Character Associations and Genetic Divergence in Cowpea [*Vigna unguiculata* (L.) Walp.]

लोबिया [*विग्ना अन्गुइकुलेटा* (एल.) वाल्प.] में लक्षण सहचर्य एवं आनुवंशिक विविधता

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By

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1. INTRODUTION

Cowpea [*Vigna unguiculata* (L.) Walp.] is an annual, autogamous leguminous crop belongs to family Leguminoseae (Mackie and Smith, 1935) with a diploid chromosome number of 2n=2x=22 (Darlington and Wylie, 1955). It is native to India (Vavilov, 1949) but tropical and central Africa is also considered as secondary centre of origin where wild races are found even now (Ng and Marechal, 1985).

Cowpea is a tropical grain legume which plays an important nutritional role in developing countries of the tropics and sub tropics, especially in Sub-Saharan Africa, Asia, Central and South America (Singh *et al.*, 1997). Cowpea has been referred to as “Poor man’s meat” because of its high protein content (20-25%). Cowpea young leaves, pods and beans contain vitamins and minerals which have fuelled its usage for human consumption and animal feeding (Nielson *et al.*,1997) and considered as one of agriculture’s oldest legume used as protein source for humans and livestock (Steele, 1972).

Dry seeds of cowpea are used to prepare several snacks and main meal dishes. It contains high amount of quality protein (23.4%), carbohydrate (60.3%), fat (1.8%) and sufficient amount of calcium (76mg/100gm), iron (57mg/100gm) and vitamins such as thiamine (0.92mg/100g.), riboflavin (0.18mg/100g.) and nicotinic acid (1.9mg/100g.) (Chatterjee and Bhattaacharya, 1986). The off-take crop of cowpea for fodder makes an important contribution to feed supplies for ruminants to maintain their health in dry season (Quin, 1997).

Besides, its use as green vegetable and food legumes it is also used for green manure and quick growing cover crop under a wide range of climatic conditions within the country. It is one of the major pulse crops grown in *kharif* season in Rajasthan and other major cowpea producing states are Karnataka, Andhra Pradesh, Uttar Pradesh and Bihar in India. The area occupied by *kharif* pulses in Rajasthan was (*Kharif*, 2013) 22,20,553 ha, with the production and productivity of 7,73,019 tonnes and 348 kg ha^{-1}, respectively, out of which the cowpea occupied 61,265 ha area, producing 33,975 tonnes of dry seeds with a productivity of 555 kg ha^{-1} (Anonymous, 2013). The major cowpea producing districts in Rajasthan are Sikar, Jhunjhunu, Jaipur, Nagaur, Ajmer, and Sirohi.

In Rajasthan cowpea is of great importance because of its short duration, high yield potential and quick growing habits along with high protein content and as cover crop which helps in conservation of soil. It is grown as an alternative crop in dry land farming. Cowpea is some time grown as a green manure for soil improvement. *In situ* decomposition of root residues of cowpea crop contributes organic matter and associated nutrients to the soil. Many experimental evidences showed that soil nitrogen level increased following cowpea crop at the rate of 40-80 kg N per ha due to symbiosis with nodulating bacteria of genus *Bradyrhizobium* that fixes atmospheric dinitrogen within the nodule (Quin, 1997). The drought hardy nature of cowpea crop enables it to maintain some growth or at least survive under dry soil conditions. This trait is also extended by the deep rooting habit of some varieties and accounts for the crop's ability to grow and yield under the semi-desert conditions (Quin, 1997). In addition, some cowpea varieties are suicidal to the germination of seeds of *Striga hermonthica,* a parasitic plant (Quin, 1997).

On account of diverse uses of cowpea the varietal requirement in term of plant type, seed type, maturity, pattern of use and growth are diverse from region to region. Therefore cowpea breeding programme has become more complex and no single variety can be suitable for all the objectives (Barrett, 1987). Thus, there is need to develop varieties suitable for a specific region and or use. However, production is constrained by low and variable grain yield, seed quality, susceptibility to diseases and pests and the absence of improved cultivars, under such circumstances genetic diversity is of great importance and plays a crucial role in focusing crop improvement.

In India sporadic breeding work on cowpea was started after 1970 under All India Co-ordinated Crop Research Programme (Jonoria and Ali, 1970 and Bapna *et al.*, 1972), but the achievements were limited. Information about genetic variability, correlation analysis, path analysis and genetic divergence are limited but the same an essential for any concerted and specific breeding programme on genetic improvement of the crop. Thus, the present investigation aims to assess the genetic correlation between various pairs of traits character associations and genetic divergence in 72 genotypes of cowpea.

Objectives:

Keeping the above facts in view, the present investigation was carried out with the following objectives.

(i) To estimate genetic variability for seed yield and its components in germplasm lines of cowpea.

(ii) To determine associations between seed yield and its components.

(iii) To determine direct and indirect effects of various component characters on seed yield.

(iv) To measure the degree of genetic divergence.

2. REVIEW OF LITERATURE

Literature on important aspects pertinent to present study has been reviewed and presented in this chapter.

2.1 Genetic Variability

Assessment of genetic variability is usually made through the estimates of genetic parameters of variation such as range, genotypic and phenotypic variance and genotypic and phenotypic coefficient of variance of the characters under consideration. The literature available on these aspects in cowpea has been reviewed and presented as under:

Nehru and Manjunath (2001) evaluated 40 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] and reported genetic variability for yield and its components. The PCV was highest for pods/plant followed by cluster/plant, primary branches/plant and yield/plant. High PCV coupled with high heritability resulted in high genetic advance expressed as per cent of mean for pods/plant and moderate for plant height, 100-seed weight and yield/plant.

Singh and Verma (2002) evaluated 600 lines of cowpea for genetic variation and correlation for 8 quantitative traits of cowpea. High coefficient of variation was recorded for seed yield, plant height, 100-seed weight and number of pods/peduncle. Moderate variation was recorded for number of days to 50% flowering and pod length. Minimum variability was observed for number of days to maturity and number of seeds/pod.

In a study, Pal *et al.* (2003) evaluated 40 diverse genotypes of vegetable type cowpea [*Vigna unguiculata* (L.) Walp.] and assessed genetic variability for 13 traits. The phenotypic coefficient of variation was greater than genotypic coefficient of variation for most of traits. Relatively high phenotypic and genotypic coefficients of variation were recorded for plant height, number of primary branches/plant, number of peduncles/plant, number of pod/plant and green pod yield/plant.

Rocha *et al.* (2003) studied genetic parameters in 23 white coat cowpea [*Vigna unguiculata* (L.) Walp.] genotypes and evaluated the agronomic traits *viz.,* number of days to initial flowering, agronomic value, number of pod/plant, pod length, number of grains/pod, weight of 100 grains and grain yield. The traits recorded highest variability for agronomic value (20.74), grain yield (19.55) and weight of 100-grains (16.87).

Venkatesan *et al.* (2003) evaluated 20 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] for 12 traits and recorded significant variation among the genotypes for all the traits studied and greatest variation was recorded for plant height. The magnitude of the PCV was higher than that of the GCV. High GCV and PCV were recorded for plant height and dry matter production.

Vineeta *et al.* (2003) evaluated 50 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] and studied genetic variation for 10 traits and reported significant genetic variation was recorded for most of the traits. The PCV was higher than their corresponding GCV. GCV and PCV values were higher for days to flowering and maturity, number of cluster and pods/plant, 100-seed weight and seed yield/plant.

In a study on 45 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] Nigude *et al.* (2004) observed a wide range of genetic variability for yield and yield components. The phenotypic variance for all 13 characters studied was higher than the genotypic variance indicating influence of environment on all the characters.

Zarger *et al.* (2005) evaluated 32 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] and estimated genetic variability, heritability and genetic advance for seven traits. Significant variation among the genotypes was evident for all the traits studied. Considerable variation was recorded for seed yield/plot, 100-seed weight, plant height, number of pods/plant, number of seeds/pod and pod length. The magnitude of the phenotypic coefficient of variation (PCV) was higher than that of the genotypic coefficient of variation (GCV) for all the traits studied. High GCV and PCV were recorded for plant height, number of pods/plant, seed yield/plot and 100-seed weight.

In cowpea high positive significant phenotypic and genotypic correlations were observed for traits *viz.,* plant height, number of branches, numbers of leaves, leaf length, leaf weight, stem weight, green fodder yield and crude protein content by Sheelamary and Gopalan (2006). Days to 50% flowering showed negative significant relationship at both the levels.

Lal *et al.* (2007) studied genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed that the high degree of variability for number of peduncles and pods/plant, pod weight and pod yield/plant. Higher estimates of heritability coupled with the higher genetic advance for number of peduncles/plant, number of days to flower, number of pods/plant and pod yield/plant indicated that heritability is mainly due to additive genetic effects.

Saini (2007) in a study on 60 genotypes of cowpea and high estimates of GCV and PCV were recorded for clusters/plant, seed yield/plant and plant height whereas, moderate estimate of PCV along with high estimate of GCV were recorded for branches/plant and pods/plant. Moderate estimates of GCV along with low estimates of PCV were recorded for pod length and seeds/pod. Rest of the characters had low estimates of PCV and GCV.

Suganthi and Murugan (2008) studied 30 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and reported a high genotypic coefficient of variation than phenotypic coefficient of variation for all the characters. Maximum phenotypic and genotypic coefficient of variation was recorded for seed yield/plant followed by pods/plant and clusters/plant. High heritability was recorded for seed yield/plant followed by seeds/pod, pod length and hundred seed weight. Genetic advance as per cent of mean was higher for seed yield/plant followed by pods/plant and clusters/plant. Seed yield had positive and significant association with pod length.

Tamgadge *et al.* (2008) evaluated 30 genotypes of cowpea *[Vigna unguiculata* (L.) Walp] and reported that the phenotypic coefficient of variation was greater than genotypic coefficient of variation, number of cluster/plant, diameter of pod and number of seeds/pod manifested high heritability coupled with low genotypic coefficient of variation and genetic advance.

Vishwanath *et al.* (2009) studied on 41 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and reported existence of relatively high degree of variability for plant height, peduncle length, number of peduncles and pods/plant, pod length, pod weight and pod yield/plant. Higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles/plant, number of days to flower and pod yield/plant indicated that heritability is mainly due to additive genetic effects.

Imran *et al.* (2010) evaluated 14 lines of cowpea [*Vigna unguiculata* (L.) Walp.] and reported significant variability among the lines. Three lines– CP/V4, CP/V2 and CP/V6 were found suitable for obtaining higher green fodder yield, whereas the lines CP/V10, CP/V5, No. 1, SA-Dandy, CP/V2, CP/V6, CP/V3, CP/V7, CP/V8, CP/VII, CP/V9 and CP/ V12 were found suitable for maximum grain yield and two lines CP/V2 and CP/V6 could be used both for fodder and grain yield and one line CP/V4 proved to be suitable exclusively for green fodder yield under rained conditions of Islamabad.

In a study on 10 cowpea [*Vigna unguiculata* (L.) Walp.] accessions Manggoel *et al.* (2012) observed significant variability for days to 50% flowering, number of peduncles/plant, flower/plant, pods/plant, seed/pod, pod length, 100-seed weight and grain yield and the phenotypic coefficient of variation and genotypic coefficient of variance were high for the traits studied, except pod length and seeds/pod.

Inuwa *et al.* (2012) conducted two different but related experiments, and observed that there were considerable variation among the lines for duration of vegetative and reproductive phases and for yield characters (*viz.*, seed/pod, number of pod/plant, weight of pod/pant and 100- seed weight).

Vavilapalli *et al.* (2013) studied the genotypic variability in 22 genotypes of bush cowpea and observed that the analysis of variance indicated the prevalence of sufficient genetic variation among the genotypes from all the characters studied. Among the genotypes VU 6 (310.41g) was the highest yielder. Pods/plant was highest in VU 8 (70.30) and pod weight in VU 20 (12.44g). The high phenotypic coefficient of variation and genotypic coefficient of variation were observed for pod weight, plant height, and pod length.

Chattopadhyay *et al.* (2014) studied 60 genotypes of vegetable cowpea (*Vigna unguiculata cv-gr.sesquipedalis)* and reported high to moderate GCV and PCV values for number of pods/plant, pod yield/plant, pod weight, number of seeds/pod and pod length.

2.2 Heritability and genetic advance

Heritability is an index of the transmission of characters from parents to their offspring (Falconer, 1960). It is generally expressed in percentage. The estimation of heritability helps the plant breeder in selection of elite genotypes. It also measures the degree of resemblance between relatives and correspondence between phenotype and breeding value. Genetic advance is the measure of genetic gain under selection. Heritability estimates along with genetic advance are more helpful in predicting the gain under selection than heritability estimates alone. Allard (1960) expressed the genetic advance as the product of selection intensity, heritability and phenotypic standard deviation of a character. The literature available on these aspects has been presented as under:

In a study on 5 cowpea cultivars (TCS-85, TCS-76, ARL-25, ECS-89 and TCS-39) Kumar *et al.* (2002) observed a wide range of genetic variability for most of the characters under study. High heritability was recorded for green fodder yield/plant, number of days to 50% flowering, plant height and dry fodder yield/plant. Genetic advance was higher for green fodder yield, plant height and number of days to 50% flowering.

Pal *et al.* (2003) evaluated 40 diverse genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] and assessed high heritability estimates with moderate to high GCV and genetic advance for plant height, peduncle length, number of primary branches/plant, number of peduncle/plant and green pods/plant, which could be improved by simple selection in the early generation. Days to 50% flowering, days to first green pod picking, pod diameter, number of seeds/pod and 100-seed weight manifested high heritability with low genotypic coefficient of variance and genetic advance.

Venkatasan *et al.* (2003) evaluated 20 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] for 12 traits *viz*., number of days to first flower, plant height, number of branches/plant, number of cluster/plant, number of pods/cluster, number of pods/plant, pod yield/plant, pod length, number of seeds/pod, 100-seed weight, seed yield/plant and dry matter production and recorded that plant height, number of pod/plant, pod length, 100-seed weight, seed yield and dry matter production were characterized by very high heritability. High heritability coupled with high genetic advance was recorded for plant height, dry matter production and seed yield indicating the importance of additive genes effects in these characters.

Vineeta *et al.* (2003) evaluated 50 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] for 10 traits *viz*., days to 50% flowering, days to maturity, plant height, number of branches/plant, number of cluster/plant, number of pods/plant, pod length, number of seeds/pod, 100-seed weight, seed yield/plant and recorded high heritability and genetic gain for seed yield/plant, number of pods/plant and cluster/plant.

Zargar *et al.* (2005) performed a study on 32 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed high heritability coupled with high genetic gain was observed for plant height (96.39 and 90.78%), number of pods/plant (67.84 and 38.39%), seed yield/plot (175.02 and 122.83%) and 100-seed weight (37.40 and 39.34%) indicating the preponderance of additive gene effects for these traits.

Malarvizhi *et al.* (2005) carried out genetic variability, heritability and genetic advance studies with 60 genotypes of fodder cowpea [*Vigna unguiculata* (L.) Walp.]. Days to 50% flowering along with twelve economic traits were studied. The analysis of variance revealed that all the 60 genotypes varied significantly for all the 13 characters indicating that there existed considerable variation for all the characters.

Girish *et al.* (2006) studied 100 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and estimated genetic variability, heritability and genetic advance for eleven quantitative characters. Wide range of variability was observed for most quantitative characters. Plant height and seed yield showed highest phenotypic and genotypic variance, while primary and secondary branches showed lowest variances. The magnitude of Phenotypic Coefficient of Variation (PCV), Genotypic Coefficient of Variation (GCV), Heritability (h^2) and Genetic Advance (GA) was high for seed yield/plant, number of pods/plant and plant height. Days to first flower opening, days to 50% flowering and days to maturity had a low genetic advance. It was inferred that a heritability value based on phenotypic expression and genetic advance is more useful in predicting actual value of selection.

Eswaran *et al.* (2007) studied the genetic variability with 30 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed high estimates of genetic variability coupled with high heritability and genetic advance for plant height at the time of first flowering, plant height at the time of 50 per cent flowering and plant height at the time of 50 per cent maturity indicating their dependability for effecting selection.

In a study on evaluation of 60 genotypes of cowpea by Saini (2007) high estimates of heritability were recorded for days to maturity, test weight and seed yield/plant whereas, moderate estimates of heritability were recorded for cluster/plant, days to 50% flowering, plant height and pods/plant. Rest of the characters showed low estimate of heritability.

Idahosa *et al.* (2010) studied genetic variability, heritability and genetic advance at Ekpoma and Lyanomo locations on 8 cowpea genotypes and observed high broad-sense heritability percentage in all the characters studied except for pod weight character which revealed low estimate of 25.5% at Lynomo location. The expected genetic advance as percentage of mean (GA %) was relatively high for pod length, pod weight, seeds/pod and 100-seed weight characters in the two locations.

In a study on 25 genotypes of cowpea Singh *et al.* (2010) observed high phenotypic and genotypic coefficient of variation coupled with high heritability and genetic advance as per cent of mean were reported for plant height, stem weight, leaves weight, biological yield, dry matter yield and green fodder productivity indicating predominance of additive gene effects in controlling these characters. Green fodder yield was significantly and positively correlated with green fodder productivity, dry matter yield, biological yield, leaves weight and stem weight.

Thorat and Gadewar (2013) studied the genetic variability, heritability and genetic advance with 30 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed that the almost all characters showed high heritability values. High heritability coupled with high genetic advances observed for plant height, number of pods/plant and number of branches/plant and high GCV observed for leaf area index followed by days to 50% flowering indicating thereby the preponderance of additive gene effects for this characters.

Vavilapalli *et al*. (2013) carried out genetic variability, heritability and genetic advance studies with 22 genotypes of bush cowpea. High heritability coupled with high genetic advance were observed for all characters studied, except days to first flowering and days to first harvest indicating these characters are governed by additive gene action. Hence, direct selection may be followed for the improvement of vegetable cowpea for these characters.

Chattopadhyay *et al.* (2014) studied 60 genotypes of vegetable cowpea (*Vigna unguiculata cv-gr.sesquipedalis)* and higher estimates of broad sense heritability coupled with higher genetic advance for number of pods/plant, pod yield/plant, pod weight, number of seeds/pod and pod length.

2.3 Correlation coefficients

Correlation coefficient is a statistical measure, which is used to find out the degree and direction of relationship between two variables. It is the independent of the unit of measurement. In plant breeding, correlation coefficient analysis is very useful as it provides measure of the mutual relationship between various plant characters and determines the component characters on which selection can be based for genetic improvement in yield through indirect selection. The literature available on this aspect has been reviewed as under:

Singh and Verma (2002) evaluated 600 lines of cowpea for 8 quantitative traits. Seed yield was positively correlated with 100-seed weight and pod length. Pod length and plant height were positively correlated with 100-seed weight. A negative correlation between 100-seed weight and number of pod/peduncle, number of days to 50% flowering and days to maturity was observed.

Venkatesan *et al.* (2003) carried out correlation analysis using 20 diversified genotypes of cowpea for 12 component characters including seed yield. Characters branches/plant, clusters/plant, pods/plant, pods/cluster and pod yield had positive correlation with seed yield both at genotypic and phenotypic level.

