GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN COWPEA [*Vigna unguiculata* (L.) Walp.]

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ABSTRACT

The present investigation entitles "Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]" was carried out to evaluate thirty genotypes of cowpea for seed yield and its component traits. The experiment was conducted in a randomized block design (RBD) with four replications at Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *kharif*-2021. The observations were recorded on traits under study *viz*., days to flowering, days to maturity, plant height (cm), number of branch per plant, number of pod per plant, number of seed per pod, pod length (cm), 100 seed weight (g), harvest index (%), protein content (%) and seed yield per plant (g).

The analysis of variance revealed that mean sum of squares due to genotypes was found significant for all the characters under study. This indicated the presence of adequate variability in the experimental material and the genotypes under study were genetically diverse. A broad range of phenotypic variability was estimated for seed yield and its components characters. On the basis of *per se* performance, best three genotypes identified *viz*., for days to flowering GC 2002, GC 2112 and GC 2007; for days to maturity GC 1501, GC 2002 and GC 2006; for lowest plant height GC 2121, GC 2118 and GC 2101, for highest plant height GC 2106, GC 2111 and GC 2113; for number of branch per plant GC 2109, GC 2116 and 2115; for number of pod per plant GC 2106, GC 2108 and GC 1501; for number of seed per pod GC 2118, GC 3 and GC 2103; for pod length GC 2108, GC 2106 and 2118; for 100 seed weight GC 2112, GC 2111 and GC 2113; for harvest index GC 2108, GC 2109 and GC 2118; for protein content GC 2002, GC 2007 and GC 2119 and for seed yield per plant GC 2108, GC 2109 and GC 2106. The values of phenotypic coefficient of variation (PCV) were slightly higher than that of genotypic coefficient of variation (GCV) for all the characters studied, indicating less influence of environment on the expression of characters under studied.

The moderate values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for 100 seed weight followed by harvest index, plant height, number of seed per pod, number of pod per plant and number of branch per plant this represented the presence of broad genetic variation for these characters and effective selection of traits is possible. Low values of GCV and PCV were observed for pod length, seed yield per plant, days to flowering, protein content and days to maturity,. This represented the presence of broad genetic variation for these characters.

The high values of heritability (broad sense) were observed in days to flowering, plant height followed by number of pod per plant, protein content, 100 seed weight, number of branch per plant, harvest index, number of seed per pod and days to maturity while, the heritability was moderate for seed yield per plant and pod length. It suggested that heritability may be due to higher contribution of the genotypic component in these characters.

The genetic advance expressed as percentage of mean values were observed high for 100 seed weight followed by harvest index, plant height, number of seed per pod, number of pod per plant, number of branch per plant. Moderate to high estimates of heritability values coupled with high genetic advance expressed as percentage of mean values were observed for 100 seed weight followed by harvest index, plant height, number of seed per pod, number of pod per plant, number of branch per plant. Moderate values of the genetic advance as percentage of mean was observed for pod length and low mean values were observed seed yield per plant, days to flowering, protein content, days to maturity. Which may be attributed to the prevalence of additive gene action which is fixable for governing the character and acquired high selective value and thus, selection pressure could profitably be applied on these traits for their judicious improvement. The selection may be effective for improvement of these traits.

The values of genotypic correlation coefficient normally, higher as compared to the proportionate phenotypic correlation coefficient. This stipulated that though there was high degree of association between the two variables at genotypic level and its phenotypic expression was collapsed by the effect of environment. The characters, seed yield per plant was found significantly high and positively correlated with number of seed per pod, number of pod per plant and pod length at both the genotypic and phenotypic levels. Thus, these characters were the most important traits and may impart considerably that respecting higher seed yield.

The genotypic path coefficient analysis estimated that pod length (1.1797), number of branch per plant (0.7733), number of seed per pod (0.4806) and number of pod per plant (0.3187) showed high and positive direct effect on seed yield per plant Plant height showed low and positive direct (0.1372) effect while, 100 seed weight exhibit negligible and positive direct (0.0708) effect on seed yield per plant. which are found to be the most important yield components. On the basis of path coefficient analysis, it can be concluded that improving seed yield per plant in cowpea, due consideration should be given to these characters during selection.

The genetic divergence was assessed by Mahalanobis D^2 statistics and grouped thirty genotypes of Cowpea into twelve clusters. The cluster II was the largest cluster having 9 genotypes followed by cluster I (6 genotypes), cluster III and V (3 genotypes), cluster VII (2 genotypes) and cluster IV, VI, VIII, IX, X, XI, XII (1 genotype). The perusal of intra- cluster and inter- cluster distance revealed that inter- cluster values were greater than intra- cluster distance values. The maximum inter- cluster distance (D^2 = 315.38) was found between cluster III and X followed by cluster XII and X (D^2 = 284.58). The minimum inter- cluster distance was observed between cluster I and II (D^2 = 72.10). The cluster IV, VI, VIII, IX, X, XI and XII contained single genotype therefore; its intra- cluster distance was Zero. Selections of parent based on large inter- cluster and intra- cluster distances for hybridization work gives a range of useful combination. Days to flowering followed by plant, 100 seed weight, number of pod per plant and protein content contributed maximum toward to the total divergence in seed yield. Based on the cluster mean value, cluster VII with genotypes GC 2106, GC 2108 were having more number of pod per plant, pod length, harvest index and seed yield per plant. The genotypes belonging to the clusters separated by high stastical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates and high heterosis. The genotypes with high value of any cluster can be used either for direct adoption for hybridization followed by selection.

An over view of the experimental results of present investigation indicated a wide spectrum of variation with respect to yield related traits among all the thirty genotypes of cowpea. From the foregoing discussion, it can be concluded that the characters coefficient of variation for GCV and PCV were found moderate for the following traits *i.e.*, 100 seed weight, harvest index, plant height, number of seed per pod, number of pod per plant and number of branch per plant. The high heritability coupled with high genetic advance was found for 100 seed weight, harvest index, plant height, number of seed per pod, number of pods per plant and number of branches per plant. This was due to less environmental influence and major effect of additive genes and therefore a selection of these traits will be more effective in improvement of crop. From the correlation and path coefficient analysis it is envisaged that number of pod per plant, number of seed per pod and pod length were most important traits which should be given more emphasis during selection programme for the improvement of seed yield in cowpea. Based on the relative magnitude of D^2 values, the thirty genotypes were grouped into twelve clusters. The cluster II exhibited maximum intera-cluster distance. Based on the genetic divergence studies, it was apprent that the maximum inter-cluster distance was observed between cluster X and III followed by X and XII indicating that the hybridization between the most diverse genotypes from these clusters would be desirable with the accumulation of favourable genes in the segregating generation. Days to flowering, plant height, 100 seed weight and number of pod per plant contributed maximum towards the total divergence in seed yield. Hence, selection for divergent parents, based on these characters would be useful for developing potential hybrids.

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CERTIFICATE – I

Date : 18/07/2022

This is to certify that the thesis entitled, **"GENETIC VARIABILITY AND CHARACTER ASSOCIATION IN COWPEA [*Vigna unguiculata* (L.) Walp]"** submitted for the degree of **MASTER OF SCIENCE (Agriculture)** in the subject of **GENETICS AND PLANT BREEDING** is a record of bonafide research work carried out by **PATEL KUNDANBEN SURYAKANT** under my guidance and supervision and that no part of this thesis has been submitted for any other degree, diploma, associateship, fellowship or other similar titles. The assistance and help received during the course of investigation have been fully acknowledged.

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Place: Sardarkrushinagar

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LIST OF ABBREVIATIONS AND SYMBOLS

\°**C**	Degree Celsius
ANOVA	Analysis of Variance
C.D	Critical Difference
C.V.	Coefficient of Variation
cm	Centimeter
Conti.	Continuous
Cov.	Covariance
CPCA	C. P. College of Agriculture
d.f.	Degree of Freedom
etc.	Etcetera
E	Environment
et al.	*Et allii* (and others)
Fig.	Figure
g	Gram
G	Genotype
GA	Genetic Advance
GAM	Genetic Advance as per cent Mean
GCV	Genotypic Coefficient of Variation
h^2**b.s**	Heritability Broad Sense
i.e.	That is
MS	Mean Square
NIR	Near Infrared
No.	Number
r	Replication
RBD	Randomized Block Design
r_g	Genotypic Correlation Coefficient
r_p	Phenotypic Correlation Coefficient
S.E.	Standard Error
S.Ed.	Standard Error of Difference
S.Em.±	Standard Error of Mean
SDAU	Sardarkrushinagar Dantiwada Agricultural University
Sr.	Serial
UPGMA	Unweighted Pair Group Method with Arithmetic Average
viz.	Which is (Namely)
e.g.	Example
vs.	Versus

σ^2_e	Variances due to Error
σ^2_g	Variances due to Genotype
σ^2_p	Variances due to Phenotype
σ^2_r	Variances due to Replication
Σp	Phenotypic Standard Deviation
=	is equal to
.	Full stop
×	Multiply
&	And
-	Minus
( )	Bracket
√	Square root
[ ]	Square bracket
,	Comma
%	Per cent
>	Greater than
<	Less than
@	At the rate of
/	Per
Σ	N-ray summation
σ	Sigma
;	Semi colon
:	Colon
µ	General Mean

I. INTRODUCTION

Pulse is a derivation from the the French word “Pottage” or “Poridge” meaning “soup (dal)”. The “Pulse Crop” generally refers to those legume species harvested primarily for dry seed that is used as both human food and animal feed. The word legume was derived from the Latin word “Legne” which mean “to collect or to gather” refers to collection of pods. Looking to the importance of pulses, the year 2016 was declared as the “International Year of Pulses” by the sixty eighth session of the United Nations General Assembly held on December 20, 2013 (FAO Report- 2019). This was done to raise awareness of the nutritional value of pulses, their contribution to sustainability and more reliable food. The fruit of a pulse crop is pod containing one to several seeds, which are high in protein, carbohydrates, fibre, minerals, and vitamins.

Cowpea [*Vigna unguiculata* (L.) Walp.], is an important multipurpose grain legume, which is widely grown under low input production system in arid region of the world. Cowpea is predominantly a self-pollinated crop, belonging to family *fabaceae* and sub family *faboideae* (Horn and Shimelis, 2020*)*. It is a short duration, photo and thermo-insensitive and most drought tolerant crop among the pulses. The primary centre of origin is an Africa (Vavilov, 1951). It is widely adopted and grown all over the world. It is commercially grown throughout India for its long green pods as a vegetable, seeds as pulses and foliage as fodder for milch animal. It is well fit in different cropping system such as cover crop, mix crop, catch crop and inter crop.

Cowpea has several vernacular names in different languages *viz*., black-eye pea, Southern pea, Lobia or Chawli (Hindi), Chowli or Choli (Gujarat), Bobbarlu or Alasandalu (Telugu), Karamani (Tamil), Chavli (Marathi) and Alasande (Kannada). The major cowpea growing countries are Nigeria, Niger, Ghana, Kenya, Uganda, Malawi, Tanzania, India, Sri Lanka, Burma, Bangladesh, Philippines, Indonesia and Thailand. In Indian context, it is a minor pulse cultivated mainly in pockets of Punjab, Haryana, Delhi, and West Uttar Pradesh along with considerable area in Rajasthan, Karnataka, Kerala, Tamilnadu, Maharashtra and Gujarat. Cowpea is cultivated in all the seasons in India. In Gujarat, it is mainly grown in Sabarkantha, Banaskantha, Mehasana, Patan, Ahemedabad, Kheda and Anand district. (Jat *et al*., 2013)

Cowpea can be grown in rainfed and irrigated condition. Because of its high protein content cowpea has been referred as “poor man’s meat”. The green tender pods contain moisture 84.6 per cent, protein 4.3 per cent, carbohydrate 8.0 per cent, fats 0.2 per cent and are also rich source of calcium, phosphorus and iron (Aykroyd, 1963). Nutrition content of mature cowpea is protein (24.8%), fat (1.9%), fibre (6.3%) and carbohydrates (63.6%) but thiamine, riboflavin and niacin are present in trace, (Davis *et. al.*, 2000). Cowpea grain contains lysine and tryptophane rich protein (Abadassi, 2015). Cowpea seed contain, on average, 53.2 ppm iron, 38.1 ppm zinc, 826 ppm calcium, 1915 ppm magnesium, 14,890 ppm potassium, and 5055 ppm phosphorus (Boukar *et al.*, 2011). It exerted health beneficial properties, including anti-diabetic, anti-cancer, anti -inflammatory and anti-hypertensive properties (Get *et al*., 2021).

Cowpea also perform well on a well-drained sandy loams or sandy soils from highly acidic to neutral condition or also performs wide variety of soils and is less tolerant in alkaline conditions (Duke, 1981). Cowpea germination is rapid at a temperature above 18°C with an optimum at 28°C (Craufurd *et al*., 1997). Seeds germination is epigeal with the cotyledons emerging from the ground. The first two leaves above cotyledons are simple and opposite, the others are alternate, petiolate and trifoliate (Pasquet and Baudoin, 2001). Peduncle that arises from the leaf axial contains commonly two or three pods and sometimes can carry four or more pods. Cowpea plant generally sets flowers 30 to 40 days after germinating with a life cycle of 60-240 days (Duke, 1981 and Miller *et al*., 1989).

Cowpea plants can be found erect, semi-erect, prostrate or climbing in their growing areas. Fruits of the cowpea plant vary in size, colour and texture; they can be erect, crescent-shaped or coiled and are usually yellow when ripe but can also be brown or purple in colour. The length of pod, which usually can reach 30 cm, contains 8-20 seeds that vary in size, shape and colour. Stems of cowpea plant are smooth or slightly hairy and sometimes tinged with purple colour. Orientation of stigma can be vertical or horizontal (Pasquet, 1993). Flowers are self-pollinating and arranged in raceme or intermediate inflorescence in alternate pair and can be white, dirty yellow, pink, pale blue or purple in colour. Length of flower ranges from 21 mmto 43 mm (Pasquet, 1993). In wild cowpea characteristics present such as perenniality, hairiness, small size of pods and seeds, pod shattering, outbreeding and bearded stigma. Cowpea primarily is self-pollinating, but outcrossing rates as high as 5 per cent have been recorded and care needs to be taken to prevent outcrossing during the production of breeder and foundation seed of cowpea (Timko *et. al. 2007*).

At present cowpea is grown over small acreage but potential possibilities exist to increase the area under this crop. There are several diverse uses of cowpea due to which the varietal requirement in terms of plant type, pod type, maturity, pattern of use and growth are required to develop to suit the diverse regions of the country. Therefore, in cowpea selection and evaluation programme has become more complex and no single variety can be recommended to full fill all the objectives (Barrett, 1987). Thus, there is a growing need to develop suitable varieties for a specific region and or use. However, the production is constrained by low and variable seed yield, seed quality, susceptibility to diseases and pests and the less availability of improved cultivars (Santos *et al*., 2014).

At Global level, the pulses are the second most important group of crops after cereals. In India pulses are grown nearly in 292.7 lakh ha with an annual production of 224.77 lakh tonnes and average productivity of 765 kg/ha (Annual Report-2019-20). In Gujarat, the area under pulses is 437.20 ha with annual production 365.70 tonnes and average productivity of 836.47 kg/ha (Annual Report-2019-20). It is, therefore, important to increase the productivity of pulse crops especially those of minor importance. The per capita per day availability of pulses in 2019 was 52.9 g per day. In India, cowpea is grown across the country primarily in southern zone. Banaskantha comes under 4th agroclimatic zone of Gujarat. Area and production of vegetable cowpea in Banaskantha district was 1950 hectare and 16575 MT, respectively (Annnual Report-2019-20)

In Gujarat, cowpea is one of the important vegetable legume crops because of its short period, high yield potential and quick growing habit along with high protein content. It is grown as an alternative crop in dry land farming because of its drought hardy nature that enables it to maintain some growth or at least survive even 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 even under the semi-desert conditions (Meena *et al*., 2015).

There are five subspecies of vegetable cowpea *viz, unguiculata*, *sesquipedali*s and *cylindrica* which are designated as cultivated and *dekindtiana* and *mensenensis* which are designated as wild (Verdcourt 1970).

Cowpea also provide fodder for livestock and improves soil fertility by fixing atmospheric nitrogen through root nodule rhizobia symbiosis. Cowpea makes considerable contribution to food and nutrition security in developing countries, especially India, as it is a cheap source of dietary protein and make up for the low protein present in widely consumed cereals and tuber crop- based food (Fatokun *et al.*, 2020). Due to unavailability of region-specific improved genotype/variety which can suit well in different cropping systems and have wider adaptability. Though the country has vast genetic variability for various traits, productivity for green pod yield has not been achieved to the highest level. Hence, the development of short duration, bushy and photo-thermo insensitive varieties/genotypes with high yield potential and quality are the main objectives for improvement in this crop.

The basic rational in any crop improvement programme is the increase yield potential. The character like yield has a complex gene action because of cumulative effect of other quantitative traits. To study it properly, different factors influencing the seed yield must be considered and evaluated with regard to their contribution towards the yield. The knowledge of variability presence in the breeding material due to genetic and non-genetic causes is a pre-requisite in the selection of the superior plant type. The information on association of attribute with seed yield and among themselves is of considerable importance in exercising selection programmes.

Good amount of diversity has been reported in cowpea for various characters, such as flowering, maturity, plant height, pods per plant, seeds per pod, length of pod, test weight, branches per plant, *etc.* It is therefore, felt necessary to study the genetic diversity in cowpea for improvement by utilizing desired traits in breeding programme. There are several diverse uses of cowpea due to which the varietal requirement in terms of plant type, pod type, maturity, pattern of use and growth are required to develop to suit the diverse regions of the country. Thus, there is a growing need to develop suitable varieties for a specific region. However, production is constrained by low and variable grain yield, grain quality, susceptibility to diseases and pests and abiotic stresses also. Thus, there is need to develop varieties suitable to fulfill all production constraints and regional requirements. Under such circumstances genetic diversity is of great importance and plays a crucial role in focusing crop improvement.

Selection of superior genotypes is proportional to the amount of genetic variability present and the extent to which the characters are inherited. Heritability indicates the relative degree to which a character is transmitted from parent to offspring. The magnitude of such estimates suggests the extent to which improvement is possible through selection. The success of any selection programme in segregating generations depends on the nature and extent of correlations between independent variables with dependent variables like yield and simultaneous selection can be carried out for more than one character to achieve the required improvement in seed yield.

Correlation and path analysis are important biometrical techniques to select traits of interest, which are heritable unless and until there is large amount of genetic variability present in the population, the breeder has little scope in breeding for high yielding varieties. The characters that are positively correlated with yield are considerably important to plant breeder for selection purpose.

Genetic diversity is very important for any crop improvement programme. The larger the genetic diversity in the crop is, more the opportunity will be for identification of the suitable parents for hybridization in the crop. Further, the genetics of the yield and its contributing traits needs to be well elucidated in a crop like cowpea, which is an autogamy by pollination, hybridization between selected parents is used to create variability. The selection of parents plays a crucial role in success of hybridization.

Multivariate analysis was done by using Mahalanobis D^2 statistic (Mahalanobis, 1936) and genotypes were grouped into different clusters following Tocher’s method (Rao, 1952). The magnitude of D^2 values suggested that there was considerable variability in the material studied, which led to genetic diversity. After testing the difference in regard to individual character through “Anova” a simultaneous test of significant difference with regard to the pooled effect of eleven characters was carried out using Wilk’s criterion (Wilk’s, 1932 and Rao, 1952).

Selection in different environment could cause greater diversity than geographical distance. Further, there was a free exchange of seed material among different regions consequently character constellations that might be associated with particular region in nature, lose their individuality under human interference.

Thus, the present investigation “Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]” aims to study genetic variability among genotypes of cowpea to achieve the target with following objectives:

1. To study the genetic variability, heritability and genetic advance for morphological traits in cowpea
2. To study the amount of genotypic and phenotypic correlation between seed yield and its attributing characters
3. To study the path analysis for assessing the direct and indirect effect of individual character on seed yield
4. To find out the genetic diversity through D^2 involving seed yield and its attributing character

II. REVIEW OF LITERATURE

The literature pertaining to the present investigation entitled "Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]" has been reviewed under following different aspects: -

2.1 Genetic variability

2.2 Heritability and genetic advance

2.3 Correlation and path analysis

2.4 Genetic divergence

2.1 Genetic variability

Variability refers to the presence of differences among the individuals of a population due to differences in their genetic constitution or the environment in which they are grown. Heritability can be defined as the ratio of the genotypic variance to phenotypic variance. Expected genetic advance represents the shift in a population towards superior side under selection pressure after single generation of selection for traits of interest.

Exploration of genetic variability in the available germplasm is pre-requisite for any successful breeding programme. The possibility of achieving improvement in any crop plants primarily depends on the magnitude of genetic variability.

Tyagi *et al.* (2000) studied genetic variability among twenty-four cowpea genotypes. High estimates for genotypic coefficients of variation were observed for days to 50 per cent flowering, plant height, seed yield per plant and days to maturity, indicating their dependability for effecting selections.

Rocha *et al.* (2003) studied genetic parameters in twenty-three white coat cowpea genotypes and evaluated the agronomic traits *viz.*, number of days to initial flowering, number of pod per plant, pod length, number of seed per pod, 100 – seed weight and seed yield. The traits recorded highest variability for seed yield (19.55%) and weight of 100- seed (16.87%).

Shahid *et al.* (2005) evaluated thirty-two genotypes of cowpea and estimated genetic variability for seven traits. Considerable variation was recorded for seed yield per plot, 100-seed weight, plant height, number of pod per plant, number of seed per 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 pod per plant, seed yield per plot and 100-seed weight.

Eswaran *et al*. (2007) studied the genetic variability with thirty genotypes of cowpea. The PCV ranged from 2.71 per cent for days to first flowering to 31.48 per cent for seed yield per plant. The PCV was high (>20%) for plant height at the time of first flowering, days to 50 per cent flowering, plant height at the time of 50 per cent flowering, seed yield per plant and total dry mater production. It was moderate (10-20%) for number of leaves at the time first flowering, number of first flowering node, height of first flowering node, height of first fruiting node, plant height at the time of 50 per cent maturity, 100 seed weight and harvest index. GCV revealed the same pattern of variability as shown by the PCV in general for all the characters. The characters' *viz.*, number of first flowering node, height of first flowering node, plant height at the time of first flowering, height of first fruiting node, plant height at the time of 50 per cent flowering, plant height at the time of 50 per cent maturity, 100 seed weight, seed yield per plant and total dry matter production showed moderately high GCV, there by suggestion that these characters could be improved genetically.

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

Adewale *et al.* (2010) studied the seed yield components of eleven cowpea genotypes to understand the sensitivity of the quantitative traits to heterozygous inherent environments. The genotypes differ significantly in seed yield and pods per plant. Significant (p 0.05) genotypic variation in pod length was recorded. Days to 50 per cent flowering, days to 95 per cent maturity, 100 seed weight and pod yield were significantly influenced by the effect of genotype, year and their interactions. Seeds per pod, 100 seed weight and pod length had fairly high relative genetic gain resulting from high GCV: PCV indicating their low sensitivity to G × E.

Futuless and Bake (2010) studied yield and yield attributes of some cowpea varieties in 2009 to determine their seed yield attributes. Data were collected on plant height, number of leaves per plant, number of branch per plant per plant, number of days to flowering, pod filling period, days to physiological maturity, pods per plant, pod length, number of seed per pod, number of pod per plant, 100 seed weight and yield per hectare. The result showed a significant difference in plant height, number of leaves per plant, number of seed per pod, number of pod per plant and no significant difference was recorded in number of branch per plant, days to flowering. Most of the yield and yield determining attributes recorded significant difference due to treatment effects.

Shimelis and Shiringani (2010) studied on genetic variability of genotypes of cowpea. The results indicated significant interactions was observed among genotypes, locations and planting dates. Genotypic variance attributed considerably i.e., ≥50% to the total phenotypic variations for days to 50 per cent flowering (50%), days to maturity (66%), numbers of productive branches per plant (53%) and seed yield (55%). A relatively greater proportion of the phenotypic variation was attributed to genotype by planting date by location interaction variance (44%) and genotype by location interaction variance (67%) for the numbers of pods per plant and hundred seed weight, respectively. The presence of considerable degree of genotypic variance among tested genotypes under various environments suggests that success in cowpea breeding could be achieved through direct phenotypic selection. Further, genotype by plating date by location interaction variance contributed a significant proportion (40%) of the total phenotypic variation in seed yield following the genotypic variance.

Manggoels *et al.* (2012) studied ten diverse accessions of cowpea for the genetic variability for yield components. The accessions showed significant variability for days to 50 per cent flowering, number of peduncles per plant, flowers per plant, pods per plant seeds per pod, pod length, 100 seed weight and seed yield. They reported the genotypic variance of these traits were higher than the environmental variance, indicating that the genotypic component was the major contributor to total variance. Phenotypic coefficient of variation and genotypic coefficient of variation were high for the traits studied, days to 50 per cent flowering, number of peduncles per plant, flowers per plant, pods per plant, seeds per pod, pod length, 100 seed weight and seed yield except pod length and seeds per pod.

Nwofia *et al.* (2012) observed genetic variability of different cowpea genotypes for yield traits to identify and select genotypes with adequate trait combination for yield improvement. Analyses of variance showed that number of seed per pod, seed weight per pod, pod length, number of branch per plant per plant, number of leaves per plant, seed yield studied in 2010 showed highly significant differences among the genotypes, while in 2011 number of seed per pod, number of pod per plant, dry matter, pod length, number of branch per plant per plant, plant height, number of leaves per plant, seed yield the attributes were highly significant except seed weight per pod that was significant at 5%.

Khan *et al.* (2013) studied the segregating populations of C-152 × V-16 cross and showed high PCV % estimates for plant height, number of branch per plant per plant, number of seed per pod, seed yield per plant and number of pod per plant. But, GCV % estimate was high for the traits like number of pod per plant and seed yield per plant.

Kumar *et al.* (2013) studied phenotypic coefficient of variation and genotypic coefficient of variation for ten quantitative characters in forty genotypes of cowpea originated from different sources. Based on the analysis, it was observed that seed yield and number of clusters had high PCV, GCV which suggested that direct selection for these traits would be fruitful in genetic improvement of cowpea. Also, morphological variations on flower colour, seed colour and seed size releaved that much variations were present in these characters. Seed colour ranged from buff, tan, cream, white, mottled, brown, dark brown and black. Flower colour *viz*., white, yellow, light violet, dark violet, shades were found in the genotypes studied.

Nwosu *et al.* (2013) studied genetic variability with five genotypes of cowpea cultivated at two agroecological environments. Analysis of variance revealed that though there was no significant interaction among the genotypes for most of the characters studied, they varied significantly for plant height, number of branch per plant per plant, days to 50 per cent flowering, days to maturity, clusters per plant, pods per cluster, pods per plant, peduncle length, pod length, dry pod weight, 100 seed weight, seeds per pod, number of seed per plant and seed yield. All the characters at each of the two locations, indicating the existence of considerable variation for these the characters. Considerable amount of genotypic and phenotypic coefficient of variation was observed for given characters.

Bhardwaj *et al*. (2014) evaluated sixty genotypes of cowpea for eleven morphological traits *viz*., plant height, leaf length, leaf width, number of branch per plant, stem girth, number of leaves, number of pod, seeds per pod, pod weight, 100 seed weight and seed yield per plant. The high range of variability was observed for plant height (117.2–261.5), number of leaves (194–568), pod weight (10–105) and seed yield per plant (3.12- 225.05) while rest of the traits showed medium range of variability. The highest value of PCV (Phenotypic coefficient of variation) and GCV (Genotypic coefficient of variation) were recorded for seed yield per plant (108.91, 108.86) followed by number of pod (66.12, 65.05), pod weight (49.1, 48.37) and 100- seed weight (28.88, 27.92).

Sapara and Javia (2014) studied genetic variability of forty genotypes of cowpea for twelve traits *viz*., days to 50 per cent flowering, days to first pod picking, number of primary branches per plant, plant height, pod length, pod width, number of pod per plant, ten pod weight, number of fresh seeds per pod, 100 fresh seed weight, green pod yield per plant and fresh pod crude protein content. Significant differences among the genotypes for all the characters studied except pod width indicating existence of ample variability in the experimental material for days to 50 per cent flowering, days to first pod picking, number of primary branches per plant, plant height, pod length, pod width, number of pod per plant, ten pods weight, number of fresh seeds per pod, 100-fresh seeds weight and fresh pod crude protein content. The estimates of genotypic and phenotypic co-efficient of variation were high for number of pod per plant, 100 fresh seed weight, plant height, 10 pod weights and green pod yield per plant. The values of phenotypic co-efficient of variation were higher than their genotypic co-efficient of variation for all the characters indicating the influence of environmental factors.

