0.955
ACM-05-7	6.27	4.315	510.0	0.059	1.030	0.061	1.005	0.043	0.736
CPD-91	10.63	4.342	668.0	0.090	1.167	0.097	0.921	0.101	1.120
GC-502	10.27	6.563	803.3	0.102	0.941	0.112	1.165	0.118	1.157
HC-08-02	6.90	2.282	76.7	0.049	1.260	0.070	1.129	0.053	1.084
KBC-1-M	9.17	1.186	220.0	0.103	1.113	0.094	0.604	0.078	0.755
CPD-83	16.33	1.484	169.3	0.141	1.101	0.120	0.774	0.139	0.987
GC-601	11.13	3.158	310.0	0.121	0.942	0.100	0.877	0.099	0.818
RC-101 (C)	10.33	2.236	260.0	0.100	1.027	0.103	1.006	0.099	0.993
GC-3 (C)	8.43	3.494	602.0	0.083	1.138	0.091	0.962	0.097	1.172
Subhra	6.83	5.354	623.3	0.040	1.444	0.084	1.451	0.102	2.557
DCP-2	11.63	4.863	127.2	0.143	1.065	0.135	0.890	0.139	0.977
DCP-6	9.53	5.698	127.7	0.104	1.078	0.103	0.916	0.097	0.931
VBN-1 (LC)	9.13	3.633	120.9	0.097	1.106	0.112	1.043	0.124	1.274
TCM-138-1	9.00	3.475	60.3	0.103	0.804	0.104	1.253	0.097	0.943
TCM-148-1	8.50	4.777	70.7	0.089	1.048	0.101	1.082	0.112	1.254
V-130	9.53	2.720	61.9	0.120	0.825	0.061	0.613	0.041	0.339
V-240	9.37	3.650	189.2	0.084	1.300	0.101	0.927	0.117	1.401
Khalleshwari(LC)	11.27	4.121	58.8	0.102	1.062	0.142	1.524	0.142	1.392

SV = Seed volume.
SD = Seed density.
HC = Hydration capacity.
HI = Hydration index.
SC = Swelling capacity.
SI = Swelling index.
100 SW = 100 seed weight.
SYP = Seed yield per plant.

PLATE II: VARIABILITY IN SEED COLOUR, SIZE AND SHAPE IN COWPEA GENOTYPES

CP-13
(CPD-103)

CP-14
(VCP-04-001)

CP-15
(VCP-04-003)

CP-16
(ACM-05-2)

CP-17
(ACM-05-7)

CP-18
(CPD-91)

CP-19
(GC-502)

CP-20
(HC-08-02)

PLATE III: VARIABILITY IN SEED COLOUR, SIZE AND SHAPE IN COWPEA GENOTYPES

CP-21
(KBC-1-M)

CP-22
(CPD-83)

CP-23
(GC-601)

CP-24
(RC-101(C))

CP-25
(GC-3(C))

CP-26
(Subhra)

(DCP-2)

(DCP-6)

PLATE IV: VARIABILITY IN SEED COLOUR, SIZE AND SHAPE IN COWPEA GENOTYPES

(VBN-1)

(TCM-138-1)

(TCM-148-1)

(V-130)

(V-240)

(KHALLESHWARI)

PLATE I: FIELD VIEW OF EXPERIMENT