Narayanankutty *et al.* (2003) studied 37 divergent genotypes of vegetable cowpea for 12 traits (*viz.,* number of days to first flower opening, leaf length, leaf width, number of days to first picking, number of pickings, yield/plant, number of pods/plant, average weight of pods, pod length, number of seeds/pod, 100-seed weight and number of days to complete flowering) and reported that the number of pods/plant, number of pickings, average weight of pods and pod length were positively and significantly correlated with yield/plant both at phenotypic and genotypic levels. Number of days to first picking showed significant negative correlation with number of pickings, yield/plant and number of pods/plant.

Venkatesan *et al.* (2003) evaluated 20 genotypes of cowpea for 10 traits, and observed that the number of branches/plant, number of clusters/plant, number of pods/cluster, number of pods/plant, and pod yield were positively correlated with seed yield at the genetic and phenotypic levels. The magnitude of genetic correlation was higher than that of phenotypic correlation. The number of clusters/plant was positively associated with number of branches/plant, number of pods/cluster and number of pods/plant, but was negatively correlated with number of days to flowering, 100-seed weight, and dry matter production. The number of branches/plant and number of pods/cluster exhibited few significant associations with the other traits.

Fifty genotypes of cowpea were evaluated by Vineeta *et al.* (2003) for 10 traits *viz.,* days to 50% flowering, days to maturity, plant height, number branches/plant, number of clusters/plant, number of pos/plant, pod length, number of seeds/pod, 100-seed weight and seed yield. Seed yield/plant was positively correlated with number of cluster/plant and pods/plant and 100-seed weight, but was negatively correlated with days to maturity.

Nigude *et al.* (2004) studied 45 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] and reported that the grain yield/plant showed highly significant and positive association for most of the characters studied except, pod length and test weight at both genotypic and phenotypic level.

Patil *et al.* (2004) evaluated 47 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and analyzed correlation for 10 yield contributing characters and revealed that the seed yield/plant had highly positive and significant correlation with number of compound leaves per plant at the phenotypic level and with leaf area/plant, dry weight of pods/plant and biological yield both at the phenotypic and genotypic level.

Pal *et al.* (2004) evaluated 40 diverse cowpea genotypes for green pod yield and 12 yield components and observed green pod yield/plant was positively and significantly associated with number of primary branches/plant, pod length, pod diameter, number of pods/plant, number of seeds/pod and 100-seed weight. Days to 50% flowering and days to first green pod picking showed significant negative correlation with green pod yield/plant, indicating that selection should be based on these traits. The negative association of these two traits with green pod yield/plant also suggested that selection for these traits will be of help to the breeders in selecting cultivar for earliness.

Kumawat and Raje (2005) evaluated 50 genotypes of cowpea *[Vigna unguiculata* (L.) Walp.] reported that the seed yield/plant had significant positive correlations with branches/plant, clusters/plant, pods/plant, biological yield/plant and harvest index. These characters also had positive correlation among themselves, except correlation of harvest index with biological yield/plant. Seed yield/plant had significantly negative correlation with days to 50% flowering and days to maturity.

Saini (2007) evaluated 60 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed that seed yield/plant had positive significant correlation with seeds/pod. Whereas it had negative significant correlation with days to maturity, In addition, days to maturity also had negative significant correlation with test weight. Days to maturity had positive significant correlation with days to 50% flowering. Among other yield attributing traits, clusters/plant and seed/pods were positively and significantly correlated with pods/plant and pod length, respectively. Clusters/plant was negatively and significantly correlated with test weight.

Alege and Mustapha (2007) conducted an experiment on 60 improved varieties of cowpea [V*igna unguiculata* (L.) Walp.] and performed studies on some qualitative and quantitative characters. Positive correlations were obtained between leaf number and stem diameter, leaf number and number of seeds/pod, number of branches and plant height. Negative correlation existed between number of pods/plant and number of seeds/pod.

Vishwanath *et al.* (2009) studied on 41 genotypes of cowpea and reported that the correlation analysis revealed the importance of number of branches/plant, number of peduncles/plant, pod length, pod weight and number of seeds/pod towards pod yield. Pod weight exerted the maximum positive direct effect on pod yield followed by number of pods/plant and pod length. It was inferred that selection pressure on these traits may lead to an overall increase in pod yield/plant.

Imran *et al.* (2010) evaluated 14 local lines of cowpea and reported that the number of branches/plant showed a significant correlation (r=0.585) with leaf area but non-significant association with number of leaves/main branch and green fodder yield and leaf area showed a negative and significant correlation (r=0.583) with pod length which is indicative of the fact that a plant having more vegetative growth *(i.e.,* leaf area) produces small pods.

Manggoel *et al.* (2012), evaluated 10 cowpea accessions and observed positive correlation between grain yield and number of peduncles/plant (r=0.716**), flowers/plant (r=0.776**), pods/plant (r=0.640*) and 100- seed weight (r=0.690*).

Cokkizgin *et al.* (2013) evaluated 6 common bean genotypes and observed that seed yield was significantly correlated with all the traits except plant height and 100-seed weight and the relationship of seed yield/plant with branch number/plant (r=0.78), pod length (r=0.51), seed number/pod (r=0.57), seed weight/pod (r=0.87), pod number/plant,(r=0.90),seed number/plant(r=0.88) and seed yield/plant (r=0.92), was positive while correlation of seed yield/plant with first pod height (r= -0.79) was negative.

In a study on 30 genotypes of cowpea Thorat and Gadewar (2013) observed that the days to maturity had highly significant positive correlation with days to 50% flowering both genotypically and phenotypically. Protein content was significant but negatively associated with days to maturity. Number of clusters/plant showed strong positive significant correlation with protein content. Pod length exhibited significant positive correlation with protein content. Number of seeds/pod exhibited positive significant correlation with protein content and strongly correlated with pod length. Seed yield/plot exhibited strong positive significant correlation with clusters/plant, number of pods/plant. It also shows moderately positive significant correlation with protein content.

Sahai *et al.* (2013) performed a study on cowpea germplasm lines and estimated correlation coefficients and path analysis coefficient of morphological as well as fodder and grain yield attributes. The study showed a high impact of direct effects of correlation (0.9714**) and suggested that going for plant types with higher biomass/plant (0.8856**), dry weight/plant (0.4598), stem girth (0.2336) number of secondary branches (0.2788), leaves/plant (0.3251), pods/plant (0.9059) and pod clusters/plant (0.7718) would be effective for improving both fodder and seed yield in cowpea.

Chattopadhyay *et al.* (2014) studied 60 genotypes of vegetable cowpea (*Vigna unguiculata cv-gr.sesquipedalis)* and reported that the genotypic correlation coefficients were higher than their phenotypic correlation coefficients in most of the cases. From the correlation and path analysis, it can be concluded that emphasis should be given on number of pods/plant and pod weight for selecting high yielding genotypes.

2.4 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient which provides effective means of finding out direct and indirect causes of association, thereby permitting a critical examination of specific forces acting to produce a given factor. The available literature on path coefficient analysis was reviewed and has been presented here:

Kumar *et al.* (2002) evaluated 5 cowpea cultivars (TCS-85, TCS-76, ARL-25, ECS-89 and TCS-39) and observed correlation and path analysis, correlation study among various component characters showed that plant height, number of branches/plant, leaf length, leaf breadth and dry fodder yield/plant were positively correlated with green fodder yield. In general, genotypic coefficients were higher than the corresponding phenotypic correlation coefficient. Path analysis showed that dry fodder yield had the highest direct positive contribution towards green fodder yield followed by number of days to 50% flowering, leaf stem ratio, number of branches, plant height, leaf breadth and leaf length, respectively.

Narayanankutty *et al.* (2003) studied 37 divergent genotypes of vegetable cowpea for 12 traits and reported that the path analysis indicated that the number of pods/plant, followed by average weight of pods and number of pickings had the greatest positive direct effect on yield. The direct effects of pod length and number of days to first picking were low, mainly due to high indirect effects via average weight of pods and number of pods/plant.

Venkatesan *et al.* (2003) evaluated 20 genotypes of cowpea for 10 traits (*viz.*, number of days to flowering, plant height, number of branches, clusters and pods/plant, number of pods/cluster, pod length, number of seeds/pod, 100-seed weight, and seed yield/plant) and analysed path analysis showed the positive direct effect of number of pods/plant, pod length, number of clusters/plant, number of seeds/pod, and 100-seed weight on seed yield.

Vineeta *et al.* (2003) studied 50 cowpea genotypes and path analysis revealed that the number of clusters, pods and seeds/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/plant. Thus, selection for higher seed yield should involve early-maturing genotypes with high 100-seed weight, and number of clusters and pods/plant.

Venkatesan *et al.* (2003) carried out path analysis using 20 diversified genotypes of cowpea for 12 component characters including seed yield. Path analysis showed positive direct effect of number of pods/plant, pod length and clusters/plant, seeds/pod and 100-seed weight on seed yield.

Nigude *et al.* (2004) studied 45 cowpea genotypes and reported correlation and path coefficients analysis for the grain yield/plant was significantly and positively associated with all the characters except, pod length and test weight at both levels. Biomass (dry weight) at harvest and harvest index had the highest direct effect on grain yield. Association of biomass with grain yield was significantly positive.

Patil *et al.* (2004) studied 47 genotypes of cowpea for 10 yield contributing characters and path coefficient analysis revealed among the biomass partitioning characters, the number of compound leaves/plant, leaf area/plant, number of inflorescences/plant, number of days to first pod maturity, and dry weight/plant had positive direct effect on seed yield/plant at both phenotypic and genotypic levels.

Peksen and Artk (2004) studied 6 genotypes of cowpea and path analysis revealed that pod length had the highest direct positive effect on seed yield/plant, followed by 100-seed weight and pods/plant. On the other hand, seed yield/plant was directly and negatively affected by first pod height and branches/plant.

Mittal and Singh (2005) studied 30 progenies of cowpea *[Vigna unguiculata* (L.) Walp.] which developed from the varietal cross Cowpea 99 x BS, for seed yield and its components (*viz.*, pods/plant, pods/cluster, pod length, seeds/pod, 100-seed weight, days to flowering and days to maturity) and observed path analysis revealed that pods/plant, pod length, 100-seed weight and days to flowering had high positive direct effects on seed yield. Pods/cluster influenced seed yield positively via pods/plant. It is concluded that seed yield in cowpea may be improved by selection of plants having more pods with bold seeds.

Kumawat and Raje (2005) studied 50 genotypes of cowpea [*Vigna unguiculata* (L.) Walp.*]* and path coefficient analysis was indicated high positive direct effect of clusters/plant, biological yield/plant and harvest index on seed yield/plant. Days to maturity had the highest positive direct effect on seed yield/plant along with significant negative correlation with seed yield/plant.

Anbumalarmathi *et al.* (2005) studied on 26 cowpea genotypes and path analysis revealed that pods/plant, seeds/pod and 100-seed weight had high direct effect on single plant yield. Clusters/plant showed high indirect effect through pods/plant on grain yield.

Lal *et al.* (2007) studied genotypes of cowpea [*Vigna unguiculata* (L.) Walp.] and observed that the correlation analysis pointed out the importance of number of peduncles/plant, number of pods/plant, average pod weight and pod length towards pod yield. Number of pods/plant exerted maximum positive direct effect on pod yield followed by pod weight, number of peduncles/plant and pod length. Selection pressure on these traits may lead to an overall increase in pod yield/plant.

Vishwanath *et al.* (2009) evaluated 41 genotypes of cowpea and reported for pod weight exerted the maximum positive direct effect on pod yield followed by number of pods/plant and pod length. Selection pressure on these traits may lead to an overall increase in pod yield/plant.

Kumari *et al*. (2010) studied 14 genotypes of cowpea collected from different states in the India for eight yield contributing characters to the study revealed that the days to maturity, number of branches/plant and number of pods/plant showed positive significant correlation with seed yield. Path coefficient analysis exhibited days to fifty per cent flowering, plant height, pods/plant showed positive direct effect on yield except days to maturity, branches/plant, seeds/pod and hundred seed weight which showed negative direct effects.

Singh *et al.* (2010) carried out path coefficient analysis with 25 genotypes of cowpea and observed that the stem weight had maximum and positive direct effect on green fodder yield at phenotypic and genotypic level followed by leaves weight and dry matter yield. Biological yield and dry matter percent had negative direct effect on green fodder yield.

Nwofia *et al.* (2012) reported that seed yield was positively and significantly correlated to number of leaves/plant, seed weight/pod, dry matter yield/plant in 2010 and number of pods/plant in 2011. Seed weight/pod and number of leaves/plant had positive direct effects on seed yield in 2010. Number of pods/plant, number of leaves/plant and pod length had positive direct effects of varying magnitude to seed yield in 2011.

Cokkizgin *et al.* (2013) evaluated 6 beans [*Vigna unguiculata* (L.)Walp.] genotypes and reported that the number of plant had positive and highest direct effect on the seed yield while seed weight/plant had negative and highest direct effect on the seed yield.

Nwofia *et al. (*2013) studied 7 genotypes of vegetable cowpea [*Vigna unguiculata* (L.) Walp.] and observed that genotypic coefficient of variation was lower than the phenotypic coefficient of variation for all the traits. Number of seeds/pod, pod length, leaf area and plant height had broad sense heritability estimates greater than 90%. Number of pods/plant showed higher positive direct effect as well as correlation on pod yield than other yield traits (0.972 and 0.936, respectively).

Number of pods/plant and seeds/plant showed negative direct effects on pod yield (-0.197, -0.01, respectively) even though they had significant positive correlation to pod yield. The indirect effects of the two traits through number of pods/plant were positive (0.46, 0.31, respectively) and high and seemed to be the cause of the significant correlation between the traits and pod yield. In conclusion, selecting vegetable cowpea genotypes high in number of pods/plant that showed high magnitude of positive direct effect on pod yield would sustain high yields. This is most likely as the trait is highly heritable and compliments others.

2.5 Genetic divergence

The variability for different characters among different genotypes of a species is known as genetic diversity. Genetic diversity arises due to geographical separation or genetic barrier to cross ability.

Several methods have been developed for measuring divergence between population using multivariate such as multiple regression discriminate function (Fisher, 1936) and D^2 statistic (Mahalanobis, 1936). Out of these methods, D^2 statistic is a powerful tool in quantifying the degree of genetic divergence among the relative contribution of different components to the total divergence. The available literature is reviewed here:

Anbuselvan *et al.* (2001) evaluated 50 genotypes of cowpea for seed yield and its component. The data subjected to D^2 statistic analysis and could group the genotypes into 4 clusters by Tocher' method. The average intra cluster D^2 values ranged between zero and 85.10. The relative contribution of different characters towards the genetic divergence showed that days to 50% flowering had maximum contribution (35.2%) followed by number of primary branches (14.5%), pod length (14.0%) and number of seeds/pod (9.1%).

Narayanankutty *et al.* (2003) studied 37 genotypes of cowpea and grouped there into eleven clusters using Mahalanobis D^2 statistics. In general, the inter cluster distances were higher than intra cluster distances. The maximum inter cluster distance was between clusters VIII and X followed by clusters VI and X and clusters VIII and IX, respectively. The intra cluster distance was maximum in cluster VII.

Nigude *et al.* (2004) evaluated 45 genotypes of cowpea by using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 5 clusters. The cluster I contained the highest 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/plant, test weight, biomass (dry weight) at harvesting and number of pods/plant had contributed considerably toward divergence.

Venkatesan *et al.* (2004) assessed genetic divergence in 20 genotypes of cowpea using Mahalanobis D^2 value and indicated considerable diversity in the material. The population was grouped into six clusters of which cluster II and III has maximum number of genotypes. Analysis corroborated the absence of parallelism between geographic origin and genetic diversity. The maximum intra cluster distance was exhibited by cluster V and minimum by cluster II. The inter cluster distance was maximum between II and VI. Cluster/plant, pods/cluster, pods/plant and seed yield/plant contributed maximum towards the total divergence.

Kumawat and Raje (2005) evaluated 50 genotypes of cowpea for seed yield and its component. D^2 analysis of the data revealed six clusters. The average intra cluster D^2 values ranged from zero to 5.622. The relative contribution of various characters towards the total genetic divergence revealed that seed yield/plant had maximum contribution followed by seeds/pod, days to 50% flowering, plant height and reproductive period.

Naher *et al.* (2005) evaluated 68 genotypes of cowpea by using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 6 clusters. The cluster II contained the highest number of accessions (32) followed by the clusters I (21), III (6), IV (4), V (4) and VI (1). No relationship was found between genetic divergence and geographical distribution of the accessions. The maximum inter-cluster divergence was found between the cluster IV and V and was minimum between II and III. The maximum intra-cluster divergence was found between accessions falling in the cluster V. On the basis of the mean performance of different clusters, accessions having acceptable yield were placed in cluster I, II and V.

Lesly *et al.* (2006) assessed genetic divergence in 169 genotypes of cowpea using D^2 statistics. The population grouped into 46 clusters revealed that the clusters (6, 8, and 9) were the largest, containing seven genotypes followed by the clusters 1,2,5,6 and 24 with six genotypes. The inter cluster distance was maximum between cluster 11 and 42 followed by cluster 34 and 42. The number of pods/plant contributed maximum divergence (14.75) which was followed by harvest index (14.74%) and days to flower termination (13.72%).

Anbumalarmathi and Nadarajan (2007) studied 26 genotypes of cowpea for nine characters assessed the divergence using Mahalanobis D^2 statistics. The genotypes were grouped into seven clusters. Cluster I was the largest with 9 genotypes and cluster VII contained only one genotype. The intra cluster distance values indicated that the genotypes of cluster VI are highly divergent among them. Maximum inter cluster distance was observed between cluster V and VII followed by cluster I and VII. Single plant yield contributed maximum towards divergence followed by 100-seed weight.

Saini (2007) performed a study on 60 genotypes of cowpea by using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 9 clusters. Intra-cluster distance was found to be low as compared to inter-cluster ones. Maximum inter-cluster distance was observed between cluster VI and IX. Days to maturity and test weight appeared to be the most important traits contributing maximum towards genetic divergence. Inter-cluster distance and mean cluster value for characters indicated that hybridization of cluster VI assessions with cluster IX assesssion would be result in marked heterosis and produce segregants with improved yield.

Sulnathi *et al.* (2007) studied genetic divergence in 56 genotypes of cowpea using D^2 statistics for thirteen yield contributing characters which showed grouping of genotypes into nine clusters.

Cluster I had the maximum number of genotypes character *viz.,* days to maturity, 100 seed weight and days to flowering were the highest contributors to D^2 values. The geographical diversity was not related to genetic diversity.

Pandey (2007) conducted a study on 44 grain cowpea for 13 characters to quantify the genetic diversity existing among them using Mahalanobis D^2 statistics. The genotypes fell into 9 clusters. Cluster strength varied from single genotypes (cluster IV to IX) to 31 genotypes (cluster I). Cluster III had minimum days to first flower opening, day to 50% flowering and stover yield/plant in addition to maximum number of pod/plant and primary branches cluster II, V, VII had maximum yield/plant, 100-seed weight, pod length and number of seed/pod, respectively, cluster II had minimum days to maturity, while cluster VII showed maximum days to maturity.