Shanko *et al.* (2014) observed adequate variability among forty-nine genotypes of cowpea. High phenotypic and genotypic coefficient of variation estimated for the characters *viz*., yield per plant, number of pod per plant and 100-seed weight indicated the scope of improvement of these characters through selection.

Vir and Singh (2014) estimated high degree of genetic variability during *kharif* and *rabi* season for seed yield per plant, 100 seed weight, pod length, number of seed per pod, number of pod per plant, number of pod per cluster, number of branch per plant per plant, number of clusters per plant, plant height, number of days to 50 per cent flowering and number of days to maturity.

Animasaun *et al.* (2015) studied ten cultivars of cowpea grown in the screen house and evaluated for genetic similarity and variability. Data were collected on vegetative, fruiting and seed characters. Proximate analysis was conducted to determine variation in nutrient composition of the seeds at harvest. The results showed considerable variations in growth and yield characters like, plant height, number of leaves, leaf length, leaf breath, stem girth, number of branch per plant per plant, number of flowering, number of days to 50 per cent flowering. Cultivars NGB/06/047, IFE BROWN 2012 and IT98K-133-1-1 had optimal growth performance with respect to fruiting and seed yield parameters. Proximate results indicated that crude protein varied from 23.42-26.78%. Ash content ranged between 3.60-4.21%, crude fiber varied from 2.10-2.98% and carbohydrates 56.10-59.59%.

Gerrano *et al.* (2015) studied genetic and phenotypic variability among the twenty-five cowpea genotypes. The experiment was laid out in a randomised complete block design with three replications. Analysis of variance for the phenotypic traits revealed that differences among genotypes were highly significant for days to 50 per cent flowering, leaf number, leaf length, leaf width, leaf area, leaf area index, number of branch per plant, plant height, fresh biomass, dry bio mass, number of pod per plant, pod length, harvest index, number of seed per pod, hundred seed weight and yield per plant. This indicated the high level of genetic variability among the cowpea genotypes studied. Genetic and phenotypic coefficient of variation were estimated for all phenotypic traits.

Khan *et al.* (2015) carried out genetic variability of one hundred ninety-six cowpea set genotypes and analysis of variance revealed significant differences among the genotypes tested for number of days to flowering, days to maturity, number of pod per plant, pod length, plant height, number of branch per plant per plant, test weight, harvest index and seed yield per plant were observed. The genotypes exhibit considerable amount of genetic variation for all the characters and it indicated the good scope for selection of suitable basic material for further improvement. PCV values were of higher magnitude than GCV for all the characters under study. The estimates of PCV and GCV were high for number of pod per plant, pod length, plant height, number of branch per plant per plant, test weight and seed yield per plant.

Khanpara *et al.* (2015) studied genetic variability in sixty diverse genotypes of vegetable cowpea. The results revealed that significant differences among the genotypes were found for days to 50 per cent flowering, days to first green pod picking, number of primary branches per plant, plant height, pod length, pod width, number of seed per pod, number of pod per cluster, pod weight, hundred fresh seed weight, number of pod per plant and green pod yield per plant. The highest range of variation was observed for green pod yield per plant followed by ten pod weight, number of pod per plant and plant height. Higher values of PCV than GCV were observed for green pod yield per plant, number of pod per plant, pod length and number of seed per pod which indicated partly interaction of the genotypes with the environment or other environmental factors influencing the expression of these characters. The values of PCV and GCV were more or less equal in the remaining characters which indicated that these characters were less influenced by the environment.

Chandrakar *et al*. (2016) studied genetic variability in twenty-one genotype of vegetable cowpea including checks, the data recorded on twenty-one characters were subjected to analysis of variance. The analysis of variance revealed highly significant differences among the genotypes were observed for plant height, number of branch per plant, first node of flowering, first flowering, 50 per cent of flowering, number of flower per plant, number of pod per plant, pod length, pod weight, days to first picking, pod setting per cent in cluster, 100 dry seed weight, fruiting duration 100 green seed weight, days to maturity and green pod yield except pod width. It indicates that sufficient variability exhisted among the genotype for the mentioned characters. The GCV value was higher for plant height, pod yield per plant indicated that these characters exhibited variability among the genotypes.

Nguyen *et al*. (2017) high genotypic coefficient of variation and phenotypic coefficient of variation was observed for biological yield per plant, followed by plant height, harvest index, number of clusters per plant, pod yield per plant, seed yield per plant, number of pod per plant, number of branch per plant per plant, pod weight and days to 50 per cent flowering of cowpea genotype. Considerable amount of genetic variability was present in the experimental material, which could be exploited for improvement of cowpea.

Sarath and Reshma (2017) studied genetic variability for twelve characters of twenty-two genotype of cowpea. The high degree of variability was observed for all the characters. High magnitude of the phenotypic coefficient of variation and genotypic coefficient of variation were observed for plant height, grain yield per plant and length of the pods. Seeds per pod and protein content exhibited low PCV and GCV. The difference between the phenotype coefficient of variation and genotype coefficient of variation were found maximum in pod weight (30.15%), followed by number of pod per plant (18.12%) and test weight (16.27%).

Sharma *et al.* (2017$_a$) observed genetic variability in thirty cowpea genotypes for days to 50 per cent flowering, number of flowers per plant, days to maturity, plant height, number of primary branches per plant, number of pod per plant, number of cluster per plant, test weight, seed yield per plant and harvest index. The estimates of genotypic parameters revealed that differences between the estimates of GCV and PCV were found least for to 50 per cent flowering, number of flowers per plant, days to maturity, number of pod per plant, number of cluster per plant and harvest. Higher estimates of GCV and PCV were observed for plant height, primary branches per plant, seed yield per plant and test weight.

Srinivas *et al.* (2017) studied genetic variability among thirty genotype of cowpea. Significant differences among the genotypes for all the characters indicating existence of ample variability in the experimental material for all the characters. High to moderate range of variation was observed for important yield components. The estimate of genotypic and phenotypic coefficient of variation were high for number of branch per plant per plant, pod yield per plant, total number of pod per plant, number of seed per pod. The values of phenotypic coefficient of variation were higher than their genotypic co-efficients of variation for all the characters indicating the influence of environmental factors.

Benjamin *et al.* (2018) studied genetic variability among twenty wild cowpea accessions. The experiment was laid in a randomized complete block design with five replicates and assessed for agro-morphological and yield parameters. The results showed significant deference in length of pod, number of pod per plant, number of seed per plant, 100 seed weight, days to first flowering, days to harvest of the morphological parameters studied. The high morphological variability observed among the wild cowpea in this study indicated the presence of good and useful traits in the crop which could be explored for its improvement.

Bhagavati *et al.* (2018) studied genetic variability among twenty-four genotypes of cowpea [*vigna unguiculata* (L) walp s.sp *sesquipedalis* verdc.]. They reported PCV was greater than GCV for all the characters indicating the influence of environment in the expression of traits. High PCV and GCV were observed for the traits like number of primary branches per plant, pod length, number of pod per plant, ascorbic acid content, 100 seed weight, pod yield per plant, pod yield per plot and pod yield per hectare.

Das *et al.* (2018) studied genetic variability in cowpea genotype, analysis of variance for the characters revealed that highly significant variations among the genotypes for yield and yield attributing characters. Further, it was observed that the parents, crosses as well as parents vs. crosses showed significant variations for pod length, seeds per pod, pods per cluster and plant height which indicated considerable effect of environment for these characters studied. Among the parents JCC-4 showed the best mean performance for seed yield per plant. Among the cross JCC-1 × JCC-4 exhibited the highest mean performance for seed yield per plant. Highest GCV was obtained for plant height.

Devi and Jayamani (2018) studied genetic variability in One hundred and eighty genotypes of cowpea, analysis of variance revealed that significant difference existed among the genotypes for the traits plant height, number of primary branches per plant, days to flowering, number of recemes per plant, peduncle length, number of pod per plant, number of cluster per plant, number of pod per cluster, days to maturity, pod length, number of seed per pod, hundred seed weight, single plant yield studied. The phenotypic coefficient of variation was higher than genotypic coefficient of variation for all the traits studied. The high estimates of GCV was found in traits *viz.*, number of pod per plant, number of clusters per plant, hundred seed weight and single plant yield. The high degree of variability was observed among the genotypes for different yield contributing traits. This could be utilized in the breeding programme for the improvement of cowpea.

Havaraddi and Deshpande (2018) studied genetic variability in advanced stabilized lines of cowpea using thirty genotypes along with two checks *viz.*, DC 15 and DCS 47-1 for eight quantitative characters. They found high range of variation for characters *viz.*, seed yield, days to fifty per cent flowering, plant height and number of pod per plant. High PCV and GCV values were recorded for the traits seed yield and number of pod per plant. Plant height showed moderate PCV and GCV values whereas, remaining traits exhibited low to moderate PCV and GCV values.

Kumar *et al*. (2018) studied for variability in cowpea, the results revealed that the phenotypic coefficient of variation was higher than their respective genotypic coefficient of variation for the traits plant height, number of primary branches per plant, number of branch per plant per plant, days to first open flower, number of pod per plant, days to first pod picking, pod length, pod diameter, number of pod per peduncle, pod weight per plant, pod yield per plot, peduncle length, number of peduncle per plant, duration of reproductive phase, number of seed per plant, number of seed per pod, 100 seeds weight, vitamin A and vitamin C studied. The widest range was recorded for pod yield per plot (3581.00- 3825.00) followed by number of seed per plant (236.97-312.73), pod weight per plant (g) (360.74-390.25), number of pod per plant (39.33-49.41), plant height (27.89-32.35), days to first open flower (40.76-45.98) and duration of reproductive phases (30.15-36.78). Phenotypic coefficient of variation was higher for number of primary branches (23.54%) followed by number of pod per peduncle (18.16 %), peduncle length (17.32 %), pod diameter (10.99 %), pod length (9.39 %), number of branch per plant per plant (8.87 %) and number of pod per plant (7.98 %). Highest genotypic coefficient of variation was observed in number of primary branches (22.81% high) followed by number of pod per peduncle (17.26 % moderate), peduncle length (16.31 % moderate), pod diameter (9.62 % low), number of branch per plant per plant (7.96 % low), number of seed per plant (7.68 % low) and pod length (7.60 % low).

Nair *et al.* (2018) studied genetic variability among twenty-five F_2 interspecific hybrids of cowpea and their fourteen parents for different fourteen traits. They reported phenotypic coefficient of variation was greater in magnitude over respective genotypic coefficient of variation for the characters *viz*, plant height, number of primary branches per plant, days to first flower, days to maturity, pod length, number of seed per pod, number of pod per cluster, number of cluster per plant, number of pod per plant, green pod yield per plant, dry pod yield per plant, 100 seed weight, harvest index, seed yield per plant studied. The estimate of PCV and GCV were high for plant height and green pod yield per plant.

Sabale *et al.* (2018) studied variability in twenty-three F_2 generations of cowpea genotypes. The results revealed that phenotypic coefficient of variation was greater than the genotypic coefficient of variation for the characters *viz.*, days to first flowering, days to maturity, plant height, number of primary branches per plant, number of cluster per plant, number of pod per cluster, number of pod per plant, pod length, number of seed per pod, hundred seed weight, harvest index and seed yield per plant. The high phenotypic and genotypic coefficient of variation was observed for seed yield per plant, number of pod per plant, number of clusters per plant and number of primary branches per plant, while lowest GCV and PCV was observed for days to first flowering and days to maturity.

Thouseem *et al*. (2018) studied on genetic variability in cowpea. The phenotypic coefficient of variation was found higher than the genotypic coefficient of variation for the traits days to 50 per cent flowering, number primary branches per plant, length of main stem, number of pod cluster per plant, number pod per cluster, number pod per plant, pod weight, pod length, pod girth, number of seed per pod, 100 seed weight, seed yield per plant and crop duration studied. The highest magnitude of GCV was observed for pod weight followed by number of pod clusters per plant, seed yield per plant, 100 seed weight, pod length, number of pod per cluster and number of pod per plant.

Gupta *et al.* (2019) studied genetic variability in cowpea among twenty-seven genotypes of cowpea were sown in randomized block design with three replications for eighteen characters. Analysis of variance showed that significant difference among the genotypes for the characters *viz*. seed germination, plant height, number of branch per plant per plant, days to first flowering, first flowering node, number of nodes on main stem, peduncle length, number of pod per cluster, days to first picking, pod length, pod diameter, average pod weight, number of pod per plant, number of seed per pod, test weight, pod yield per plant, pod yield and pod borer infestation percentage indicated the diverse genetic nature of base population. The coefficient of phenotypic variation was slightly greater than those of genotypic variation for almost all the characters showed that the existing variation is mainly governed by the genotypic factor and there is little influence of environment in the expression of the character.

Magashi *et al*. (2019) studied genetic variability for quantitative traits in seven varieties of cowpea, the results indicated that highly significant difference in the plant height, number of days to 50 per cent flowering, number of days to maturity, number of pod per plant, pod length, number of seed per plant and 100 seed weight and significant at seedling height and number of branch per plant per plant. Similarly, IAR1074 was found high performance in terms of most of the quantitative traits under study. However, sampea 8 has the highest mean performance at nutritional level (carbohydrate and protein content). It was concluded that, all the seven cowpea genotypes were water stress tolerant and produced considerable yield that contained significant nutrients. It was recommended that IAR1074 should be grown for yield, while sampea 8 should be grown for protein supplements.

Meenatchi *et al.* (2019) studied genetic variability parameters *viz.*, phenotypic coefficient of variation (PCV) and genotypic coefficient of variation for yield and yield attributing traits such as days to 50 per cent flowering, plant height, number of clusters per plant, number of branch per plant per plant, number of pod per plant, pod length, number of seed per pod, hundred seeds weight and seed yield per plant in nine F_2 populations of cowpea genotypes. High level of PCV and GCV were observed for number of branch per plant per plant, number of clusters per plant, number of pod per plant and single plant yield. Low level of PCV and GCV were obtained for all the crosses except for cross CO4 × VCP-09-024. Results suggest that quantitative traits like number of branch per plant per plant, number of clusters per plant, number of pod per plant and single plant yield can be used as selection criteria for yield improvement in F_2 population of cowpea.

Nkoana *et al.* (2019) studied genetic variability to evaluate agronomic performance of twenty-eight cowpea germplasm and select the candidate accessions for breeding population and cultivation by small-scale farmers in South Africa. Data were collected on the agronomic traits including days to 50 per cent flowering, days to 95 per cent maturity, hundred seed weight, leaf area index, number of branch per plant per plant, number of internodes per plant, number of seed per plant, plant height, number of pod per plant, pod length, dry biomass weight per plant, seed yield per plant and grain yield per hectare. Highly significant differences were observed among the accessions for the trait days to 50 per cent flowering, days to 95 per cent maturity, hundred seed weight, leaf area index, number of primary branches, number of internodes per plant, number of seed per pod, plant height, number of pod per plant, pod length, dry biomass weight per plant, grain yield per plant and grain yield per hectare. The seed yield per hectare correlated positively and significantly with number of pod per plant and grain yield per plant showing a scope for simultaneous improvement of yield and yield related traits.

Sharma *et al.* (2019) studied genetic variability for twenty-two diverse genotype of cowpea. Maximum phenotypic and genotypic coefficients of variation were observed for seed yield per plant followed by number of clusters per plant, number of pod per plant, pod length, number of seed per pod, green pod weight per plant and plant height. This indicated the presence of high magnitude of genetic variability in the material for these characters.

Verma *et al.* (2019) studied genetic variability in F_2 generation of twenty-four hybrids of cowpea and observed. Wide range of variability was observed for plant height, number of branch per plant per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seed per pod, 100 seed weight and pod yield per plant, except number of branch per plant per plant and pod width. The high genotypic coefficient of variation and phenotypic coefficient of variation was recorded for characters like number of pod per cluster (PCV only), number of pod per plant, pod weight and 100 seed weight indicating high variability available in the germplasm for these characters for further improvement. Moderate GCV and PCV was observed for plant height, number of branch per plant per plant, flowers per cluster, pods per cluster (GCV only), percent pod set, pod length, pod width (PCV only), number of seed per pod and low GCV and PCV recorded for pod yield per plant, plant height, branches per plant, pod length and seeds per pod whereas, days to first flowering, days to 50 per cent flowering, days to first harvest, days to last harvest and pod width (GCV only)

Yadav and dudduker (2019) studied thirty cowpea genotypes along with one check (Pant lobia-5) for genetic variability. Analysis of variance showed highly significant differences among (29+1check) cowpea genotypes for thirteen yield contributing characters studied. Highest genotypic and phenotypic coefficient of variation were recorded for pods per plant, primary branches per plant, pod length and plant height, thus scope for genetic improvement through selection for these characters. Moderate for days to 50 per cent fowering, clusters per plant, seeds per pod, seed index, seed yield per plant and low for days to 50 per cent pod filling, days to maturity, biological yield per plant and harvest index.

Chaudhary *et al.* (2020) studied genetic variability for yield and yield attributes of thirty cowpea cultivars in randomized block design with three replications and reported genotypic coefficient of variation and phenotypic coefficient of variation were observed highest for seed yield per plant (55.51% and 57.14% respectively) followed by number of pod per plant (45.49% and 47.42% respectively), leaf area per plant (38.15% and 39.34% respectively) and number of seed per pod (20.74% and 23.56% respectively). Moderate estimates of genotypic and phenotypic coefficient of variation were observed for test weight, pod length and number of branch per plant per plant. While lowest estimates of genotypic and phenotypic coefficient variation were observed for plant height, days to maturity, days to flowering and protein content.

Pandiyan *et al.* (2020) studied phenotypic and genotypic variability of twenty-eight cowpea entries for days to 50% flowering, days to maturity, plant height, number of pod per plant, number of cluster per plant, number of seed per pod, 100 seed weight and seed yield. The highest range of genotypic and phenotypic coefficient of variation in the yield attributing parameters like number of pod per plant and number of cluster per plant in the selected genotypes is highly essential for plant breeding. Moderate PCV for days to 50 per cent flowering, plant height, number of seed per pod, 100 seed weight and low for days to maturity.

Purohit *et al.* (2020) studied forty-two genotypes including five checks of seed cowpea. Analysis of variance showed the presence of significant amount of variability in all the characters *viz*., days to 50 per cent flowering, plant height, leaf length, leaf width, peduncle length, pod length, number of pod per cluster, number of pod per plant, number of seed per pod, 100 seed weight, protein content, yield per plant, yield per plot and yield per hectare. The estimate high phenotypic and genotypic variance was observed for yield per hectare. High estimate of PCV and GCV was observed for yield per plot.

Ugale *et al*. (2020) studied genetic variability in thirty-one genotypes of cowpea. The observations were recorded on 12 characters *viz.*, plant height, number of primary branches per plant, days to 50 per cent flowering, number of pod per plant, number of seed per pod, mean pod weight, pod length, pod width, days to first pod harvest, 100 seed weight (g), pod yield per plant, pod yield per hectare. Analysis of variance and mean performance for pod yield and its components revealed significant differences among all the genotypes for all the characters there by indicating presence of variability in genotypes studied. GCV and PCV values were at par with one another for most of the characters which indicated that the influence of the environment on the trait was very negligible. The genotypic and phenotypic coefficient of variation were high (>20%) for the characters pod yield per hectare, plant height, number of primary branches per plant, pod length. Moderate (10-20%) for number of pod per plant, number of seed per pod, 100 seed weight and low (<10%) for day to 50% flowering, mean pod weight, pod width, days to first pod harvest and pod yield per plant. The differences between PCV and GCV values were less indicating that these traits were less influenced by environment and could be improved by following phenotypic selection.

Panchta *et al.* (2021) studied fourteen genotypes of cowpea for genetic variability. The genotypes were found significantly different for all the characters, which indicated scope for further genetic studies. The phenotypic coefficient of variation estimates was invariably higher than their corresponding genotypic coefficient of variation values. High GCV and PCV were observed for seed yield per plot, days to 50% flowering, days to maturity and plant height suggesting that selection based on these characters would facilitate successful isolation of desirable types.

Thapa *et al.* (2021) studied the genetic variability in twelve cowpea genotypes and revealed that all the genotypes were significantly different for an early stand, 50 per cent flowering days, 90 per cent maturity days, pods per plant, seeds per plant, final plant stand, 100 seed weight, grain yield except for plant height. Genotypes such as IT10K-815-5, IT10K-973-1, IT82-1337 and IT10K-973-1 were promising cowpea genotypes having high PCV for traits such as seeds per pod, pods per plant, plant height and grain yield, considered for selection in further yield improvement program. Moderate for 50 per cent flowering days, hundred seed weight and low for early stand, 90 per cent maturity days, final stand.

Yasin *et al.* (2021) studied genetic variability among thirty-six cowpea genotypes based on morpho-agronomic traits. Analysis of variance for fourteen quantitative traits showed significant differences among the cowpea genotypes. High phenotypic and genotypic coefficient of variation for seed yield, biomass yield, plant height, number of secondary branches per plant, number of pod pet plant, number of seed per plant. Moderate for hundred seed weight, harvest index, pod length, number of seed per pod and low for days to first flower opening, days to 50 per cent flowering, days to maturity.

2.2 Heritability and genetic advance

Heritability is a good index of the transmission of quantitative characters from parents to their offspring, it has relative role in heredity in the expression of phenotypes (Falconer, 1989 and Allard, 1961).

Roquib and Patnaik (1990) reported high estimates of heritability (broad sense) and genetic advance in cowpea for plant height, number of seed per pod, primary branches, pod length and breadth, days to 50 per cent flowering and maturity and seed yield per plant. The estimates of heritability in the broad sense and genetic advance were high for plant height at days to maturity, lateral leaflet area and days to 50% flowering but genetic advance estimates were moderate for terminal leaflet area and effective root nodules on main root 65 days after sowing.

Tyagi *et al.* (2000) reported high heritability and genetic advance for days to 50 per cent flowering, plant height, seed yield per plant and days to maturity, indicating their dependability for effecting selections.

Shahid *et al.* (2005) observed high heritability coupled with high genetic gain for plant height, number of pod per plant, seed yield per plot and 100-seed weight indicating the of additive gene effects for these traits.

Eswaran *et al.* (2007) observed 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 effective selection.

Adewale *et al.* (2010) reported high heritability and genetic advance in cowpea. Heritability (broad sense) for days to 95 per cent maturity, number of pod per plant, number seeds per pod, 100 seed weight, days to 50 per cent flowering, pod yield, grain yield and pod length and also reported that seeds per pod, 100 seed weight and pod length had fairly high relative genetic gain resulting from high heritability and repeatability, indicating their low sensitivity to G × E interaction.

Shimelis and Shiringani (2010) observed high heritability for days to maturity (66%); moderate for seed yield per plant (55%), number of branch per plant per plant (53%), days to 50 per cent flowering (50%) and low for number of pod per plant (23%) and 100 seed weight (11%). The relatively moderate to high heritability values for some of the traits were noted owing to the greater contribution of genotypic variance among the tested lines. Accordingly, cowpea breeders can achieve higher selection efficiency through direct phenotypic selection for reduced days to 50 per cent flowering and maturity, increased productive branches per plant and high seed yield. The low heritability of the number pods per plant and hundred seed weight necessitates indirect selection via other agronomic traits.

Manggoel *et al.* (2012) studied ten diverse accessions of cowpea for the heritability and genetic advance for different traits like days to 50 per cent flowering, number of peduncles per plant, flowers per plant, pods per plant, seeds per pod, pod length, 100-seed weight and grain yield. They reported high broad sense heritability (63.16- 96.74%) indicated the presence of additive gene effects.

Khan *et al.* (2013) noticed high heritability for test weight, number of branch per plant per plant and seed yield. The genetic advance as a percentage of mean estimates were high for the traits plant height, number of branch per plant per plant, flowers per cluster, pods per cluster, per cent pod set, days to last harvest, pod length, pod weight, number of seed per pod, 100 seed weight and pod yield per plant except pod width.

Kumar *et al*. (2013) studied heritability and genetic advance for ten quantitative characters in forty genotypes of cowpea from different sources. Based on the analysis, they observed seed yield and number of clusters per plant had high heritability and genetic advance as percent of mean, which suggested that direct selection for these traits would be fruitful in genetic improvement of cowpea.

Nwosu *et al.* (2013) studied five genotype of cowpea for heritability and genetic advance as per cent of mean. They reported that high heritability with genetic advance as a per cent of mean for clusters per plant, pods per plant, peduncle length, pod length, dry pod weight, hundred seed weight, seeds per pod, number of seed per plant and seed yield per plant indicating that these traits were controlled by additive genetic effects and could be dependable for grain improvement in cowpea.

Thorat and Gadewar (2013) studied thirty genotypes of cowpea for heritability and genetic advance. Almost all fifteen characters *viz.*, days to 50 per cent flowering, days to maturity, plant height, number of branch per plant per plant, leaf area index, chlorophyll content (45 DAS), chlorophyll content (65 DAS), protein content %, number of cluster per plant, number of pod per plant, pod length, number of seed per pod, 100 seed weight, seed yield per plant and seed yield per plot showed high heritability values. High heritability coupled with high genetic advance was observed for plant height, number of pod per plant and number of branch per plant per plant.

Pandey e*t al.* (2014) observed higher estimates of heritability coupled with the higher genetic advance for plant height, number of peduncles per plant, number of pod per plant and pod yield per plant indicated that these traits are under the control of additive genes in cowpea.

Sapara and Javia (2014) studied heritability and genetic advance of forty cowpea genotypes for twelve traits and reported high heritability along with high genetic advance expressed as percentage of mean for the characters number of primary branches per plant, plant height, pod length, pod width, number of pod per plant, ten pod weight, number of fresh seeds per pod, 100 fresh seed weight, green pod yield per plant and fresh pod crude protein content.

Shanko *et al.* (2014) observed heritability and genetic advance in forty-nine diverse cowpea genotypes. The estimates of high heritability in broad sense and genetic advance for the characters *viz.*, yield per plant, number of pod per plant and 100-seed weight indicated the scope of improvement of these characters through selection.

Vir and Singh (2014) reported the moderate to high heritability coupled with moderate to high expected genetic advance for days to flower, number of pod per plant and pod yield per plant in cowpea.

Khan *et al.* (2015) evaluated cowpea genotype for heritability and genetic advance as per cent of mean. They reported high heritability with high genetic advance as per cent of mean for number of pod per plant, number of seed per pod, pod length, plant height, number of branch per plant per plant, test weight and seed yield per plant. These characters are governed by additive gene action and one should go for direct selection for these traits to improvement in future.

Khanpara *et al.* (2015) revealed high heritability along with high genetic advance for green pod yield per plant, plant height, pod length, pod width, number of seed per pod, number of pod per plant, ten pod weight, number of pod per cluster and hundred fresh seed weight indicating that these traits were mainly governed by additive gene action.

Chandrakar *et al.* (2016) studied variability in cowpea genotypes and highest heritability was recorded for the characters plant height (60 DAS), days of maturity, fruiting duration, 50 per cent flowering, pod setting per cent per plant, 100 dry seed weight and 100-green seed weight.

Nguyen *et al*. (2017) reported high heritability coupled with high genetic advance for characters *viz*., biological yield per plant followed by plant height, harvest index, number of clusters per plant, seed yield per plant, pod yield per plant, number of branch per plant per plant, pod weight, days to 50 per cent flowering, 100 seed weight, number of seed per pod, days to maturity and pod length indicated additive gene effects. Hence, simple selection could be effective for further improvement in these characters.

Sarath and Reshma (2017) studied heritability and genetic advance as a per cent of mean for twelve characters in cowpea. They reported high magnitude of heritability and genetic advance for plant height, seed yield per plant and length of pods. Seeds per pod and protein content exhibited high heritability and low genetic gain.

Sharma *et al* (2017_a) observed maximum heritability and genetic advance for test weight followed by plant height, biological yield per plant, seed protein content, primary branches per plant and pods per plant. These characters are governed by additive gene action and one should go for direct selection for these traits to improve breeding programme in future.

Srinivas *et al.* (2017) studied heritability and genetic advance for thirty genotypes of cowpea for sixteen traits. Significant differences among the genotypes for the characters indicating existence of ample variability in the experimental material for the characters. High heritability along with high genetic advance was observed for number of branch per plant per plant, pod yield per plant, total number of pod per plant, number of seed per pod indicating scope for improvement through selection breeding programme.