Dahiya *et al.* (2007) evaluated 80 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 9 distinct clusters. All the clusters had more than 5 genotypes except cluster IX, which was mono-genotypic. The analysis of variance revealed significant differences for days to flowering, days to maturity, plant height, number of branches/plant, number of clusters/plant, number of pods/plant, pod length, seeds/pod, seed yield/plant, 100-seed weight, biological yield and harvest index based on the pooled analysis of 2 years data.

Valarmathi *et al.* (2007) evaluated 68 genotypes of cowpea which included 60 genotypes from *Vigna unguiculata subsp. unguiculata* and 8 genotypes from *Vigna unguiculata subsp.*

sesquipedalis for nine quantitative characters using Mahalanobis D^2 analysis. All the accessions were grouped into twelve clusters, in which cluster I was the largest having 47 genotypes from subspecies *unguiculata*. Subspecies *unguiculata* was grouped in seven distinct clusters, whereas the genotypes of subspecies *sesquipedalis* were grouped in five other distinct clusters. Days to maturity had the greatest contribution to genetic divergence, followed by 100-seed weight, while the number of branches/plant and the number of seeds/pod contributed least among the accessions.

Dalsaniya *et al.* (2009) evaluated 60 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 12 clusters. Inter cluster distance and mean cluster character values indicated that hybridization of cluster X variety(JCPL-134) with cluster IV varieties(JCPL-1,JCPL-13,and JCPL-21) and cluster V varieties(JCPL-50 and JCPL-133) with cluster III varieties(JCPL-26 and JCPL-131) exhibit high heterosis and also result in transgressive segregants with higher yield and cluster X had higher cluster mean value for yield and other desired character like leaf area, ten pods weight, number of pods/plant and green pod yield/plant etc.

Nagalakshmi *et al.* (2010) assessed 66 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 23 clusters for 12 quantitative traits. The Cluster I had the maximum number of genotypes i.e. 22 and cluster XXIII had only one genotype. Intra cluster distance analysis revealed that the minimum intra cluster distance was observed in the cluster II. The inter-cluster distance (D) was found to be the maximum between the clusters XXII and XXIII and the same was minimum between clusters II and V. The results indicated that grain yield/plant contributed maximum to the total divergence followed by 100-seed weight and days to 50% flowering. Number of branches/plant had least contribution to the total divergence followed by petiole length. The existence of wide genetic diversity among the types chosen from the same geographical location was obviously seen. In the study, the variety Vellayani local had the maximum value for plant height and pod length and thereby distinguished from other varieties and it is present singly in the cluster XXIII. Hence it is proved to be widely divergent, since its yield is high, it can be used for further crossing and yield improvement. The cluster XVIII had the highest cluster mean values for number of clusters/plant and the cluster XIV has the highest mean value for grain yield/plant.

Singh *et al.* (2013) evaluated 46 genotypes of cowpea by using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 8 clusters. The widest inter-cluster distance was found between cluster V and VIII (8.629) followed by cluster II and VIII (8.490), cluster I and VIII (6.439) and soon. Thus, genotypes of cluster VIII showed maximum genetic divergence with cluster V and II. The genotypes of cluster VIII showed maximum genetic divergence with cluster V followed by Cluster II hence, the genotypes belonging to cluster VIII and cluster V may be selected for generating genetic variability and hybridization. Cluster II having two genotypes was found to be the best performing for agronomic characters followed by cluster I with three genotypes and cluster V with three genotypes.

Tigga and Tandekar (2013) conducted a study on 22 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes could be grouped into four clusters. Non-overlapping clusters showed genetic diversity rather than geographical diversity. 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). Thus, 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.

Vavilapalli *et al.* (2014) evaluated 32 genotypes of cowpea using Mahalanobis D^2 statistics and the genotypes could be grouped into 6 clusters, where clusters I was the largest, containing eleven genotypes followed by the clusters III (5 genotypes) and cluster II with three genotypes. The inter cluster distance was maximum between cluster III and VI followed by cluster III and V. Based on inter cluster distance and *per se* performance of genotypes, the entries *viz.*, VU 1, VU 2, VU6, VU 8 and VU 21 were selected, which could be intercrossed to recover good recombinants and desirable segregants. The pod yield/plant contributed maximum divergence (66.23%) which was followed by pod weight (20.78%) and plant height (8.23%).

Chattopadhyay *et al.* (2014) evaluated 60 genotypes of cowpea using Mahalanobis D^2 statistics and reported that genotypes could be grouped into 7 clusters. The top three characters which contributed most towards the genetic divergence were number of seeds/pod, pod yield/plant and pod weight. Cluster II had genotypes with high pod productivity, while the genotypes in Cluster III flowered much earlier. Crossing between genotypes within these groups could produce highly productive and early maturing cowpea genotypes.

In a study on 40 genotypes of cowpea Brahmaiah *et al.* (2014) used Mahalanobis D^2 statistics for 18 quantitative characters to estimate the genetic diversity. The genotypes were grouped into 6 clusters. The cluster strength varied from single genotype (Clusters III, IV and V) to 25 genotypes (Cluster I). Clusteres IV and VI had high inter cluster distance. Clusters II, III and I had maximum 100-seed weight, number of seeds/pod and seed yield respectively. Cluster IV had maximum seedling vigour index, germination per cent, peduncle length, number of clusters/plant and number of primary branches. The genotypes from clusters IV and IV may be inter crossed to obtain high variation.

3. MATERIALS AND METHODS

The experimental material for the present investigation entitled **"Character associations and genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]"** consisted of 72 genotypes (including 3 checks) of cowpea. These genotypes were received from AICRP on Arid Legume Trial and the collection maintained at S.K.N. College of Agriculture, Jobner, (Jaipur). The list of genotypes used in the study is given in Table 3.1. The 72 genotypes were evaluated in a Randomized Completely Block Design (RCBD) with three replications during *Kharif* season of 2013 at Agriculture Research Farm, S.K.N. College of Agriculture, Jobner. Each genotype was sown in a single row plot of 4 m. length. The row to row distance and plant to plant distance were kept at 30 cm and 10 cm, respectively. All the recommended package of practices were followed to raise a healthy crop. Meteorological data during the period of crop production are given in Table 3.2 and figure 1.

3.1 Observations recorded

The observations on 10 morphological traits were recorded on a random sample of 10 competitive plants selected for each genotype in each replication except days to 50% flowering and days to pod maturity which were recorded on plot basis. Mean value of 10 plants were used for statistical analysis. The methodology followed for taking observation on different characters is described below:

3.1.1 Days to 50% flowering

The numbers of days taken from the date of sowing to anthesis in 50% of total plants in each plot were recorded as days to 50% flowering.

Table 3.1: List of genotypes & checks used in the study

S.No.	Cowpea accessions	Source
1.	CPD-108	IVT-1 CAZRI trial 2009
2.	GC-525	IVT-1 CAZRI trial 2009
3.	GC521	IVT-1 CAZRI trial 2009
4.	PGCP-6	IVT-1 CAZRI trial 2009
5.	JOB-129 (Mutant of RC-101)	IVT-1 CAZRI trial 2009
6.	CP-107	IVT-1 CAZRI trial 2009
7.	CPD-105	IVT-1 CAZRI trial 2009
8.	PHULE-CP-5040	IVT-1 CAZRI trial 2009
9.	PHULE-CP-5030	IVT-1 CAZRI trial 2009
10.	RC-101	Check variety
11.	GC-3	Check variety
12.	CPD-115	IVT- I CAZRI trial 2010
13.	GC-723	IVT- I CAZRI trial 2010
14.	DCS-47-1	IVT- I CAZRI trial 2010
15.	GC-501	IVT- I CAZRI trial 2010
16.	GC-703	IVT- I CAZRI trial 2010
17.	GC-3	Check variety
18.	NBC-2	IVT- I CAZRI trial 2010
19.	CPD-118	IVT- I CAZRI trial 2010
20.	NBC-1	IVT- I CAZRI trial 2010
21.	NBC-3	IVT- I CAZRI trial 2010
22.	JOB-129 (Mutant of RC-101)	IVT- I CAZRI trial 2010
23.	SUBHARA	IVT- I CAZRI trial 2010
24.	GOA LOACAL	IVT- I CAZRI trial 2010
25.	PGCP-12	IVT- I CAZRI trial 2010
26.	CPD-119	IVT- I CAZRI trial 2011
27.	JOB-11 (Mutant of RC-101)	IVT- I CAZRI trial 2011
28.	JOB-80BR (Mutant of RC-101)	IVT- I CAZRI trial 2011
29.	KBC-4	IVT- I CAZRI trial 2011
30.	CPD-121	IVT- I CAZRI trial 2011
31.	GC-817	IVT- I CAZRI trial 2011
32.	KBC-5	IVT- I CAZRI trial 2011
33.	GC-3	Check variety
34.	PTB-1	IVT- I CAZRI trial 2011
35.	CPD-83	IVT- I CAZRI trial 2011
36.	GC-815	IVT- I CAZRI trial 2011
37.	GC-810	IVT- I CAZRI trial 2011
38.	DC-15	IVT- I CAZRI trial 2011

39.	HC-38	IVT- I CAZRI trial 2011
40.	JOB-129 (Mutant of RC-101)	IVT- State Trial Durgapura 2011
41.	CPD-119	IVT- State Trial Durgapura 2011
42.	CPD-103	IVT- State Trial Durgapura 2011
43.	JOB-80BR (Mutant of RC-101)	IVT- State Trial Durgapura 2011
44.	CPD-132	IVT- State Trial Durgapura 2011
45.	CPD-121	IVT- State Trial Durgapura 2011
46.	CPD-134	IVT- State Trial Durgapura 2011
47.	GC-3	Check variety
48.	CPD-127	IVT- State Trial Durgapura 2011
49.	CPD-142	IVT- State Trial Durgapura 2011
50.	CPD -136	IVT- State Trial Durgapura 2011
51.	CPD-78	IVT- State Trial Durgapura 2011
52.	CPD-83	IVT- State Trial Durgapura 2011
53.	RC-19	Check variety
54.	CPD-115	IVT- State Trial Durgapura 2011
55.	CPD- 118	IVT- State Trial Durgapura 2011
56.	CPD- 129	IVT- State Trial Durgapura 2011
57.	CPD- 77	IVT- State Trial Durgapura 2011
58.	CPD- 108	IVT- State Trial Durgapura 2011
59.	RC-101	Check variety
60.	Mutant-1 (Mutant of RC-19)	Dept. Cowpea Research,SKNCOA
61.	Mutant-2 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
62.	Mutant-3 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
63.	Mutant-4 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
64.	Mutant-5 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
65.	Mutant-6 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
66.	Mutant-7 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
67.	Mutant-8 (Mutant of RC-19)	Dept. Cowpea Research,SKNCOA
68.	Mutant-9 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
69.	Mutant-10 (Mutant of RC-19)	Dept. Cowpea Research,SKNCOA
70.	Mutant-11 (Mutant of RC-19)	Dept. Cowpea Research,SKNCOA
71.	Mutant-12 (Mutant of RC-101)	Dept. Cowpea Research,SKNCOA
72.	RC19	Check variety

Table 3.2: Weekly mean meteorological observations recorded during the crop season (July to Oct. 2013)

SMW*	**Period**		**Temperature**		**Relative humidity (%)**	**Evaporatio (mm)**	**Rainfall (mm)**
	From	**To**	**Max. Temp (^{0}C)**	**Min. Temp (^{0}C)**			
27	02.07.13	08.07.13	35.3	26.3	72	6.2	31.8
28	09.07.13	15.07.13	33.4	24.8	75	5.3	8.60
29	16.07.13	22.07.13	33.7	25.4	78	4.9	38.6
30	23.07.13	29.07.13	32.3	25.9	81	3.9	52.0
31	30.07.13	05.08.13	31.5	25.2	85	3.8	37.0
32	06.08.13	12.08.13	30.0	24.4	89	3.1	62.4
33	13.08.13	19.08.13	29.7	24.5	90	3.2	88.0
34	20.08.13	26.08.13	31.5	23.7	81	3.5	34.4
35	27.08.13	02.09.13	32.9	22.8	70	5.8	-
36	03.09.13	09.09.13	33.9	20.2	61	6.7	-
37	10.09.13	16.09.13	37.1	22.7	55	8.0	-
38	17.09.13	23.09.13	35.5	21.7	63	6.8	1.80
39	24.09.13	30.09.13	31.3	23.7	79	4.8	19.0

* Standard meteorological week number

3.1.2 Days to maturity

The numbers of days taken from the date of sowing to yellowing of about 50% pods in each plot were recorded as days to maturity.

3.1.3 Plant height (cm)

Plant height was measured in centimeter from the ground level to the tip of the main axis of the ten plants at the maturity and was averaged.

3.1.4 Primary branches per plant

The number of pod bearing branches arising from the main axis at the time of maturity were recorded for each of the ten plants and averaged.

3.1.5 Pods per plant

The number of pods per plant from all the ten plants were counted and averaged.

3.1.6 Pod length (cm)

The length of such pod which had arisen from first node of the first branch from each selected plant were measured in centimeter and averaged.

3.1.7 Seeds per pod

The numbers of seeds were counted for the same pod which had been used to measure the pod length. The mean value was recorded as number of seeds per pod.

3.1.8 100-seed weight (g)

A sample of 100 seeds drawn from the pooled yield of the selected plants in each replication, and its weight was recorded in grams.

3.1.9 Pod wall proportion (%).

Plant architectural components like pod wall proportion (PWP) and pod filling index (PFI) also influence seed yield (Huyghe, 1998). Strategies to reduce the PWP in order to increase harvest index of the reproductive compartment (seeds and pod walls combined) is considered a potential breeding method for higher seed yield (Huyghe and Ney, 1997). Pod wall proportion is an index obtained by dividing the weight of pod wall by the weight of whole pod and multiply by hundred. It may be affected by the specific weight of the pod walls (which reflects variations in either wall thickness or wall density, or both) and by the weight of the seed in the pod.

3.1.10 Seed yield per plant (g)

After harvesting and threshing, clean seeds obtained from each plant were weighed in grams and averaged out for a single plant.

3.2 Statistical analysis

3.2.1 Analysis of variance (ANOVA)

The data were subjected to analysis of variance using random model to determine the significance of differences among genotypes following standard statistical procedures as suggested by Singh and Choudhary (1995). The structure of analysis of variance (ANOVA) is given in Table 3.3.

Table 3.3: Analysis of variance (ANOVA)

Source	d.f.	Mean Squares	Expectation of mean squares
Replications	(r-1)	MSr	$\sigma^2 e + g\,\sigma^2 r$
Genotypes	(g-1)	MSg	$\sigma^2 e + r\,\sigma^2 g$
Error	(r-1) (g-1)	MSe	$\sigma^2 e$

Total	(rg – 1)

Where,

d.f. = Degrees of freedom

r = Number of replications

g = Number of genotypes

MSr = Mean sum of squares due to replications

MSg = Mean sum of squares due to genotypes

MSe = Mean sum of squares due to error

$\sigma^2 g$ = Variance due to genotypes (including checks)

$\sigma^2 e$ = Variance due to error

3.2.2 Mean

The general mean was computed by summing the data of all the treatments over all the three replications for each character using following formula.

$$\bar{X} = \Sigma\bar{X} / N$$

Where,

$\sum\bar{X}$ = Mean variance of i^{th} genotype

N = Total number of genotypes

3.2.3 Range

The lowest and highest mean value for each character was taken as range.

3.2.4 Standard error of mean

Standard error of difference between two mean was calculated as per following formula:

$$SEm\pm = \sqrt{\frac{2MSe}{}}$$

Where,

r = number of replication

MSe = MSS due to error

3.2.5 Coefficient of variation (CV)

The experimental coefficient of variation (CV) for various characters was calculated by the following formula:

$$CV\ (\%) = \sqrt{\frac{MSe}{}} \quad X\ 100$$

Where,

MSe = Error variance

$\bar{X}$ = Grand total

3.2.6 Critical difference (CD)

Critical difference was calculated by following formula:

$$CD = \sqrt{\frac{2EMS}{r}} \text{ x } t\text{ - value.}$$

t-value = table value of error difference at 5% level of significance

Where,

r = number of replications

EMS = error mean sum of squares

3.2.7 Estimation of genetic parameters of variation

3.2.7.1 Genotypic, phenotypic and environmental variances:

3.2.7.1.1 Genotypic variance ($\sigma^2 g$)

The genotypic variance (VG or $\sigma^2 g$) is the variance due to the genotypes present in the population. The formula used for calculation of genotypic variance was,

$$\text{Genotypic variance } (\sigma^2 g) = \frac{(MSt - MSe)}{r}$$

Where,

MSt = Mean square due to genotypes

MSe = Mean square due to error

r = Number of replications

3.2.7.1.2 Phenotypic variance ($\sigma^2 p$)

Phenotypic variance ($\sigma^2 p$) denotes the total variance present in a population for particular character and was calculated by following formula

$$\text{Phenotypic variance } (\sigma^2 p) = \sigma^2 g + \sigma^2 e$$

Where,

σ^2g = Genotypic variance

σ^2e = Mean sum of squares due to error

3.2.7.1.3 Environmental variance (σ^2e)

The environmental variance (σ^2e) is the variance due to environmental deviation.

σ^2e = MSe

3.2.7.2 Coefficient of variation

The estimation of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV) and error/environmental coefficient of variation (ECV) was done as per the formula given by Johnson *et al.*, (1955) and Burton (1952).

$$\text{GCV (\%)} = \sqrt{\frac{\sigma_g^2}{\quad}} \qquad \text{X}$$

$$\text{PCV (\%)} = \sqrt{\frac{\sigma_p^2}{\quad}} \qquad \text{X}$$

$$\text{ECV (\%)} = \sqrt{\frac{\sigma_e^2}{\quad}} \qquad \text{X}$$

Where,

σ^2p = Phenotypic variance

σ^2g = Genotypic variance

σ^2e = Error variance

$\bar{X}$ = Grand mean

3.2.8 Heritability in broad sense

The heritability in broad sense (h^2_{bs}) was estimated as the ratio of genotypic variance to the total variance. It was calculated by the formula given by Johnson *et al*. (1955) and Hanson *et al*. (1956).

$$h^2_{bs} = \frac{\sigma^2 g}{\sigma^2 p} \times 100$$

where,

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance

h^2_{bs} = Heritability in broad sense

3.2.9 Computation of expected genetic advance (GA)

The expected genetic advance (GA) for each character was estimated by the formula as given by Johnson *et al*. (1955).

$$G.A. = k \times h^2_{bs} \times \sigma p$$

Where,

G.A. = Expected genetic advance

h^2_{bs} = Heritability in broad sense

σp = Phenotypic standard deviation

K = Standardized selection differential. Its value is a constant for a given selection intensity. It was taken as 2.06 at 5% selection intensity in present investigation.

To compare the expected genetic advance for different characters, it was expressed as percentage of mean:

$$\text{GA (as \% of mean)} = \frac{\text{GA}}{\overline{X}} \text{X100}$$

Whereas,

$\overline{X}$ = Grand mean

3.2.10 Estimation of correlation coefficient

Correlation coefficient were worked out between different pairs of characters as well as with yield as per the method described below. For computing genotypic and phenotypic correlation coefficient analysis of covariance was carried out in all possible paired combination of characters. The structure of the analysis of covariance is presented in Table 3.4.