Viswanatha and yogesh (2017) evaluated cowpea genotype for variability and they observed the genetic advance estimates were medium to high (17.34% to 87.94%) for all the characters. Seed yield contributed maximum towards the total diversity (48.05%) followed by days to 50 per cent flowering (21.08%), test weight (17.68 %), days to physiological maturity (3.58 %), plant height (3.49 %), pod length (1.69 %), number of clusters per plant (1.35 %), number of pod per plant (1.07 %), number of seed per pod (0.75 %) and lowest contribution was noted from number of branch per plant per plant (0.05 %).

Bhagavati *et al.* (2018) studied heritability and genetic advance among twenty-four genotypes of cowpea [*vigna unguiculata* (L) walp s.sp *sesquipedalis* verdc.] for twenty-four different traits. They reported high heritability coupled with high genetic advance for vine length, number of primary branches per plant, number of nodes per plant, pod length, number of clusters per plant, number of pod per plant, pod ascorbic acid content, 100-seed weight, pod yield per plant, pod yield per plot and pod yield per hectare indicated that these traits were under the control of additive gene action.

Das *et al.* (2018) studied heritability and genetic advances for different cowpea genotypes and they reported highest heritability for hundred seed weight and expected genetic advance was found highest for plant height.

Devi *et al.* (2018) observed high heritability for plant height, days to 50 per cent flowering, number of racemes per plant, peduncle length, number of pod per plant, number of clusters per plant, days to maturity, pod length, hundred seed weight and single plant yield. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, number of racemes per plant, peduncle length, number of pod per plant, number of clusters per plant, pod length, hundred seed weight and single plant yield.

Havaraddi and Deshpande (2018) observed high heritability coupled with high genetic advance as per cent over mean for seed yield, number of pod per plant and plant height. Characters such as days to 50 per cent flowering and days to maturity showed high heritability and low genetic advance as per cent over mean. Moderate heritability with moderate genetic advance as per cent over mean was recorded by number of seed per pod and hundred seed weight. However, pod length recorded moderate heritability and low genetic advance as per cent over mean.

Kumar *et al.* (2018) reported highest broad sense heritability for number of primary branches per plant (0.94%), followed by number of pod per peduncle (0.90%), peduncle length (0.89%), number of seed per plant (0.80%), number of branch per plant per plant (0.81%) number of pod per plant (0.78%), pod diameter (0.77%) and number of seed per pod (0.70%). The maximum genetic advance was recorded for pod yield per plot (79.08%) fallowed by number of seed per plant (40.10%), pod weight per plant (9.86%), number of pod per plant (5.51%), duration of reproductive phase (2.77%), peduncle length (2.29%) and number of pod per peduncle (2.20%).

Nair *et al*. (2018) evaluated twenty-five F_2 interspecific hybrids of cowpea and their fourteen parents and observed high heritability and genetic advance as per cent of mean for plant height, green pod yield per plant, seed yield per plant, pod length and number of pod per plant. These characters were governed by additive gene action.

Sable *et al*. (2018) studied heritability and genetic advance for twenty-three F_2 generation and high heritability with high genetic advance as percentage of mean was observed for seed yield per plant, number of pod per plant, plant height, number of primary branches per plant, hundred seed weight and harvest index. It indicated that these characters governed by additive gene action and made it suitable for direct selection.

Singh *et al.* (2018a) studied heritability and genetic advance in cowpea. A collection of thirty-two cowpea genotypes were evaluated for eleven quantitative characters. High estimate of heritability was found for plant height and number of pod per plant. High genetic advance was observed for number of pod per plant and minimum in leaf length.

Thouseem *et al*. (2018) reported high heritability coupled with high genetic advance for days to 50 per cent flowering, length of main stem, number of pod clusters per plant, number of pod per cluster, pod weight, pod length, pod girth, number of seed per pod and 100 seed weight. High heritability was observed for number of primary branches per plant, number of pod per plant and seed yield per plant.

Gupta *et al.* (2019) studied twenty-seven diverse cowpea genotypes and depicted high heritability coupled with high genetic advance for pod yield per plant, plant height, pod yield per hacter, number of pod per plant and number of nodes on the main stem indicated direct selection was more effective for further improvement.

Meenatchi *et al*. (2019) studied broad sense heritability and genetic advance as per cent of mean for yield and yield attributing traits in nine F_2 populations of cowpea. The results revealed that high heritability and high genetic advance of mean were recorded for plant height, pod length, seeds per pod, hundred seeds weight and single plant yield.

Sharma *et al.* (2019) studied twenty-two genotype of cowpea and observed high heritability coupled with high genetic advance in characters *viz.*, seed yield per plant, plant height, days to 80 per cent maturity, green pod weight, days to 50 per cent flowering and pods per plant indicated that these traits were mostly controlled by additive gene action.

Verma *et al.* (2019) studied heritability coupled with genetic advance in cowpea and found higher value for plant height, number of branch per plant per plant, flowers per cluster, pods per cluster, per cent pod set, days to harvest, pod length, pod weight, number of seed per pod, 100-seed weight and pod yield per plant.

Yadav *et al.* (2019) reported high heritability for biological yield (97%), seed yield (95%), number of pod per plant (94%), 100 seed weight (93%), pod length (93%), days to 50 per cent flowering (84%) and days to 50 per cent pod setting (92%). Number of pod per plant (h^2=94%, GAM=79.50%), number of primary branches per plant (h^2=81%, GAM=53.02%), plant height (h^2=82%, GAM=43.89%), 100 seed weight (h^2=93%, GAM=37.49%) showed high heritability with high genetic advance. These results suggest the preponderance of additive gene action in the expression of these characters and showed ample scope of selection.

Chaudhary *et al.* (2020) reported high heritability coupled with high genetic advance for number of pod per plant, number of seed per pod, pod length, test weight, seed yield per plant and leaf area per plant specified that these characters were governed by the additive action of polygene and might be considered at selection criteria.

Mofokeng *et al.* (2020) observed heritability ranged from 37.27% (grain yield) to 97.2% (hundred seed weight) and high heritability values for traits such as days to 50 per cent flowering, number of primary branches per plant, number of seed per pod, number of pod per plant and green pod yield per plant. Genetic advance value ranged from 71.86% (number of branch per plant per plant) to 2242.6% (number of seed per pod) followed by pod weight, grain yield, pod number per plant and days to flowering.

Pandiyan *et al.* (2020) reported high heritability and low genetic advance as percentage of mean for days to 50 per cent flowering, days to maturity and plant height suggesting that selection based on these characters could be effective.

Purohit *et al.* (2020) found high heritability with high genetic advance for plant height, yield per hectare and yield per plant. Moderate heritability and genetic advance were observed for days to 50 per cent flowering while, low heritability with low genetic advance exhibited by leaf length.

Ugale *et al*. (2020) observed high heritability coupled with high genetic advance as per cent of mean for traits *viz*., plant height, number of primary branches per plant, days to 50 per cent flowering, number of pod per plant, number of seed per pod, mean pod weight, pod width, days to first pod harvest, 100 seed weight, pod yield per plant and pod yield per hectare except days to 50 per cent flowering and pod width indicating that these characters were less influenced by environmental effects and these characters were governed by additive genes and selection will be rewarding for improvement of such traits.

Thapa *et al*. (2021) studied the heritability in twelve cowpea genotypes and results indicated that all the genotypes were significantly different for an early stand, 50 per cent flowering days, 90 per cent maturity days, pods per plant, seeds per plant, final stand, 100 seed weight, seed yield except for plant height. Genotypes such as IT10K-815-5, IT10K-973-1, IT82-1337 and IT10K-973-1 were promising cowpea genotypes having high heritability along with genetic advance for traits such as seeds per pods, pods per plants, plant height, hundred grain weight and grain yield, considered for selection in further yield improvement programme.

2.3 Correlation and path analysis

The correlation coefficient is an index of the proportion of causes common in the genesis of two variables to the total and not the causes themselves (Bowely, 1920). Path coefficient measure the influence of one variable on another from particular point of view. Correlation helps in identifying suitable plant types and plant breeding procedure and path analysis helps in assessing the relatively contribution of yield components on seed yield.

Tyagi *et al.* (2000) studied genetic parameters in twenty-four cowpea genotypes. Seed yield per plant had high significant positive correlation with days to 50 per cent flowering, plant height, pod length, number of pod per plant, seed weight, pod and 100-seed weight both at phenotypic and genotypic levels. The path coefficient analysis indicated that higher seed weight per pod, number of pod per plant and 100-seed weight are important for effecting selection.

Rocha *et al*. (2003) studied genetic parameters in twenty-three white coat cowpea genotypes. They reported that genotypic correlations was usually larger than phenotypic and environment correlations. The indirect selection through number of pod per plant, number of seed per pod, weigh of 100-seed traits provides larger probability of genetic gains for seed yield.

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

Eswaran *et al.* (2007) studied on thirty genotypes of cowpea and reported seed yield per plant had high significant positive correlation with total dry matter production and harvest index both at phenotypic and genotypic levels. The path coefficient analysis indicated that plant height at the time of first flowering, plant height at the time of 50 per cent flowering, plant height at the time of 50 per cent maturity and total dry matter production are important for effective section.

Bhardu and Navale (2011) noticed that seed yield per plant found significant and positive correlation with number of pod per plant, biomass at harvest, number of branch per plant per plant, test weight, pod length and vine length. Number of pod per plant showed highest magnitude of direct effect on seed yield per plant followed by test weight, biomass at harvest and number of branch per plant per plant in cowpea.

Cholin *et al.* (2010) reported that number of clusters per plant and pods per plant had positive correlation with seed yield whereas, clusters per plant, pod length and test weight had a positive direct effect on seed yield and days to maturity has negative direct effect on seed yield in cowpea.

Manggoel *et al.* (2012) studied ten diverse accessions of cowpea and reported positive correlation between seed yield and number of peduncles per plant (r = 0.716**), flowers per plant (r = 0.776**), pods per plant (r = 0.640*) and 100- seed weight (r = 0.690*). Path analysis showed high positive direct effects of number of peduncles per plant (p = 0.94), flowers per plant (p = 1.40) and 100-seed weight (p = 1.45). Numbers of peduncles per plant, flowers per plant, pods per plant and 100-seed weight were identified as selection criteria for obtaining good parental lines in cowpea breeding programs.

Udensi and Ikpeme (2012) reported that genotypic correlation coefficients were high and more significant than the phenotypic and environmental correlation coefficients. Path coefficient analysis showed that number of pod per plant had the highest direct effects to cowpea seed yield (0.588). This was followed by number of seed per pod (0.366), leaf area at 5 weeks (0.366), pod length and 100 seed weight (0.316), respectively in cowpea.

Khan *et al.* (2013) revealed number of pod per plant and number of seed per pod had significant positive correlation among themselves in C-152 × V-16 and C-152 × HC-03-02 both the crosses studied. It may be inferred that these traits had strong influence on seed yield per plant. Since, the characters were inter-correlated among themselves; selection for any one of the traits will result in the improvement of other trait thereby, resulting in increased seed yield.

Kumar *et al*. (2013) studied the correlation coefficients at phenotypic and genotypic levels for different characters of cowpea. The results revealed that the seed yield per plant showed significant and positive association with plant height, number of clusters, number of pod, pod length and number of seed per pod while, it was negatively correlated with primary branches and 100 seed weight.

Thorat and Gadewar (2013) studied variation in thirty genotypes of cowpea. Days to maturity had highly significant positive correlation with days to 50 per cent flowering both genotypically and phenotypically. Protein content is significant but negatively associated with days to maturity. Number of clusters per plant showed strong positive significant correlation with protein content. Pod length exhibited significant positive correlation with protein content. Number of seed per pod exhibited positive significant correlation with protein content and strongly correlated with pod length. Seed yield per plot exhibited strong positive significant correlation with clusters per plant, number of pod per plant it also showed moderately positive significant correlation with protein content. Component traits for seed yield *viz.* number of pod per cluster and number of clusters per plant appears to provide reliable criteria for effective selection in cowpea.

Anamika and Tajane (2014) studied path coefficient analysis of cowpea genotypes. The results indicated that number of pod per plant, 100 seed weight and number of seed per pod had high positive direct effect on seed yield per plant and these traits had significant and positive correlation with seed yield per plant.

Bhardwaj *et al*. (2014) evaluated sixty genotypes of cowpea for eleven morphological traits *viz*., plant height, leaf length, leaf width, number of branch per plant, stem girth, number of leaves, number of pod, seeds per pod, pod weight, 100 seed weight and seed yield per plant. The genotypic correlation coefficient was higher in magnitude than the phenotypic correlation co-efficient. Seed yield per plant was highly significant and positively correlated with number of pod per plant (0.92, 0.90), pod weight (0.90, 0.89), 100- seed weight (0.57, 0.55), leaf length (0.56, 0.90), leaf width (0.27, 0.11) and number of seed per pod (0.22, 0.14) at phenotypic and genotypic level, respectively in cowpea.

Pandey *et al.* (2014) studied on correlation analysis in cowpea and they pointed out the importance of number of branch per plant per plant, peduncles per plant, pods per plant, pod length, pod weight and number of seed per pod towards pod yield in cowpea.

Santos *et al.* (2014) studied correlations and direct and indirect effects of yield components is important for the selection of promising parental and segregating populations. The character showed low to moderate possibility of gain from indirect selection, with greater possibility for success when joining multiple character and a genotype of better performance.

Sapara and Javia (2014) studied the genotypic and phenotypic correlations in forty genotypes of vegetable cowpea. The genotypic and phenotypic correlations agreed closely with each other. Yield contributing character number of pod per plant had positive and highly significant association with green pod yield per plant at phenotypic level. Phenotypic interrelationship between days to 50 per cent flowering and days to first pod picking was negatively significant with green pod yield. The genotypic and phenotypic path analysis revealed the high to moderate direct effect of green pod yield per plant with number of pod per plant and pod length. Therefore, number of pod per plant and pod length was important component for improving green pod yield in vegetable cowpea.

Shanko *et al.* (2014) studied on correlation and path analysis in cowpea. They reported that seed yield exhibited positive and significant environmental correlation with number of primary branches per plant, number of secondary branches per plant, days to 50 per cent flowering, number of pod per plant, number of seed per pod and plant height. Path analysis revealed that, yield per plant exerted the maximum positive direct effect on seed yield followed by number of pod per plant, while number of secondary branches per plant, days to flowering, days to maturity and number of seed per pod exhibited negative direct effect phenotypically. In addition, genotypic path analysis revealed that, maximum direct effect on seed yield was exerted by number of pod per plant and yield per plant. However, days to 50 per cent flowering, days to maturity, number of secondary branches per plant and number of seed per pod exerted negative direct effect on seed yield. Thus, yield per plant and number of pod per plant could be used as a selection index for cowpea improvement.

Vir and Singh (2014) studied correlation and path coefficient for number of seed per pod, number of pod per plant, number of pod per cluster, number of clusters per plant, days to 50 per cent flowering and days to maturity and reported positive and significant correlations with seed yield per plant in cowpea.

Meena *et al.* (2015) studied the correlations and path coefficients for ten quantitative characters among seventy-two cowpea germplasm. Seed yield per plant had positive significant correlation with days to 50 per cent flowering, plant height, primary branches per plant, pods per plant, pod length, seeds per pod and 100 seed weight at both genotypic and phenotypic levels. Path coefficient analysis revealed that primary branches per plant and 100 seed weight had high direct positive effect on seed yield per plant at both genotypic and phenotypic levels. Pod length, days to maturity, 100 seed weight and pod wall proportion had high positive direct effects on seed yield per plant at only genotypic level. Correlation and path analysis indicated that for increasing seed yield in cowpea direct selection should be carried out for higher value of primary branches per plant, pods length, days to maturity and 100 seed weight.

Patel *et al.* (2016) studied on thirty-two diverse genotypes of cowpea for correlations and path coefficient for different traits *viz.*, days to 50 per cent flowering, number of branch per plant per plant, number of clusters per plant, pod length, number of seed per pod, number of pod per plant, plant height at final harvest, sugar content, shelling, crop duration, green pod yield per plant, green pod yield per hectare. Association analysis between green pod yield per plant and other eleven quantitative characters revealed that green pod yield per plant was highly significant and positively correlated with pod length (r_g=0.456), (r_p=0.312) and sugar content (r_g= 0.269), (r_p= 0.217) at both genotypic and phenotypic level. Path coefficient analysis indicate the highest positive direct effect on green pod yield per plant by pod length (0.716) followed by days to 50 per cent flowering (0.645), shelling % (0.398), number of pod per plant (0.289), sugar content (0.219) and plant height at final harvest (0.204).

Sharma *et al.* (2016) studied correlation coefficient and path analysis on sixty genotypes of cowpea. They reported yield contributing traits *viz.*, biological yield per plant, number of pod per plant, number of flowers per plant, test weight, number of pod per cluster, pod length, number of seed per pod, number of clusters per plant, harvest index and plant height due to their direct high positive association with seed yield. The trait days to maturity had negative and non-significant correlation with seed yield per plant there by indicating selection for early maturity would give drought tolerant and drought avoiding genotypes affecting the seed yield positively in cowpea. Path analysis revealed that, seed yield per plant can be improved practicing selection for biological yield per plant, harvest index, number of pod per plant, days to 50 per cent flowering, number of flowers per cluster, number of primary branches per plant, number of seed per pod, test weight and plant height as they contributed directly to the seed yield per plant. It indicated the possibilities of simultaneous improvement of these traits by selection. This in turn, would improve the seed yield, since they were positively correlated with the seed yield.

Dinesh *et al.* (2017) studied correlation and path analysis in early segregating generation of cowpea. Two genetically diverse parents (C-152 × V-57817) were crossed and advanced to F_3 generation. The magnitude of variation, heritability, genetic advance, association of component characters and path coefficient analysis were estimated in a set of 194 F_3 progenies. The traits having high heritability and significant positive correlation with the grain yield can be utilized for indirect selection for genetic improvement. Results suggests that traits like number pods per plant and 100 seeds weight could be used as selection criteria for seed yield improvement in segregating populations of cowpea.

Nguyen *et al.* (2017) studied correlation and path coefficient analysis in thirty cowpea genotypes. Correlation analysis indicated that seed yield per plant exhibited highest and positive significant correlation with pod yield per plant, followed by number of pod per plant, number of clusters per plant, number of pod per cluster, harvest index, number of seed per pod, number of branch per plant per plant and pod weight. Harvest index, biological yield per plant, pod yield per plant, number of seed per pod and number of pod per plant reflected high direct and positive effect on seed yield. If the selection is made for any of these components, the improvement in seed yield could be achieved.

Sharma *et at.* (2017$_b$) studied correlation and path analysis in thirty genotypes of cowpea. Correlation and path analysis indicated that for increasing seed yield in cowpea direct selection should be carried out for higher values of biological yield per plant, harvest index, pod length and primary branches per plant. The direct and indirect effects of different characters on seed yield per plant were worked out using path coefficient analysis. Among the different contributing characters high positive direct effects on seed yield per plant were exhibited by biological yield (1.228), harvest index (0.828), pod length (0.109), number of branch per plant per plant (0.107) and clusters per plant (0.55) at genotypic level and positive direct effects on seed yield per plant were exhibited by biological yield (0.973), harvest index (0.711), days to 50 per cent flowering (0.077), pod length (0.066) and ranches per plant (0.063) at phenotypic level.

Srinivas *et al.* (2017) studied thirty genotypes of cowpea for phenotypic and genotypic correlation coefficient and revealed that pod yield per plot was significantly and positively correlated with number of branch per plant per plant (0.7659), number of nodes (0.5523), pod length (0.3960), number of seed per pod (0.2815), number of cluster per plant (0.550), number of pod per plant (0.547), number of pod per cluster (0.524), plant height (0.437) and protein content (0.2871). However, days for 50 per cent flowering (-0.2081) showed significantly and negatively correlated with pod yield per plot. Other characters *viz.*, days taken for first flowering (- 0.1946), pod diameter (-0.1035) showed negative non significantly correlated with pod yield per plot.

Das *et al.* (2018) reported correlation and path analysis for yield per plant was positively and significantly correlated with clusters of pod per plant at both genotypic and phenotypic levels. Seed yield per plant was negatively correlated with pods per cluster and hundred seed weight at both genotypic and phenotypic levels. Path analysis revealed that clusters of pod per plant, primary branches and seed yield per pod exhibited high positive direct effect on seed yield per plant at phenotypic level and at genotypic level clusters of pod per plant, pods per cluster, number of primary branches, seed yield per pod and plant height had the maximum direct effect on seed yield.

Manisha *et al.* (2018) studied correlation and path analysis in F_5 generation of cowpea for fifteen characters. The characters like number of pod per plant, number of pod per cluster, primary branches per plant, number of cluster per plant, pod length, pod diameter, average pod weight, leaf area had highly significant positive correlation with pod yield per plot both genotypic and phenotypic levels, which indicating dependence of these characters on each other. Path coefficient analysis revealed that the characters number of pod per plant, 100 seed weight, primary branches per plant, plant height, pod length, number of seed per pod positive direct effect on pod yield per plot. While the trait like number of pod per cluster, number of cluster per plant, pod diameter, pod length, average, pod weight, primary branches per plant,100 seed weight, plant height and leaf area contributed indirect effect towards the yield.

Patel *et al.* (2018) studied correlation and path analysis in cowpea. The experimental materials consisting sixteen genotypes of cowpea. The maximum correlation coefficient at genotype and phenotypic levels were observed for average pod yield per plot. At genotypic level, highest positive direct effect towards pod yield per plant was showed by plant height (2.0266) followed by number of seed per plant (2.0180), pod length (1.3435), days to first pod picking (1.3398), number of pod per peduncle (1.2163), vitamin-A (1.2087), number of primary branches per plant (1.0063), pod diameter (cm) (0.8480) and days to first open flower (0.3174). Highest negative effect towards pod yield per plant was showed by number of peduncle per plant (-3.8261) followed by vitamin-C (-2.5669), number of seed per plant (-1.8234), pod weight per plant (-1.8234), number of pod per plant (-1.2892), number of branch per plant per plant (-0.4917) and number of seed per pod

Walle *et al.* (2018) studied correlation and path coefficient analysis of cowpea to determine the nature and extent of phenotypic and genotypic correlation and path coefficient analysis among eighteen quantitative traits. A total of three hundred and twenty-four cowpea land races were tested in 18 × 18 simple lattice designs. The magnitude of genotypic correlations was higher than phenotypic correlations in traits; this implies that the traits under consideration were genetically controlled. Seed yield was positively and highly significantly correlated with all the traits at phenotypic and genotypic levels, indicated the presence of strong inherited association between seed yield and the other seventeen traits. Genotypic direct and indirect effects were higher than the phenotypic direct and indirect effects indicated that the other traits had a strong genetically inherited relationship with seed yield.

Kalambe *et al.* (2019) studied path analysis for quantitative traits in twenty-two cowpea germplasm lines including two checks and observations were recorded on twelve characters *viz.*, plant height, number of primary branches per plant, days to 50 per cent flowering, number of pod per plant, number of seed per pod, mean pod weight, pod length, pod width, days to first pod harvest, 100 seed weight, pod yield per plant and pod yield per hectare. The magnitude of genotypic correlation was higher than phenotypic correlation for all the traits that indicated inherent association between various characters. In the present findings significant positive phenotypic correlation of pod yield per plant was observed with number of pod per plant and pod weight indicating that these characters are the primary yield determinant in cowpea.

Sharma *et al*. (2019) reported positive correlation of seed yield per plant with pod length, number of cluster per plant and pods per plant while, number of primary branches, days to 50 per cent flowering and days to 80 per cent maturity exhibited negative correlation with seed yield per plant at genotypic and phenotypic level, where as positive correlation of those characters with yield directly enhance yield of cowpea.

Waghmare *et al*. (2019) studied correlation and path analysis in thirty genotypes of cowpea using randomized block design with two replications. The phenotypic and genotypic correlation coefficient revealed that seed yield per plant was significantly and positively correlated with dry matter yield per plant (0.8502), harvest index (0.8082), 100 seed weight (0.6377), number of pod per plant (0.4413) and number of seed per pod (0.2815). However, plant height (-0.0022) showed significantly and negatively correlated with seed yield per plant. The character pod length (-0.2377) showed negative non-significantly correlated with seed yield per plant. Path coefficient analysis of different yield and yield contributing traits on number of pod per plant, number of seed per pod, pod length, hundred seed weight and harvest index exhibited positive direct effects on seed yield per plant.

Yadav and Duddukur (2019) studied on genotypic and phenotypic correlation coefficients of cowpea for thirteen characters. The traits *viz.*, days to 50 per cent flowering, days to 50 per cent pod setting, pods per plant, 100 seed weight, harvest index and biological yield showed highly significant positive association with seed yield at both phenotypic and genotypic levels. While plant height showed significant negative association with seed yield at both phenotypic and genotypic levels. Days to maturity is significant positive association with the seed yield at genotypic level.

Chaudhary *et al.* (2020) observed significant positive correlation between seed yield per plant and number of pod per plant, number of seed per pod, number of branch per plant per plant, pod length and plant height. Whereas, negative significant correlation was observed between seed yield per plant with days to flowering and days to maturity. In present study pod length recorded the highest positive direct effect on seed yield per plant followed by number of branch per plant per plant and number of pod per plant. While, days to flowering had highest negative direct effect on seed yield per plant. Both correlation and path analysis indicated that number of pod per plant, number of seed per pod, number of branch per plant per plant and pod length were the major direct effect contributors to seed yield.

Detroja *et al.* (2020) studied on direct and indirect path coefficient values in cowpea. Maximum positive correlation depicted by pod yield per plant with harvest index followed by chlorophyll content, plant height and nitrogen content of pods at phenotypic level. While, negative correlation was exerted with the number of leaves, primary branches, days to 50 per cent flowering and secondary branches. The path analysis depicted protein content of green pod having higher positive direct effect followed by harvest index and total dry weight whereas, nitrogen content of green pod had negative direct effect on green pod yield per plant followed by secondary branches, the number of leaves and nitrogen content in plant part.

Kumar *et al.* (2020) evaluated one hundred and two Indian cowpea genotypes based on twelve quantitative characters for association between yield and its contributing traits. Single plant yield showed significant positive correlation with traits *viz.*, number of clusters per plant, number of pod per plant, pod length, number of seed per pod, number of pod per cluster and hundred seed weight. The highest inter correlation was obtained between number of clusters per plant and number of pod per plant. Path analysis revealed that, the highest direct effect on single plant yield was obtained by number of pod per plant followed by hundred seed weight and number of seed per pod. The highest positive indirect effect on single plant yield was observed in number of clusters per plant through number of pod per plant. Hence, selection based on the traits *viz.*, number of clusters per plant, number of pod per plant, number of seed per pod, hundred seed weight and pod length would be highly rewarding in cowpea yield improvement program

Mofokeng *et al.* (2020) studied direct and indirect path coefficient values of agronomic traits in cowpea. The high direct path coefficient value 0.71 for pod weight per plant with highly significant correlation with seed yield was observed. The genotypic coefficient of variation was moderate for number of branch per plant, number of seed per pod and high for number of seed per plant and pod weight per plant.

Nagalakshmi *et al.* (2020) studied the correlation coefficients among twelve quantitative characters and analysed the direct and indirect effects of these characters on seed yield by path coefficient analysis in sixty-six genotypes collected from various agroclimatic zones of India. The study revealed that seed yield was positively and significantly correlated with number of pod per plant (0.40), peduncle length (0.38), number of clusters per plant (0.31), number of seed per pod (0.29), number of leaves per plant (0.28), number of branch per plant per plant (0.27) and days to 50 per cent flowering (0.19). Hundred seed weight (-0.44) and pod length (-0.1) were negatively correlated with seed yield. Number of seed per pod (0.34), peduncle length (0.26), plant height (0.23), number of branch per plant per plant (0.15), number of clusters per plant (0.12), number of pod per plant (0.12) and days to 50 per cent flowering (0.07) exerted a direct positive association with seed yield. The results of correlation and path analysis suggests that seeds per pod, pod length and number of branch per plant per plant were the important characters for selection in cowpea.

patil *et al.* (2020) studied on five crosses of cowpea in randomized block design with two replications. The character seed yield per plant had positive and highly significant correlated with number of pod per plant (0.8906), harvest index (0.8758), 100 seed weight (0.7123) and pod length (0.3114) at phenotypic level. Similarly at phenotypic level it showed negative nonsignificant correlation with days to 50 per cent flowering (-0.0159) while, days to maturity (-0.3005) had negative significant correlation. Positive and highly significant correlation was reported between seed yield per plant and number of pod per plant (1.0080) followed by harvest index (0.8652), 100 seed weight (0.7685) at genotypic level. Genotypically negative highly significant correlation was reported with days to maturity (-0.4294) and negative nonsignificant correlation with days to 50 per cent flowering (-0.0413). Path coefficient analysis revealed positive direct effect of number of pod per plant, days to initiation of flowering and hundred seed weight at both genotypic and phenotypic level. Whereas, characters *viz.*, days to maturity, number of clusters per plant, number of pod per cluster and plant height at genotypic level and characters *viz.*, number of branch per plant per plant and pod length were having direct positive effect on seed yield per plant at phenotypic level.

Panchta *et al.* (2021) reported number of seed per pod had positive and significant correlation at genotypic level with seed yield per plot. The traits like number of seed per pod, number branches per plant and days to maturity showed direct effect on seed yield per plot.

2.4 Genetic divergence

Information on the extent and nature of interrelation among character help in formulating efficient scheme of multiple traits selection. Beside this, knowledge of the naturally occurring diversity in a population help to identify diverse group of genotype that can be used for hybridization programme. This naturally occurring diversity in agronomic importance traits is studied through D^2 analysis (Mahalanobis, 1936).

Backlyaranl *et al.* (2000) observed the nature and magnitude of genetic divergence assessed in thirty-two genotypes of cowpea using Mahalanobi's D^2 value and indicated that considerable diversity in the material studied. The population was grouped into six clusters, cluster IV had the maximum number of genotypes. The intra and inter cluster average of values indicated maximum statistical distance between cluster I and V followed by III and V. The geographical diversity was not related to genetic diversity. Single plant yield, harvest index and earliness in flowering contributed considerably an accounted of 80 per cent of total divergence.

Kumari *et al.* (2000) studied fifty genotypes of cowpea grouped in to thirteen clusters by Mahalanobls D^2 statistics. The genotypes, IT -86-F-310-6 and IT-87-0-272 had distinct identity with respect to yield attributes. Hybridization between genotypes of cluster VIII and XIII should result in desirable combinations leading to development of usual genetic stocks and varieties. Among the yield attributing characters, seeds per pod, number of branch per plant, number of pod per cluster and pod length were the important traits responsible for the divergence recorded.

Kumawat and Raje (2005) studied genetic divergence for seed yield and its component in cowpea. The data were subjected to D^2 analysis and grouped into different clusters following Tocher's method. The fifty genotypes were grouped in to six clusters. The average intra cluster D^2 values ranged from 0.00 to 5.622. The relative contribution of various characters towards the total genetic divergence revealed that seed yield per plant had maximum contribution followed by seeds per pod, days to 50 per cent flowering, plant height and reproductive period.

Suganthi *et al.* (2007) studied genetic divergence analysis among thirty genotypes of cowpea and the results indicated the existence of considerable diversity. These genotypes were grouped into eleven clusters. The cluster III was largest and consisted of seven genotypes followed by cluster X of four, cluster II, IV, V and VIII (three in each), cluster I and VII (two in each) and clusters VI, IX and XI consisting of only one genotype in each. Maximum inter cluster D^2 value was observed between I and XI, indicating that the genotypes included in these clusters had maximum divergence. The diversity among the genotypes measured by inter-cluster distance was adequate for improvement of cowpea by hybridization and selection. The genotypes included in these diverse clusters may be used as promising parents for hybridization to obtain better segregants in cowpea.

Valarmathi *et al.* (2007) studied sixty-nine cowpea genotypes, which included sixty genotypes from *Vigna unguiculata ssp. unguiculata* and eight genotypes from *Vigna unguiculata ssp. sesquipedalis* which were evaluated for nine quantitative characters and replication-wise means were subjected to Mahalonobis D^2 analysis. All the accessions were grouped into twelve clusters, in which cluster I was the largest having forty-seven genotypes from sub species unguiculata. Unguiculata were grouped in seven distinct clusters, whereas the genotypes of *Sesquipedalis* were grouped in five other distinct clusters. Days to maturity contributed maximum to the genetic divergence followed by hundred seed weight and characters namely number of branch per plant per plant and number of seed per pod and total exhibited least contribution among the accessions.

Dalsaniya *et al.* (2009) studied sixty genotypes of cowpea for diversity among the genotypes which were grouped into twelve clusters revealing the presence of considerable diversity in the material. The clustering pattern of the varieties usually did not confirm to geographical distribution. Inter cluster distance and mean cluster character values indicated that hybridization of cluster-X variety with cluster-IV varieties and cluster-V varieties with cluster-III varieties would exhibit high heterosis and also result in transgressive segregants with higher yield. It was also noted that genotypes of cluster-X which had higher cluster mean values for yield and other desired characters like leaf area, ten pods weight, number of pod per plant and green pod yield per plant. could be directly tested in multilocation trials for their suitability or could be used as a donor parent in breeding programme. The characters like plant height, green pod yield per plant, protein content and leaf area were found to contribute much to the total genetic divergence in cowpea.

Nagalakshmi *et al.* (2010) studied sixty-six genotypes of cowpea and investigated the extent of genetic diversity through twelve quantitative traits. Mahalanobis D^2 analysis established the presence of wide genetic diversity among these genotypes by the formation of 23 clusters. Cluster I had the maximum number of genotypes *i.e.,* 22 and cluster 23 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 per plant contributed maximum to the total divergence followed by hundred seed weight and days to 50 per cent flowering. Number of branch per plant per 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. The cluster XVIII had the highest cluster mean values for number of clusters per plant and the cluster XIV has the highest mean value for grain yield per plant. These two clusters may be utilized in crossing programme which may yield in a wide spectrum of variability and selection for seed yield in the subsequent generations. The clustering pattern of the varieties in the present study clearly indicated that there was no parallelism between genetic and geographic diversities.

Nancee *et al*. (2013) studied genetic divergence based on D^2 values of forty-six genotypes were grouped into eight clusters containing two to fifteen genotypes. These clusters consisted of genotypes with different geographical origins and indicated no correlation between genetic and geographical divergence. 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. Thus, to generate desirable genetic variability, the crossing between cluster II, I and V genotypes would be useful. It is suggested that hybridization among genotypes of above said clusters would produce segregants for more than one economic character which can serve as parents of hybrids. The number of seed per pod contributed highest towards divergence.

Ahamed *et at.* (2014) studied genetic diversity among eleven cowpea germplasm. Mahalanobis generalized distance (D^2) analysis was used to group the cowpea genotypes. Considering the mean values, the germplasm were grouped into four clusters. Maximum numbers (four) genotypes were included in cluster III and a minimum number (two) genotypes were included in both cluster II and IV. Among the clusters, the highest inter-cluster distance was obtained between the cluster IV and II (23.952) and the lowest one was obtained between II and I (6.753). The maximum value of inter-cluster distance indicated that genotypes belonging to cluster IV were far diverged from those of cluster II.

Brahmaiah *et al.* (2014) studied forty cowpea genotypes for eighteen quantitative characters to estimate the genetic diversity existing among them by using Mahalanobis D^2 statistics. The genotypes were grouped into six clusters. The cluster strength varied from single genotype (Clusters III, IV and V) to 25 genotypes (Cluster I). Clusters IV and VI had high inter cluster distance. Clusters II, III and I had maximum 100-seed weight, number of seed per pod and seed yield, respectively. Cluster IV had maximum seedling vigour index, germination per cent, peduncle length, number of clusters per plant and number of primary branches.

Sandeep *et al.* (2014) studied genetic divergence in fifty diverse genotypes of cowpea. All the fifty genotypes were grouped into twelve clusters. Cluster I was largest comprising of twenty-seven genotypes followed by Cluster II with twelve genotypes, cluster IV with three genotypes and cluster III, V, VI, VII and VIII, IX, X, XI, XII were represented each by single genotype. Intra-cluster D^2 values ranged from 0 to 38.06. The inter-cluster D^2 values ranged from 44.08 to 276.55. The maximum inter cluster distance was observed between VII and XII clusters followed by clusters IV and XII and cluster X and VII. The maximum contribution towards genetic divergence is by days to 50 per cent flowering.

Chandrakar *et al*. (2016) studied the genetic divergence among twenty-one genotypes of vegetable cowpea and showed low quantum of divergence. They were grouped into five clusters on the basis of D^2 analysis. Maximum number of genotypes (nine) was accommodated in cluster - II. The average inter and intra cluster divergence (D) values had also been calculated. The intra-cluster distance varied from 0.00 to 5.04. The maximum intra cluster distance was shown by cluster I (5.04) followed by cluster V, cluster II, cluster III and cluster IV. The maximum inter cluster distance was observed in between cluster I and V (5.04). The cluster III showed maximum value for mean green pod yield followed by cluster IV. Crossing between the genotypes of maximum two clusters appeared to be most promising to combine the desirable characters.

Shrinivas *et al.* (2016) studied thirty genotypes of cowpea to understand the extent of genetic diversity through sixteen traits. Mahalanobis's D^2 analysis established the presence of wide genetic diversity among these genotypes which were grouped into six clusters. The cluster I was largest and consisted of 21 genotypes followed by cluster III of 5 genotypes and clusters II, IV, V and VI consisting of only one genotype each. Maximum inter cluster D^2 value was observed between VI (6987.85) and III (4806.87), indicating that the genotypes included in these clusters had maximum divergence. The diversity among the genotypes measured by inter-cluster distance was adequate for improvement of cowpea by hybridization and selection.

Nguyen *et al*. (2017) evaluated thirty genotypes, which were grouped into six clusters. Cluster pattern revealed that cluster I and II were the largest groups, each has the eight genotypes, followed by cluster III (six genotypes), cluster V (four genotypes), cluster IV (three genotypes) and cluster VI (1 genotype). The maximum intra-cluster D^2 value was shown by cluster V (19.85) followed by cluster III (19.35), cluster IV (18.49) and cluster I (15.63). The intra-cluster D^2 values ranged from 15.63 (cluster I) to 19.85 (cluster V). Highest inter-cluster D^2 values among genotypes existed between clusters III and VI (52.08), followed by clusters III and V (45.99), clusters IV and V (43.62) and clusters II and III (41.21). There were high variations among six clusters for all characters *viz*. plant height, days to 50 per cent flowering, days to maturity, number of branch per plant per plant, number of cluster per plant, number of pod per cluster, number of pod per plant, pod length, pod breadth, pod weight, pod yield per plant, number of seed per pod, hundred seeds weight, seed yield per plant, biological yield per plant, harvest index and seed protein content. Cluster V revealed the highest mean value for almost desirable seed yield characters *i.e.* seed yield per plant, number of clusters per plant, number of pod per plant, harvest index, seed protein content and early in maturity. Cluster III exhibited superior characters of biological yield and plant height. On the contrary, cluster VI had smallest mean values for almost important characters.

Patel *et al*. (2017) evaluated thirty-two cowpea genotypes evaluated for twelve quantitative characters to estimate the genetic diversity existing among them using Mahalanobis D^2 statistics. The genotypes were grouped into eight clusters. The cluster strength varied from single genotype (Clusters IV, V, VI, VII and VIII) to 12 genotypes (Cluster II). The maximum inter-cluster distance (D^2= 35.43) was observed between cluster-VI and VIII. Clusters II, III and I maximum 100-seed weight, number of seed per pod and seed yield, respectively. Cluster VIII had the highest mean value for the characters *viz*., number of pod per plant, number of green pods per plant and green pod yield per hectare, while the cluster III had a lowest mean value for days to 50 per cent flowering. On the basis of inter cluster distances, cluster VIII was found to be more divergent. Therefore, it was concluded that the genotypes belonging to these cluster should be inter-crossed in order to generate more variability.

Viswanatha *et al*. (2017) studied one hundred and sixty-nine genotypes of cowpea using Mahalanobis D^2. The genotypes were grouped in to eight clusters, of which maximum intra cluster distance was exhibited by cluster VI and minimum by cluster II. The inter cluster distance was maximum between cluster II and IV. The genotypes from cluster II and IV, which have high and low cluster means for majority of the characters. Therefore, genotypes from same regions are not recommended for hybridization because of close genetic background which was evident from the result showing genotypes belonging to same cluster.

Singh *et al*. (2018_b) evaluated thirty-eight accessions of cowpea for nine quantitative characters to estimate the genetic diversity among them by using Mahalanobis D^2 statistics during *kharif* 2013 (E_1) and *Kharif* 2014(E_2). The genotypes were grouped into ten clusters in E_1 and into five clusters in E_2 environment. In E_1 environment, the cluster strength varied from single genotype (Cluster III, IV, V VI, VIII, IX and X) to 16 genotypes (Cluster II), while in E_2 environment, it varied from single genotype (Cluster III, IV and V) to 19 genotypes (cluster I). Clusters VII and X had highest inter-cluster distance in E_1 and cluster II and III had highest inter-cluster distance in E_2 environment. The maximum mean value for seed yield per plant, number of pod per plant and number of clusters per plant was showed by genotypes of clusters VII in E_1 environment and by genotypes of cluster IV for the traits number of seed per pod, pod length and plant height in E_2 environment. On the basis of inter-cluster distances, cluster VII and X in E_1 environment and cluster II and III in E_2 environment were found to be most divergent. Cluster VII had the genotype with the highest mean value for number of seed yield per plant, number of pod per plant and number of clusters per plant in E_1 environment, while cluster I had the genotypes which showed maximum mean value for seed yield per plant, number of pod per plant, peduncle length and number of clusters per plant in E_2 environment. Therefore, it was concluded that these clusters and their genotypes could be intercrossed in order to achieve more variability.

Gupta *et al*. (2019) studied on twenty-seven cowpea genotypes for genetic divergence using D^2 statistinc and grouped into six clusters. Out of the six clusters, cluster I was largest comprising of eleven genotypes followed by cluster III with five, cluster IV with four, cluster II and V with three genotypes each and cluster VI with single genotype. Inter-cluster distance values ranged from 606.110 to 1837.922. Maximum intra cluster distance was observed between cluster II and cluster V (1837.922) followed by between cluster IV and cluster VI (1675.503), between cluster I and cluster V (1360.086) and between cluster III (1277.398) and cluster IV (1231.772). The highest D^2 distance help breeder in a selection of the parental line for initiating any hybridization programme. Thus, the lines from cluster V and cluster II will give the maximum variation followed by the crosses made between the lines of cluster VI and IV and cluster II and cluster III and cluster IV

Rai *et al.* (2020) studied thirty cowpea genotypes for analyse the genetic divergence of twelve characters. These genotypes were clustered into eight distinct groups using Mahalanobis D^2 statistic and Tocher's method. Cluster I and cluster II were the largest comprised of twelve genotypes each. Cluster III, IV, V, VI, VII and VIII were monogenotypic indicating wide diversity from the rest and also from each other. The maximum intra cluster D^2value was observed within cluster II followed by cluster I suggesting that genotypes present in these clusters might have different genetical constitution. The highest inter cluster distance was registered between cluster II and cluster III followed by cluster II and cluster V and cluster II and cluster IV indicating wide divergence among these clusters. The crossing among the genotypes of these divergent clusters could be used in hybrid development programme of cowpea.

Panchta *et al.* (2021) studied sixty genotypes of fodder cowpea for the genetic diversity. They were grouped into ten clusters indicating high genetic divergence among cowpea genotypes. The clustering pattern showed that geographic diversity is not an index of genetic diversity. Intra cluster distance exhibited a range of 13.59 to 16.01. The maximum inter-cluster distance (D) was noticed between cluster I and X. It was least between cluster V and VI. Based on the inter cluster distance and cluster mean for various characters, it could be seen that the cluster I, II, IX and X were the most divergent from the other clusters. The genotypes from these clusters may possibly be utilized for hybridization programme. Dry matter yield, green fodder yield and plant height contributed highly towards the genetic divergence among the types studied.

Thapa *et al.* (2021) studied the twelve cowpea genotypes for genetic divergence and results indicated that cluster I consisted of six genotypes, cluster II consists of two genotypes and cluster III consisted of four genotypes. The genotypes belongs to cluster I have highest hundred seed weight and lowest plant height and lowest seed yield. Cluster II genotypes have highest pod per plants, lowest final stands and seed per pods along with highest grain yield. Similarly genotypes of III cluster have highest early stands and final stands, seeds per pods and maturity days, yielder plant, late flowering and lowest for pods per plants and lowest hundred seed yield.

Yasin *et al.* (2021) studied genetic diversity among cowpea genotypes based on morpho-agronomic traits. Thirty-six cowpea genotypes were tested using a simple lattice design. On the basis of cluster analysis, thirty-six genotypes, based on the 14 quantitative traits, were grouped into six clusters. I, II, IV, V, III and VI, each with nine, eight, seven, seven, three and two genotypes, respectively. The highest inter-cluster distance was noticed between cluster III and VI (4265.10) followed by cluster III and V (3569.30), cluster IV and VI (3365.38) suggesting wide diversity between them. Cluster III was found to be promising for yield and its major component traits, while the genotypes in Cluster VI had for earlier flowering and maturity. Therefore, clusters III, V and VI genotypes could be used as directly in multi-location trials for their suitability to be released for successful cowpea production or could be source materials for obtaining desirable new recombinants for early maturity and higher yield in South Ethiopia.

III. MATERIAL AND METHODS

The present investigation work on "Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]". The experiment was conducted at Agronomy Instructional Farm, Chimanbhai Patel College of Agriculture, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *kharif* 2021 0 at Agronomy Instructional Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Geographically, Sardarkrushinagar is situated at 240 - 19' North latitude and 720 - 19' East longitude with an altitude of 154.52 meter above the mean sea level. The soil of experimental sight is sandy loam in texture with a pH of 7.5 and and it is situated in North Gujarat Agro-climatic Zone. The weather condition during crop season was favorable for the crop showed in Appendix-A.

The details of the material used, methods adopted and statistical analysis followed during the investigation are described as below.

3.1 Experimental materials

The experimental materials used for study consisted of thirty genotypes of s of diverse geographic and genetic origin of cowpea. These were procured from the Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. The list of thirty cowpea genotypes is given in Table 3.1

Table 3.1 : Genotypes included in the study

Sr. No.	Name of genotypes	Sr. No.	Name of genotypes
1.	GC 3	**16.**	GC 2111
2.	GC 4	**17.**	GC 2112
3.	GC 5	**18.**	GC 2113
4.	GC 6	**19.**	GC 2114
5.	GC 1501	**20.**	GC 2115
6.	GC 2101	**21.**	GC 2116
7.	GC 2102	**22.**	GC 2117
8.	GC 2103	**23.**	GC 2118
9	GC 2104	**24.**	GC 2119
10.	GC 2105	**25.**	GC 2120
11.	GC 2106	**26.**	GC 2121
12.	GC 2107	**27.**	GC 2002
13.	GC 2108	**27.**	GC 2006
14.	GC 2109	**29.**	GC 2007
15.	GC 2110	**30.**	GC 1905

3.2 Methodology

3.2.1 Experimental design

A set of thirty diverse genotypes of cowpea were sown in a randomized block design (RBD) with four replications during *kharif* 2021. Sowing was done on 16th July, 2021. Each genotype was accommodated in a single row of 4 m length with a spacing 45 cm between row and 15 cm between plants. All the recommended crop production and protection practices were followed to raise the good crop.

3.2.2 Sowing and cultural practices

The land selected for the experiment was sandy loam soil which brings to fine tilth. The fertilizer @ 20kg N and 40 kg P_2O_5/ha were applied as a basal dose at the time of sowing. The operations like thinning, weeding, hoeing and plant protection measures were carried out regularly to ensure satisfactory crop growth. Given the treatment of pendimethalin herbicide as pre-emergence.

3.3 Observations recorded

Five competitive plants per genotype were randomly selected for recording observation on following characters in each replication and averages were worked out for statistical analysis. For the characters like days to flowering and days to maturity observation were recorded on plot basis.

3.3.1 Days to flowering

Number of days from the date of sowing to the date on which 50 per cent of the plants flowered in each entry in each replication on plot basis was recorded.

3.3.2 Days to maturity

Number of days taken from the date of sowing to 80 per cent of the physiological maturity of crop was recorded as days to maturity on plot basis in each genotypes for each replication.

3.3.3 Plant height (cm)

The plant height was recorded from ground level to the tip of main stem at maturity in randomly selected five plants and averaged out.

3.3.4 Number of branch per plant

The number of pod bearing branch per plant of the randomly selected five plants was counted at the time of maturity.

3.3.5 Number of pod per plant

The number of well filled pod per plant was counted from five randomly selected plants at maturity and averaged out.

3.3.6 Number of seed per pod

This observation was recorded by taking the seeds of randomly selected five pods from a randomly selected five plants and the average of five pods was estimated.

3.3.7 Pod length (cm)

The length of five randomly selected pods on randomly selected five plants was measured and the average was worked out.

3.3.8 100 seed weight (g)

Hundred seeds were randomly counted from the bulk of seeds harvested from five randomly selected plants of each genotype and weighed in grams.

3.3.9 Seed yield per plant (g)

Seeds from randomly selected five competitive plants were harvested, threshed, cleaned, weighed and averaged out on plant basis in gram.

3.3.10 Harvest index (%)

The ratio of grain yield (g) to total dry matter of plant was considered as harvest index and expressed in percentage. It was calculated using the formula of Donald and Hamblin (1976) for each genotype in each replication.

Harvest index calculated by using following formula:

$$\text{Harvest Index (\%)} = \frac{\text{Economic yield per plant (g)}}{\text{Biological yield per plant (g)}} \times 100$$

3.3.11 Protein content (%)

One-gram grinded seed powder (floor) was weighed on electronic balance and taken for estimation of seed protein content with the help of Instalab 600 NIR analyzer and expressed in percentage.

3.4 Statistical procedure

The mean values of five randomly selected observational plants for thirty-two different genotypes were used for statistical analysis. The following statistical parameters were worked out for presentation of the data on different quantitative attributes.

3.4.1 Analysis of variance
3.4.2 Genetic variability parameters
3.4.3 Correlation coefficient
3.4.4 Path coefficient analysis
3.4.5. Genetic divergence

3.4.1 Analysis of variance

The data recorded for all the characters were subjected to analysis of variance with the formula suggested by Panse and Sukhatme (1978). The statistical model used for analysis of the present investigation is described below.

$$Y_{ij} = \mu + a_i + b_j + e_{ij}$$

Where,

Y_{ij} = Yield of j^{th} genotype in i^{th} replication,

μ = General mean,

a_i = Effect of i^{th} replication,

b_j = Effect of j^{th} genotype, and

e_{ij} = Uncontrolled variation associated with i^{th} replication and j^{th} genotype.

For all the characters under study, the mean values of five randomly selected plants were used for statistical analysis. The data recorded for different characters were subjected to analysis of variance. Different components of variance *viz.*, phenotypic, genotypic and environmental variances were estimated. Different parameters of genetic variability were computed by standard statistical procedures. The phenotypic and genotypic correlations were also estimated. The genotypic correlations were subjected to path coefficient analysis. The analysis of variance was done as suggested by Panse and Sukhatme (1978).

Table 3.2 : Analysis of variance for experimental design

Source of variation	d.f.	MSS	Expected mean square
Replications	(r-1)	MSr	$\sigma^2_e + t\ \sigma^2_r$
Genotypes	(t-1)	MSt	$\sigma^2_e + r\ \sigma^2_g$
Error	(r-1) (t-1)	MSe	σ^2_e
Total	(rt-1)	-	-

Where,

r = Number of replications,

g = Number of genotypes,

σ^2_e = Variances due to error,

σ^2_r = Variances due to replication,

σ^2_g = Variances due to genotypes,

MSr = Mean sum of square for replication,

MSt = Mean sum of square for genotypes, and

MSe = Mean sum of square for error.

The standard error for differences between treatments mean was calculated from ANOVA table.

$$\text{S.Em.}\pm = \sqrt{\frac{\sigma_e^2}{r}}$$

Where,

S.Em. = Standard Error of Mean,

$\sigma^2{}_e$ = Error Mean Square, and

r = Number of replications.

The critical difference to compare the mean values of various genotypes was calculated by using the following formula.

$$\text{C.D.} = \sqrt{2} \times \text{S.Em.} \times t_{0.05} \text{ at error d.f.}$$

Where,

C.D. = Critical difference

S.Em. = Error Mean Square,

r = Number of replication, and

t = Table 't' value at error d.f.

The Coefficient of Variation (C.V. %) was calculated by using the following formula :

$$\text{C.V.}\,\% = \frac{\sqrt{\text{MSe}}}{\bar{X}} \times 100$$

Where,

C.V. = Coefficient of variation,

MSe = Mean sum of square of error, and

$\bar{X}$ = General mean.

3.4.2 Genetic variability parameters

[i] Mean

It is computed by dividing the sum of all observations in a sample by their number.

$$\bar{X} = \frac{\Sigma X_{ij}}{n}$$

Where,

$\bar{X}$ = General mean,

X_{ij} = Any observation in i^{th} replication and j^{th} genotype, and

n = Number of observations.

[ii] Range

It is the difference between maximum value and minimum value in a particular character. The genotypic, phenotypic and environmental components were estimated as explained by Johnson *et al.* (1955).

$$\text{Range} = \text{Maximum value} - \text{Minimum value}$$

[iii] Genotypic variance (σ^2_g)

The genotypic variance is contributed by genetic cause or the occurrence of difference among individuals due to differences in their genetic make-up. Following formula was used.

$$\text{Genotypic variances } (\sigma^2_g) = \frac{\text{Genotypic M S} - \text{Error M S}}{\text{Number of replications (r)}}$$

[iv] Environmental variance

Following formula was used.

$$\text{Environmental variances } (\sigma^2_e) = \text{Mean square of error (MSe)}$$

[v] Phenotypic variance

It is the sum of the variances contributed by genetically causes and environmental factors and is calculated as under.

$$\text{Phenotypic variance } (\sigma^2_p) = \text{Error variance } (\sigma^2_e) + \text{Genotypic variance } (\sigma^2_g)$$

[vi] Coefficient of variation

The coefficient of phenotypic and genotypic variations was calculated by the formula suggested by Burton (1952).

(a) Phenotypic Coefficient of Variation (PCV)

The phenotypic coefficient of variation, which measures the magnitude of phenotypic variation present in a particular character. It was estimated as per the formula suggested by Burton (1952).

$$\text{PCV\%} = \frac{\sqrt{\sigma^2 p}}{\text{Mean } (\overline{X})} \times 100$$

Where,

$\sigma^2 p$ = Phenotypic variance, and

$\overline{X}$ = Mean of a character.

(b) Genotypic Coefficient of Variation (GCV)

The genotypic coefficient of variation, which measures the magnitude of genetic variation present in a particular character. It was estimated as per the formula suggested by Burton (1952).

$$\text{GCV\%} = \frac{\sqrt{\sigma^2 g}}{\text{Mean } (\bar{X})} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance, and

$\bar{X}$ = Mean of a character.

GCV and PCV were categorized as low, moderate and high by following Shivasubramanian and Menon (1973). It is as follows :

0-10 % = Low

10-20 % = Moderate

20 % and above = High

[vii] Heritability (Broad Sense) h^2 (bs)

It is the proportion of phenotypic variability that is due to genetic reasons. It was calculated by using the formula proposed by Allard (1961).

$$h^2(\text{bs})\ \% = \frac{\text{Genotypic variance } (\sigma^2 g)}{\text{Phenotypic variance } (\sigma^2 p)} \times 100$$

Where,

$\sigma^2 g$ = Genotypic variance, and

$\sigma^2 p$ = Phenotypic variance.

Heritability percentage was categorized as demonstrated by Robinson (1966). It is as follows :

0-30 % = Low

30-60 % = Moderate

60 % and above = High

[viii] Expected genetic advance (GA)

Expected genetic advance represents the shift in a population towards superior side under some selection pressure after single generation of selection. It could be calculated by using the methodology suggested by Allard (1961) at 5 per cent selection intensity using the constant ‘K’ as 2.06.

$$G.A. = h^2 (b) \times K \times \sigma_p$$

Where,

G.A. = Genetic Advance.

h^2(bs) = Heritability (Broad sense).

K = Selection intensity at 5 per cent = 2.06, and

σ_p = Phenotypic standard deviation.

[ix] Genetic advance expressed as per cent of mean (Genetic gain)

The expected genetic advance as expressed in per cent of mean was calculated by the method suggested by Johnson *et al.* (1955).

$$\text{Genetic gain \%} = \frac{\text{Expected genetic advance (G.A.)}}{\text{Mean } (\bar{X})} \times 100$$

The genetic advance as per cent mean was categorized as suggested by Johnson *et al.* (1955). It is as follows :

0-10 %	=	Low
10-20 %	=	Moderate
20 % and above	=	High

3.4.3 Correlation coefficient

Correlation coefficients measure the relationship between two or more series of variables. The genotypic correlation coefficient provides a measure of genotypic association between different characters, while phenotypic correlation includes both genotypic as well as environmental influences.