Table 3.4: Analysis of covariance and expectations of mean sum of cross products between characters x and y

Source	d.f.	Mean Squares	Expectation of mean squares
Replications	(r-1)	MSPr	
Genotypes	(g-1)	MSPg	$Cov\ e_{xy} + r.\ Cov\ g_{xy}$
Error	(r-1) (g-1)	MSPe	Cov e_{xy}
Total	(rg – 1)		

Form the above table the expected mean sum of products were estimated as given below.

Where,

Error covariance ($\mathrm{Cov}\ e_{xy}$) = MSPe

Genotypic covariance ($\mathrm{Cov}\ g_{xy}$) = (MSPg-MSPe)/r

Phenotypic covariance ($\mathrm{Cov}\ p_{xy}$) =$\mathrm{Cov}\ g_{xy}$ +$\mathrm{Cov}\ e_{xy}$

The genotypic and phenotypic correlation coefficients were calculated from the phenotypic and genotypic components of variances and covariance as described by Singh and Choudhary (1995) and as per formula given by Johnson *et al*. (1955).

Genotypic correlation (r_g) between characters x and y

$$r_g = \frac{\mathrm{Cov}\ g_{xy}}{\sqrt{(\sigma^2 g.\ \text{of X}).\ (\sigma^2 g.\ \text{of Y})}}$$

Phenotypic correlation (r_p) between characters x and y

$$r_p = \frac{\mathrm{Cov}\ p_{xy}}{\sqrt{(\sigma^2 p.\ \text{of X}).\ (\sigma^2 p.\ \text{of Y})}}$$

Environment correlation (r_e) between characters x and y

$$r_e = \frac{\mathrm{Cov}\ e_{xy}}{\sqrt{(\sigma^2 e.\ \text{of X}).\ (\sigma^2 e.\ \text{of Y})}}$$

Where,

σ^2g and σ^2p represented the genotypic and phenotypic variance, respectively. The estimates of correlation coefficient were compared with the ‘r’ values given in the ‘r’ Table (Fisher and Yates, 1938) at error degree of freedom.

3.2.11 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient. It measures the direct and indirect contribution of independent variable on dependent variable and it allows splitting the total correlation coefficient between two variables into components of direct and indirect effects.

The estimation of direct and indirect effects was calculated by the path coefficients analysis as suggested by Wright (1921) and as elaborated by Dewey and Lu (1959) at both phenotypic and genotypic levels. The following sets of simultaneous equation were formed and solved for estimated the various direct and indirect effects.

$$r_{1y} = p_{1y} + r_{12}\, p_{2y} + r_{13} p_{3y} + -------------- + r_{1i}\, p_{iy}$$

$$r_{2y} = r_{12}\, p_{1y} + p_{2y} + r_{23}\, p_{3y} + -------------- + r_{2i}\, p_{iy}$$

$$\vdots$$

$$\vdots$$

$$\vdots$$

$$r_{10y} = r_{1.10}\, p_{1y} + r_{2\,.10}\, p_{2y} + r_{3.\,10}\, p_{3y} + -------------- + p._{10.y}$$

Where,

r_{1y} to $r._{10.y}$ = Phenotypic correlation coefficient effects between causal factors 1 to 10 and dependent characters Y.

r_{12} to $r_{1.10}$ = Phenotypic correlation coefficient among causal factors themselves and

p_{1y} and $p._{10.y}$ = Direct effects of characters 1 to 10 on character Y. The independent characters *viz.*,

1. Days to 50% flowering
2. Days to maturity
3. Plant height (cm)
4. Primary branches per plant
5. Pods per plant
6. Pod length (cm)
7. Seeds per pod
8. 100-seed weight (g)
9. Pod wall proportion (%)
10. Seed yield per plant (g)

3.2.11.1 Residual effect

Residual effect measures the contribution of the unidentified factors on dependent variable and was obtained by the following formula.

$$\text{Residual effect } (P_{ry}) = \sqrt{1 - \Sigma p_{iy}\, r_{iy}}$$

Whereas,

p_{iy} = Direct effect of i^{th} character on seed yield per plant

r_{iy} = Correlation of i^{th} traits with seed yield per plant.

3.2.12 Multivariate analysis

The genetic divergence among 72 entries was estimated by Mahalanobis D^2 statistic (generalized distance) as suggested by Rao (1952). For this estimation, 10 characters *viz.*, Days to 50% flowering, days to maturity, plant height (cm), primary branches per plant, pods per plant, pod length (cm), seeds per pod, test weight (g), pod wall proportion (%) and seed yield per plant (g) were considered. The calculation of D^2 values involved the following steps (Singh and Choudhary, 1985);

3.2.12.1 Test of significance (Wilk's criterion)

Using the 'V' statistic which in turn utilizes Wilk's criterion (^) a simultaneous test of differences between mean values of a number of correlated variables was done as described by Rao (1952) and explained by Singh and Choudhary, (1995).

$$\text{Wilk's criterion } (\wedge) = \frac{[W]}{[W + Q]}$$

Where,

W = Determination of error matrix

W+Q = Determination of error + genotypes matrix

Determinations for error + genotypes were calculated by using the error + genotypes variance and covariance matrix by following the "Pivotal condensation method". The significance of Lambda was tested by Chi square χ^2 as,

$$\chi^2 = \text{V (State)} = -\text{M} \log_e \wedge$$

Where,

$$M = n - \frac{(p + q + 1)}{2}$$

n = degree of freedom for error plus treatment

p = Number of characters or variables

q = Degree of freedom for treatment

e = 2.7183

χ^2 = Chi square

$\log_e \wedge = 2.3026 \log_e \wedge$

$$\text{So V (State)} = \left[n - \frac{(p + q + 1)}{2}\right] 2.3026 \log 10$$

V (State) is distributed as χ^2 with p x q degree of freedom. For calculating χ^2 value for more than one hundred degree of freedom following formula was used,

$$\chi^2 \text{ as } Z = (2\chi^2)^{1/2} - (2\wedge - 1)^{1/2}$$

3.2.12.2 Computation of D^2 values

The transformation of correlated variables into uncorrelated variables and computation of D^2 values were carried out.

3.2.12.3 Test of significance of D^2 values

The D^2 value obtained for a pair of population was taken as the calculated value of χ^2 for 'P' degree of freedom where "p" is the number of characters considered.

3.2.12.4 Group constellation

In the present study, a method suggested by K. D. Tocher (Rao, 1952) for grouping the different lines into clusters was used. Two population having smallest (D^2 values) distance from each other were considered. A third population having smallest average D^2 values from the first two populations was added. Then considered the nearest fourth population and so it was done for the remaining ones. At certain stage when it was felt that after adding only of the remaining entries, there was abrupt increase in the average D^2, that population was not added in that cluster and another cluster was formed. In this way clusters were formed till all the population were included into one or the other cluster.

3.2.12.5 Average inter and intra cluster distance

Average intra-cluster distance was calculated as follows,

Average intra-cluster distance = ΣDi^2 / n

Where,

Di^2 = the sum of D^2 values between all possible combinations,

n = lines included in a cluster

Average inter-cluster distances were calculated between all possible combinations of the clusters as follows:

Average inter-cluster distance between ith and jth cluster

$$= \Sigma Di^2 / (ni.nj)$$

Where,

Di^2 as the sum of D^2 values of all possible pairs of combination between the lines of ith and jth clusters and "ni and nj" are the number of lines included into ith and jth cluster, respectively.

3.2.12.6 Cluster mean

The cluster mean was calculated by summing all the mean values of each genotypes belonging to a particular for each traits cluster, which was then divided by number of genotypes and thus cluster mean was obtained for each character.

3.2.12.7 Computation of data

All the data were analysed on computer using Windostate version 8.1 from indostate services, Hyderabad licensed to NRCSS, Tabiji (Ajmer).

4. EXPERIMENTAL RESULTS

The experimental results of the present investigation have been presented under following subheads:

4.1 Analysis of variance

4.2 Variability parameters

4.3 Character association

4.4 Path coefficient analysis

4.5 Genetic divergence

4.1 Analysis of variance

Analysis of variance was carried out for each character separately and has been presented in Table 4.1. Analysis of variance revealed highly significant difference among genotypes including checks for all the traits studied indicated that considerable amount of genetic variability was present in the experimental material which can be exploited for improvement of seed yield in cowpea.

4.2 Variability parameters

The general mean, range and variability parameters for each character are given in Table 4.2. The mean performances of different genotypes used in study in respect of different characters are shown in Annexure 1.

The range for plant height appeared to be relatively wide whereas those for primary branches/plant, pods/plant, seeds/pod and seed yield/plant was relatively narrow. Days to 50% flowering ranged from 35.33 days (Mutant-3) to 50.73 days (GOA LOCAL) with mean value of 40.34 days. Days to maturity ranged from 63.00 days (CPD-115, GC-723) to 75.67 days (DCS-47-1, GOA LOCAL) with mean value of 67.78 days. Plant height ranged from 25.73 cm (Mutant-10) to 101.17 cm (CPD-118) with mean value of 49.00 cm. Primary branches/plant ranged from 3.03 (CPD-77) to 6.10 (DCS-47-1) with mean value of 4.28. Pods/plant ranged from 3.07 (PTB-1) to 6.83 (CPD-115) with mean value of 4.46. Pod length ranged from 9.40 cm (PHULE-CP-5030) to 20.47 cm (GOA LOCAL) with mean value of 11.98 cm. Seeds/pod ranged from 7.43 (GC-817) to 15.63 (GOA LOCAL) with mean value of 10.82. 100-seed weight ranged from 5.69 g (Mutant-2) to 17.34 g (GOA LOCAL) with mean value of 9.81 g. Pod wall proportion ranged from 16.66 % (Mutant-12) to 50.30 % (CPD-118) with mean value of 30.29. Seed yield/plant ranged from 2.61 g (Mutant-7) to 5.23 g (CPD-103) with mean value of 3.76 g. The range was wider for the character of plant height where it was narrow for the character of seed yield/plant.

Phenotypic and genotypic variances were estimated for all the characters studied. The phenotypic variances for all the characters were invariably higher than respective genotypic variance. The phenotypic variance ranged from 0.50 (Primary branches/plant and seed yield/plant) to 378.44 (Plant height). The highest estimate of the phenotypic variance was recorded for plant height (378.44) followed by pod wall proportion (41.27) days to maturity (14.32) and days to 50% flowering (10.16). The genotypic variance ranged from 0.30 (Primary branches/plant) to 358.69 (Plant height). The highest estimate of phenotypic and genotypic variance was recorded for plant height whereas it was lowest for Primary branches/plant.

Table 4.1: Analysis of variance for different characters in cowpea

S.No	Characters	Mean sum of squares			SEm±	C.D.
		Replication (d.f.=2)	Genotypes (d.f.=71)	Error (d.f.=142)		
1.	Days to 50% flowering	3.34	21.15**	4.66	1.25	3.48
2.	Days to maturity	2.35	25.41**	8.78	1.71	4.78
3.	Plant height (cm)	23.10	1095.81**	19.76	2.57	7.17
4.	Primary branches/plant	0.59	1.10**	0.20	0.26	0.73
5.	Pods/plant	0.58	1.65**	0.33	0.33	0.93
6.	Pod length (cm)	1.73	10.21**	0.61	0.45	1.26
7.	Seeds/pod	0.86	6.49**	0.58	0.44	1.23
8.	100-seed weight (g)	0.13	19.30**	0.27	0.30	0.84
9.	Pod wall proportion (%)	0.38	117.86**	2.97	1.00	2.78
10.	Seed yield/plant (g)	0.06	1.21**	0.14	0.21	0.60

** Significant at the p= 0.01

Table 4.2: Genetic parameters of variation for different characters in cowpea

Characters	Mean	Range	Variance		Coefficient of Variance			Broad sense heritability (h^2_{bs}) (%)	Genetic advance	Genetic advance (GA) as % of mean
			Genotypic	Phenotypic	(ECV)	(GCV)	(PCV)			
Days to 50% flowering	40.34	35.33-50.33	5.50	10.16	5.35	5.81	7.90	54.11	3.55	8.80
Days to maturity	67.78	63.00-75.67	5.54	14.32	4.37	3.47	5.58	38.70	3.02	4.45
Plant height (cm)	49.00	25.73-101.17	358.69	378.44	9.07	38.65	39.70	94.78	37.98	77.52
Primary branches/plant	4.28	3.03-6.10	0.30	0.50	10.55	12.77	16.57	59.43	0.87	20.28
Pods plant	4.46	3.07-6.83	0.44	0.77	12.93	14.86	19.69	56.90	1.03	23.08
Pod length (cm)	11.98	9.40-20.47	3.20	3.81	6.51	14.93	16.28	84.02	3.38	28.19
Seeds/pod	10.82	7.43-15.03	1.97	2.55	7.04	12.98	14.76	77.24	2.54	23.49
100-seed weight (g)	9.81	5.69-17.34	6.35	6.61	5.28	25.68	26.21	95.95	5.08	51.81
Pod wall proportion (%)	30.29	16.66-50.30	38.30	41.27	5.62	20.49	21.24	93.01	12.28	40.70
Seed yield/plant (g)	3.76	2.61-5.23	0.36	0.50	9.91	15.93	18.76	72.08	1.05	27.85

ECV= Environmental Coefficient of Variance, GCV= Genotypic Coefficient of Variance, PCV= Phenotypic Coefficient of Variance

The PCV & GCV were estimated for all the characters. The values of PCV for all the characters were higher than the values of their respective GCV. The highest PCV estimate was recorded for plant height (39.70%) followed by 100-seed weight (26.21%), pod wall proportion (21.24%), pods/plant (19.69%), seed yield/plant (18.76%), primary branches/plant (16.57%), pod length (16.28%) and seeds/pod (14.76%). Days to 50% flowering and days to maturity recorded minimum PCV value of 7.90% and 5.58%, respectively.

The highest GCV estimate was recorded for plant height (38.65%) followed by 100-seed weight (25.68%), pod wall proportion (20.49%), seed yield/plant (15.93%), pod length (14.93%), pods/plant (14.86%), seeds/pod (12.98%) and primary branches/plant (12.77%). Relatively lower GCV estimate were recorded for days to 50% flowering (5.81%) and days to maturity (3.47%).

Heritability in broad sense was estimated for all the characters. Heritability estimates varied from 38.70% (Days to maturity) to 95.95% (100-seed weight). High estimates of heritability were observed for the characters like 100-seed weight (95.95%) followed by plant height (94.78%), pod wall proportion (93.01%), pod length (84.02%), and seeds/pod (77.24%). Whereas, estimates of heritability were moderate for seed yield/plant (72.08%), primary branches/plant (59.43%), pods/plant (56.90%) and days to 50% flowering (54.11%). The heritability estimate was low for days to maturity (38.70%).

Expected genetic advance ranged from 0.12 (Pod wall proportion) to 37.98 (Plant height). The highest estimate of expected genetic advance was recorded for plant height (37.98) followed by 100-seed weight (5.08).

Expected genetic advance as per cent of mean was calculated for all the characters which ranged from 4.45% (Days to maturity) to 77.52% (Plant height). The higher estimate of expected genetic advance as per cent of mean was recorded for plant height (77.52%) followed by 100-seed weight (51.81%). Whereas, moderate estimate of genetic advance as per cent of mean were recorded for pod wall proportion (40.70%) followed by pod length (29.19%) and seed yield/plant (27.85%). Rest of the characters *viz.*, seeds/pod (23.49%), pods/plant (23.08%), primary branches/plant (22.28%), days to 50% flowering (8.80%) and days to maturity (4.45) had low estimates of expected genetic advance as per cent of mean.

4.3 Character association

Phenotypic and genotypic correlation coefficients between different pairs of characters were computed and are presented in Table 4.3 and 4.4. Significance of only phenotypic correlation coefficient was tested. In general, the genotypic correlation, were higher in magnitude than their respective phenotypic correlation coefficient for most of the characters pairs. The directions of phenotypic and genotypic correlation coefficient were similar for most of the characters combinations.

Seed yield/plant had significant positive correlation for all characters *viz.,* days to 50% flowering (r=0.15*), plant height (r=0.29**), primary branches/plant (r=0.26**), pods/plant (r=0.22**), pod length (r=0.32**), seeds/pod (r=0.39**) and 100-seed weight (r=0.23**) except, days to maturity and pod wall proportion.

Table 4.3: Phenotypic correlation coefficient between different characters in cowpea

Characters	Days to maturity	Plant height	Primary branches/ plant	Pods plant	Pod length	Seeds/ pod	100-seed weight	Pod wall proportion	Seed yield/plant
Days to 50% flowering	**0.67****	0.09	0.28**	-0.33**	0.47**	0.41**	0.27**	-0.01	0.15*
Days to maturity		**0.01**	0.12	-0.14*	0.34**	0.29**	0.12	-0.03	0.12
Plant height			**0.10**	0.09	0.30**	0.27**	0.08	0.08	0.29**
Primary branches/plant				**-0.02**	0.19**	0.16*	0.10	-0.06	0.26**
Pods/plant					**-0.23****	-0.21**	-0.28**	0.18**	0.22**
Pod length						**0.85****	0.44**	-0.02	0.32**
Seeds/pod							**0.38****	0.02	0.39**
100-Seed weight								**-0.26****	0.23**
Pod wall proportion									-0.08

*** Significant at the p= 0.05 and ** Significant at the p= 0.01**

Table 4.4: Genotypic correlation coefficient between different characters in cowpea

Characters	Days to maturity	Plant height	Primary branches/plant	Pods/plant	Pod length	Seeds/pod	100-seed weight	Pod wall proportion	Seed yield/plant
Days to 50% flowering	**0.84**	0.12	0.43	-0.45	0.73	0.64	0.37	-0.00	0.21
Days to maturity		**0.06**	0.21	-0.27	0.57	0.59	0.20	-0.06	0.25
Plant height			**0.14**	0.12	0.34	0.31	0.08	0.09	0.34
Primary branches/plant				**-0.07**	0.28	0.24	0.16	-0.10	0.43
Pods plant					**-0.35**	-0.32	-0.39	0.28	0.20
Pod length						**0.97**	0.48	-0.02	0.39
Seeds/pod							**0.43**	0.04	0.46
100-Seed weight								**-0.27**	0.27
Pod wall proportion									0.04

Days to 50% flowering had significant positive correlation with days to maturity (r=0.65**), primary branches/plant (r=0.28**), pod length (r=0.47**), seeds/pod (r=0.41**), 100-seed weight (0.27**) while significant negative correlation with pods/plant (r= -0.33**). Days to maturity had significant positive correlation with pod length (r=0.34**), seeds/pod (r=0.29**), 100-seed weight (r=0.16**) while significant negative correlation with pods/plant (r= -0.14*). Plant height had significant positive correlation with pod length (r=0.30**), seeds/pod (r=0.27**). Primary branches/plant had significant positive correlation with pod length (r=0.19**), seeds/pod (r=0.16*). Pods/plant had significant positive correlation with pod wall proportion (r= 0.18**) while significant negative correlation with pod length (r= -0.23**), seeds/pod (r= -0.21**) and 100-seed weight (r= -0.28**). Pod length had significant positive correlation with seeds/pod (r=0.85**), 100-seed weight (r=0.44**). Seeds/pod had significant positive correlation with 100-seed weight (r=0.38**). 100-seed weight had significant negative correlation with pod wall proportion (r= -0.26**).

4.4 Path coefficient analysis

To assess the direct and indirect effects of various characters on seed yield per plant, path coefficient analysis was carried out by taking seed yield per plant as dependent variable and their yield components as independent variables. The results of path coefficient analysis are presented in Table 4.5 and 4.6.

Table 4.5: Phenotypic path coefficients of various characters on seed yield per plant

Characters	**Days to 50% flowering**	**Days to maturity**	**Plant height**	**Primary branches/ plant**	**Pods/ plant**	**Pod length**	**Seeds /pod**	**100-seed weight**	**Pod wall proportion**	**Correlation with seed yield/plant**
Days to 50% flowering	**0.03**	0.02	0.02	0.05	-0.11	-0.06	0.17	0.04	0.00	0.15*
Days to maturity	0.02	**0.03**	0.00	0.02	-0.05	-0.05	0.12	0.02	0.00	0.12
Plant height	0.00	0.00	**0.16**	0.02	0.03	-0.04	0.11	0.01	-0.01	0.29**
Primary branches/plant	0.01	0.00	0.02	**0.18**	-0.01	-0.03	0.07	0.02	0.01	0.26**
Pods/plant	-0.01	0.00	0.01	0.00	**0.35**	0.03	-0.09	-0.04	-0.02	0.22**
Pod length	0.01	0.01	0.05	0.03	-0.08	**-0.13**	0.36	0.07	0.00	0.32**
Seeds/pod	0.01	0.01	0.04	0.03	-0.07	-0.11	**0.43**	0.06	0.00	0.39**
100-seed weight	0.01	0.00	0.01	0.02	-0.10	-0.06	0.16	**0.16**	0.03	0.23**
Pod wall proportion	0.00	0.00	0.01	-0.01	0.06	0.00	0.01	-0.04	**-0.12**	-0.08

Diagonal figures represent direct effects
Phenotypic residual effect= 0.66
* Significant at the p= 0.05 and ** Sig`1nificant at the p= 0.01

Table 4.6: Genotypic path coefficients of various characters on seed yield per plant

Characters	Days to 50% flowering	Days to maturity	Plant height	Primary branche s/plant	Pods/ plant	Pod length	Seeds/ pod	100-seed weight	Pod wall proportion	Correlation with seed yield/plant
Days to 50% flowering	**-2.21**	1.26	0.01	0.35	0.04	1.72	-1.07	0.11	0.00	0.21
Days to maturity	-1.85	**1.51**	0.00	0.17	0.02	1.34	-0.98	0.06	-0.02	0.25
Plant height	-0.26	0.09	**0.05**	0.11	-0.01	0.81	-0.51	0.02	0.04	0.34
Primary branches/plant	-0.96	0.31	0.01	**0.80**	0.01	0.66	-0.40	0.05	-0.04	0.43
Pods/plant	1.06	-0.41	0.01	-0.06	**-0.09**	-0.84	0.54	-0.12	0.12	0.20
Pod length	-1.61	0.85	0.02	0.22	0.03	**2.36**	-1.63	0.15	-0.01	0.39
Seeds/pod	-1.41	0.88	0.02	0.19	0.03	2.29	**-1.68**	0.13	0.02	0.46
100-seed weight	-0.82	0.30	0.00	0.13	0.03	1.14	-0.72	**0.30**	-0.11	0.27
Pod wall proportion	0.01	-0.09	0.00	-0.08	-0.02	-0.05	-0.06	-0.08	**0.41**	0.04

Diagonal figures represent direct effects
Genotypic residual effect= 0.49

A perusal of data indicated that the magnitude of genotypic path coefficient was higher than the magnitude of phenotypic path coefficient. However the directions of direct effects both at phenotypic and genotypic levels were not same in some cases. The result of path analysis is presented below.

4.4.1 Direct effects

At phenotypic levels the high positive direct effects on seed yield/plant were exhibited by seeds/pod (0.43), pods/plant (0.35) and primary branches/plant (0.18) whereas, high negative direct effects were exhibited by pod length (-0.13) and pod wall proportion (-0.12).

At genotypic levels the high positive direct effects on seed yield/plant were exhibited by pod length (2.36), days to maturity (1.51), primary branches/plant (0.80) and pod wall proportion (0.41) whereas, high negative direct effects were exhibited by days to 50% flowering (-2.21) seeds/pod (-1.68) and pods/plant (-0.09).

4.4.2 Indirect effects

At phenotypic level days to 50% flowering had high positive indirect effect via seeds/pod (0.17) whereas, it had negative indirect effects via pods/plant (-0.11), days to maturity had high positive indirect effect via seeds/pod (0.12) whereas, it had negative indirect effects via pods/plant and pod length (-0.05), plant height had high positive indirect effect via seeds/pod (0.11) whereas, it had negative indirect effects via pod length (-0.04), primary branches/plant had high positive indirect effect via seeds/pod (0.07) whereas, it had negative indirect effects via pod length (-0.03), pods/plant had high positive indirect effect via pod length (0.03) whereas, it had negative indirect effects via seeds/pod (-0.09), pod length had high positive indirect effect via seeds/pod (0.36) whereas, it had negative indirect effects via pods/plant (-0.08), seeds/pod had high positive indirect effect via 100-seed weight (0.06) whereas, it had negative indirect effects via pod length (-0.11), 100-seed weight had high positive indirect effect via seeds/pod (0.16) whereas, it had negative indirect effects via pods/plant (-0.10) and pod wall proportion had high positive indirect effect via pods/plant (0.06) whereas, it had negative indirect effects via 100-seed weight (-0.04).

At genotypic level days to 50% flowering had high positive indirect effect via pod length (1.72) whereas, it had negative indirect effects via seeds/pod (-1.07), days to maturity had high positive indirect effect via pod length (1.34) whereas, it had negative indirect effects via days to 50% flowering (-1.85), plant height had high positive indirect effect via primary branches/plant (0.11) whereas, it had negative indirect effects via seeds/pod (-0.51), primary branches/plant had high positive indirect effect via pod length (0.66) whereas, it had negative indirect effects via days to 50% flowering (-0.96), pods/plant had high positive indirect effect via seeds/pod (0.54) whereas, it had negative indirect effects via pod length (-0.84), pod length had high positive indirect effect via days to maturity (0.85) whereas, it had negative indirect effects via seeds/pod (-1.63), seeds/pod had high positive indirect effect via pod length (2.29) whereas, it had negative indirect effects via days to 50% flowering (-1.41), 100-seed weight had high positive indirect effect via pod length (1.14) whereas, it had negative indirect effects via days to 50% flowering (-0.82) and pod wall proportion had high positive indirect effect via days to 50% flowering (0.01) whereas, it had negative indirect effects via days to maturity (-0.09).

4.5 Genetic divergence

The knowledge of genetic divergence provides us a sound scientific basis for the selection of genotypes to be used in hybridization programme for further improvement. The D^2 analysis was carried out to estimate genetic divergence among the 72 genotypes (including 3 checks) of cowpea. The generalized D^2 values were calculated for each pair of genotypes in all possible combinations.

4.5.1 Grouping of genotypes into various clusters

All the genotypes were grouped into various clusters by Tocher method (Rao, 1952). The genotypes were grouped into 9 distinct clusters Table 4.7 and dendrogram obtained in figure 2. Cluster I contained maximum number of genotypes i.e. 33 genotypes followed by cluster II which contained 11 genotypes, cluster IV contained 3 genotypes, cluster V contained 4 genotypes, cluster VI contained 9 genotypes, cluster VII contained 8 genotypes, cluster VIII contained 2 genotypes and cluster III and cluster IX contained only one genotype each.

4.5.2 Mean values of cluster

Perusal of Table 4.8 indicated that mean values for different characters in different clusters varied considerably. The results showed that range was of wider divergence for the characters plant height followed by pod wall proportion and narrow divergence for the characters primary branches/plant and pods/plant. Days to 50% flowering ranged from 37.67 days (cluster III) to 50.33 days (cluster IX). Days to maturity ranged from 65.33 days (cluster III) to 75.67 days (cluster IX). Plant height ranged from 30.53 cm (cluster III) to 90.90 cm (cluster III). Primary branches/plant ranged from 3.50 (cluster III) to 5.18 (cluster IV). Pods/plant ranged from 3.50 (cluster IX) to 5.05 (cluster VIII). Pod length ranged from 11.03 cm (cluster V) to 20.47 cm (cluster IX). Seeds/pod ranged from 10.10 (cluster I) to 15.63 (cluster IX). 100-seed weight ranged from 7.97 g (cluster II) to 17.34 g (cluster IX). Pod wall proportion ranged from 20.12 (cluster V) to 47.70 (cluster VIII). Seed yield/plant ranged from 3.38 g (cluster V) to 4.49 g (cluster IV).

4.5.3 Intra and inter- cluster distances

The average intra and inter cluster distance (D$\sqrt{= D^2}$) were calculated from the D^2 values of the respective genotypes within and between the clusters. A perusal of data presented in Table 4.9 indicated that the intra cluster distance (D^2) ranged from zero to 6.63 (43.96). Inter cluster distance (D^2) ranged from 5.56 (30.91) to 19.39 (375.97). The maximum intra cluster distance was observed within cluster VI followed by cluster VII. The maximum inter cluster distance was observed between cluster VIII and cluster V followed by cluster IX and cluster VIII and cluster VIII and cluster VII.

4.5.4 Contribution of individual character to divergence

Contribution of individual character toward divergence was the highest estimated for seed yield/plant (35.81%) followed by 100-seed weight (29.07%) and plant height (19.33%). Days to maturity (0.16%) contributed least towards total divergence (Table 4.10).

Table 4.7: Number of clusters along with included genotypes

Clusters	No. of genotypes	Genotypes
I	33	GC-723, GC-810, CPD-127, CPD-134, JOB-11, CPD- 129, MUTANT-7, CPD-108, GC-3, GC-3, GC-3, MUTANT-5, CPD-119, CPD-115, CPD-105, CPD-132, GC-703, JOB-80BR, CP-107, JOB-80BR, CPD-121, CPD-119, JOB-129, CPD-108, GC-501, MUTANT-9, GC-817,PHULE-CP-5030, CPD-77, CPD-142 , PHULE-CP-5040, JOB-129, RC-101
II	11	RC-19, RC-19, MUTANT-6, SUBHARA, MUTANT-8, MUTANT-4, MUTANT-1, RC-101, GC-521, CPD-115, PGCP-6
III	1	JOB-129
IV	3	KBC-4, DC-15, KBC-5,
V	4	MUTANT-3, MUTANT-11, MUTANT-10, MUTANT-12,
VI	9	CPD-118, CPD-103, CPD-136, GC-3, CPD-121, PTB-1, MUTANT-1, DCS-47-1, HC-38
VII	8	GC-525, NBC-1, GC-815, NBC-2, PGCP-12, NBC-2, CPD-83, CPD-83
VIII	2	CPD-78, CPD-118
IX	1	GOA LOCAL

Table 4.8: Mean value of different characters in different clusters

Characters	Clusters								
	I **(33)**	**II** **(11)**	**III** **(1)**	**IV** **(3)**	**V** **(4)**	**VI** **(9)**	**VII** **(8)**	**VIII** **(2)**	**IX** **(1)**
Days to 50% flowering	39.77	39.45	37.67	46.44	38.67	40.81	41.54	38.33	50.33
Days to maturity	67.10	67.45	65.33	73.33	68.67	68.07	67.96	65.83	75.67
Plant height (cm)	41.01	43.18	30.53	53.18	40.47	78.67	46.12	90.90	88.63
Primary branches/plant	4.18	4.04	3.50	5.18	4.49	4.53	4.40	4.25	4.40
Pods/plant	4.40	5.00	4.23	4.12	4.56	4.49	4.00	5.05	3.50
Pod length (cm)	11.25	11.60	11.57	15.79	11.03	12.61	12.77	12.38	20.47
Seeds/pod	10.10	10.88	10.80	14.16	10.47	11.20	11.43	11.55	15.63
100-seed weight (g)	9.24	7.97	11.93	9.54	8.42	9.16	14.93	10.07	17.34
Pod wall proportion (%)	29.09	37.11	31.09	39.10	20.12	28.07	26.80	47.70	25.02
Seed yield/plant (g)	3.42	3.96	4.17	4.49	3.38	4.28	3.97	4.22	4.27

Table 4.9: Average inter and intra cluster distance based on corresponding D^2 values

Clusters	No. of genotypes	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**
I	33	**4.57**	7.33	5.56	9.93	7.11	7.69	8.54	14.52	13.95
		(20.88)	(53.73)	(30.91)	(98.60)	(50.55)	(59.14)	(72.93)	(210.83)	(194.60)
II	11		**4.81**	6.36	6.59	11.88	8.91	11.24	10.47	15.93
			(23.14)	(40.45)	(43.43)	(141.13)	(79.39)	(126.34)	(109.62)	(253.76)
III	1			**0.00**	8.08	9.93	8.78	6.95	12.7	13.13
				(0.00)	(65.29)	(98.60)	(77.09)	(48.30)	(161.29)	(172.40)
IV	3				**3.12**	14.68	9.77	11.54	8.35	13.67
					(9.73)	(215.50)	(95.45)	(133.17)	(69.72)	(186.87)
V	4					**4.52**	9.84	10.62	19.39	15.41
						(20.43)	(96.83)	(112.78)	(375.97)	(237.47)
VI	9						**6.63**	9.99	12.63	12.27
							(43.96)	(99.80)	(159.52)	(150.55)
VII	8							**6.45**	15.54	9.95
								(41.60)	(241.49)	(99.00)
VIII	2								**5.09**	16.8
									(25.91)	(282.24)
IX	1									**0.00**
										(0.00)

Table 4.10: Contribution of each character to divergence

S.No.	Source	Times ranked 1st	Contribution %
1	Days to 50% flowering	8	0.31%
2	Days to maturity	4	0.16%
3	Plant height (cm)	494	19.33%
4	Primary branches/plant	18	0.70%
5	Pods/plant	15	0.59%
6	Pod length (cm)	109	4.26%
7	Seeds/pod	9	0.35%
8	100-seed weight (g)	743	29.07%
9	Pod wall proportion (%)	164	6.42%
10	Seed yield/plant (g)	992	38.81%

5. DISCUSSION

Cowpea is one of the major pulse crops grown in *kharif* season in Rajasthan. It produces sufficient amount of biomass and seed yield per plant in semi-arid region because it s drought tolerant crop with spreading indeterminate growth habit. It has high protein content (20-25%) and can be used as dal, vegetable and in various confectionary preparations.

In Rajasthan cowpea is of great importance because of its short duration, high yield potential and quick growing habits along with high protein content. The crop is also known to provide quick and thick cover on ground and thus help in conservation of soil. No single cowpea variety can be suitable for all conditions (Barrett, 1987) due to its several diverse uses making the varietal requirement diverse in term of plant height, seed type, maturity and pattern of use which very extremely from region to region and has made breeding programme for cowpea more complex. Thus, there is need to develop varieties suitable for a specific region. However, production is constrained or low due to several reasons, such as poor fertility, lack of fertilizer application, susceptibility to diseases and pests and the absence of improved cultivars, under such circumstances genetic diversity is of great importance and plays a crucial role in focusing crop improvement.

The knowledge about the genetic variability and character association is the prime requirement in a breeding programme as it decides the selection criteria and breeding strategy. Moreover, identification of high yielding genotypes and the genotypes having superior performance for component characters which are positively associated with seed yield and genotypes which are genetically more diverse is also important because these may be used as parents in hybridization programme. Hence, the present investigation aimed to assess the genetic correlation between various pairs of traits character associations and genetic divergence in 72 genotypes of cowpea to determine the selection criteria on the basis of association analysis and determine the degree of divergence for improvement in seed yield. In view of the above facts the experimental findings of the present investigation have been discussed with respect to the available literature.

5.1 Variability parameters

Information about genetic variation existing within the genetic material is vital in assessing the potential for successful selection and breeding for increased seed yield because genetic variability is essential to realize response to selection pressure. Thus, genetic variability was estimated for seed yield and its components. Analysis of variance indicated highly significant differences among the genotypes for all the characters studied, which indicated that the material used had considerable genetic variability. Similar finding were also reported by Venkatesan *et al*. (2003), Vineeta *et al.* (2003) and Zargar *et al.* (2005). The significant difference among the genotypes for the characters studied indicated that the genotypes, if intermated could provide better combination in segregating generation.

5.1.1 Mean and Range

Genotypes exhibited wide range for mean and variance for almost all the characters studied. Similar finding were also reported by Kandaswami *et al.* (1989), Sharma and Singhania (1992), Rewale *et al.* (1995), Ahmed *et al.* (2000), Anbuselven *et al.* (2000), Grish *et al.* (2006) and Dhanasekar *et al.* (2010). Genotypes having high mean for specific characters were identified and it revealed that CPD-103, GC-525, DC-15, CPD-78, PGCP-6 and CPD-118 had high mean and appeared to be *at par* with each other and were found significantly superior to all the checks for seed yield/plant. The mean performance of genotypes for days to 50% flowering was 40.34 days which were close to the performance exhibited by checks. This trait could be taken as an index of maturity period. Assumes early flowering as desirable, the genotypes Mutant-3, Mutant-4, JOB-129 and Mutant-9 appeared to have lower days to flowering than checks. It is worth mentions that all the genotypes are mutants of RC-101 (Personal communicated, Dr. K. Ram Krishna). Genotypes - GC-723, CPD-118, JOB-80BR and GC-810 appeared to have early maturity than checks. Genotypes CPD-118 had highest mean value for plant height, but dwarfness is desirable therefore, Mutant-10, JOB-80BR, Mutant-2, Mutant-9 and JOB-129 genotypes were found to be superior over checks of RC-101, RC-19 and GC-3. Primary branches/plant is one of the important component traits of seed yield/plant. The genotypes DCS-47-1, DC-15 and CPD-103 were found to be superior over checks of RC-101, RC-19 and GC-3. Regarding pods/plant, the genotypes CPD-115, Mutant-6 and CPD-78 were better than the checks RC-101 and GC-3. GOA LOCAL, PTB-1, DC-15 and KBC-4 were superior for pod length over the checks. Seeds/pod is also an important trait as it directly influences seed yield/plant. GOA LOCAL, PTB-1 and KBC-4 genotypes had superior performance over the checks. 100-seed weight like seeds/pod is also important component traits of seed yield/plant. About one third of the test genotypes have higher magnitude for this trait. However, GOA LOCAL, CPD-83 and NBC-1 genotypes have significantly different from the checks in the positive direction. The genotypes had lower values of pod wall proportion *viz.*, Mutant-12, GC-525, Mutant-11, CPD-77 and Mutant-10 over the checks. These genotypes with specific desirable characters can be utilized in hybridization programme in order to get superior recombinants in segregating generations.

5.1.2 Phenotypic and genotypic variance

The existence of considerably higher genetic variability was also revealed by higher phenotypic and genotypic variance for all the characters studied. The phenotypic variance was higher than their respective genotypic variance for all the characters studied indicating the influences of environment on the expression of these traits.