For this purpose, analysis of covariance for all possible pairs of eleven characters was carried out using the procedure of Panse and Sukhatme (1978).

Table 3.3 : Analysis of variance for correlation coefficient

Source	d.f.	Mean square of products (M.S.)	Expectation of mean square of products
Replications	(r-1)	MSP_1	$Cov_exy + gCov_rxy$
Genotypes	(g-1)	MSP_2	$Cov_exy + rCov_gxy$
Error	(r-1) (g-1)	MSP_3	Cov_exy
Total	(rg-1)	-	-

Where,

r = Number of replications,

g = Number of genotypes,

Cov_exy = Environmental component of covariance,

Cov_rxy = Replication component of covariance,

$Cov_g\ xy$ = Genotypes components of covariance,

MSP_1 = Mean square products for replication,

MSP_2 = Mean square products for genotypes, and

MSP_3 = Mean square product for error.

The components of covariance were estimated by equating the observed mean sum of products with their expectations as shown below.

$$Cov_g xy = \frac{(MSP2-MSP3)}{r}$$

$$Cov_e xy = MSP_3$$

$$Cov_p xy = Cov_g xy + Cov_e xy$$

Where,

$Cov_g xy$ = Genotypic components of covariance,

$Cov_e xy$ = Environmental components of covariance, and

$Cov_p xy$ = Phenotypic components of covariance.

The genotypic (r_g) and phenotypic (r_p) correlation coefficient were calculated as under by adopting the procedure explained by Al-Jibouri *et al.* (1958).

(a) Genotypic correlation coefficient :-

$$r_g(XY) = \frac{Cov_g\ (XY)}{\sqrt{\sigma_g^2(X)} \times \sqrt{\sigma_g^2(Y)}}$$

(b) Phenotypic correlation coefficient :-

$$r_p(XY) = \frac{Cov_p\ (XY)}{\sqrt{\sigma_p^2(X)} \times \sqrt{\sigma_p^2(Y)}}$$

Where,

$r_g(xy)$ and $r_p(xy)$ are genotypic and phenotypic correlation coefficient for a pair of trait x and y, respectively.

$Cov_g(xy)$ and $Cov_p(xy)$ are genotypic and phenotypic covariance for a pair of characters x and y, respectively.

The phenotypic correlation was tested using the method suggested by Fisher and Yates (1963).

3.4.4 Path coefficient analysis

The cause and effect, interrelationship between two variables cannot be estimated from simple correlation coefficient analysis. Path coefficient is a standardized partial regression coefficient and measures the direct and indirect influence of one variable upon another thereby permitting the separation of correlation coefficient into the component of direct and indirect effects. Therefore, the path coefficient analysis was carried-out according to the method suggested by Wright (1921) and used by Dewey and Lu (1959). Genotypic correlation coefficients of twelve variables with seed yield per plant were used to estimate the path coefficients for the direct effects of various independent characters on seed yield per plant.

The path coefficients were obtained by solving a set of simultaneous equations as below.

$$r_{ny} = P_{ny} + r_{n2} \,.\, P_{2y} + r_{n3}.\, P_{3y} + r_{n4}.\, P_{4y} + \ldots\ldots + r_{nx} \,.\, P_{xy}$$

Where,

r_{ny} = Represents correlation coefficient between one component character and seed yield per plant,

P_{ny} = Represents the path coefficient between the character and seed yield per plant, and

r_{n2}, r_{n3}... r_{nx} = Represents correlation coefficient between that character and other yield component in turn.

The following correlation matrix was formed,

Matrix-A **Matrix-B** **Matrix-C**

$$\begin{pmatrix} r_1y \\ r_2y \\ r_3y \\ : \\ : \\ : \\ r_ny \end{pmatrix} = \begin{pmatrix} r_{11} & r_{12}.......r_{1n} \\ r_{21} & r_{22}.......r_{2n} \\ r_{31} & r_{31}.......r_{3n} \\ : & : \quad : \\ : & : \quad : \\ : & : \quad : \\ r_{n1} & r_{n2} \quad r_{nn} \end{pmatrix} \times \begin{pmatrix} p_1y \\ p_2y \\ p_3y \\ : \\ : \\ : \\ p_ny \end{pmatrix}$$

Or A = B × C

Where,

r_{11}...rnn

r_{12}, r_{21} and so on = Correlation between two component characters, and

r_{1y}, r_{2y} and so on = Correlation between component characters and seed yield per plant.

The technique given by Goulden (1962) was followed for inversion of the ‘B’ matrix using partitioning method of matrix inversion.

Path coefficients (Pij) were obtained as follows.

$$P_{ij} = (B^{-1}) \times (A)$$

Where,

(B^{-1}) is the inverse of mutual correlation matrix of character.

The indirect effects for a particular character through other characters were obtained by multiplication of direct path and particular correlation coefficient between those two characters, respectively.

$$\text{Indirect effect} = r_{ij} \times P_{ij}$$

Where,

i = 1, 2, 3, ...,....,..,., n

j = 1, 2, 3, ...,..,..,..., n

P_{ij} = $P_1y \times P_2y \times P_3y \times .... \times P_ny$

Path coefficient (P_{ij}), correlation coefficient (r_{ij}) and residual factors (R) were diagrammatically presented. The residual factor *i.e.,* variation in yield unaccounted for by these associations was calculated with the following formula.

$$\text{Residual factor (R)} = \sqrt{1 - R^2}$$

Where,

R^2 = $(P_{1y}\, r_{1y} + P_{2y}\, r_{2y} + ... + P_{ny}.r_{ny})$,

$P_{1y}, P_{2y}, ..., P_{ny}$ = Direct path values

r_{1y}, r_{2y}, r_{ny} = Correlation coefficient.

The path coefficient value was categorized as suggested by (Lenka and Mishra, 1973).

0.00 to 0.09 = Negligible

0.10 to 0.19 = Low

0.20 to 0.29 = Moderate

0.30 to 0.99 = High

More than 1.00 = Very high

3.4.5. Genetic divergence

Mahalanobis (1936) D^2 statistic was used for assessing the genetic divergence between different populations. The D^2 analysis was carried out using the data recorded on germplasms. Mahalanobis generalized distance (D^2) between any two populations is given by the formula.

$$D^2=\Sigma\lambda^{ij}\sigma^{ij}$$

Where,

D^2 = Square of generalized distance,

λij = Reciprocal of the common dispersal index,

Σi = $\mu i1 - \mu i2$,

Σj = $\mu j2 - \mu j1$, and

M = General mean.

Since the formula for computation requires inversion of higher order determinants, transformation of the original correlated unstandardized character mean (Xs) to standardize uncorrelated variable (Ys) was done to simplify the computational procedure. The D^2 values were obtained as the corresponding uncorrelated (Ys) values of any two uncorrelated genotypes (Rao, 1952).

3.4.5.1 Group constellation based on D^2

Grouping of the genotypes in different clusters was done by using Tocher's method (Rao, 1952). The criterion used for clustering in this method is that any two genotypes belonging to the same cluster should on an average show a smaller D^2 values than those belonging to different clusters.

To start with, two genotypes having smallest average D^2 value between them were considered, to which a third genotype having smallest average D^2 value from these genotypes was added. Next, the nearest fourth genotypes were considered, and this procedure was continued. At a certain stage, when it was felt that inclusion of a genotype result in abrupt increase in the average D^2 of the genotypes (for that cluster), that genotype was not included in the cluster. In a similar way the other clusters were formed. This procedure was continued till all the genotypes were included in one cluster or the other cluster. After the formulation of the clusters, average intra-cluster distance (D) was calculated by using the formula.

$$D = \sqrt{\Sigma Di^2 / n}$$

Where,

ΣDi^2 = Sum of distance between all possible combinations of the populations included in the cluster, and

N = Number of population in a cluster.

The inter and inter-cluster distance was calculated by Tocher's method as suggested by Rao (1952) to form the clusters. This criterion was based on the principles that any two populations belonging to the same cluster should at least on the average show smaller D2 than belonging to different clusters. For graphical presentation average intra-cluster values were used to obtain manual relationship between clusters.

3.4.5.2Cluster means:

Cluster means were calculated for individual character on the basis of mean performance of the genotypes included in the cluster.

IV. RESULTS AND DISCUSSION

The experimental results obtained from the present investigation on "Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]" are presented and discussed here under the following sub-headings.

4.1 Analysis of variance for experimental design

4.2 Analysis of variability components

4.3 Estimation of correlation coefficients

4.4 Path coefficient analysis

4.5 Genetic divergence using D^2 statistics

4.1 Analysis of variance for experimental design

The analysis of variance for all the eleven characters in thirty genotypes was carried out in a randomized block design. The results obtained are presented in Table 4.1. The result revealed highly significant for all the traits *viz.*, days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, number of seed per pod, 100 seed weight, protein content and seed yield per plant. This is indicating that the existence of tremendous variability in the experimental material under study and there may be a scope for improvement of these traits through selection.

Table 4.1 Analysis of variance for experimental design

Sr. No.	Characters	Mean sum of square		
		Replications	**Genotypes**	**Environmental**
Degree of Freedom:		**3**	**29**	**87**
1	Days to flowering	0.41	12.02**	0.32
2	Days to maturity	1.79	7.23**	0.79
3	Plant height (cm)	1.67	260.52**	7.27
4	Number of branch per plant	0.17	3.60**	0.23
5	Number of pod per plant	0.00	12.24**	0.43
6	Number of seed per pod	0.31	11.61**	0.81
7	Pod length (cm)	0.19	6.28**	1.25
8	100 seed weight (g)	0.04	21.92**	0.93
9	Protein content (%)	0.25	3.07**	0.11
10	Harvest index (%)	37.98	465.05**	31.19
11	Seed yield per plant (g)	1.90	6.69**	1.17

*, ** Significant at 5% and 1% level of significance, respectively.

4.2 Analysis of variability components

Analysis of variance (ANOVA) may not reveal that the mean square of genotypes was found highly significant for all the characters under study which indicated highly significant differences among the cowpea genotypes for eleven characters *viz.,* days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, number of seed per pod, pod Length, 100 seed weight, protein content, seed yield per plant and harvest index, which revealed the existence of variability in the experimental material and this could be accessed through standardizing the phenotypic and genotypic variances by obtaining coefficient of variability.

The genetics of metric character centers on the study of its variation. The amount of variation is measured and expressed as the variance. Further, it is essential to separate out the environmental influence from the total variability. This indicates the accuracy with which genotype can be identified by its phenotypic performance. The estimates of heritability alone fail to indicate the response to selection. Therefore, the heritability estimates appeared to be more meaningful when accompanied by estimates of genetic advance.

Best six *per se* performing genotypes (Table 4.2) for days to flowering [GC 2002 (39.25), GC 2112 (39.50), GC 2007 (39.50), GC 2120 (39.75), GC 2118 (40.50) and GC 1905 (40.75)], days to maturity [GC 1501 (60.25), GC 2002 (61.50), GC 2006 (61.50), GC 2007 (62.00), GC 2120 (62.25) and GC 2101 (62.50)], lowest plant height [GC 2121 (35.97 cm), GC 2118 (39.19 cm), GC 2101 (39.89 cm), GC 2105 (41.66 cm), GC 3 (44.21 cm) and GC 2110 (47.77 cm)], highest plant height [GC 2106 (69.22 cm), GC 2111 (68.89 cm), GC 2113 (63.66 cm), GC 2107 (61.83 cm), GC 2119 (61.42 cm) and GC 2108 (60.90 cm)], number of branch per plant [GC 2109 (10.45), GC 2116 (9.40), GC 2115 (9.15), GC 2108 (9.00), GC 2113 (8.90) and GC 2107 (8.80)], number of pod per plant [GC 2106 (18.19), GC 2108 (17.74), GC 1501 (17.17), GC 2006 (16.24), GC 2109 (15.95) and GC 2007 (15.49)], number of seed per pod [GC 2118 (14.59), GC 3 (14.44), GC 2103 (14.34), GC 2120 (13.44), GC 2109 (13.40) and GC 2006 (13.39)], pod length [GC 2108 (15.29 cm), GC 2106 (15.27 cm), GC 2118 (14.53 cm), GC 2101 (14.45 cm), GC 2109 (14.09 cm) and GC 1905 (14.09 cm)], 100 seed weight [GC 2112 (16.17 g), GC 2111 (16.14 g), GC 2113 (15.44 g), GC 2109 (15.37 g), GC 2103 (15.27 g) and GC 4 (15.17 g)], harvest index [GC 2108 (73.18 %), GC 2109 (70.43 %), GC 2118 (70.37 %), GC 2006 (70.08 %), GC 2106 (69.51 %) and GC 3 (69.26 %)], protein content [GC 2002 (24.19 %), GC 2007 (23.75 %), GC 2119 (23.72 %), GC 2101 (23.53 %), GC 2006 (23.32 %) and GC 2107 (23.07 %)], seed yield per plant [GC 2108 (21.70 g), GC 2109 (20.35 g), GC 2106 (20.23 g), GC 2006 (19.98 g), GC 2118 (19.60 g), and GC 3 (19.58 g)].

Table 4.2 : Best six *per se* performing genotypes

Sr. No.	Characters	Name of genotype	Mean
1	**Days to flowering**	GC 2002	39.25
		GC 2112	39.50
		GC 2007	39.50
		GC 2120	39.75
		GC 2118	40.50
		GC 1905	40.75
2	**Days to maturity**	GC 1501	60.25
		GC 2002	61.50
		GC 2006	61.50
		GC 2007	62.00
		GC 2120	62.25
		GC 2101	62.50
3	**Plant height (cm)**	Lowest:-	
		GC 2121	35.97
		GC 2118	39.19
		GC 2101	39.89
		GC 2105	41.66
		GC 3	44.21
		GC 2110	47.77
		Highest: -	
		GC 2106	69.22
		GC 2111	68.89
		GC 2113	63.66
		GC 2107	61.83
		GC 2119	61.42
		GC 2108	60.90
4	**Number of branch per plant**	GC 2109	10.45
		GC 2116	9.40
		GC 2115	9.15
		GC 2108	9.00
		GC 2113	8.90
		GC 2107	8.80
5	**Number of pod per plant**	GC 2106	18.19
		GC 2108	17.74
		GC 1501	17.17
		GC 2006	16.24
		GC 2109	15.95
		GC 2007	15.49
6	**Number of seed per pod**	GC 2118	14.59
		GC 3	14.44
		GC 2103	14.34
		GC 2120	13.44
		GC 2109	13.40
		GC 2006	13.39

Table 4.2 Continue...

Table 4.2 Continue...

Sr. No.	Characters	Name of genotype	Mean
7	**Pod length (cm)**	GC 2108	15.29
		GC 2106	15.27
		GC 2118	14.53
		GC 2101	14.45
		GC 2109	14.09
		GC 1905	14.09
8	**100 seed weight (g)**	GC 2112	16.17
		GC 2111	16.14
		GC 2113	15.44
		GC 2109	15.37
		GC 2103	15.27
		GC 4	15.17
9	**Harvest index (%)**	GC 2108	73.17
		GC 2109	70.43
		GC 2118	70.37
		GC 2006	70.08
		GC 2106	69.51
		GC 3	69.26
10	**Protein content (%)**	GC 2002	24.19
		GC 2007	23.75
		GC 2119	23.72
		GC 2101	23.53
		GC 2006	23.32
		GC 2107	23.07
11	**Seed yield per plant (g)**	GC 2108	21.70
		GC 2109	20.35
		GC 2106	20.23
		GC 2006	19.98
		GC 2118	19.60
		GC 3	19.58

The ratio of genotypic variance to the phenotypic variance is known as broad sense heritability. It is generally expressed in per cent. Thus, heritability is the heritable portion of phenotypic variance. It is a good index of the transmission of characters from parents to their offspring (Falconer, 1981). Improvement in the mean genotypic value of selected plants over the parental population is known as genetic advance. It is the measure of genetic gain under selection. The success of genetic advance under selection depends on three main factors *viz.*, genetic variability, heritability and selection intensity (Allard, 1961).

The mean performance of thirty cowpea genotypes under study for eleven traits were presented in Appendix II. The estimate of genotypic (σ^2g) and phenotypic (σ^2p)

Plate I: General view of experimental plot variances of each character as well as other genetic components narrated in Table 4.3. The PCV value was higher than GCV value for all the traits indicating that the apparent variation was not only due to genotype, but also due influence of environment on the phenotypic expression of traits (Fig. 4.1). Whereas, the Heritability h^2_b (%), Genetic advance GA (%) and Genetic advance per cent of mean GAM (%) narrated in Table 4.3 and Figure 4.1.

4.2.1 Days to flowering

4.2.1.1 Mean performance

The wide range of variability was recorded for days to flowering from 39.25 to 45.75 days with a general mean of 42.48 days. Minimum days to flowering were observed in genotype GC 2002 (39.25) followed by GC 2112 (39.50) and GC 2107 (39.50), GC 2120 (39.75), GC 2118 (40.50), GC 1905 (40.75), respectively. Maximum days to flowering recorded in GC 2109 (45.75) followed by GC 2108 (45.00), GC 2110 (44.75), GC 5 (44.50), GC 3 (44.25) and GC 2114 (45.25), respectively.

4.2.1.2 Variance components

The magnitude of genotypic variance, phenotypic variance and environmental variance were observed 2.92, 3.24 and 0.32 respectively. The genotypic variance contributed more proportion to the total phenotypic variance suggesting the phenotypic variance mainly due to genotypic variance. There was low influence of environment on days to flowering. The narrow difference between genotypic and phenotypic variance were also reported by Sharma *et al.* (2017_b), Bhagavati *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.1.3 Genotypic and phenotypic coefficients of variation

Days to flowering depicted low GCV (4.02 %) and PCV (4.24 %) indicate variability present in material and simple selection would be desirable for improvement of this character. Eswarna *et al.* (2007), Kumar *et al.* (2013), Khanpara *et al.* (2015), Sharma *et al.* (2017_b), Bhagavati *et al.* (2018), Das *et al.* (2018), Yadav *et al.* (2019) and Chaudhary *et al.* (2020) were reported low GCV and PCV value in cowpea.

4.2.1.4 Heritability and genetic advance (% of mean)

The high heritability (90.00 %) coupled with low genetic advance as per cent of mean (7.86 %) was recorded for days to flowering revealed that the non-additive effects of genes and selection may not be effective. The high heritability along with low genetic advance as per cent of mean were also reported by Khanpara *et al.* (2015), Sharma *et al*. (2017$_b$), Das *et al*. (2018), Sharama *et al*. (2019), Chaudhary *et al.* (2020) for days to flowering.

4.2.2 Days to maturity

4.2.2.1 Mean performance

The general mean for days to maturity was 63.52 days with a range from 60.25 to 66.00 days. The genotypes GC 1501 (60.50 days) was earliest in the maturity followed by GC 2002 and GC 2006 (61.50 days), GC 2007 (62.00 days), GC 2120 (62.25 days) and GC 2101 (62.50 days). The late maturity genotypes were GC 2109 (66 days) followed by GC 2108 (65.75 days) and GC 2110 (65.75 days).

4.2.2.2 Variance components

The magnitude of genotypic variance, phenotypic variance and environmental variance were observed 1.60, 2.40 and 0.80, respectively. The genotypic variance (1.60) contributed more proportion to the total phenotypic variance (2.40) suggesting the phenotypic variance mainly due to genotypic variance. It indicates that there is little influence of environment on expression of days to flowering. The present findings are in accordance with earlier results reported by Sharma *et al*. (2017$_b$), Bhagavati *et al.* (2018) and Chaudhary *et al*. (2020)

4.2.2.3 Genotypic and phenotypic coefficients of variation

Low values of GCV (1.99 %) and PCV (2.44 %) observed for days to maturity, which indicate the presence of low genetic variability in the population for this trait. The present findings are in accordance with earlier results reported by Bhagavati *et al.* (2018), Das *et al.* (2018), Yadav *et al.* (2019) and Chaudhary *et al.* (2020).

4.2.2.4 Heritability and genetic advance (% of mean)

Days to maturity exhibited high heritability (67.02 %) along with low genetic advance as per cent of mean (3.37 %) indicated that heritability is due to non-additive gene and selection may be not be effective. The high heritability along with low genetic advance as per cent of mean were also reported by *viz.*, Bhagavati *et al.* (2018), Das *et al.* (2018), Sharma *et al.* (2019) and Chaudhary *et al.* (2020)

4.2.3 Plant height (cm)

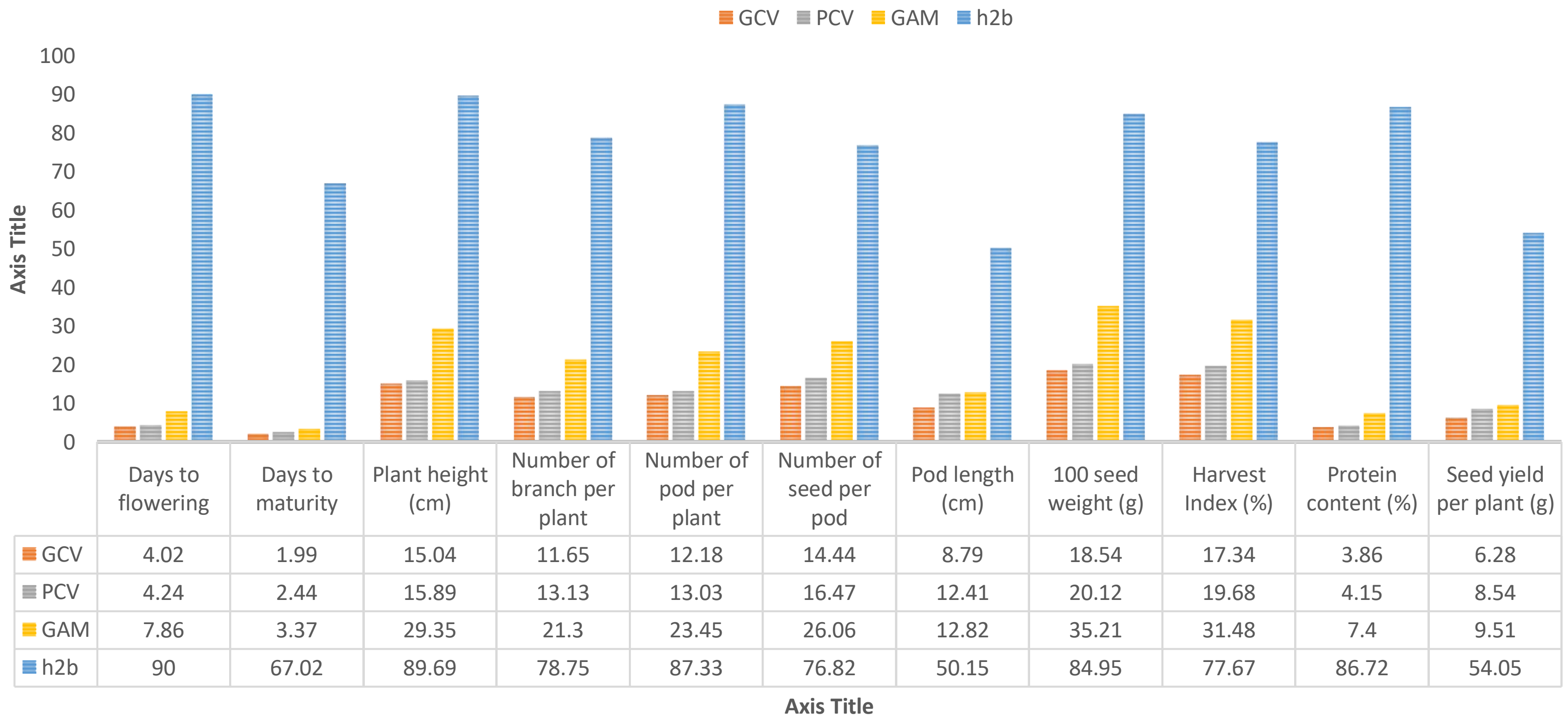
4.2.3.1 Mean performance

Among the genotypes, significant differences were recorded for plant height. The range for plant height was observed from 35.97 cm (GC 2121) to 69.22 cm (GC 2106). Maximum plant height was observed in genotype GC 2106 (69.22 cm) followed by GC

Table 4.3 : Genetic parameters of variation for seed yield and its contributing characters in cowpea

Sr. No.	Characters	Genetic parameters									
		Mean	Range	σ^2_g	σ^2_p	σ^2_e	GCV (%)	PCV (%)	h^2_b (%)	GA	GAM (%)
1	**Days to flowering**	42.48	39.25-45.75	2.92	3.24	0.32	4.02	4.24	90.00	3.34	7.86
2	**Days to maturity**	63.52	60.25-66.00	1.60	2.40	0.80	1.99	2.44	67.02	2.14	3.37
3	**Plant height (cm)**	52.88	35.97-69.22	63.31	70.58	7.27	15.04	15.89	89.69	15.52	29.35
4	**Number of branch per plant**	7.88	5.95-10.45	0.84	1.07	0.23	11.65	13.13	78.75	1.68	21.30
5	**Number of pod per plant**	14.10	11.09-18.19	2.95	3.38	0.43	12.18	13.03	87.33	3.31	23.45
6	**Number of seed per pod**	11.38	7.34-14.59	2.70	3.51	0.81	14.44	16.47	76.82	2.97	26.06
7	**Pod length (cm)**	12.76	11.09-15.29	1.25	2.50	1.25	8.79	12.41	50.15	1.64	12.82
8	**100 seed weight (g)**	12.35	8.59-16.17	5.24	6.17	0.93	18.54	20.12	84.95	4.35	35.21
9	**Harvest Index (%)**	60.05	33.50-73.17	108.46	139.65	31.19	17.34	19.68	77.67	18.91	31.48
10	**Protein content (%)**	22.26	20.74-24.19	0.74	0.85	0.11	3.86	4.15	86.72	1.65	7.40
11	**Seed yield per plant (g)**	18.30	14.96-21.70	1.38	2.55	1.17	6.28	8.54	54.05	1.79	9.51

*, ** significant at 5 % and 1 % level of significance, respectively.



	Days to flowering	Days to maturity	Plant height (cm)	Number of branch per plant	Number of pod per plant	Number of seed per pod	Pod length (cm)	100 seed weight (g)	Harvest Index (%)	Protein content (%)	Seed yield per plant (g)
GCV	4.02	1.99	15.04	11.65	12.18	14.44	8.79	18.54	17.34	3.86	6.28
PCV	4.24	2.44	15.89	13.13	13.03	16.47	12.41	20.12	19.68	4.15	8.54
GAM	7.86	3.37	29.35	21.3	23.45	26.06	12.82	35.21	31.48	7.4	9.51
h2b	90	67.02	89.69	78.75	87.33	76.82	50.15	84.95	77.67	86.72	54.05

Fig. 4.1:- Graphical representation of environment, GCV, PCV, heritability (h^2_b) and genetic advance as percent of mean for eleven character in cowpea

2111 (68.89 cm), GC 2113 (63.66 cm), GC 2107 (61.83 cm) and GC 2119 (61.42 cm). Phenotypically dwarfness was observed in genotype GC 2121 (35.97 cm) followed by GC 2118 (39.19 cm), GC 2101 (39.89 cm), GC 2105 (41.66 cm), GC 3 (44.21 cm) and GC 2110 (47.77 cm). The general mean of plant height was 52.88 cm.

4.2.3.2 Variance components

The magnitude of genotypic variance (63.31), environmental variance (7.27) and phenotypic variance (70.58) were found, which suggested the phenotypic variance mainly due to genotypic variance. It indicates that there is little influence of environment on expression of days to maturity. The present findings are in accordance with earlier results reported by Khanpara *et al.* (2015), Sharma *et al.* (2017$_b$) and Chaudhary *et al.* (2020).

4.2.3.3 Genotypic and phenotypic coefficients of variation

The genotypic (15.04 %) and phenotypic (15.89%) coefficients of variation were moderate for plant height. The little difference between GCV and PCV value revealed negligible influence of environment on the expression of plant height. The present findings are in accordance with earlier results reported by Kumar *et al.* (2013), Khanpara *et al.* (2015) and Chaaudhary *et al.* (2020).

4.2.3.4 Heritability and genetic advance (% of mean)

The high heritability (89.67 %) coupled with high per cent of mean genetic advance (29.35 %) indicated the possibility of improving and fixing this character through selection due to additive gene effect. Similar result was also observed by Khanpara *et al.* (2015), Sarath and Reshma (2017), Sharma *et al.* (2017$_b$), Das *et al.* (2018), Sharama *et al.* (2019), Yadav *al.* (2019), Chaudhary *et al.* (2020)

4.2.4 Number of branch per plant

4.2.4.1 Mean performance

The range for number branch per plant was noticed from 5.95 (GC 1905) to 10.45 (GC 2109). The genotypes GC 2109 had the maximum number of branch per plant (10.45) followed by GC 2116 (9.40), GC 2115 (9.15), GC 2108 (9.00), GC 2113 (8.90), GC 2107 (8.80) showed superior performance for number of branch per plant. The general mean of number branch per plant was 7.88.