5.1.3 Phenotypic and genotypic coefficient of variance (PCV & GCV)

The PCV was higher than the values of their respective GCV for all the characters studied which indicated the positive effects of environment in enhancing character expression among genotypes at phenotypic level. High estimates of GCV and PCV were recorded for the characters *viz.,* plant height followed by 100-seed weight and pod wall proportion which indicated the presence of high amount of genetic variability for these characters. Thus, selection may be effective for these characters because the response to selection is directly proportional to the variability present in the experimental material. These finding were consistent with those of Singh and Verma (2002), Venkatesen *et al.* (2003), Zargar *et al.* (2005), Saini (2007), Manggol *et al.* (2012) and Chattopadhyay *et al.* (2014).

5.1.4 Heritability and expected genetic advance

The knowledge of heritability estimate of quantitative characters is very important as phenotypic expression of a genotype may be altered by environment at various stages of its development. The response of selection depends upon the relative magnitude of heritable variation present in relation to the phenotypic variation. In the present investigation, high heritability estimates were observed for the characters studies *viz.,* 100-seed weight followed by plant height, pod wall proportion, pod length, seeds/pod, seed yield/plant. Similar observations were recorded by Damarany (1994), Ram *et al.* (1994), Vineeta *et al.* (2003) and Idahosa *et al*. (2010). High heritability indicated closeness of respective σ_p^2 and σ_g^2 values thereby, low environmental effects on the expression of these characters. Thus, phenotypic selection may be effective for these characters.

Heritability estimates alone do not provide reliable information about the gene action governing the expression of a particular character and also do not provide the information of the amount of genetic progress that would result from the selection of best individuals. Johanson *et al*. (1955) had pointed out that the heritability estimates along with genetic advance was more useful than the heritability estimates alone in predicting the response to selection.

Relative comparison of heritability coupled with genetic advance as per cent of mean over the characters indicated that characters 100-seed weight and plant height had high heritability estimates coupled with high genetic advance as per cent of mean. Panse (1957) suggested that the genotypic variation for such characters is probably due to high additive genetic effects and are least influenced by environment. High estimates of heritability and genetic advance as per cent of mean for 100-seed weight and plant height were also reported by Ramesh and Sangwan (2000) and Zargar *et al.* (2005). These characters also had high GCV and PCV. Thus, selection could be expected to effect desirable improvement in two traits.

Another characters, pod wall proportion, seed yield/plant and pod length had high heritability coupled with moderate genetic advance as per cent of mean which indicated these characters was mainly under the control of non-additive gene action. Similar finding was reported by Bachiyarani and Nadarajan (1996) and Rangaiah *et al.* (1999).

Seeds/pod had high heritability coupled with low genetic advance as per cent of mean indicated these characters may be governed by non-additive gene action that indicated least or complete absence of response to selection for this character. Similar finding was reported by Mathur (1995).

5.2 Character association

Genetic correlation provides information about degree and direction of association between two characters. It may result due to genetic causes such as pleiotropic effect or linkage or it may also due to environment causes. The magnitude and direction of correlation coefficient varies with the genetic material and the environment in which the genetic material is evaluated. The magnitude and direction of correlation helps in judging how improvement in one characters will cause simultaneous change in the other characters.

High magnitude of positive correlation coefficient at genotypic level between seed yield and its component characters is important for indirect selection for seed yield/plant. Since suitable test for significance of genotypic correlation coefficient is not available therefore, major emphasis has been put on phenotypic correlation coefficient. The estimate of correlation was compared with the ‘r’ values given in the ‘r’ Table (Fisher and Yates, 1938) at error degree of freedom. In general, the genotypic correlation coefficient were greater than their phenotypic correlation coefficient which indicated higher degree of association between two characters at genotypic levels, the magnitude of phenotypic correlation coefficient decreased due to the effect of environment.

In the present investigation, seed yield/plant had significant positive correlation for all characters *viz.,* days to 50% flowering, plant height, primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight except, days to maturity and pod wall proportion. Similar finding reported by Tiwari and Gautam (1989), Thiagarajan and RajashKaran (1989), Tamilselven and Das (1994), Sawant (1994), Mathur (19950, Tyagi *et al,* (2000), Venkatesen *et al.* (2003), Patil *et al.* (2004), Kumawat and Raje (2005) and Manggol *et al.* (2012). On the basis of association analysis it can be concluded that seeds/plant is the major components of seed yield/plant. This character should be considered as potential selection for improvement in seed yield.

Primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight had significant positive correlation with seed yield/plant. This indicated that selection for higher values of these characters will be effective in increasing the seed yield/plant. While, days to 50% flowering, plant height and pod wall proportion had significant positive correlation which again indicated that selection for lower values of these characters will be effective in increasing the seed yield/plant. Summarized features of correlation are presented in Table 5.1.

Table 5.1: Character association and interrelationship between different characters

Characters	**Significant positive correlation**	**Significant negative correlation**
Days to 50% flowering	Days to maturity, plant height, primary branches/plant, pod length, seeds/pod, 100-seed weight and seed yield/plant	Pods/plant
Days to maturity	Pod length and seeds/pod	Pods/plant
Plant height (cm)	Pod length, seeds/pod and seed yield/plant	-
Primary branches/plant	Pod length , seeds/pod and seed yield/plant	-
Pods/plant	Pod wall proportion and Seed yield/plant	Pod length, seeds/pod and 100-seed weight
Pod length (cm)	Seeds/pod, 100-seed weight and seed yield/plant	-
Seeds/pod	100-seed weight and seed yield/plant	-
100-seed weight (g)	Seed yield/plant	Pod wall proportion
Pod wall proportion (%)	-	-

5.3 Path coefficient analysis

The correlation analysis does not provide a clear picture of interrelationship of different characters influencing seed yield/plant. The expression of complex characters like seed yield/plant depends upon the interplay of a number of components characters. Thus, path coefficient analysis was carried out by taking seed yield/plant as dependent variable to partition the correlation coefficient into direct and indirect effects in order to determine the contribution of different characters towards the seed yield/plant. The path coefficient analysis at genotypic level has been discussed in view of the available literature.

In the present investigation, high positive direct effects on seed yield/plant were exerted by seeds/pod, pods/plant, primary branches/plant, pod length and days to maturity whereas, high negative direct effects were exerted by pod length, pod wall proportion, days to 50% flowering, seeds/pod and pods/plant. These observations were in agreement with those of Tyagi and Koranne (1988), Patil *et al.* (1989), Altinbas and Sepetogly (1993), Kalaiyarasi and Papanisamy (2001), Vineeta *et al.* (2003) and Anbumalarmathi et *al.* (2005). Seed yield/plant had significant positive correlation for characters *viz.,* days to 50% flowering, plant height, primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight.

The results suggested that primary branches/plant, pods/plant and seeds/pod can be used as reliable parameter for seed yield in cowpea. Primary branches/plant had high positive indirect effect via seeds/pod while negative indirect effects via pod length. Pods/plant had high positive indirect effect via pod length while negative indirect effects via seeds/pod. Seeds/pod had high positive indirect effect via 100-seed weight while negative indirect effects via pod length. Primary branches/plant, pods/plant and seeds/pod with higher magnitude while, days to 50% flowering, days to maturity, pod wall proportion and 100-seed weight with low magnitude can be used as reliable parameter for seed yield in cowpea.

5.4 Genetic divergence

The knowledge of genetic divergence provides us a sound scientific basis for the selection of genotypes to be used in hybridization programme for further improvement. The breeders sometimes make a choice of good parents based on visual examination of desirable attributes but, a more rational approach is to base the selection on combining ability effects and F_1 heterosis (Arunchalam,1989). Maximum hetrosis is expressed in F_1 hybrid between parents which are genetically more divergent (within units). Generally, divergence study is performed to make search for superior and divergent parents for any hybridization programme. Therefore, while selecting parents for a crossing programme, two points are considered:

1. The choice of clusters with maximum group distance, and
2. Selection of one or two genotypes from already chosen clusters.

Crossing of genetically diverse parents may provide improved progenies due to assembling of desirable genes scattered in these parents.

In the present investigation, 72 genotypes collected from different places were clubbed into 9 clusters. This indicated that genotypes were and much divergent. While cluster I contained maximum number of genotypes i.e. 33 genotypes, cluster II contained 11 genotypes, cluster IV contained 3 genotypes, cluster V contained 4 genotypes, cluster VI contained 9 genotypes, cluster VII contained 8 genotypes, cluster VIII contained 2 genotypes and cluster III and cluster IX contained one genotype in the sense that they has solitary entry.

The maximum inter cluster distance was observed between cluster VIII and cluster V followed by cluster IX and cluster VIII and cluster VIII and cluster VII. Maximum intra cluster distance was observed within cluster VI followed by cluster VII. Since clusters III and IX had solitary entry, intra cluster distance was zero. Intra cluster distance was less compared to inter cluster distance. Theoretically, one can anticipate maximum expression of heterosis in hybrids obtained by crossing of genotypes having maximum genetic distance. Inter cluster distance and mean cluster values for characters indicated that hybridization of clusters VIII (CPD-78 and CPD-118) with clusters V assessions (Mutant-3, Mutant-11, Mutant-10 and Mutant-12) would result in marked heterosis and produce segregants with improved yield.

In selecting genotypes from the already chosen group, important characteristics like disease resistance, earliness, quality or even performance of particular character should also be considered (Choudhary *et al.,* 1975). The mean performance of already formed clusters with respect to all the significant characters could not be taken into consideration simultaneously. It was imperative therefore, to consider characters having high contribution to total divergence. Seed yield/plant followed by 100-seed weight and plant height contributed maximum towards total divergence. These observations were in agreement with those of Usakumari *et al*. (2000), Kumawat and Raje (2005), Anbumalamarthi and Nadarajan (2007) and Nagalakshmi *et al.* (2010). Thus, it was concluded that best performing genotypes from cluster VIII and cluster V could be hybridized to generate superior progenies in segregating generations.

5.5 Plant breeding implications

Significant genetic variability was present in the material for seed yield and its components which indicated the possibility of improvement in seed yield. Genotypes with high mean performance for specific characters were identified, which indicated that the genotypes may be used in breeding programme.

Consideration of genetic parameters of variation indicated that high estimate of PCV and GCV were recorded for plant height followed by 100-seed weight and pod wall proportion. Further, joint consideration of GCV, PCV and heritability estimates along with genetic advance as per cent of mean indicated that characters plant height and 100-seed weight under the control of additive gene effects Thus, direct selection of this character in segregating generation will be responsive. On consideration of correlation coefficient and path coefficient analysis it revealed that direct selection for higher values of primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight and lower values of days to 50% flowering, days to maturity, pod wall proportion and plant height will be effective improving seed yield/plant.

On simultaneous consideration of genetic parameters of variation, correlation coefficient and path analysis it revealed that direct selection for higher values pods/plant and seeds/pod in segregating generation will be highly responsive in improving seed yield/plant. Seed yield/plant (35.81%) followed by 100-seed weight (29.07%) and plant height (19.33%) appeared to be the most important traits contributing maximum towards genetic divergence. Inter cluster distance and mean cluster values for characters indicated that hybridization of clusters VIII assessions with clusters V assessions would result in marked heterosis and produce segregants with improved yield.

One interesting point that emerged from the study that certain mutants of checks varieties RC-101 and RC-19 were included in the study. Cluster V was comprised only of the mutant genotypes whereas cluster III had only one genotype which was a mutant of RC-101. This indicates these mutants were considerable diverged from their parents and can be identified in the clustering revealed by D^2 analysis. Another interesting point to note in the study was repetition of certain checks, mutants and genotypes GC-3, RC-101, RC-19, JOB-129, JOB-80BR, CPD-121, CPD-83, CPD-119, CPD-118, CPD-115, and CPD-108. During clustering it was found repeated checks and genotypes were included in the same cluster. However, in case of GC-3, RC-101, CPD-118, CPD-115, JOB-129 and CPD-121 which were found in different clusters, latter observation may be attributed to an experimented error arising from fertility gradient.

Thus, on the basis of present investigation it can be concluded that sufficient amount of genetic variability was present in the genetic material. This variability can be exploited by carrying out hybridization involving genotypes having superior performance for the components characters determining seed yield/plant. Thus, direct selection should be carried out for higher values of primary branches/plant, pods/plant and seeds/pod in segregating generation for improving seed yield/plant. The mean performance of top 10 genotypes based on seed yield/plant and early maturity, respectively (Table: 5.2 and 5.3).

Table 5.2: The mean performance of top 10 genotypes based on seed yield/plant

S.No	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Pods /plant	Pod length (cm)	Seeds /pod	100-seed weight (g)	Pod wall proportion (%)	Seed yield/plant (g)
1.	CPD-103	40.33	67.33	92.17	5.43	5.37	12.03	10.53	9.20	23.98	5.23
2.	GC-525	39.67	68.33	38.57	4.23	5.00	11.30	10.80	14.26	19.01	5.19
3.	DC-15	48.67	73.53	50.53	5.60	4.10	15.87	13.63	10.02	35.14	4.98
4.	CPD-78	38.33	66.33	80.63	4.83	5.67	12.93	11.80	11.49	43.11	4.91
5.	PGCP-6	40.33	68.00	40.50	4.27	4.60	15.27	14.43	10.23	29.93	4.70
6.	CPD-118	39.67	64.00	83.83	4.87	4.47	11.47	10.33	9.45	28.85	4.68
7.	DCS-47-1	48.33	75.67	45.23	6.10	3.17	14.67	12.03	9.43	24.47	4.65
8.	CPD-115	41.33	70.33	61.60	4.23	6.83	11.07	10.83	8.14	40.18	4.62
9.	CPD-121	39.33	66.23	61.37	5.37	5.17	12.03	10.90	11.44	27.28	4.55
10.	NBC-1	40.33	67.67	35.87	4.60	3.43	11.50	10.30	15.48	25.36	4.52

Table 5.3: The mean performance of top 10 genotypes based on early maturity

S.No	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Pods/plant	Pod length (cm)	Seeds /pod	100seed weight (g)	Pod wall proportion (%)	Seed yield/plant (g)
1	GC-723	38.67	63.00	36.33	4.20	3.97	10.97	9.93	9.26	30.19	2.88
2	CPD-118	39.67	64.00	83.83	4.87	4.47	11.47	10.33	9.45	28.85	4.68
3	GC-810	38.33	64.00	35.57	3.87	4.30	11.67	10.83	9.04	29.70	3.35
4	JOB-80BR	38.67	64.33	26.40	4.40	4.57	12.00	11.23	11.07	28.01	3.46
5	CPD-127	38.67	64.33	37.23	4.40	4.73	11.93	10.93	9.59	26.70	3.77
6	RC-19	38.33	64.33	43.87	4.40	4.43	12.27	11.97	8.04	41.08	3.60
7	PHULE-CP-5040	41.33	64.33	33.30	3.57	3.93	11.53	10.23	9.18	34.88	3.65
8	Mutant-3	35.33	64.67	46.90	4.30	5.17	10.10	9.73	6.68	22.69	3.39
9	JOB-129	37.67	64.67	30.70	4.17	5.57	11.13	10.13	10.76	32.45	4.13
10	NBC-3	39.67	64.67	31.70	4.77	3.93	11.20	10.27	14.17	33.89	3.99

6. SUMMARY AND CONCLUSION

The present investigation entitled **"Character associations and genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]"** was conducted at Agriculture Research Farm, S.K.N. College of Agriculture, Jobner, during *kharif* season 2013 with the objectives of estimating the extent of genetic variation, degree of association, path coefficient analysis and genetic divergence among 72 genotypes including 3 checks of cowpea. Genotypes were evaluated in a Randomized Completely Block Design (RCBD) with three replications for seed yield per plant and its component characters with a view to decide breeding strategy and also to determine selection criteria for improving seed yield/plant in cowpea. Observation were recorded on days to 50% flowering, days to maturity, plant height (cm), primary branches/plant, pods/plant, pod length (cm), seeds/pod, 100-seed weight (g), pod wall proportion (%) and seed yield/plant (g). The data obtained were subjected to statistical analysis and results obtained are summarized below:

1. Analysis of variance indicated considerable amount of genetic variability among the genotypes for all the characters studied. The high estimates of genotypic and phenotypic variance were recorded for plant height followed by pod wall proportion.
2. The PCV were higher than their respective GCV for all the characters studied. High estimates of GCV and PCV were recorded for plant height followed by 100-seed weight and pod

wall proportion. Whereas, moderate estimate of PCV and GCV were recorded for seed yield/plant followed by pods/plant, pod length, primary branches/plant and seeds/pod and lower estimate of PCV and GCV for days to 50% flowering and days to maturity.

3. High estimates of heritability were recorded for 100-seed weight followed by plant height, pod wall proportion, pod length, and seeds/pod. Whereas, estimates of heritability were moderate for the characters seed yield/plant, primary branches/plant, pods/plant and days to 50% flowering. The heritability estimate was low for days to maturity.
4. The characters 100-seed weight and plant height had high heritability estimates along with high genetic advance as per cent of mean which indicated a major role of additive gene action for this character, whereas, seed yield/plant, pod length and pod wall proportion had high heritability along with moderate genetic advance as per cent of mean which indicated that character was mainly governed by non additive gene action. Seeds/pod had high heritability along with low genetic advance as per cent of mean which indicated major role of non additive gene action. Days to maturity had low estimates of genetic advance as per cent of mean which indicated least or complete absence of response to selection for these characters.
5. Correlation analysis in phenotypic level indicated that seed yield/plant had significant positive correlation for all the characters *viz.*, days to 50% flowering, plant height, primary

branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight except, days to maturity and pod wall proportion. In addition, days to 50% flowering and days to maturity had significant positive correlation with pod length, seeds/pod and 100-seed weight. Among other yield attributing traits primary branches/plant had significant positive correlation with pod length and seeds/pod and pods/plant had significant positive correlation with pod wall proportion. Seeds/pod had significant positive correlation with 100-seed weight.

6. Path coefficient analysis revealed that seed yield/plant can be improved upon by direct selection for more number of primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight and lower values of days to 50% flowering, days to maturity, plant height and pod wall proportion.
7. Simultaneous consideration of genetic parameters of variation, correlation coefficient and path analysis indicated that selection for primary branches/plant, pods/plant, seeds/pod and seed yield/plant in segregating generation will be effective for improvement in seed yield in cowpea.
8. The D^2 statistics was used to measure degree of divergence among genotypes. All the genotypes were grouped into 9 clusters. Intra cluster distance was found to be low as compared to inter cluster distance. The maximum inter cluster distance was observed between cluster VIII and V followed by IX and VIII. Seed yield/plant and 100-seed weight appeared to be the most important traits contributing maximum towards genetic

divergence. Inter cluster distance and mean cluster values for characters indicated that hybridization of clusters VIII assessions with clusters V assessions would result in marked heterosis and produce segregants with improved yield.

9. Comparison of genotypes with checks indicated that the genotypes Mutant-3 and Mutant-4 for days to 50% flowering, GC-723 and CPD-118 for early maturity, Mutant-10 and JOB-80BR for plant height, DCS-47-1 and DC-15 for primary branches/plant, CPD-115 and Mutant-6 for pods/plant, GOA LOCAL and PTB-1 for pod length, GOA LOCAL and PTB-1 for seeds/pod, GOA LOCAL and CPD-83 for 100-seed weight, Mutant-12 and GC-525 for pod wall proportion and CPD-103, GC-525 and DC-15 were superior for seed yield/plant over the checks.