4.2.4.2 Variance components

The genotypic variance (0.84) contributed more proportion to the total phenotypic variance (1.07) suggesting the phenotypic variance mainly due to genotypic variance. It indicates that there is a little influence of environment on number of branch per plant. The present findings are in accordance with earlier results reported by Sharma *et al.* (2017$_b$), Bhagavati *et al.* (2018) and Kumar *et al.* (2018).

4.2.4.3 Genotypic and phenotypic coefficients of variation

Number of branch per plant showed moderate GCV (11.65 %) and PCV (13.13 %) value, which indicate moderate variability present in population and simple selection may be rewarding. The present finding was close in conformity with finding of Kumar *et al*. (2013), Khanpara *et al*. (2015), Sarath and Reshma (2017), Sharma *et al*. (2017$_b$), Bhagavati *et al*. (2018), Sharama *et al*. (2019), Yadav *et al*. (2019) and Chaudhary *et al*. (2020).

4.2.4.4 Heritability and genetic advance (% of mean)

The high heritability (78.75 %) coupled with high genetic advance as per cent mean (21.30 %) exhibited for number of branch per plant indicates heritability is due to additive gene influence. Thus, improvement and fixing of this character through selection could be fruitful. The present findings were close in conformity with finding of Khanpara *et al*. (2015), Sarath and Reshma (2017), Sharma *et al*. (2017$_b$), Bhagavati *et al*. (2018), Kumar *et al*. (2018), Thouseem *et al*. (2018), Sharama *et al*. (2019) and Yadav *et al*. (2019).

4.2.5 Number of pod per plant

4.2.5.1 Mean performance

The wide range for number of pod per plant was observed from 11.09 (GC 2102) to 18.19 (GC 2106). The genotype GC 2106 had the highest number of pod per plant (18.19) followed by GC 2108 (17.74), GC 1501 (17.17), GC 2006 (16.24), GC 2109 (15.95), GC 2007 (15.49) and GC 2104 (15.24). The general mean of number of pod per plant was 14.10.

4.2.5.2 Variance components

The magnitude of genotypic variance (2.95), phenotypic variance (3.38) and environmental variance (0.43). The genotypic variance contributed more proportion to the total phenotypic variance suggesting the phenotypic variance mainly due to genotypic variance. It indicates the little influence of environment on expression of number of pod per plant. The present findings confirmed with the result of Sharma *et al*. (2017$_b$) and Kumar *et al*. (2018).

4.2.5.3 Genotypic and phenotypic coefficients of variation

The estimates of GCV (12.18 %) and PCV (13.03 %) were high for number of pod per plant, which indicate the moderate variability present in population and simple selection would be desirable for improvement of this character. The present findings confirmed the report of Kumar *et al.* (2013), Sharma *et al.* (2017$_b$), Pandiyan *et al.* (2019), Verma *et al*. (2019) and Ugale *et al*. (2020).

4.2.5.4 Heritability and genetic advance (% of mean)

Number of pod per plant depicted high heritability (87.33 %) coupled with high genetic advance as per cent of mean (23.45 %) suggesting that the predominance of additive gene action were largely responsible for the reflection of this character. Thus, direct selection could be fruitful. Similar results were also obtained by Khanpara *et al.* (2015), Sarath and Reshma (2017), Sharma *et al*. (2017$_b$), Bhagavati *et al*. (2018), Das *et al*. (2018), Kumar *et al*. (2018), Thouseem *et al*. (2018), Sharma *et al*. (2019) and Yadav *et al*. (2019).

4.2.6 Pod length (cm)

4.2.6.1 Mean performance

Genotypes exhibited significant differences for pod length. The range for pod length was observed from 11.09 cm (GC 1501) to 15.29 cm (GC 2108). The genotype GC 2108 exhibited the longest pod length (15.29 cm) followed by GC 2106 (15.27 cm), GC 2118 (14.53 cm), GC 2101 (14.45 cm), GC 2109 (14.09 cm) and GC 1905 (14.09 cm). The general mean of pod length was 12.76 cm.

4.2.6.2 Variance components

The results revealed that the magnitude of genotypic variance (1.25), phenotypic variance (2.50) and environmental variance (1.25). The environmental variance and genotypic variance contribute equal proportion to the total phenotypic variance. It indicates that the environment is playing a significant role in the expression of this character. Selection for the improvement of this character will be ineffective. The present findings confirmed the report of Kumar *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.6.3 Genotypic and phenotypic coefficients of variation

Pod length showed low value of GCV (8.79 %) and moderate value of PCV (12.41 %). The GCV value was equal to ECV and lower than PCV values indicated environment play major role in expression of this trait. Simple selection will not be rewarding. The similar finding was earlier reported by Kumar *et al*. (2013), Khanpara *et al*. (2015), Sarath and Reshma (2017), Das *et al*. (2018), Kumar *et al*. (2018) and Sharama *et al*. (2019).

4.2.6.4 Heritability and genetic advance (% of mean)

Pod length exhibited low heritability (50.15 %) along with moderate genetic advance as per cent of mean (12.82 %) indicating that non-additive gene action present and highly environment role in this trait. Thus, direct selection may not be desirable for pod length. The similar finding was earlier reported by Kumar *et al.* (2013), Khanpara *et al.* (2015), Das *et al.* (2018) and Sharma *et al.* (2019).

4.2.7 Number of seed per pod

4.2.7.1 Mean performance

The range for number of seed per pod was found from 7.34 (GC 2101) to 14.59 (GC 2118). Highest number of seed per pod was found in genotype GC 2118 (14.59) followed by GC 3 (14.44), GC 2103 (14.34), GC 2120 (13.44), GC 2109 (13.40) and GC 2006 (13.39). The general mean for number of seed per pod was 11.38.

4.2.7.2 Variance components

The results revealed that the magnitude of genotypic variance (2.70), phenotypic variance (3.51) and environmental variance (0.81), which suggested the genotypic variance contributed more proportion to the total phenotypic variance. It indicates the little influence of environment on expression of number of seed per pod. The present findings are in accordance with the results of Khanpara *et al.* (2015), Bhagavati *et al.* (2018), Kumar *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.7.3 Genotypic and phenotypic coefficients of variation

The estimates of genotypic coefficients variation (14.44 %) and phenotypic coefficients variation (16.47 %) it was moderate for number of seed per pod. Which indicate the high variability present in population and simple selection would be desirable for improvement of this character. The similar trends were also observed by Kumar *et al.* (2013), Khanpara *et al.* (2015), Bhagavati *et al.* (2018), Das *et al.* (2018), Kumar *et al.* (2018), Thouseem *et al.* (2018) Yadav *et al.* (2019).

4.2.7.4 Heritability and genetic advance (% of mean)

Number of seed per pod exhibited high heritability (76.82 %) along with high genetic advance as per cent of mean (26.06 %) indicated role of additive gene on reflection of this character and selection would be effective. Similar result was found by Khanpara *et al.* (2015), Sarath and Reshma (2017), Kumar *et al.* (2018), Sharma *et al.* (2019) and Chaudhary *et al.* (2020).

4.2.8 100 seed weight (g)

4.2.8.1 Mean performance

The variation for 100 seed weight was found highly significant. The range for 100 seed weight was observed from 8.59 g (GC 2006) to 16.17 g (GC 2112). Maximum 100 seed weight was recorded by genotype GC 2112 (16.17 g) followed by GC 2111 (16.14 g), GC 2113 (15.44 g), GC 2109 (15.37 g), GC 2103 (15.27 g) and GC 4 (15.27 g). The general mean of 100 seed weight was 12.35 g.

4.2.8.2 Variance components

The magnitude of genotypic variance (5.24), phenotypic variance (6.17) and environmental variance (0.93), which suggested the which suggested the genotypic variance contributed more proportion to the total phenotypic variance suggesting the phenotypic variance mainly due to genotypic variance. It indicates the little influence of environment on expression of 100 seed weight. Selection for this character is effective. Sharma *et al.* (2017$_b$), Kumar *et al.* (2018) and Chaudhary *et al.* (2020) were also reported same result for 100 seed weight.

4.2.8.3 Genotypic and phenotypic coefficients of variation

The values of GCV (18.54 %) and PCV (20.11 %) were moderate. There was not as much difference between GCV and PCV values indicated less influence of environment on the expression of this trait. Sharma *et al.* (2017$_b$), Sarath and Reshma (2017), Sharma *et al.* (2019) and Chaudhary *et al.* (2020) were also reported same trend for 100 seed weight.

4.2.8.4 Heritability and genetic advance (% of mean)

100 seed weight showed high heritability (84.95 %) coupled with high genetic advance as per cent mean (35.21 %), which indicated role of additive gene action on reflection of this character and selection would be effective. Similar result was found by Kumar *et al.* (2013), Sharma *et al.* (2017$_b$), Kumar *et al.* (2018), Sharma *et al.* (2019), Yadav *et al.* (2019) and Chaudhary *et al.* (2020).

4.2.9 Harvest index (%)

4.2.9.1 Mean performance

Genotypes exhibited highly significant differences for harvest index. The range for harvest index was observed from 33.50 % (GC 2002) to 73.17 % (GC 2108). The maximum harvest index showed in genotype GC 2108 (73.17 %) followed by GC 2109 (70.43 %), GC 2118 (70.37 %), GC 2006 (70.08 %) and GC 2106 (69.51 %) genotypes. The general mean of harvest index was 60.05 per cent.

4.2.9.2 Variance components

The magnitude of genotypic variance, phenotypic variance and environmental variance were observed 108.46, 139.65 and 31.19, respectively. The results revealed that the genotypic variance (108.46) contributed more proportion to the total phenotypic variance (139.65) suggesting the phenotypic variance mainly due to genotypic variance. It indicates the low influence of environment on harvest index. Selection for improvement of this character will be beneficial. Khanpara *et al.* (2015), Sharma *et al.* (2017$_b$) and Das *et al.* (2018) also observed similar results for harvest index.

4.2.9.3 Genotypic and phenotypic coefficients of variation

The genotypic coefficients of variation (17.34 %) and phenotypic coefficients of variation (19.68 %) were moderate for harvest index. Which indicates moderate variability present in population. The least difference between GCV and PCV value revealed less influence of environment on the expression of this trait. Similar result was found by Sharma *et al.* (2017$_b$).

4.2.9.4 Heritability and genetic advance (% of mean)

Harvest index showed high heritability (77.67 %) accompanied with high genetic advance as per cent of mean (31.48 %), suggesting predominance of additive gene effect and selection for improvement of such character would be useful. Similar result was found by Sharma *et al.* (2017$_b$), Das *et al.* (2018) and Thouseem *et al.* (2018).

4.2.10 Protein content (%)

4.2.10.1 Mean performance

The variation among the genotypes for protein content was highly significant. The range for protein content was observed from 20.74 % (GC 2112) to 24.19 % (GC 2002). The genotype GC 2002 (24.19 %) showed highest protein content followed by GC 2007 (23.75 %), GC 2119 (23.72 %), GC 2101 (23.53 %) and GC 2006 (23.32 %). The general mean of protein content was 22.26 per cent.

4.2.10.2 Variance components

The magnitude of genotypic variance (0.74), phenotypic variance (0.85) and environmental variance (0.11) were found low for protein content. The genotypic variance contributed more proportion to the total phenotypic variance suggesting the phenotypic variance is mainly due to genotypic variance. It indicates the little influence of environment on protein content. The present finding is in accordance with Bhagavati *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.10.3 Genotypic and phenotypic coefficients of variation

The genotypic coefficients of variation (3.86 %) and phenotypic coefficients of variation (4.15 %) were low for protein content. It indicates the low variability present in population and simple selection not be effective. The low genotypic and phenotypic coefficient of variation for protein content was reported by Sarath and Reshma (2017), Bhagavati *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.10.4 Heritability and genetic advance (% of mean)

The high heritability (86.72 %) along with low genetic advance (7.40 %) was found for protein content which indicated, the presence of non-additive gene effect and selection for protein content may not be beneficial. Similar result was found by Bhagavati *et al.* (2018) and Chaudhary *et al.* (2020).

4.2.11 Seed yield per plant (g)

4.2.11.1 Mean performance

Seed yield per plant ranged from 14.67 g (GC 2102) to 22.63 g (GC 2108). The next high yielding genotype was GC 2108 (21.70 g) followed by GC 2109 (20.35 g), GC 2106 (20.23 g) and GC 2006 (19.98 g), GC 2118 (19.60 g), GC 3 (19.58 g). Genotype GC 2112, GC 2115, GC 2103, GC 2113, GC 2116 had also higher value for one or two of its yield contributing traits *viz.*, early maturity, number of pod per plant, number of seed per pod, 100 seed weight and harvest index. The general mean of seed yield per plant was 18.30 g.

4.2.11.2 Variance components

The genotypic variance (1.38) contributed more proportion to the total phenotypic variance (2.55) suggesting the phenotypic variance mainly due to genotypic variance. There was low influence of environment on seed yield per plant. Selection for improvement of this character will be beneficial. The present findings are in accordance with earlier results obtained by Kumar *et al.* (2018).

4.2.11.3 Genotypic and phenotypic coefficients of variation

The results revealed that low GCV (6.28 %) and low PCV (8.54 %) value for seed yield per plant. This indicate low variability present in material and simple selection would be desirable for improvement this character. Similar results were found by Thorat and Gadewar (2013), Kumar *et al.* (2018) and Yadav *et al.* (2019) for seed yield per plant.

4.2.11.4 Heritability and genetic advance (% of mean)

The moderate heritability (54.05 %) is accompanied with low genetic advance as per cent of mean (9.51 %) which indicates heritability is due to non-additive gene effect and selection may not be effective. The present findings are in accordance with earlier results obtained by Kumar *et al.* (2013), Thouseem *et al*. (2018) and Ugale *et al.* (2020) for seed yield per plant.

The phenotypic (σ^2p), genotypic (σ^2g) and environmental (σ^2e) components of variance were computed for all the characters and was presented in Table 4.3. The highest genotypic and phenotypic variances were observed for harvest index (108.46 and 139.65) followed by plant height (63.31 and 70.58). The phenotypic and genotypic variances were lowest for 100 seed weight (5.24 and 6.17), number of seed per pod (2.70 and 3.51), number of pod per plant (2.95 and 3.38), days to flowering (2.92 and 3.24), days to maturity (1.60 and 2.40), seed yield per plant (1.38 and 2.55), pod length (1.25 and 2.50), number of branch per plant (0.84 and 1.07) and protein content (0.74 and 0.85).

The data indicated that the genotypic variances accounted for most of the total phenotypic variances in case of days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, number of seed per pod, 100 seed weight, harvest index, protein content and seed yield per plant. The results suggested that there was good agreement between phenotypic and genotypic variances for these traits and hence selection based on phenotypic value would be reliable for improving these traits. The environmental variation was low for various traits ranging from 0.11 (protein content) to 31.19 (harvest index).

The estimates of genotypic and phenotypic coefficient of variation revealed higher contribution of genotypic variation to total variation for the trait which indicate high variability present in population and simple selection would be desirable for improvement of these characters. While harvest index, plant height, number of seed per pod, number of pod per plant, number of branch per plant were moderate in genotypic coefficients of variation and phenotypic coefficients of variation, which indicate moderate variability present in population. Days to flowering, days to maturity, protein content and seed yield per plant depicted low value of genotypic and phenotypic coefficients of variation which indicate low variability present and simple selection for these traits not desirable in given population. Pod length contain low genotypic coefficient of variation and moderate phenotypic coefficient of variation, which indicate simple selection will not be rewarding. 100 seed weight exerted moderate genotypic coefficient of variation and high phenotypic coefficient of variation which indicate moderate to high variability present in population and simple selection may be rewarding.

The high heritability coupled with high genetic advance indicated that heritability in genotypes were due to additive gene effects indicating better scope for the improvement in the characters by effective selection of genotypes. The traits, plant height, number of branch per plant, number of pod per plant, number of seed per pod, 100 seed weight and harvest index were exhibited high heritability with high genetic advance which could be effectively improved by selection.

4.3 Correlation coefficient analysis

Correlation coefficient analysis measures the mutual relationship between component characters and determines the component characters on which selection can be used for genetic improvement in the yield. The association between characters that can be directly observed is the phenotypic correlation. The genotypic correlation that may be due to pleiotropic action of genes or linkages or more likely both permit the prediction of correlated response and evaluation of the relative influence of one character on the other.

The genotypic and phenotypic correlation coefficients are estimated among eleven characters using 30 genotypes of cowpea to find out the association of seed yield per plant and other seed yield related characters (Table 4.4 and 4.5).

The perusal of the data revealed that the correlation at the genotypic as well as phenotypic levels has the same trend for most of the traits studied. The magnitude of genotypic correlation coefficient were relatively higher than the corresponding phenotypic correlation coefficient in almost all the traits paired indicated the inherent association between various characters.

4.3.1 Days to flowering

Days to flowering showed highly significant and positive correlated with days to maturity (r_g = 0.5616** and r_p = 0.4207**), number of brach per plant (r_g = 0.463** and r_p = 0.4271**), pod length (r_g = 0.5001** and r_p = 0.3468**) at both genotypic and phenotypic level, while, seed yield per plant (r_g = 0.2706 and r_p = 0.1938*), number of pod per plant (r_g = 0.2075 and r_p = 0.2042*), 100 seed weight (r_g = 0.2558 and r_p = 0.2124*) and harvest index (r_g = 0.2349 and r_p = 0.2099*) were significant at only phenotypic level exhibited late flowered genotypes produced more yield. This results supported by Kumar *et al.* (2013), Sapara and Javia (2014), Gerrano *et al*. (2015) and Sharma *et al.* (2017$_a$) for seed yield per plant; for number of branch per plant and pod length by Sapara and Javia (2014), Shanko *et al.* (2014) and Das *et al.* (2018) at both genotypic and phenotypic levels; for number of branch per plant and seed yield per plant by Meena *et al.* (2015) at both genotypic and phenotypic levels. Number of branch per plant by Thorat and Gadewar (2013), Sharma *et al.* (2017$_a$) and Sharma *et al*. (2019) at both genotypic and phenotypic level indicated early flowered genotypes were matured early and late flowered genotypes matured late, which result supported by Thorat and Gadewar (2013), Shanko *et al.* (2014), Meena *et al.* (2015), Sharma *et al.* (2017$_b$) and Yadav and Duddukur (2019) for days to maturity. While, plant height (r_g = 0.1716 and r_p = 0.1793) and number of seed per pod (r_g = 0.0334 and r_p = 0.0156) positive and non-significant correlated at at both genotypic and phenotypic levels. Similar result was also recorded by Shanko *et al.* (2014), Meena *et al*. (2015), Sharma *et al.* (2017$_b$) for plant height positive and non-significantly correlated at genotypic level and significantly correlated at phenotypic level. Similar result observed by Shanko *et al.* (2014) and Sharma *et al.* (2017$_b$); Only number of pod per plant by Sharma *et al*. (2019) and Mofokeng *et al*. (2020); While, protein content negatively and non-significantly correlated with days to flowering (r_g = -0.1882 and r_p = -0.1671) at both genotypic and phenotypic levels. Similar result was observed by Thorat and Gadewar (2013).

4.3.2 Days to maturity

Days to maturity showed positive and highly significant correlation with number of branch per plant (r_g = 0.4915** and r_p = 0.3851**), 100 seed weight (r_g = 0.728** and r_p = 0.5474**) and pod length (r_g = 0.6992** and r_p = 0.3854**) at both genotypic and phenotypic levels while, plant height (r_g = 0.2094 and r_p = 0.1798*) and harvest index (r_g = 0.2917 and r_p = 0.1798*) significant at only phenotypic level, which result supported by Sapara and Javia (2014) and Sharma *et al.* (2017$_b$). This character was positive and non-significant correlated with number of seed per pod (r_g = 0.0719 and r_p = 0.0967) and seed yield per plant (r_g = 0.1994 and r_p = 0.1556) at both genotypic and phenotypic levels, respectively, Similar result was observed for plant height by Sapara and Javia (2014), Sharma *et al*. (2017$_b$), Meena *et al*. (2019) and Sharma *et al*. (2019); Days to maturity negative and highly significant correlated with protein content (r_g = -0.5464** and r_p = -0.3901**) at both genotypic and phenotypic levels. This character also negatively and non-significantly correlated with number of pod per plant (r_g = -

0.0874 and r_p = -0.0362) at both genotypic and phenotypic levels, Similar result was observed for number of pod per plant by Sapara and Javia (2014), Meena *et al*. (2015), Sharma *et al.* (2017_b) and Sharma *et al.* (2019). While, negatively and highly significantly correlation was observed by Thorat and Gadewar (2013); for seed yield per plant by Sharma *et al*. (2017_b) and 100 seed weight by Sapara and Javia (2014) and Yadav and Duddukur (2019); Days to maturity showed a positive and significant correlation with seed yield per plant at both genotypic and phenotypic levels, respectively, indicating that high expression of this trait delayed flowering.

4.3.3 Plant height (cm)

Plant height showed positive and non-significant correlation with number of branch per plant (r_g = 0.2864 and (r_p = 0.2652**) and harvest index (r_g = 0.2985 and r_g = 0.2536**) at genotypic levels and positive and highly significant correlated at only phenotypic level, which result supported by Meena *et al.* (2015)**,** Sharma *et al.* (2017_b), Sharma *et al*. (2019) and Yadav and Duddukur (2019); Plant height showed positive and non-significantly correlation with number of pod per plant (r_g = 0.1951 and r_p = 0.1704), 100 seeds weight (r_g = 0.2291 and r_p = 0.1705), pod length (r_g = 0.0826 and r_p = 0.0466), number of seed per pod (r_g = 0.026 and r_p = 0.0356) and seed yield per plant (r_g = 0.2451 and r_p = 0.2085*) at both genotypic and phenotypic levels. Similar conclusion drawn for number of pod per plant by Meena *et al*. (2015), Sharma *et al*. (2017_b), Sharma *et al*. (2019); for 100 seeds weight Meena *et al*. (2015)**;** for number of seed per pod by Sharma *et al*. (2017_b) and Yadav *et al*. (2018)**;** Sharma *et al*. (2017_b) and Das *et al*. (2018) also reported similar results for and seed yield per plant. This character showed negative and non-significant correlation with protein content at genotypic level (r_g = -0.2372), while negative and highly significantly at phenotypic level (r_p = -0.0898**). Similar results for pod length were observed by Yadav and Duddukur (2019).

4.3.4 Number of branch per plant

This character showed positive and non-significant correlattion with seed yield per plant (r_g = 0.3259 and r_p = 0.2137*) and 100 seed weight (r_g = 0.351 and r_p = 0.2846**) at genotypic level, while positive and highly significant correlated at phenotypic level. Similar result obtained by Shanko *et al.* (2014) for seed yield per plant and Sharma *et al*. (2017_b) for 100 seed weight; Number of branch per plant was positive and non-significant correlated with number of pod per plant (r_g = 0.0509 and r_p = 0.047) and pod length (r_g = 0.0212 and r_p = 0.0614) at both genotypic and phenotypic levels, which was supported by Sharma *et al.* (2019) and Yadav and Duddukur (2019) for number of pod per plant. number of branch per plant showed negatively and non-significantly correlated with number of seed per pod (r_g = -0.0104 and r_p = -0.0023), protein content (r_g = -0.1127 and r_p = -0.0897) and also harvest index (r_g = -0.0153 and r_p = -0.0061) at both genotypic and phenotypic levels, which was supported by Sharma *et al.* (2017_b). Meena *et al.* (2015) for pod length, number of seed per pod and seed yield per plant.

4.3.5 Number of pod per plant

This character was positive and highly significant correlated with seed yield per plant (r_g = 0.6716* and r_p = 0.4692**) at both genotypic and phenotypic levels. Similar result obtained by Thorat and Gadewar (2013), Sharma *et al.* (2017_b), Gupta *et al.* (2019) and Yadav and Duddukur (2019) for seed yield per plant. Number of pod per plant was positive and non-significant correlated with harvest index (r_g = 0.2092 and r_p = 0.1659), number of seed per pod (r_g = 0.1131 and r_p = 0.0891), pod length (r_g = 0.2338 and r_p = 0.1476) and protein content (r_g = 0.0348 and r_p = 0.0285) at both genotypic and phenotypic levels, which exhibited seed yield per plant can be improved if selection is carried out for a greater number of pod with high harvest index. This result is in accordance with Sharma *et al.* (2017_b) and Yadav and Duddukur (2019) for harvest index; by Sharma *et al.* (2017_b) for protein content. This character also showed negative and non-significant correlation with 100 seed weight (r_g = -0.0558 and r_p = -0.0394) at both genotypic and phenotypic levels. Similar findings were also obtained by Thorat and Gadewar (2013) and Shanko *et al.* (2014) for number of seeds per pod; Thorat and Gadewar (2013) and Meena *et al.* (2015) for 100 seed weight.

4.3.6 Pod length (cm)

Pod length was positive and highly significant correlated with seed yield per plant (r_g = 0.5147** and r_p = 0.3332**) and harvest index (r_g = 0.4363* and r_p = 0.2693**) at both genotypic and phenotypic levels. The result for 100 seed weight was supported by Thorat and Gadewar (2013) and Das *et al.* (2018). While, this character was positive and non-significant correlated with 100 seed weight (r_g = 0.281 and r_p = 0.1536) at both genotypic and phenotypic levels. Which was also concluded by Thorat and Gadewar (2013), Meena *et al.* (2015), Gupta *et al.* (2016), Sharma *et al.* (2019) for seed yield per plant. This character was negative and non-significant correlated with protein content at only genotypic level (r_g = -0.2687) and while negative with significant correlated at phenotypic level (r_p = -0.1933*).

4.3.7 Number of seed per pod

Number of seed per pod was positive and highly significant correlated with seed yield per plant (r_g = 0.5369** and r_p = 0.3534**) and harvest index (r_g = 0.4363* and r_p = 0.3566**) at both genotypic and phenotypic levels. Similar result obtained by Kumar *et al*. (2013), Meena *et al.* (2015) and Waghmare *et al.* (2019) for seed yield per plant. This indicated that selection for strains having more seed per pod would lead to increase in 100 seed weight that ultimately leads to increase in seed yield per plant. This character was positive and non-significant correlated with pod length (r_g = 0.2035 and r_p = 0.1298) at both genotypic and phenotypic levels, which was also found by Thorat and Gadewar (2013). Number of seed per pod was negative and non-significant correlated with protein content (r_g = -0.105 and r_p =-0.0677) at both genotypic and phenotypic levels, whereas negative and non- significant correlated with 100 seed weight (r_g = 0.106 and r_p =-0.0106) at only phenotypic level. Similar conclusion drawn by Thorat and Gadewar (2013) and Sharma *et al.* (2017_b), for 100 seed weight;

4.3.8 100 seed weight (g)

100 seed weight showed positive and non-significant correlation with seed yield per plant (r_g = 0.0278 and r_p = 0.0083) at both genotypic and phenotypic levels. This character showed negative and non-significant correlation with harvest index (r_g = -0.0089 and r_p = 0.0022) at genotypic level, while positive at phenotypic level, it was expressed that genotypes having higher 100 seed weight produced high seed yield per plant. This result supported by Thorat and Gadewar (2013) and Meena *et al.* (2015), Sharma *et al.* (2017_b), Sharma *et al.* (2019) for seed yield per plant. Which indicate that the genotypes having greater seed size had high 100 seed weight compared to bold seeded genotypes. Similar results at phenotypic level were also concluded by Thorat and Gadewar (2013); Which was also supported by Sharma *et al.* (2017_b) for harvest index; This character was negatively and highly significantly correlated with protein content (r_g = -0.4912** and r_p = -0.4443**) at both genotypic and phenotypic levels. Which was supported by Sharma *et al.* (2017_b).

Table 4.4: Genotypic (r_g) correlation coefficients among eleven characters of cowpea for seed yield per plant

Sr. No.	Characters	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of pod per plant	Number of seed per pod	Pod length	100 seed weight	Protein content	Harvest Index	Seed yield per plant
1	**Days to flowering**	1	0.5616 **	0.1716	0.463 **	0.2075	0.0334	0.5001**	0.2558	-0.1882	0.2349	0.2706
2	**Days to maturity**		1	0.2094	0.4915 **	-0.0874	0.0719	0.6992**	0.728 **	-0.5464**	0.2917	0.1994
3	**Plant height**			1	0.2864	0.1951	0.026	0.0826	0.2291	-0.2372	0.2985	0.2451
4	**Number of branch per plant**				1	0.0509	-0.0104	0.0212	0.351	-0.1127	-0.0153	0.3259
5	**Number of pod per plant**					1	0.1131	0.2338	-0.0558	0.0348	0.2092	0.6716*
6	**Number of seed per pod**						1	0.2035	0.0106	-0.105	0.4363*	0.5369**
7	**Pod length**							1	0.281	-0.2687	0.413*	0.5147**
8	**100 seed weight**								1	-0.4912**	-0.0089	0.0278
9	**Protein content**									1	-0.3069	-0.0249
10	**Harvest index**										1	0.1535
11	**Seed yield per plant**											1

*, ** significant at 0.05 % and 0.01 % level of significance, respectively.

Table 4.5: Phenotypic (r_p) correlation coefficients among eleven characters of cowpea for seed yield per plant

Sr. No.	Characters	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of pod per plant	Number of seed per pod	Pod length	100 seed weight	Protein content	Harvest Index	Seed yield per plant
1	**Days to flowering**	1	0.4207**	0.1793	0.4271 **	0.2042 *	0.0156	0.3468**	0.2124 *	-0.1671	0.2099*	0.1938*
2	**Days to maturity**		1	0.1798*	0.3851 **	-0.0362	0.0967	0.3854**	0.5474**	-0.3901**	0.2143*	0.1556
3	**Plant height**			1	0.2652 **	0.1704	0.0356	0.0466	0.1705	-0.2066 *	0.2536**	0.2088*
4	**Number of branch per plant**				1	0.047	-0.0023	0.0614	0.2846**	-0.0897	-0.0061	0.2137*
5	**Number of pod per plant**					1	0.0891	0.1476	-0.0394	0.0285	0.1659	0.4692**
6	**Number of seed per pod**						1	0.1298	-0.0106	-0.0677	0.3566**	0.3534**
7	**Pod length**							1	0.1536	-0.1933 *	0.2693**	0.3332**
8	**100 seed weight**								1	-0.4443**	0.022	0.0083
9	**Protein content**									1	-0.2647**	0.0053
10	**Harvest Index**										1	0.084
11	**Seed yield per plant**											1

*, ** significant at 0.05 % and 0.01 % level of significance, respectively.

4.3.9 Harvest index (%)

Harvest index showed positive and non-significant correlated with seed yield per plant (r_g = 0.1535 and r_p = 0.084) at both genotypic and phenotypic levels indicated that seed yield per plant can be improved by selecting genotypes having high harvest index. Similar results were also obtained by Gerrano *et al.* (2015) and Sharma *et al.* (2017_b). Yadav and Duddukur (2019) reported positive and highly significant correlation with seed yield per plant at both genotypic and phenotypic level.

4.3.10 Protein content (%)

Protein content was negatively and non-significantly correlated with seed yield per plant (r_g = -0.0249 and r_p = 0.005386) at genotypic, while positive and non-significant at phenotypic levels. This character also showed negative and non-significant correlation with harvest index at only genotypic level (r_g = -0.3069) and was negatively but highly significant at phenotypic level (r_p = -0.2647**). This result was in accordance with result obtained by Sharma *et al.* (2017_b) and Naguyen *et al.* (2017) for seed yield per plant.

4.3.11 Seed yield per plant (g)

Seed yield per plant exhibited highly significant and positive correlation with number of seed per pod (r_g = 0.5369** and r_p = 0.3534**), number of pod per plant (r_g = 0.6716* and r_p = 0.4692**) and pod length (r_g = 0.5147** and r_p = 0.3332**) at both genotypic and phenotypic levels, similar result was observed by Kumar *et al.* (2015), Meena *et al.* (2015) for number of seed per pod; Thorat and Gadewar (2013), Meena *et al.* (2015), Sharma *et al.* (2017_b), Gupta *et al.* (2019) and Yadav and Duddukur (2019) for number of pod per plant; Thorat and Gadewar (2013), Meena *et al.* (2015) and Gupta *et al.* (2019) for pod length; Seed yield per plant showed positive and non-significant correlation with number of branch per plant (r_g = 0.3259 and $r_{p=}$ 0.2137*), days to flowering (r_g = 0.2706 and r_p = 0.1556**) and plant height (r_g = 0.2451 and $r_{p=}$ 0.2088*) at genotypic level while, significant and positive correlated at phenotypic level. Similar result reported by Kumar *et al.* (2013), Sapara and Javia (2014), Gerrano *et al.* (2015) and Sharma *et al.* (2017_a) for days to flowering, which was also reported by Sharma *et al.* (2017_b) and Das *et al.* (2018) for plant height and Shanko *et al.* (2014) for number of branch per plant; Seed yield per plant exhibited non-significant and positive correlation with days to maturity (r_g = 0.1994 and $r_{p\,=}$ 0.1556), 100 seed weight (r_g= 0.0278 and r_p = 0.0083) and harvest index (r_g = 0.1535 and r_p = 0.084) at both genotypic and phenotypic levels. Similar result observed by Thorat and

Gadewar (2013), Meena *et al.* (2015), Sharma *et al.* (2017_b) and Sharma (2019) for 100 seed weight; Sharma *et al.* (2017_b) for harvest index; Sapara and Javia (2014) and Sharma *et al.* (2017_a) for days to maturity. Seed yield per plant had negative and non-significant correlation with protein content (r_g= -0.0249 and r_p = 0.0053) at genotypic level, while positive correlated at phenotypic level. Similar result reported by Sharma *et al.* (2017_b) and Nguyen *et al.* (2017) for protein content.

Generally, the nature of inter trait correlations may enhance or retard the selection progress. A positive association indicates that the selection for improvement in one of the yield components would result in concomitant increase in one or more components.

4.4. Path coefficient analysis

Path analysis breaks correlation between traits into their direct and indirect effects on the economic product, permitting a critical examination of specific trait contributing individually and collectively to produce the total effect. It also helps to measure the relative importance of each trait. Path analysis, in this study was carried out using the estimates of genotypic coefficients. The analysis of correlation coefficient together with information on path coefficient helps in identification of suitable character for proper weightage to be given to each trait during selection. Such an analysis of genotypes under study provided precise indication of the trait that may contribute towards increased total seed yield and also outlined the possible directions to be followed in the future breeding programme for improvement in these traits.

The estimates of direct and indirect effects of various traits on total seed yield per plant are presented in Table 4.6 and Figure 4.2.

4.4.1 Days to flowering *vs.* seed yield per plant (g)

The genotypic correlation between days to flowering and seed yield per plant was positive and non-significant (r_g = 0.2706). However, the direct effect of this character on seed yield per plant was moderate and negative (-0.2014). Days to flowering exhibited high and positive indirect effects on seed yield per plant *via* pod length (0.5900) and number of branch per plant (0.3581). Days to flowering exhibited negligible and positive indirect effects on seed yield per plant *via* number of pod per plant (0.0661), protein content (0.0378), plant height (0.0235), 100 seed weight (0.0245) and number of seed per pod (0.0160). Days to flowering exerted high and negative indirect effects on seed yield per plant *via* days to maturity (-0.5518) and days to flowering exhibited negligible and negative indirect effects on seed yield per plant *via*

harvest index (-0.0860).

Meena *et al.* (2015) and Walle *et al.* (2018) had also recorded negative direct effects of days to flowering on seed yield per plant in cowpea. Days to flowering showed positive indirect effects on seed yield per plant *via*, plant height, number of branch per plant, number of pod per plant and pod length was recorded by Sapara and Javia (2014), Sharma *et al.* (2017$_b$), Walle *et al.* (2018) and Yadav and Duddukur (2019). While negative indirect effect on seed yield per plant *via* days to maturity and harvest index recorded by Walle *et al.* (2018) and Yadav and Duddukur (2019). Days to flowering showed positive indirect effects on seed yield per plant *via.,* number of pod per plant was recorded by Meena *et al.* (2015), Sharma *et al.* (2017$_b$), Mofokeng *et al.* (2020) and Nagalakshmi *et al.* (2020), while pod length was recorded by Sapara and Javia (2014) and Meena *et al.* (2015); and protein content was recorded by Sapara and Javia (2014); Similar result was observed by Sapara and Javia (2014), Meena *et al.* (2015); Yadav and Duddukur (2019), Mofokeng *et al.* (2020 and Nagalakshmi *et al.* (2020) for 100 seed weight and for harvest index by Sharma *et al.* (2017$_b$).

4.4.2 Days to maturity *vs.* seed yield per plant (g)

The genotypic correlation between days to maturity and seed yield per plant was positive and non-significant (r_g = 0.1994) and its direct effect on seed yield per plant was also low and negative (-0.1131). Days to maturity showed high and positive indirect effects on seed yield per plant *via* pod length (0.8249) and number of branch per plant (0.3800). Days to maturity showed low and positive indirect effects on seed yield per plant *via* protein content (0.1100) also showed negligible and positive indirect effects on seed yield per plant *via* 100 seed weight (0.0515), number of seed per pod (0.0345) and plant height (0.0287). Days to maturity indicated low and negative indirect effects on seed yield per plant *via* days to flowering (-0.1131), harvest index (-0.1069) also exhibit negligible and negative indirect effects on seed yield per plant *via* number of pod per plant (-0.0278).

Sapara and Javia (2014), Sharma *et al.* (2017$_b$), Walle *et al.* (2018), Yadav and Duddukur (2019) also recorded negative direct effects of days to maturity on seed yield per plant in cowpea. It showed positive indirect effects on seed yield per plant *via* number of seed per pod and 100 seed weight by Sapara and Javia (2014) and Yadav and Duddukur (2019); for protein content by Sapara and Javia (2014); Similar results for days to maturity with of number of branch per plant by Sapara and Javia (2014) and Meena *et al.* (2015); for plant height by Sharma *et al.* (2017_b), Walle *et al.* (2018) and Yadav and Duddukur (2019); while negative indirect effects on seed yield per plant *via* days to flowering and harvest index were recorded by Yadav and Duddukur (2019) and Walle *et al.* (2020); for pod length recorded by Sapara and Javia (2014) and Sharma *et al.* (2017_b) and for harvest index by Sharma *et al.* (2017_b).

4.4.3 Plant height (cm) *vs.* seed yield per plant (g)

The genotypic correlation between plant height and seed yield per plant was found positive and non-significant (r_g = 0.2451) and its direct effect on seed yield per plant was also low and positive (0.1372). Plant height exhibited moderate and positive indirect effects on seed yield per plant *via* number of branch per plant (0.2214) and also exhibit negligible and positive indirect effects on seed yield per plant *via* pod length (0.0973), number of pod per plant (0.0621), protein content (0.0477), 100 seed weight (0.0162), number of seed per pod (0.0125). Plant height exhibited moderate and negative indirect effects on seed yield per plant *via* days to maturity (-0.2057) and showed low and negative indirect effects *via* harvest index (-0.1093) and negligible effect *via* days to flowering (-0.0345).

Meena *et al.* (2015) and Nagalakshmi *et al.* (2020) had also recorded positive direct effects of plant height on seed yield per plant in cowpea. Plant height showed positive indirect effects on seed yield per plant *via* number of branch per plant similar results found by Sapara and Javia (2014), Meena *et al.* (2015), Sharma *et al.* (2017_b), Yadav and Duddukur (2019), Nagalakshmi *et al.* (2020) and; for number of pod per plant and number of seed per pod by Sharma *et al.* (2017_b); for protein content by Sharma *et al.* (2017_b) and Sapara and Javia (2014); for pod length by Meena *et al.* (2015) and Sapara and Javia (2014); While negative indirect effects on seed yield per plant *via* days to flowering and days to maturity was recorded by Sapara and Javia (2014), Meena *et al.* (2015) and Yadav and Duddukur (2019); for 100 seed weight by Yadav and Duddukur (2019) and Nagalakshmi *et al.* (2020) and for harvest index by Sharma *et al.* (2017_b).

4.4.4 Number of branch per plant *vs.* seed yield per plant (g)

Number of branch per plant showed positive and non-significant (r_g =0.3259) association with seed yield per plant at genotypic level. Its direct effect on seed yield per plant was high and positive (0.7733), similar result obtained by Sapara and Javia (2014), Meena *et al.* (2015), Sharma *et al.* (2017_b) and Mofokeng *et al.* (2020).

Number of branch per plant exhibited negligible and positive indirect effects on seed yield per plant *via* plant height (0.0393), pod length (0.0250), 100 seed weight (0.0248), protein content (0.0226), number of pod per plant (0.0162) and harvest index (0.0056). This result was in accordance with result obtained by Meena *et al*. (2015), Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020) for number of seed per pod. While low and negative indirect effect on seed yield per plant *via* days to flowering, this result was in accordance with result obtained by Sapara and Javia (2014), Meena *et al*. (2015) and Mofokeng *et al*. (2020); for plant height by Meena *et al*. (2015) and Nagalakshmi *et al*. (2020). Number of branch per plant exhibited high and negative indirect effects on seed yield per plant *via* days to maturity (-0.4828). This character also exhibited negligible and negative indirect effects on seed yield per plant *via* days to flowering (-0.0932) and number of seed per pod (-0.0049). This was in accordance with the result obtained by Sapara and Javia (2014), Meena *et al*. (2015), Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020) for number of pod per plant; for pod length Meena *et al*. (2015) and Sapara and Javia (2014); for protein content Sharma *et al*. (2017_b) and Sapara and Javia (2014). for 100 seed weight by Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020) and for harvest index by Sharma *et al*. (2017_b).

4.4.5 Number of pod per plant *vs.* seed yield per plant (g)

Number of pod per plant showed positive and significant (r_g =0.6716) association with seed yield per plant at genotypic level. Its direct effect on seed yield per plant was high and positive (0.3187). Number of pod per plant exhibited moderate and positive indirect effects on seed yield per plant *via* pod length (0.2758). This character exhibited negligible and positive indirect effects on seed yield per plant *via* days to maturity (0.0858), number of seed per pod (0.0543), number of branch per plant (0.0394), plant height (-0.0113). It showed negligible and negative indirect effects on seed yield per plant *via* harvest index (-0.0766), days to flowering (-0.0417), protein content (-0.0070) and 100 seed weight (-0.0039). The result obtained in the present investigation clearly indicate that improvement of seed yield is simultaneously possible through selection of plants having more number pod per plant.

Walle *et al*. (2018), Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020) recorded positive direct effects of number of pod per plant on seed yield per plant in cowpea. Number of pod per plant exhibited positive indirect effects on seed yield per plant *via* days to maturity supported by Sapara and Javia (2014), Yadav and Duddukur

(2019), Sharma *et al*. (2017$_b$), Walle *et al*. (2018) and Nagalakshmi *et al*. (2020) and for pod length by Sharma *et al*. (2017$_b$) and Walle *et al*. (2018); for number of seed per pod by Sharma *et al*. (2017$_b$), Walle *et al*. (2018) and Yadav and Duddukur (2019); for plant height by Sapara and Javia (2014), Meena *et al*. (2015), Mofokeng *et al*. (2020); for 100 seed weight by Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020); for harvest index by Sharma *et al*. (2017$_b$). While, negative indirect effects on seed yield per plant *via* plant height and days to flowering by Sapara and Javia (2014) and Sharma *et al*. (2017$_b$); for number of branch per plant by Mofokeng *et al*. (2020); and for protein content by Sapara and Javia (2014). The result obtained in the present investigation clearly indicate that improvement of seed yield is simultaneously possible through selection of plants having a greater number of branch per plant.

4.4.6 Pod length (cm) *vs.* seed yield per plant (g)

The genotypic correlation between pod length and seed yield per plant was positive and highly significant (r_g = 0.5147) and its direct effect on seed yield per plant was also very high and positive (1.1797). Meena *et al*. (2015), Sharma *et al.* (2017$_b$), Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020) recorded positive direct effects of pod length on seed yield per plant in cowpea. Pod length exhibited negligible and positive indirect effects on seed yield per plant *via*, number of seed per pod (0.0978), number of pod per plant (0.0745), protein content (0.0540), 100 seed weight (0.0199), number of branch per plant (0.0163), and plant height (0.0113). These results supported by Sharma *et al*. (2017$_b$) and Nagalakshmi *et al*. (2020) for seed yield per plant; for number of branch per plant by Meena *et al*. (2015), Sharma *et al.* (2017$_b$) and Nagalakshmi *et al*. (2020); for number of pod per plant by Meena *et al.* (2015); for protein content and harvest index recorded by Sharma *et al.* (2017$_b$) and Yadav and Duddukur (2019), respectively; This character show high and negative indirect effects on seed yield per plant *via* days to maturity (-0.6870), while low and negative indirect effects on seed yield per plant *via* harvest index (-0.1513) and days to flowering (-0.1007). Which was supported by Meena *et al*. (2015), Sharma *et al.* (2017$_b$), and Yadav and Duddukur (2019); for days to maturity and 100 seed weight by Sapara and Javia (2014), Sharma *et al.* (2017$_b$) and Yadav and Duddukur (2019); for plant height by Sapara and Javia (2014), Meena *et al.* (2015), Sharma *et al.* (2017$_b$), Yadav and Duddukur (2019) and Nagalakshmi *et al*. (2020).

4.4.7 Number of seed per pod *vs.* seed yield per plant (g)

Number of seed per pod showed positive and highly significant (r_g =0.5369) association with seed yield per plant at genotypic level. Its direct effect on seed yield per plant was high and positive (0.4806). Which was also found by Nagalakshmi *et al.* (2020). Number of seed per pod exhibited moderate and positive indirect effects on seed yield per plant *via* pod length (0.2400), while negligible and positive indirect effect on seed yield per plant *via* number of pod per plant (0.0360), protein content (0.0211), plant height (0.0035) and 100 seed weight (0.0007). These results were supported for number of pod per plant by Meena *et al.* (2015) and Sharma *et al.* (2017_b); for protein content by Sharma *et al.* (2017_b); for pod length by Yadav and Duddukur (2019) and plant height by Meena *et al.* (2015), Yadav and Duddukur (2019), Mofokeng *et al.* (2020). Number of seed per pod showed low and negative indirect effect on seed yield per plant *via* harvest index (-0.1598), while negligible negative indirect effect on seed yield per plant *via* days to maturity (-0.0706), number of branch per plant (-0.0080) and days to flowering (-0.0067). The same result earlier reported by for days to flowering by Meena *et al.* (2015), Yadav and Duddukur (2019) and Nagalakshmi *et al.* (2020); for plant height by Sharma *et al.* (2017_b) and Nagalakshmi *et al.* (2020); for days to maturity by Walle *et al.* (2018); for number of branch per plant by Meena *et al.* (2015), Sharma *et al.* (2017_b), Yadav and Duddukur (2019) and Nagalakshmi *et al.* (2020) and for 100 seed weight by Walle *et al.* (2018) and Yadav and Duddukur (2019).

4.4.8 100 seed weight (g) *vs.* seed yield per plant (g)

The genotypic correlation between 100 seed weight and seed yield per plant exhibited positive and non-significant (r_g = 0.0278) and its direct effect on seed yield per plant was also negligible and positive (0.0708). Which was supported by Sapara and Javia (2014), Sharma *et al.* (2017_b), Walle *et al.* (2018) and Nagalakshmi *et al.* (2020). 100 seed weight exhibited high and positive indirect effects on seed yield per plant *via* pod length (0.3315), while moderate and positive indirect effects on seed yield per plant *via* number of branch per plant (0.2714). It was also concluded by Meena *et al.* (2015) and Yadav and Duddukur (2019) for number of seed per pod; for protein content and harvest index by Sharma *et al.* (2017_b); This character showed negligible and negative indirect effects on seed yield per plant *via* protein content (0.0988), plant height (0.0314), harvest index (0.0032) and number of seed per pod (0.0051). 100 seed weight exhibited high and negative indirect effects on seed yield per plant *via* days to maturity (-0.7152), while negligible high and negative indirect effects on seed yield per plant *via* days to flowering (-0.0515) and number of pod per plant (-0.0178). The same result for days to flowering was recorded by Sharma *et al.* (2017$_b$) and Nagalakshmi *et al.* (2020); for days to maturity by Sapara and Javia (2014), Meena *et al.* (2015) and Sharma *et al.* (2017$_b$); for pod length by Meena *et al.* (2015) and for number of pod per plant by Nagalakshmi *et al.* (2020).for plant height by Sapara and Javia (2014), Meena *et al.* (2015), Sharma *et al.* (2017$_b$) and Mofokeng *et al.* (2020).

4.4.9 Harvest index (%) *vs.* seed yield per plant (g)

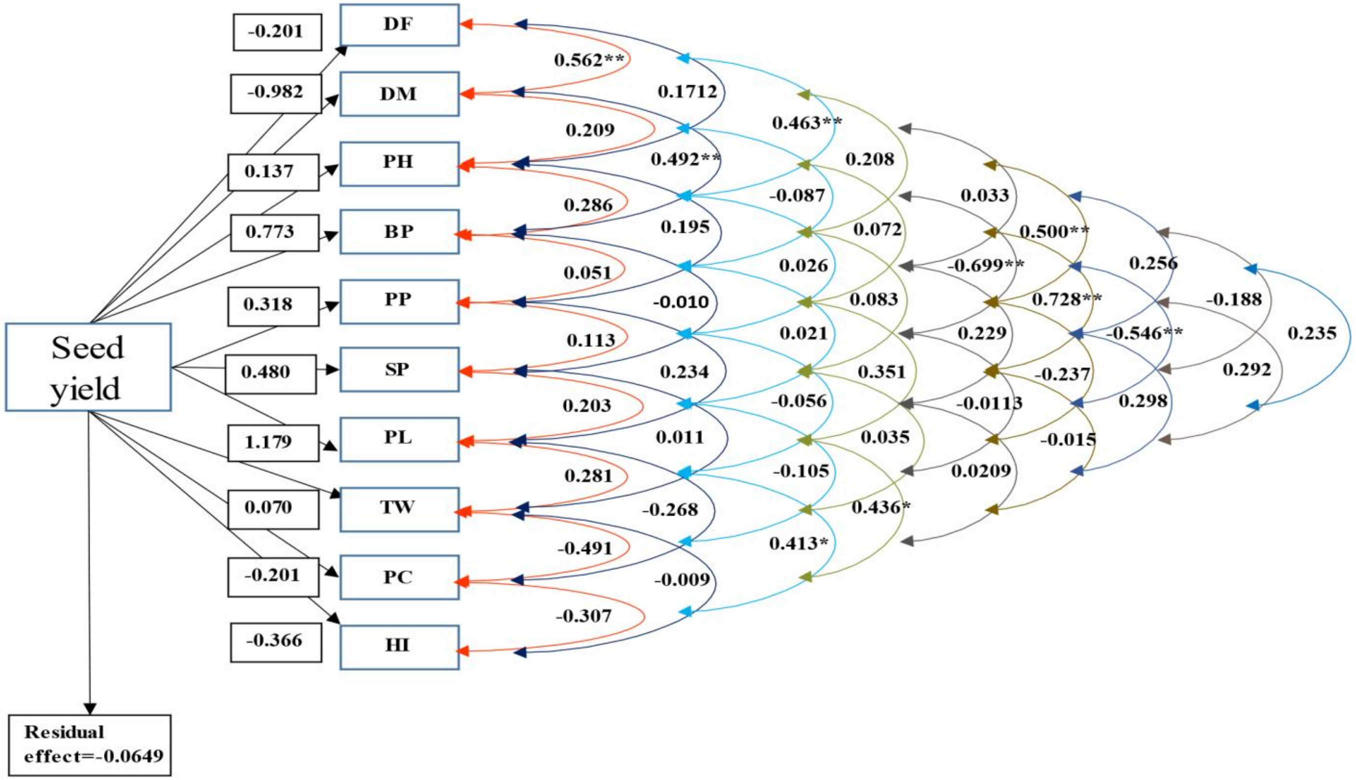
The genotypic correlation coefficient between harvest index and seed yield per plant was positive and non-significant (r_g = 0.1535). However, the direct effect of this character on seed yield per plant was high and negative (-0.3664). This result was supported by Sharma *et al.* (2017$_b$). Harvest index exhibited high and positive indirect effect on seed yield per plant *via* pod length (0.4872) also showed moderate and positive indirect effect on seed yield per plant *via* number of seed per pod (0.2097), while negligible and positive indirect effects on seed yield per plant *via* number of pod per plant (0.0666), protein content (0.0341) and plant height (0.0409). This character exhibited moderate and negative indirect effect on seed yield per plant *via* days to maturity (-0.2866) while, negligible and negative indirect effects on seed yield per plant *via* days to flowering (-0.0473), number of branch per plant (-0.0118) and 100 seed weight (-0.0006). Harvest index exhibited negative indirect effects of on seed yield per plant *via* days to flowering, days to maturity, plant height, pod length, number of branch per plant, 100 seed weight, protein content and positive indirect effects on seed yield per plant *via*, number of pod per plant and number of seed per pod were earlier reported by Sharma *et al.* (2017$_b$); and for days to maturity, plant height, number of pod per plant and pod length by Yadav and Duddukur (2019).

Table 4.6: Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect (above and below diagonal) effects of different characters on seed yield per plant

Sr. No.	Characters	Days to flowering	Days to maturity	Plant height	Number of branch per plant	Number of pod per plant	Number of seed per pod	Pod length	100 seed weight	Protein content	Harvest Index	Seed yield per plant
1	**Days to flowering**	**-0.2014**	-0.5518	0.0235	0.3581	0.0661	0.0160	0.5900	0.0181	0.0378	-0.0860	0.2706
2	**Days to maturity**	-0.1131	**-0.9825**	0.0287	0.3800	-0.0278	0.0345	0.8249	0.0515	0.1100	-0.1069	0.1994
3	**Plant height**	-0.0345	-0.2057	**0.1372**	0.2214	0.0621	0.0125	0.0973	0.0162	0.0477	-0.1093	0.2451
4	**Number of branch per plant**	-0.0932	-0.4828	0.0393	**0.7733**	0.0162	-0.0049	0.0250	0.0248	0.0226	0.0056	0.3259
5	**Number of pod per plant**	-0.0417	0.0858	0.0267	0.0394	**0.3187**	0.0543	0.2758	-0.0039	-0.0070	-0.0766	0.6716*
6	**Number of seed per pod**	-0.0067	-0.0706	0.0035	-0.0080	0.0360	**0.4806**	0.2400	0.0007	0.0211	-0.1598	0.5369**
7	**Pod length**	-0.1007	-0.6870	0.0113	0.0163	0.0745	0.0978	**1.1797**	0.0199	0.0540	-0.1513	0.5147**
8	**100 seed weight**	-0.0515	-0.7152	0.0314	0.2714	-0.0178	0.0051	0.3315	**0.0708**	0.0988	0.0032	0.0278
9	**Protein content**	0.0379	0.5368	-0.0325	-0.0871	0.0110	-0.0504	-0.3170	-0.0347	**-0.2013**	0.1124	-0.0249
10	**Harvest Index**	-0.0473	-0.2866	0.0409	-0.0118	0.0666	0.2097	0.4872	-0.0006	0.0617	**-0.3664**	0.1535

Residual effect = -0.065

Fig. 4.2 Genotypic path diagram for seed yield per plant



Where,

DF: Days to Flowering, **DM**: Days to Maturity, **PH**: Plant Height (cm), **BP**: Number of Branches Per Plant, **PP:** Number of Pods Per Plant, **SP**: Number of Seeds Per Pod, **PL**: Pod Length (cm), **TW:** 100 Seed Weight, **PC**: Protein Content, **HI**: Harvest Index.

4.4.10 Protein content (%) *vs.* seed yield per plant (g)

The genotypic correlation coefficient between protein content and seed yield per plant was negatively and non-significant (r_g = -0.0249). However, the direct effect of this character on seed yield per plant was moderate and negative (-0.2013). The similar result obtained by Nguyen *et al*. (2017). Protein content exhibited high and positive indirect effects on seed yield per plant *via* days to maturity (0.5368), while low and positive indirect effects on seed yield per plant *via* harvest index (0.1124). This character showed negligible and positive indirect effects on seed yield per plant *via* days to flowering (0.0379) and number of pod per plant (0.0110). Protein content exhibited high and negative indirect effect on seed yield per plant *via* pod length (-0.3170) while, negligible and negative indirect effect on seed yield per plant *via* number of branch per plant (-0.0871), number of seed per pod (-0.0504), 100 seed weight (-0.0347) and plant height (-0.0325). The similar result for days to flowering, days to maturity, plant height, pod length and harvest index obtained by Nguyen *etl al*. (2017). Which also concluded by Sapara and Javia (2014) and Yadav and Duddukur (2019) for plant height, number of pod per plant and 100 seed weight.; This indicate that improvement of both seed yield per plant and protein content are simultaneously not possible as the character associated them are negatively correlated with seed yield per plant.