10. Conclusively, from the result of parents study it is possible to identify useful parents for hybridization and recover even better segregants with high seeds yield/plant and other attributes such as earliness.

BIBLIOGRAPHY

Ahmed, N., Hatam, M. and Amanullah 2000. Yield potential of cowpea germplasm collected from FATA and neglected pockets of NWEP. *Sarhad Journal of Agriculture,* 16(1):7-11.

Alege, G. O. and Mustapha, O. T. 2007. Characterization studies and yield attributes of some varieties of cowpea [*Vigna unguiculata* (L.) Walp.]. *Ethnobotanical Leaflets,* 11:113-121.

Allard, R. W. 1960. Principles of plant breeding. *John Wiley and Sons Inc.,* New York, 104-254.

Altinbas, M. and Sepetoglu, H. 1993. A study to determine components affecting seed yield in cowpea [*Vigna unguiculata* (L.) Walp.]. *Populasyonumdadone verimini etkileyen ogelerin berlirlenmes uzerinde bircalisma doga turk tarum ve ormancilik dergisi,* 17(3):775-784.

Anbumalarmathi, J. and Nadarajan, N. 2007. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Journal of Ecobiology*, 19(2):129-132.

Anbumalarmathi, J., Sheeba, A. and Deepasankar, P. 2005. Genetic variability and interrelationship studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *Research on Crops,* 6(3):517-519.

Anbuselvam, Y., Manivannan, N., Saravanan, K. and Ganesan, J. 2001. Studied on genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Madras Agriculture Journal,* 87(4-6):343-345.

Annonymous, 2013. Directorate of Agriculture, Karishi Pant Bhawan, Jaipur (Rajasthan).

Arunachalam, V. 1989. Genetic basis of plant breeding. In: Plant Breeding, Theory and Practice. V. L. Chopra (eds.). *Oxford and IBH Publishing Co. Pvt. Ltd.*, New Delhi, 1-18.

Bachiyarani, S. and Nadarajan, N. 1996. Variability study in cowpea. *Legume Research*, 19(1):59-61.

Bapna, C. S., Joshi, S N. and Kabaria, M. M. 1972. Correlation studies on yield and agronomic characters in cowpea*. Indian Journal of Agronomy*, 17: 321-324.

Barrett, R. P. 1987. Integrating leaf and seed production strategies for cowpea [*Vigna unguiculata* (L.) Walp.] M.Sc. *Thesis*, Michigan State University, East, Lansing, M. I. USA, 391-396.

Brahmaiah, M., Jhansi R. K., Sunil, N. and Keshavulu K. 2014. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.] for yield components and seed quality parameters. *Electronic Journal of Plant Breeding*, 5(1):170-111.

Burton, G. M. 1952. Quantitative inheritance in grasses. *Sixth International Grassland Congress,* 277-285.

Chatterjee, B. N. and Bhattacharya, K. K. 1986. Principle and practices of grain legume production. *Oxford and IBH publishing Co. Ltd.,* New Delhi.

Chattopadhyay, A., Rana, N. P., Seth, T., Das, S., Chatterjee, S. and Dutta, S. 2014. Identification of selection indices and choosing of parents for vegetable cowpea (*Vigna unguiculata cv-gr. sesquipedalis*) breeding programme. *Legume Research*, 37(1):19-25.

Choudhary, B., Bhat, B. N. and Singh, V. P. 1975. Genetic diversity in cluster bean. *Indian Journal of Agriculture Sciences*, 45:530-535.

Cokkizgin, A., Colkesen, M., Idikut, L., Ozsisli, B. and Girgel, U. 2013. Determination of relationship between yield components in bean by using path coefficient analysis. *Greener Journal of Agricultural Science*, 3(2):85-89.

Dahiya, O. P., Singh, D. and Mishra, S. K. 2007. Correlation and path coefficient analysis in cowpea *[Vigna unguiculata* (L.) Walp.]. *Journal of Arid Legumes*, 4(2):127-129.

Dahiya, O. P., Singh, D. and Mishra, S. K. 2007. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Journal of Arid Legumes*, 4(1):62-65.

Dalsaniya, S. B., Poshiya,V. K., Savaliya,J. J., Pansuriya, A. G. and Davada, B. K. 2009. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 32(4):250-254.

Damarany, A. M. 1994. Estimates of genotypic and phenotypic correlation, heritability and potence of gene set in cowpea [*Vigna unguiculata (*L.) Walp.]. *Assiut Journal of Agricultural Sciences,* 25(4):1-8.

Darlington, C. D. and Wylie, A. P. 1955. Chromosome atlas of flowering plants. *George Allen and Unwin Ltd*. London.

Dewey, O. R. and Lu, K. H. 1959. A correlation and path coefficient analysis of components of crested wheatgrass seed production. *Agronomy Journal,* 57:515-518.

Dhanasekar, P., Reddy, K. S. and Pandey, R. N. 2010. Discerning the genetic variation of pod wall proportion and pod filling index in cowpea. *Journal of food legumes*, 23(1):9-13.

Eswaran, R. S., Kumar, T. and Venkatesan, M. 2007. Genetic variability and association of component characters for earliness in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 30 (1):17-23.

Falconer, D. S. 1960. Introduction of quantitative genetics. *Longman, New York*, 160-183.

Fisher, R. A. 1936. The use of multiple measurements in taxonomic problems. *Annals of Eugenics*, 7:179–188.

Fisher, R. A. and Yates, F. 1938. Statistical tables for Biological, Agricultural and Medicinal Research. *Published by Oliver and Boyd, Edinburgh and London*, 63.

Girish, G., Viswanatha, K. P., Manjunath, A. and Yogesh, L. N. 2006. Genetic variability, heritability and genetic advance analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Environment and Ecology*, 24(4):1172-1174.

Hanson, C. H., Robinson, H. F. and Comstock, R. E. 1956. Biometrical studies of yield in segregating population of *Korean lespedeza*. *Agronomy Journal,* 48:268-272.

Huyghe, C. 1998. Genetics and genetic modifications of plant architecture in grain legumes: a review. *Agronomie,* 18: 383-411.

Huyghe, C. and Ney, B. 1997. Effects on yield and produce quality. *In: problems and prospects for winter sowing of grain legumes in Europe, AEP, Paris*, 77-82.

Idahosa, D. O., Alika, J. E. and Omoregie, A. U. 2010. Genetic variability, heritability and expected genetic advance as indices for yield and yield components selection in cowpea [*Vigna unguiculata* (L.) Walp.]. *Academia Arena*, 2(5):22-26.

Imran, M., Hussain, A., Hussain, S., Khan, S., Bakhsh, A., Zahid, M. S. and Baig, D. 2010. Character association and evolution of cowpea germplasm for green fodder and grain yield under rainfed conditions of Islamabad. *Sarhad Journal of Agricultural,* 26:3.

Inuwa, A. H., Ajeigbe, H. A., Muhammed, S. G., Mustapha, Y. 2012. Genetic variability and heritability of some selected cowpea [*Vigna unguiculata* (L.) Walp.] lines.

Johnson, H. W., Robinson, H. F. and Comstock , R. F. 1955. Estimation of genetic environmental variability in soybean. *Agronomy Journal,* 47: 314-318.

Jonoria, M. P. and Ali. M. A. 1970. Correlation and regression studies in cowpea. *JNKVV Research Journal*, 4:15-19.

Kalaiyarasi, R. and Palanisamy, G. A. 2001. A study on character association and path analysis in F_4 generation of cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 24(1):36-39.

Kumar, S., Tyagi, I. D., Kumar, S. and Singh, B 2002. Analysis of fodder yield components in segregating generation of cowpea *[Vigna unguiculata* (L.) Walp]. *Progressive Agriculture,* 2(1):22-25.

Kumari, R. U., Usharani, K. S., Suguna, R. and Anandakumar, C. R. 2010. Relationship between the yield contributing characters in cowpea for grain purpose *[Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding*, 1(4):882-884.

Kumawat, K. C. and Raje, R S. 2005. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Journal of Arid Legumes*, 2(1):25-27.

Kumawat, K. C. and Raje, R. S. 2005. Association analysis in cowpea *[Vigna unguiculata* (L.) Walp.]. *Journal of Arid Legumes*, 2(1):47-49.

Lal, H., Rai, M., Karan, S., Verma, A. and Ram, D. 2007. Multivariate hierarchical clustering of cowpea germplasm [*Vigna unguiculata* (L.) Walp.]. *Acta Horticulture,* 752.

Lesly, W. D., Uma, M. S. and Salimath, P. M. 2006. Genetic diversity in cowpea. *Indian Journal of Plant Genetic Resources,* 19(1).

Mackie, W. W. and Smith, F. L. 1935. Evidence of field hybridization in beans. *Journal American Society Agronomy*, 27:903-908.

Mahalanobis, P. C. 1936. On the generalized distance in statistics. *Proceeding of the National Institute of Science of India*, 12:49-55.

Malarvizhi, D., Swaminathan, C., Robin, S. and Kannan, K. 2005. Genetic variability studies in fodder cowpea. *Legume Research,* 28(1):52-54.

Manggoel, W., Uguru, M. I., Ndam, O. N., and Dasbak, M. A. 2012. Genetic variability, correlation and path coefficient analysis of some yield components of ten cowpea [Vigna unguiculata (L.) Walp.] accessions. *Journal of Plant Breeding and Crop Science,* 4(5):80-86.

Mathur, R. 1995. Genetic variability and correlation studies in segregating generation of cowpea. *Madras Agricultural Journal*, 82(2):150-152.

Mittal, V. P. and Singh, P. 2005. Component analysis of seed yield and other characters in cowpea. *Journal of Arid Legumes*, 2(2):408-409.

Nagalakshmi, R. M., Usha Kumari, R. and Boranayak, M. B. 2010. Assessment of genetic diversity in cowpea *[Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding,* 1(4):453-461.

Naher, Z., Rabbani, M. G., Rahaman, E. H. and M. S. 2005. Study on genetic diversity for quantitative characters in cowpea [*Vigna unguiculata (L.)* Walp.]. *Bangladesh Journal of Training and Development*, 18(1/2):135-140.

Narayanankutty, C., Mili, R. and Jaikumaran, U. 2003. Variability and genetic divergence in vegetable cowpea. *Journal of Maharashtra Agricultural Universities*, 28(1):26-29.

Nehru, S. D. and Manjunath, A. 2001. Genetic variability for yield and accessory character in cowpea [*Vigna unguiculata (*L.) Walp.]. *Indian Agriculturist*, 45(1-2):99-101.

Ng, N.Q. and Marechal, R. 1985. Cowpea taxonomy, origin and germplasm. In: Cowpea research, production and utilization. Singh, S.R. and Rachie, K.O. (eds*.)* Wiley*,* New York*,* 11-21.

Nielsen, S., Ohler, T. and Mitchell 1997. Cowpea leaves for human consumption, production, utilization and nutrient composition. In: *Advances in Cowpea Research*. Singh, B., Raj., Mohan., D. Dashiell, K. and Jackai, L. (Eds) International Institute of Tropical Agriculture (IITA) and Japan International Research Centre for Agricultural Sciences (JIRCAS), Ibadan*,* Nigeria, 326-332.

Nigude, A. D., Dumbre, A. D. and Lad, D. B. 2004. Genetic diversity studies in cowpea. *Journal of Maharashtra Agricultural Universities,* 29(3):250-252.

Nigude, A. D., Dumbre, A. D., Lad, D. B. and Bangar, N. D. 2004. Genetic variability and correlation studies in cowpea. *Journal of Maharashtra Agricultural University,* 29(1):30-33.

Nigude, A. D., Dumbre, A. D., Sushir, K. V., Patil, H. E. and Chavhan, A. D. 2004. Correlation and path coefficient analysis in cowpea*. Annuals of Plant Physiology*, 18(1):71-75.

Nwofia, G. E., Nwanebu, M. and Agbo, C.U. 2012. Variability and inter relationship between yield and associated traits in cowpea [*Vigna unguiculata* (L.) Walp.] as influenced by plant populations*. World Journal of Agricultural Sciences*, 8(4):396-402.

Nwofia, G. E., Ogbonna, N. D. and Agbo, C. U. 2013. Path analysis and heritability estimates of yield and yield components in vegetable cowpea as influenced by planting season. *American-Eurasian Journal of Agricultural & Environmental Sciences*, 13(9):1283-1289.

Pal, A. K., Maurya, A. N., Singh, B., Ram, D. and Kumar, S. 2003. Genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata (L.*) Walp.]. *Orissa Journal of Horticulture*, 31(1):94-97.

Pal, A. K., Singh, B., Maurya, A. N. and Sanjay K. 2004. Correlation and path analysis in cowpea [*Vigna unguiculatia* (L.) Walp.]. *South Indian Horticulture*, 52(1/6):82-88.

Pandey, I. 2007. Genetic diversity in grain cowpea *[Vigna unguiculata* (L.) Walp.]. *Legume Research*, 30(2):92-97.

Panse, V. G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Plant Breeding and Genetics,* 17(2):318-328.

Patil, A. R., Bendale, V. W., Bhave, S. G. and Mehta, J. L. 2004. Correlation and path analysis studies of biomass partitioning characters in cowpea [*Vigna unguiculata* (L.) Walp.]. *Orissa Journal of Horticulture*, 32(1):19-22.

Patil, S.J., Venugoipal, R., Goud, J. V. and Parameshwar , R. 1989. Correlation and path coefficient analysis in cowpea*.* *Karnataka Journal of Agricultural Sciences,* 2(3):170-175.

Peksen, E. and Artk, C. 2004. Comparison of some cowpea [*Vigna unguiculata* (L.) Walp.]. Genotypes from Turkey for seed yield and yield related characters. *Journal of Agronomy,* 3(2):137-140.

Quin, F. M. 1997. Introduction. In: *Advances in Cowpea Research*. Singh, B.B., Ral., Mohan, Deshiell,K. and Jackai, L.E.N. (Eds.). IITA/JIRCAS, IITA*,* Ibadan*,* Nigeria, IX-XV.

Ram, T., Anasari, M. M. and Sharma, T. V. R. S. 1994. Relative reference of cowpea genotypes in rainfed condition of Andman and their genetic parameters analysis for seed yield. *Indian Journal of Pulse Research*, 7 (1):72-75.

Ramesh kumar and Sangwan, R. S. 2000. Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.]. *Annuals of Biology*, 16(2):181-183.

Rangaiah, S., Nehru, S. D. and Mahadeva, P. 1999. Genetic studies in two cross derivates of cowpea [*Vigna unguiculata* (L.) Walp.]. *Mysore Journal of Agricultural Sciences*, 33(3):125-129.

Rao, C. R. 1952. Advanced statistical methods of Biometrical Research, *John Willley and Sons, New York*, 226-272.

Rewale, A.P., Birari, S. P. and Jamadagni, B. M. 1995. Genetic variability and heritability in cowpea. *Agricultural Science Digest*, 15(2):73-76.

Rocha, M. de. M., Campelo, J. E. G., Freire, filho F. R., Ribeiro, V. Q., Lopes, A. C. de A. and de A. Lopes A. C. 2003. Estimates of genetic parameters in white coat cowpea genotypes. *Revista Cientifica Rural*, 1:135-141.

Sahai, G., Malaviya, D. R. and Singh, U. P. 2013. Morphological Traits Association with Fodder and Seed Yield in Cowpea *[Vigna Unguiculata* (L.) Walp.]. *Journal of Environmental Biology*, 34 (1).

Saini, P. P. 2007. Character associations and genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *M.Sc. (Ag.) Thesis,* SKRAU, Bikaner Campus, Jobner.

Sawant, D. S. 1994. Association and path analysis in cowpea. *Annals of Agricultural Research*, 15(2):143-139.

Sharma, C. D. and Singhania, D. L. 1992. Performance of cowpea [*Vigna unguiculata* (L.) Walp.] genotypes for fodder traits. *Annals of Agricultural Research,* 15(2):65-66.

Sheelamary, S. and Gopalan, A. 2006. Association studies for yield and its related traits of fodder cowpea in F_4 generation. *Journal of Applied Sciences Research*, 2(9):584-586.

Singh, B. B., Mohan Raj, D. R., Dashiell, K. E. and Jackai Len 1997. *Advances in Cowpea Research*, IITA- JIRCAS, Ibadan, Nigeria.

Singh, M. K. and Verma, J. S. 2002. Variation and character association for certain quantitative traits in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm. *Forage Research,* 27(4):251-253.

Singh, N., Rana, M. K., Pratap, P. S., Ranjan, R., Sah, M. and Sah, J. N. 2013. Study of genetic divergence on vegetable cowpea [*Vigina ungiculata* (L.) Walp.]. *Indian Society of Vegetable Science,* National Symposium on Abiotic and Biotic Stress Management in Vegetable Crops.

Singh, R. K. and Choudhary, B. P. 1995. Biometrical methods in quantitative genetic analysis. *Kalyani Publisher*, New Delhi. 215-238.

Singh, S. B., Singh, A. K. and Singh, A. P. 2010. Genetic variability, trait relationship and path analysis for green fodder yield and its components in cowpea [*Vigna unguiculata* (L.) Walp.] under rainfed environment. *Progressive Agriculture*, 10(1).

Steele. W. M. 1972. Cowpea in Africa. Doctroal *Thesis*, University of Reading, United Kingdom.

Suganthi, S. and Murugan, S. 2008. Association analysis in cowpea *[Vigna unguiculata* (L.) Walp.]. *Legume Research*, 31(2):130-132.

Suganthi, S., Murugan, S. and Venkatesan, M. 2007. D^2 analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 30(2):145-147.

Tamgadge, S., Dod, V. N., Mahorkar, V. K. and Peshattiwar, P. D. 2008. Genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp.]. *Asian Journal of Horticulture,* 3(1):30-32.

Tamilselvam, A. and Das, L. D. V. 1994. Correlation studies in cowpea [*Vigna unguiculata (*L.) Walp.] for seed yield. *Madras Agricultural Journal*, 76 (8):445-446.

Thiyagarajan, K. and Rajashkaran, S. 1989. Studies on character association and path coefficient analysis in cowpea [*Vigna unguiculata (*L.) Walp.]. *Madras Agricultural Journal*, 76(1):10-14.

Thorat, A. and Gadewar, R. D. 2013. Variability and correlation studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal for Environmental Rehabilitation and Conservation*, 4(1):44-49.

Tigga, K. and Tandekar, K. 2013. Genetic divergence for yeild and quality components in cowpea [*Vigna unguiculata* (L.) Walp.]. *Trends in Bio-sciences*, 6(5):555-557.

Tiwari, A. K. and Gautam, M. C. 1989. Correlation and path coefficient analysis in cowpea [*Vigna unguiculata (*L.) Walp.]. *Indian Journal of Horticulture*, 46(4):516-527.

Tyagi, P. C. and Koranne, K. D. 1988. Correlation and path coefficient analysis in cowpea [*Vigna unguiculata (*L.) Walp.]. *Indian Journal of Agricultural Science*, 58(1):57.

Tyagi, P. C., Kumar, N. and Agarwal, M. C. 2000. Genetic variability and association of component characters for seed yield in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 23(2):92-96.

Ushakumari, R., Backiyarani, S. and Dhanakodi, C. V. 2000. Character contribution to diversity in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 23(2):122-125.

Valarmathi, G., Surendran, C. and Muthiah, A. R. 2007. Genetic divergence analysis in subspecies of cowpea (*Vigna unguiculata ssp. unguiculata* and *Vigna unguiculata ssp. sesquipedalis*). *Legume Research*, 30(3):192-196.

Vavilapalli, S. K., Celine, V. A. and Sreelathakumai, I. 2014. Genetic divergence analysis in vegetable cowpea [*Vigna unguiculata subsp. unguiculata* (L.) Walp.] genotypes. *Legume Genomics and Genetics*, 5(2).

Vavilapalli, S. K., Celine, V. A., Duggi, S., Padakipatil, S. and Magadum, S. K. 2013. Genetic Variability and Heritability Studies in Bush Cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Genomics and Genetics*, 4(4).

Vavilov, N. I. 1949. The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanica,* 13:1-54.

Venkatesan, M., Prakash, M. and Ganesan, J. 2003. Correlation and path analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 26(2):105-108.

Venkatesan, M., Prakash, M. and Ganesan, J. 2003. Genetic variability, heritability and genetic advance analyses in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research*, 26(2):155-156.

Venkatesan, M., Veeramani, N., Thangavel, P. and Ganesan, J. 2004. Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]. *Legume Research,* 27(3):223-225.

Vineeta K., Arora, R. N. and Singh, J. V. 2003. Variability and path analysis in grain cowpea. *Advances in Arid Legumes Research*, 59-62.

Vishwanath, H., Rai, M., Rai, N. and Ram, D. 2009. Hierarchical clustering and character association studies in cowpea [*Vigna unguiculata (*L.) Walp.]. *Indian Journal of Plant Genetic Resources,* 22(1).

Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research,* 20:257-287.

Zargar, S. A. and Tahirali, M. A. 2005. Genetic variability, heritability and genetic advance for seed yield and component traits in cowpea [*Vigna unguiculata* (L.) Walp.]. *National Journal of Plant Improvement,* 7(2):85-87.

CHARACTER ASSOCIATIONS AND GENETIC DIVERGENCE IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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Abstract

A field experiment was conducted during *kharif* 2013 to evaluate 72 genotypes of cowpea to estimate genetic variability, characters association and direct and indirect effects of different characters on seed yield and to assess genetic divergence.

Analysis of variance indicated existence of significant genetic variability for all the characters studied. High values of genotypic and phenotypic variance were recorded for plant height followed by pod wall proportion. High estimates of GCV and PCV were recorded for plant height followed by 100-seed weight and pod wall proportion. Whereas, moderate estimate of PCV and GCV were recorded for seed yield/plant followed by pods/plant, pod length, primary branches/plant and seeds/pod and lower estimate of PCV and GCV for days to 50% flowering and days to maturity.

High estimates of heritability along with high genetic advance as per cent of mean was recorded for 100-seed weight and plant height which indicated major role of additive gene action in the expression of these characters while high heritability along with moderate genetic

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advance as per cent of mean was recorded for pod wall proportion, seed yield/plant and pod length which indicated these characters was mainly governed by non additive gene action. Seed yield/plant had significant positive correlation for all characters *viz.,* days to 50% flowering, plant height, primary branches/plant, pods/plant, pod length, seeds/pod and 100-seed weight except, days to maturity and pod wall proportion.

Path coefficient analysis revealed that seeds/pod, pods/plant and primary branches/plant exhibited high direct positive effect on seed yield/plant. Pod length and pod wall proportion had high negative direct effects on seed yield/plant. Simultaneous consideration of genetic parameters of variation, correlation and path coefficient analysis indicated that direct selection should be carried out for higher values of seeds/pod to increase seed yield/plant.

Grouping of genotypes was performed through D^2 statistics (Mahalanobis). All the 72 genotypes were grouped into 9 clusters. Two characters seed yield/plant (35.81%) and 100-seed weight (29.07%) had maximum contribution towards genetic divergence. Intra cluster distance was found to be low as compared to inter cluster distance. The maximum inter cluster distance was observed between cluster VIII and V followed by IX and VIII. It was concluded that crossing between clusters VIII (CPD-78 and CPD-118) and clusters V (Mutant-3, Mutant-11, Mutant-10 and Mutant-12) could produce elite progenies in segregating generation. Conclusively, from the result of parents study it is possible to identify useful parents for hybridization and recover even better segregants with high seeds yield/plant and other attributes such as earliness.

लोबिया [*विग्ना अन्गुइकुलेटा* (एल.) वाल्प.] में लक्षण सहचर्य एवं आनुवंशिक विविधता

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मुख्य सलाहकार

अनुक्षेपण

लोबिया के 72 जीन प्ररूपों का खरीफ 2013 के दौरान विभिन्नता आकलन, बीज उपज का उसके समागमों के साथ लक्षण सहचर्य एवं परोक्ष एवं अपरोक्ष प्रभावों के निर्धारण एवं जननीक विविधता का मुल्यांकन करने के लिए प्रयोग किया गया।

विभिन्नता विशलेषण ने सभी अध्ययन किये गये लक्षणों के लिए सार्थक विभिन्नता दर्शाई। जीन प्ररूपों में पादप ऊंचाई एवं 100 बीजों का भार के लिए लक्षण एवं आनुवंशिक विविधता के लिए उच्च मान देखा गया। जीन प्ररूपों में पादप ऊचाई, 100 बीजों का भार एवं फली भित्ति अनुपात के लिए लक्षण एवं आनुवंशिक विविधता गुणांक का उच्च मान देखा गया। जबकि बीज उपज/पादप, फलियॉ/पादप, फली लम्बाई, प्राथमिक शाखाऐं/पादप एवं बीज/फली के लिए आनुवंशिक एवं लक्षण विविधता गुणांक का आंकलन मध्यम स्तर का अभिलेखित किया गया। 50 प्रतिशत पुष्पन एवं पादप परिपक्वता के लिए लक्षण एवं आनुवंशिक विविधता गुणांक के लिए निम्न मान किया गया।

100 बीजों का भार एवं पादप लम्बाई के लिए उच्च वंशानुगति के साथ माध्य प्रतिशत के रूप में उच्च आनुवंशिक प्रगति का अनुमान अभिलेखित किया गया, जिसने इन लक्षणों की अभिव्यक्ति में युग्मित जीन क्रिया का मुख्य योगदान दर्शाया जबकि फली भित्ति अनुपात, बीज उपज/पादप एवं फली लम्बाई के लिए माध्य प्रतिशत के रूप में मध्यम

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आनुवंशिक प्रगति के साथ उच्च वंशानुगति आकलन अभिलेखित की गई। जिसने इन लक्षणों का मुख्य रूप से अयुग्मित जीन क्रिया द्वारा नियन्त्रित होना दर्शाया। बीज उपज/पादप का पादप परिपक्वता एवं फली भित्ति अनुपात के छोड़कर 50 प्रतिशत पुष्पन, पादप ऊँचाई, प्राथमिक शाखाऐं/पादप, फलियां/पादप, फली लम्बाई, बीज/फली एवं 100 बीजों का भार के साथ सार्थक धनात्मक सहसम्बन्ध पाया गया।

पथ गुणांक विशलेषण ने यह प्रकट किया की बीज/फल, फलियॉ/पादप एवं प्राथमिक शाखाएँ/पादप ने बीज उपज/पादप के प्रति धनात्मक प्रभाव प्रदर्शित किया। फली लम्बाई एवं फली भित्ति अनुपात में बीज उपज/पादप के साथ उच्च प्रत्यक्ष ऋणात्मक प्रभाव दिखाया। विभिन्नता के आनुवंशिक मापदण्डों, सहसम्बध विश्लेषण एवं पथ गुणाक विश्लेषण को एक साथ विचार करने से यह निष्कर्ष निकला की बीज उपज/पादप में वृद्धि के लिए बीज/फली के उच्च मापों का प्रत्यक्ष वरण किया जाना चाहिए।

जीन प्ररूपों का समूहीकरण D^2 सांख्यकों द्वारा किया गया। सभी 72 जीन प्ररूप नौ विभिन्न समूहों में समूहित हुए। बीज उपज/पादप (35.81 प्रतिशत) एवं 100 बीजों का भार (29.07 प्रतिशत) का योगदान आनुवंशिक विविधता की ओर अधिकतम रहा। अन्तः समूह की दूरिया अंतर समूह की दूरियों की तुलना में कम पाई गई। अधिकतम अंतर समूह दूरी समूह 8 एवं समूह 5 तथा इसके बाद समूह 9 एवं समूह 8 के बीच पाई गई। इससे यह निर्ष्कष निकला की समूह 8 (सी.पी.डी.–78 एवं सी.पी.डी. –118) एवं समूह 5 (उत्परिवत–3, उत्परिवत–11, उत्परिवत–10 एवं उत्परिवत–12) के जीन प्ररूप को आपस में संयोजित कराने पर ये विसयोजी पीढीयों में सर्वात्तम संतति को उत्पन्न कर सकते है। निर्णायक रूप से यह संस्तृति की जाती है कि प्रस्तुत अध्ययन के आधार पर चयन किये गये अच्छे जनकों को संकरण में उपयोग कर एवं उच्च विसयोजक के साथ उच्च बीज उपज/पादप और अन्य गुणों जैसे शीघ्र परिपक्वन प्राप्त करना संभव हो सकता है।

Annexure-I

List of mean performance of the genotypes and checks used in study

S. No	Genotypes	Days to 50% flowering	Days to maturity	Plant height (cm)	Primary branches/plant	Pods/ plant	Pod length (cm)	Seeds/ pod	100-seed weight (g)	Pod wall proportion (%)	Seed yield/ plant (g)
1.	CPD-108	39.67	67.67	42.57	3.73	4.27	11.03	10.80	9.54	32.12	3.00
2.	GC-525	39.67	68.33	38.57	4.23	5.00	11.30	10.80	14.26	19.01	5.19
3.	GC521	38.33	66.33	65.83	4.97	4.90	10.97	11.03	8.72	31.73	4.50
4.	PGCP-6	40.33	68.00	40.50	4.27	4.60	15.27	14.43	10.23	29.93	4.70
5.	JOB-129	38.67	68.33	28.87	4.27	5.53	11.03	10.10	10.97	32.58	3.31
6.	CP-107	41.67	70.33	40.13	4.20	4.83	11.23	9.57	9.73	31.88	3.61
7.	CPD-105	40.00	68.67	40.60	4.10	3.73	10.07	9.43	10.45	23.73	4.30
8.	PHULE-CP-5040	41.33	64.33	33.30	3.57	3.93	11.53	10.23	9.18	34.88	3.65
9.	PHULE-CP-5030	40.33	68.33	31.40	4.10	4.00	9.40	9.37	9.69	21.90	3.61
10.	RC-101	41.33	70.00	44.17	3.50	3.70	10.93	10.17	8.63	32.96	4.09
11.	GC-3	43.00	67.00	48.17	4.50	5.30	10.27	9.57	9.68	27.26	3.71
12.	CPD-115	40.00	63.00	53.10	4.37	4.43	9.47	8.63	6.79	29.42	2.91
13.	GC-723	38.67	63.00	36.33	4.20	3.97	10.97	9.93	9.26	30.19	2.88
14.	DCS-47-1	48.33	75.67	45.23	6.10	3.17	14.67	12.03	9.43	24.47	4.65
15.	GC-501	43.00	72.67	48.07	4.67	3.83	11.80	10.17	11.02	34.09	3.18
16.	GC-703	40.67	64.67	51.73	4.97	3.70	10.00	9.23	10.03	31.78	3.20
17.	GC-3	41.00	65.00	35.87	4.70	3.57	10.73	9.53	8.34	25.16	3.25

Cont....

8.	NBC-2	46.00	72.33	36.20	3.50	3.60	10.83	9.80	14.69	30.98	2.69
9.	CPD-118	39.67	64.00	83.83	4.87	4.47	11.47	10.33	9.45	28.85	4.68
0.	NBC-1	40.33	67.67	35.87	4.60	3.43	11.50	10.30	15.48	25.36	4.52
1.	NBC-3	39.67	64.67	31.70	4.77	3.93	11.20	10.27	14.17	33.89	3.99
2.	JOB-129	37.67	64.67	30.70	4.17	5.57	11.13	10.13	10.76	32.45	4.13
3.	SUBHARA	40.33	67.00	43.91	3.77	4.15	10.87	10.03	6.60	38.39	3.13
4.	GOA LOACAL	50.33	75.67	88.63	4.40	3.50	20.47	15.63	17.34	25.01	4.27
5.	PGCP-12	40.33	65.33	37.13	3.97	3.80	15.33	12.73	15.48	22.43	3.42
6.	CPD-119	40.00	66.00	48.50	4.07	5.13	11.53	10.30	7.87	31.14	4.05
7.	JOB-11	38.33	66.67	43.77	3.93	3.93	12.60	10.73	8.35	29.21	3.08
8.	JOB-80BR	39.00	68.00	44.43	4.33	4.03	11.50	9.80	11.18	31.29	3.11
9.	KBC-4	47.33	74.00	51.47	5.38	4.37	16.07	14.50	8.53	39.84	4.05
0.	CPD-121	39.33	64.67	53.40	4.60	4.93	11.97	10.37	11.51	30.04	3.38
1.	GC-817	38.33	65.00	40.27	4.13	5.03	10.93	7.43	6.34	30.81	2.72
2.	KBC-5	43.33	72.67	57.53	4.57	3.90	15.43	14.33	10.07	41.05	4.45
3.	GC-3	39.67	68.33	38.63	3.80	3.47	12.83	11.90	8.21	24.53	3.58
4.	PTB-1	42.33	67.33	71.40	3.70	3.07	16.83	15.03	11.14	23.92	4.33
5.	CPD-83	40.67	68.00	84.27	3.97	3.77	14.90	13.10	16.71	22.35	4.39
6.	GC-815	44.67	72.00	31.47	4.97	3.63	13.33	12.90	13.25	25.80	3.88
7.	GC-810	38.33	64.00	35.57	3.87	4.30	11.67	10.83	9.04	29.70	3.35
8.	DC-15	48.67	73.33	50.53	5.60	4.10	15.87	13.63	10.02	35.14	4.98

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9.	HC-38	39.33	68.33	83.90	3.93	4.97	11.53	10.17	7.16	36.92	4.22
40.	JOB-129	37.67	65.33	30.53	3.50	4.23	11.57	10.80	11.93	31.34	4.17
41.	CPD-119	38.67	65.00	53.03	5.17	4.70	11.77	10.10	7.76	29.99	3.56
42.	CPD-103	40.33	67.33	92.17	5.43	5.37	12.03	10.53	9.20	23.98	5.23
43.	JOB-80BR	38.67	64.33	26.40	4.40	4.57	12.00	11.23	11.07	28.01	3.46
44.	CPD-132	40.00	69.33	56.97	4.50	3.87	10.80	10.27	10.25	27.43	3.68
45.	CPD-121	39.33	66.33	61.37	5.37	5.17	12.03	10.90	11.44	27.28	4.55
46.	CPD-134	41.00	68.00	35.83	4.63	3.87	11.93	10.73	9.06	29.02	2.85
47.	GC-3	39.00	66.00	100.87	4.13	3.90	11.83	10.80	7.99	27.42	3.70
48.	CPD-127	38.67	64.33	37.23	4.40	4.73	11.93	10.93	9.59	26.70	3.77
49.	CPD-142	39.33	69.33	60.00	3.43	4.70	11.87	10.83	8.44	27.82	2.61
50.	CPD -136	39.33	69.67	80.97	3.77	4.67	11.77	10.77	10.66	29.58	3.46
51.	CPD-78	38.33	66.33	80.63	4.83	5.67	12.93	11.80	11.49	43.11	4.91
52.	CPD-83	41.00	65.33	73.77	5.17	4.80	13.73	11.50	15.40	31.71	3.67
53.	RC-19	38.33	64.33	43.87	4.40	4.43	12.27	11.97	8.04	41.08	3.60
54.	CPD-115	41.33	70.33	61.60	4.23	6.83	11.07	10.83	8.14	40.18	4.62
55.	CPD- 118	38.33	65.33	101.17	3.67	4.43	11.83	11.30	8.65	50.30	3.53
56.	CPD- 129	39.33	68.00	36.00	4.53	4.30	10.93	9.73	7.64	29.12	3.19
57.	CPD- 77	38.33	69.33	47.40	3.03	4.93	12.23	10.53	11.20	21.07	4.19

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58.	CPD- 108	39.67	69.67	32.37	4.03	3.97	11.53	10.53	8.84	35.83	2.94
59.	RC-101	36.67	65.33	29.63	3.07	5.27	10.63	9.53	9.51	39.75	3.77
60.	Mutant-1	40.33	68.00	88.30	3.47	5.63	11.33	10.20	5.93	25.37	3.65
61.	Mutant-2	40.00	69.33	26.73	3.60	5.47	11.13	10.40	5.69	38.22	3.63
62.	Mutant-3	35.33	64.67	46.90	4.30	5.17	10.10	9.73	6.68	22.69	3.39
63.	Mutant-4	37.67	65.00	38.20	3.60	5.23	10.23	9.43	6.73	33.00	4.05
64.	Mutant-5	38.67	68.33	35.97	4.13	5.40	10.80	9.63	6.95	25.36	3.55
65.	Mutant-6	40.67	69.00	42.13	4.77	5.83	11.37	10.00	7.14	37.42	4.08
66.	Mutant-7	42.00	70.67	34.93	3.27	4.10	11.27	10.17	8.55	31.15	2.61
67.	Mutant-8	41.33	69.67	38.97	4.13	3.43	11.83	10.70	9.23	35.82	3.91
68.	Mutant-9	38.00	67.67	27.70	4.63	4.87	11.60	10.33	9.01	31.32	4.31
69.	Mutant-10	40.00	68.33	25.73	4.37	3.50	10.13	9.80	8.80	21.65	2.83
70.	Mutant-11	39.67	72.33	40.17	4.47	5.13	11.33	11.17	7.91	20.01	3.96
71.	Mutant-12	39.67	69.33	49.07	4.83	4.43	12.53	11.17	10.30	16.66	3.33
72.	RC19	39.00	67.67	43.60	3.67	4.90	12.00	11.30	7.70	39.20	3.53
	Mean ($\overline{X}$)	**40.34**	**67.78**	**49.00**	**4.28**	**4.46**	**11.98**	**10.82**	**9.81**	**30.29**	**3.76**
	CV	**5.35**	**4.37**	**9.07**	**10.55**	**12.93**	**6.51**	**7.04**	**5.28**	**5.69**	**9.91**
	SEm±	**1.25**	**1.71**	**2.57**	**0.26**	**0.33**	**0.45**	**0.44**	**0.30**	**1.00**	**0.21**
	CD at 5%	**3.48**	**4.78**	**7.17**	**0.73**	**0.93**	**1.26**	**1.23**	**0.84**	**2.78**	**0.60**