Direct effect of any component characters on seed yield per plant gave an idea about reliability of indirect selection to be made through that character to bring the improvement in yield. If both the correlation coefficient and the direct effect were high and positive then correlation explained its true relationship and a selection for that character would be effective. If the correlation coefficient was positive but the direct effect was negative or negligible in such relations the indirect causal factors are to be considered simultaneously for selection. When correlation coefficient was negative but the direct effect was positive and high in such cases direct selection for such traits would be practiced to reduce the undesirable direct effect.

The residual effect determined how best the causal factors account for the variability of the dependent factors, the seed yield in these case if the value of residual effect was moderate or high, it indicated that the character studied were some other attributes which contributed for yield.

Based on findings of the present investigation the most desirable ideotype of cowpea for seed yield must possess early flowering, more number of pod per plant, number of seed per pod, high 100 seed weight. Selection on the basis of these criteria would improve the efficiency of selection programme.

4.5 Genetic divergence using D^2 analysis

The selection of parents based on individual attributes may be advantageous as compared to base on several important components collectively especially if the aim is to seek improvement in complex quantitative traits such as seed yield. The genetic diversity existing in the population helps in the selection of suitable parents for the breeding program. Plant breeders are always interested to assess the genetic diversity among the germplasm, varieties or advance breeding material available with them, so as to utilize them in direct breeding programme because (a) genetically diverse parents are likely to produce high heterotic effects and (b) the distantly related parents within the same species when utilized in cross breeding are likely to produce wider spectrum of variability. Mahalanobis's D^2 statistics is therefore employed to assess the amount of genetic diversity and a rational choice of potential parents for the breeding programme. Hence, D^2 analysis was carried out following procedure given by Rao (1952). The results of the study are presented below under the following heads.

4.5.1 Distribution of genotypes into clusters

Grouping of the genotypes was carried out by the Tocher's method (Rao, 1952) with the assumption that the genotypes within the cluster have smaller D^2 values among themselves than those from groups belonging to different clusters. In all, twelve clusters were formed from 30 genotypes. The distributions of genotypes into twelve clusters are presented in Table 4.7.

The cluster II was the largest cluster containing nine genotypes. Cluster I have six genotypes. Cluster III and V have three genotypes, cluster VII contains two genotypes and cluster IV, VI, VIII, IX, X, XI and XII include one genotype. Dalsania *et al.* (2009) observed similar type distribution of genotype into twelve clusters.

The clustering pattern showed that genotypes from different source were clubbed into one group and also genotypes of same source forming different cluster indicated no relationship between geographical and genetic divergence. Murthy and Arunachalam (1966) stated that genetic drift and selection in different environment could cause greater diversity than geographical distance.

Table 4.7: Distribution of genotypes evaluated for seed yield into different cluster of cowpea

Sr. No.	Cluster	Number of genotypes	Name of genotypes
1	**I**	**6**	GC 3, GC 4, GC 5, GC 2114, GC 2117, GC 1905
2	**II**	**9**	GC 6, GC 2102, GC 2103, GC 2104, GC 2107, GC 2110, GC 2115, GC 2113, GC 2116
3	**III**	**3**	GC 1501, GC 2006, GC 2007
4	**IV**	**1**	GC 2119
5	**V**	**3**	GC 2101, GC 2105, GC 2121
6	**VI**	**1**	GC 2118
7	**VII**	**2**	GC 2106, GC 2108
8	**VIII**	**1**	GC 2109
9	**IX**	**1**	GC 2120
10	**X**	**1**	GC 2111
11	**XI**	**1**	GC 2112
12	**XII**	**1**	GC 2002

4.5.2 Intra and Inter cluster average distances

The intra and inter-cluster D^2 values among twelve clusters are given in Table 4.6. The square root of average D^2, which was an approximate measure of divergence between groups and had been used to denote the distance.

Intra cluster average D^2 values ranged from 0.00 to 59.13. Among the clusters, cluster II had the maximum intra-cluster distance (D^2 =59.13), followed by cluster VII (D^2=50.04), cluster I (D^2=49.67), cluster V (D^2=45.83), cluster III (D^2=42.42). The zero intra-clusters distance was observed for cluster IV, VI, VIII, IX, X, XI and XII (D^2= 0.00). These seven clusters were a solitary cluster.

The largest inter cluster distance was observed between cluster X and cluster III (D^2= 315.38) followed by cluster XII and X (D^2= 284.58), cluster X and V (D^2= 266.58), cluster XII and VII (D^2= 259.17), cluster XII and VIII (D^2= 255.63), cluster IX and VIII (D^2= 249.56), cluster VII and V (D^2= 237.17), cluster VIII and III (D^2= 222.95), cluster VII and VI (D^2= 222.45), cluster XI and VIII (D^2= 203.36), cluster X and VIII (D^2= 199.09), while the minimum inter-cluster distance was observed between clusters II and I (D^2= 72.10), clusters I and VI (D^2= 76.83), clusters I and V (D^2= 86.04), clusters II and III (D^2= 6.11) and clusters IV and II (D^2= 92.85).

Inter-cluster distances were higher than intra-cluster distances which indicated the existence of substantial diversity among the genotypes. The selection of parents for crossing from divergent clusters may result in heterotic expression for yield and quality traits.

4.5.3 Cluster means of various characters

The mean performance of clusters for eleven characters is presented in Table 4.9. A considerable amount of inter cluster variation was observed among the days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, pod length, number of seed per pod, 100 seed weight (g), harvest index (%), protein content (%) and seed yield per plant (g).

The results indicated that cluster means for 11 characters showed considerable differences among the clusters for all the characters.

It is imperative from the results that character wise contribution differs from cluster to cluster, so far improvement of a particular character can be carried out by utilizing genotypes from the respective cluster having the highest mean values for it. Thus, clustering pattern deciding the cross combinations which may generate the highest variability for various traits. The superior genotypes for the breeding program can also be selected based on cluster means and inter cluster distance.

4.5.3.1 Days to flowering

The cluster means observed for days to flowering was varied from 39.25 days (cluster XII) to 45.75 days (cluster VIII). The genotypes of clusters XII (39.25 days) appeared to be early in flowering followed by cluster XI (39.50 days), cluster IX (39.75 days), cluster VI (40.50 days), cluster III (40.92 days), while the mean of cluster VIII (45.75 days) was highest imitated by cluster VII (44.25 days) and cluster X (43.50 days) indicating late flowering.

4.5.3.2 Days to maturity

The cluster means for days to maturity varied from 61.25 (cluster III) to 66.00 days (cluster VIII). Cluster mean for days to maturity revealed that cluster III (61.25 days) was earlier to mature imitated by cluster XII (61.50 days), cluster IX (62.25 days), cluster V (62.75) and cluster IV (63.00 days), while cluster VIII (66.00 days) was late mature followed by cluster X and XI (65.25 days).

Table 4.8: Average intra and inter cluster D^2 value of 30 genotypes of cowpea

Clusters	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**	**XII**
I	**49.67**											
II	72.10	**59.13**										
III	113.48	146.33	**42.42**									
IV	93.37	92.85	89.84	**0**								
V	86.04	99.86	140.90	133.32	**45.83**							
VI	76.83	103.65	135.15	148.24	98.29	**0**						
VII	133.76	129.69	161.68	151.42	237.17	222.45	**50.04**					
VIII	120.44	100.55	222.95	187.79	161.63	149.65	115.11	**0**				
IX	118.45	116.35	89.66	108.32	180.27	103.81	190.67	249.56	**0**			
X	164.72	113.85	315.38	152.14	266.58	243.41	151.37	199.09	196.02	**0**		
XI	154.69	110.02	157.08	135.16	179.40	152.48	138.80	203.36	93.48	136.07	**0**	
XII	172.71	139.71	116.92	79.74	132.53	159.45	259.17	255.63	145.10	284.58	174.92	**0**

4.5.3.3 Plant height (cm)

The range of cluster means for this character varied from 39.17 (cluster V) to 68.89 cm (cluster X). Cluster mean for plant height revealed that cluster X (68.89 cm) had tall plants followed by cluster VII (65.06 cm), cluster IV (61.42 cm), cluster IX (59.11 cm) and cluster II (54.38 cm). The dwarf plant was observed in cluster V (39.17 cm) followed by cluster VI (39.18 cm).

4.5.3.4 Number of branch per plant

The range of cluster means for number of branch per plant varied from 7.05 (cluster I) to 10.45 (cluster VIII). The genotypes with maximum number of branch were found in cluster VIII (10.45) followed by cluster XI (8.40), cluster II (8.39), cluster VII (8.15), and cluster IX (7.95). The lowest number of branch per plant was observed in cluster I (7.05) imitated by cluster III (7.22).

4.5.3.5 Number of pod per plant

The range of cluster means for this character varied form 11.34 (cluster X) to 17.97 (cluster VII). The cluster VII (17.97) recorded the maximum number of pod per plant followed by cluster III (16.30), cluster VIII (15.95) and cluster XI (14.69). The cluster X (11.34) showed least number of pod per plant imitated by cluster VI (12.44).

4.5.3.6 Pod length (cm)

The cluster mean observed for pod length varied from 11.44 cm (cluster XII) to 15.28 cm (cluster VII). The cluster VII (15.28 cm) recorded the highest cluster mean for pod length followed by cluster VI (14.53 cm), cluster VIII (14.09 cm), cluster X (13.98 cm) and cluster I (13.31 cm). The lowest cluster mean for pod length was recorded by cluster XII (11.44 cm) followed by cluster III (11.57 cm).

4.5.3.7 Number of seed per pod

The cluster means for this character ranged from 8.72 (cluster V) to 14.59 (cluster VI). The cluster VI (14.59) recorded the higher mean for number of seed per pod followed by cluster IX (13.44), cluster VIII (13.40), cluster VII (11.81) and cluster XII (11.74), while the cluster V (8.72) recorded minimum number of seed per pod imitated by cluster XI (9.27).

4.5.3.8 100 seed weight (g)

The cluster means for 100 seed weight ranged from 9.19 g (cluster IX) to 16.16 g (cluster XI). The cluster XI (16.16 g) showed highest mean for 100 seed weight followed by cluster X (16.14 g), cluster VIII (15.37 g) and cluster VII (14.38 g). The lowest mean for 100 seed weight was shown by cluster IX (9.19 g) followed by cluster III (9.51 g).

4.5.3.9 Harvest index (%)

The cluster mean observed for harvest index was varied from 33.50 % (cluster XII) to 71.34 % (cluster VII). The cluster VII (71.34 %) recorded the highest cluster mean for harvest index followed by cluster VIII (70.43 %), cluster VI (70.37 %) and cluster IX (68.65 %). The lowest cluster mean for harvest index was recorded by cluster XII (33.50 %) followed by cluster II (56.15 %).

4.5.3.10 Protein content (%)

The cluster mean observed for protein content was varied from 20.74 % (cluster XI) to 24.19 % (cluster XII). The cluster XII (24.19 %) recorded the highest cluster mean for protein content followed by cluster IV (23.72 %), cluster III (23.02 %) and cluster V (22.75 %). The lowest cluster mean for protein content was exhibited by cluster XI (20.74 %) imitated by cluster X (20.77 %).

4.5.3.11 Seed yield per plant (g)

The cluster means for seed yield per plant ranged from 17.11 g (cluster IV) to 20.96 g (cluster VII). The cluster VII (20.96 g) showed highest mean for seed yield per plant followed by cluster VIII (20.35 g), cluster VI (19.60 g) and cluster III (19.22 g). The lowest mean for seed yield per plant was shown by cluster IV (17.11 g) followed by cluster V (17.74 g).

Wider ranges of mean values among the clusters were recorded for different traits. The cluster III had the lowest mean values and desirable rating for earliness maturity (61.25 days). The cluster VI had highest mean value for number of seed per pod (14.59).

Table 4.9: Cluster mean for seed yield and its components in cowpea

C	DF	DM	PH	NBPP	NPPP	NSPP	PL	TW	PC	HI	SYPP
I	43.29	63.58	50.60	7.05	13.93	11.74	13.31	10.90	22.25	64.26	18.54
II	42.94	63.92	54.38	8.39	13.36	11.48	12.30	13.36	22.01	56.15	18.52
III	40.92	61.25	53.00	7.22	16.30	11.57	11.57	9.51	23.02	66.08	19.22
IV	41.75	63.00	61.42	7.45	13.04	10.14	11.96	11.57	23.72	66.68	17.11
V	42.33	62.75	39.17	7.75	13.79	8.72	12.39	11.49	22.75	42.60	17.74
VI	40.50	64.25	39.18	7.36	12.44	**14.59**	14.53	12.12	22.33	70.37	19.60
VII	44.25	64.75	65.06	8.15	**17.97**	11.81	**15.28**	14.38	21.62	**71.34**	**20.96**
VIII	**45.75**	**66.00**	51.80	**10.45**	15.95	13.40	14.09	15.37	22.58	70.43	20.35
IX	39.75	62.25	59.11	7.95	12.64	13.44	11.82	9.19	21.37	68.65	18.79
X	43.50	65.25	**68.89**	7.85	11.34	10.59	13.98	16.14	20.77	65.58	17.92
XI	39.50	65.25	54.11	8.40	14.69	9.27	12.25	**16.16**	20.74	66.84	18.02
XII	39.25	61.50	52.42	7.90	13.09	11.74	11.44	12.64	**24.19**	33.50	18.83

Highest value in bold and lowest in underline.

DF= Days to flowering, **DM** = Days to maturity**,** **PH**= Plant height (cm), **NBPP**= Number of branch per plant, **NPPP**= Number of pod per plant, **PL**= Pod length (cm), **NSPP**= Number of seed per pod, **TW**= 100 seed weight (g), **HI**= Harvest index (%), **PC**= Protein content (%), **SYPP**= Seed yield per plant (g).

The cluster VII had the highest mean values for the number of pod per plant (17.97), pod length (15.28 cm), harvest index (71.34 %) and seed yield per plant (20.96 g). Cluster VIII had a desirable high rating for number of branch per plant (6.98). Cluster X had a desirable high rating for plant height (68.89 cm). Cluster XI had a highest mean value for 100 seed weight (16.16 g), cluster XII had the lowest mean values and desirable rating for earliness flowering (39.25 days) and protein content (24.19 %).

4.5.4 Relative contribution of each character towards diversity

The components of D^2 due to each character variable were ranked I being assigned to the highest value. The total of these ranks over all possible [n (n − 1)/2] = 435 combinations would provide indirect information about the order of priority in terms of the percentage contribution of the character to the total divergence. These percentages are presented in Table 4.10 and Fig 4.3

Table 4.10: Relative contribution of different characters towards genetic diversity in cowpea genotypes evaluated for seed yield

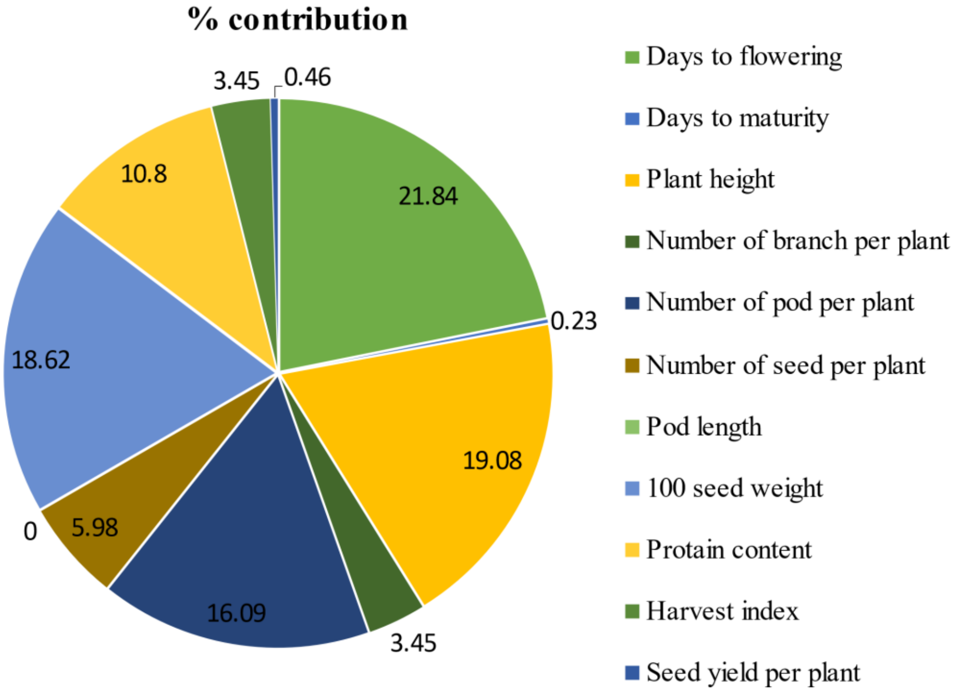
Sr. No.	Characters	Time ranked 1st	Contribution to divergence %
1	Days to flowering	95	21.84%
2	Days to maturity	1	0.23%
3	Plant height (cm)	83	19.08%
4	Number of branch per plant	15	3.45%
5	Number of pod per plant	70	16.09%
	Number of seed per pod	26	5.98%
7	Pod length (cm)	0	0%
8	100 seed weight (g)	81	18.62%
9	Protein content (%)	47	10.80%
10	Harvest index (%)	15	3.45%
11	Seed yield per plant (g)	2	0.46%

Among all the characters, days to flowering (21.84 %) contributed maximum to the diversity by taking the first rank 95 times out of 435 combinations, followed by plant height (19.08 %) with 83 times, 100 seed weight (18.62 %) with 81 times, number of pod per plant (16.09 %) with 70 times. While, protein content (10.80 %)

with 47 times, number of seed per pod (5.98 %) with 26 times, harvest index and number of branch per plant (3.45 %) with 15 times, seed yield per plant (0.46 %) with 2 times, days to maturity (0.23 %) with 1 times and pod length (0 %) with 0 times out of 435 combinations contributed minimum towards total genetic divergence.

In the present study, days to flowering (21.84 %), plant height (19.08 %) and 100 seed weight (18.62 %) were the main contributors to the total divergence. These traits may play important role for germplasm collection and evaluation. Shrinivas *et al.* (2016) and Vishwanatha *et al.* (2017) also observed high diversity for days to flowering and moderate to low contribution towards the total divergence were observed for days to maturity, protein content, number of branch per plant, plant height, number of seed per pod and 100 seed weight. Nagalakshmi *et al.* (2010) for days to flowering, 100 seed weight and seed yield per plant. Patel *et al.* (2017) also reported highest diversity for number of pod per plant. and Gupta *et al*. (2019) for 100 seed weight.

Fig. 4.3: Graphical representation of per cent (%) contribution towards genetic divergence by eleven characters to Cowpea



Thirty genotypes showed abundant variation among with respect to quantitative traits. Based on mean performance, genotypes GC 2108, GC 2109, GC 2118, GC 2006 and GC 2106 were superior for overall the characters under study. Based on heritability, days to flowering, days to maturity, plant height, number of branch per plant, number of pod per plant, number of seed per pod, 100 seed weight, protein content, harvest index were exhibited high heritability which could be effectively improved by selection. It could be also concluded that number of branch per plant, number of pods per plant, number of seed per pod, pod length and 100 seed weight were positive correlation coefficient and positive direct effect. Based on the cluster mean value, cluster VII with genotypes GC 2106, GC 2108 were having a greater number of pod per plant, pod length, harvest index and seed yield per plant. Whereas, inter-cross of the genotype clusters III (GC 1501, GC 2006, GC 2007) and cluster X (GC 2111) would be effective for creating wide spectrum of variability and improving seed yield in cowpea.

The success of the plant breeding programme depends largely on the choice of appropriate parents. It is expected that the utilization of divergent parents in hybridization results in promising recombinants. The genetic improvement mainly depends on the amount of genetic variability present in the population.

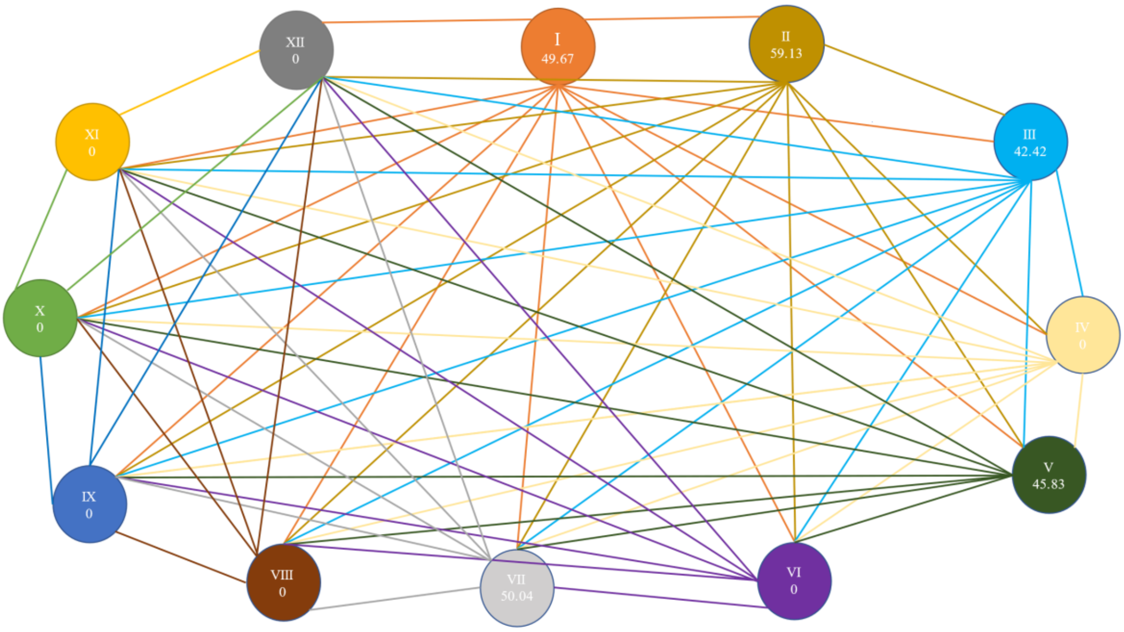


Fig. 4.4: Intra and inter-cluster distance for thirty genotypes in cowpea

V. SUMMARY AND CONCLUSIONS

The present investigation work on “Genetic variability and character association in cowpea [*Vigna unguiculata* (L.) Walp.]” The experiment was conduct at Agronomy Instructunal Farm, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar during *kharif* 2021 with following objectives,

1. To study the genetic variability, heritability and genetic advance for morphological trait in cowpea
2. To study the amount of genotypic and phenotypic correlation between seed yield and its attributing character
3. To study the path analysis for assessing the direct and indirect effect of individual character on seed yield
4. To find out the genetic diversity through D^2 involving seed yield and its attributing characters

The experimental material included of thirty diverse genotypes of cowpea collected from Pulses Research Station, Sardarkrushinagar Dantiwada Agricultural University, Sardarkrushinagar. Genotypes were planted on 16th July, 2021 at Agronomy Instructunal Farm in randomized block design (RBD) with four replications. Each genotype was sown at spacing of 45 cm between row and 15 cm between plants with row length of four meter. Data were recorded on five randomly selected plants of each entry per replication for traits under study except days to flowering and days to maturity, where observations were recorded on plot basis. The method prescribed by Panse and Sukhatme (1978) was followed to determine variability and correlation coefficient by Al-Jibouri (1958) and path analysis as per method suggested by Deway and Lu (1959) and genetic diversity analysis by Mahalanobis, (1936). The genotypes were evaluated to study the magnitude of genetic variability in traits *viz.* days to flowering, days to maturity, plant height (cm), number of branches per plant, number of pods per plant, number of seed per pod, pod length (cm), 100 seed weight (g), seed yield per plant (g), harvest index (%) and protein content (%)

Per se performance of genotypes was ranged for days to flowering (39.25) to (45.75) days, days to maturity (60.25) to (66.00) days, plant height (35.97 cm) to (69.22 cm), number of branch per plant (5.95) to (10.45), number of pod per plant

(11.09) to (18.19), number of seed per pod (7.34) to (14.59), pod length (11.09 cm) to (15.29 cm) 100 seed weight (8.59 g) to (16.17 g), harvest index (33.50 %) to (73.17 %), protein content (20.74 %) to (24.19 %) and seed yield per plant (14.96 g) to (21.70 g). Best five genotypes for days to flowering GC 2002 (39.25), GC 2112 (39.50), GC 2007 (39.50), GC 2120 (39.75) and GC 2118 (40.50); for days to maturity GC 1501 (60.25), GC 2002 (61.50), GC 2006 (61.50), GC 2007 (62.00) and GC 2120 (62.25); for lowest plant height GC 2121 (35.97 cm), GC 2118 (39.19 cm), GC 2101 (39.89 cm), GC 2105 (41.66 cm) and GC 3 (44.21 cm) for highest plant height GC 2106 (69.22 cm), GC 2111 (68.89 cm), GC 2113 (63.66 cm), GC 2107 (61.83 cm) and GC 2119 (61.42 cm); for number of branch per plant GC 2109 (10.45), GC 2116 (9.40), GC 2115 (9.15), GC 2108 (9.00) and GC 2113 (8.90); for number of pod per plant GC 2106 (18.19), GC 2108 (17.74), GC 1501 (17.17), GC 2006 (16.24) and GC 2109 (15.95); for number of seed per pod GC 2118 (14.59), GC 3 (14.44), GC 2103 (14.34), GC 2120 (13.44) and GC 2109 (13.40); for pod length GC 2108 (15.29 cm), GC 2106 (15.27 cm), GC 2118 (14.53 cm), GC 2101 (14.45 cm) and GC 2109 (14.09 cm); for 100 seed weight GC 2112 (16.17 g), GC 2111 (16.14 g), GC 2113 (15.44 g), GC 2109 (15.37 g) and GC 2103 (15.27 g).; for harvest index GC 2108 (73.17 %), GC 2109 (70.43 %), GC 2118 (70.37 %), GC 2006 (70.08 %) and GC 2106 (69.51 %); for protein content GC 2002 (24.19 %), GC 2007 (23.75 %), GC 2119 (23.72 %), GC 2101 (23.53 %) and GC 2006 (23.32 %); and for seed yield per plant GC 2108 (21.70 g), GC 2109 (20.35 g), GC 2106 (20.23 g) GC 2006 (19.98 g) and GC 2118 (19.60 g)].

The analysis of variance revealed that mean sum of squares due to genotypes was found significant for all the traits under studied. This indicated the presence of adequate amount of variability in the experimental material and the genotypes under study showed genetically diverse.

A broad range of phenotypic variability was recorded for seed yield per plant and its components traits. The values of phenotypic coefficient of variation (PCV) were slightly higher than that of genotypic coefficient of variation (GCV) for all the characters under studied in similar trends, indicating less influence of environment on the expression of traits.

The moderate values of genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were recorded for 100 seed weight (18.54 and 20.12) followed by harvest index (17.34 and 19.68), Plant height (15.04

and 15.89), number of seed per pod (14.44 and 16.47), number of pod per plant (12.18 and 13.03) and number of branches per plant (11.65 and 13.13). This represented the presence of broad genetic variation for these characters and effective selection of traits is possible. Which showed the influence of environment for expression of these traits. The low values of GCV and PCV were observed for pod length (8.79 and 12.41), seed yield per plant (6.28 and 8.54), days to flowering (4.02 and 4.24), protein content (3.86 and 4.15) and days to maturity (1.99 and 2.44) respectively.

The high values of heritability (broad sense) were observed in days to flowering (90.00 %) followed by plant height (89.69 %), number of pod per plant (87.33 %), protein content (86.72 %), 100 seed weight (84.95 %), seed yield per plant (84.86 %), number of branch per plant (78.75 %), harvest index (77.67 %), number of seed per pod (76.82 %) and days to maturity (67.02 %) suggested that heritability due to higher contribution of the genotypic component in these characters. The heritability was moderate for seed yield per plant (54.05 %) and pod length (50.15 %).

The genetic advance expressed as percentage of mean values were observed high for 100 seed weight (35.21 %) followed by harvest index (31.48 %), plant height (29.35 %), number of seed per pod (26.06 %), number of pod per plant (23.45 %) and number of branch per plant (21.30 %). While moderate values of the genetic advance as percentage of mean were observed for pod length (12.81 %) and lowest genetic advance as percentage of mean were observed for seed yield per plant (9.51), days to flowering (7.86 %), protein content (7.40 %) and days to maturity (3.37 %).

Moderate to high estimates of heritability values coupled with high genetic advance expressed as percentage of mean values were recorded for 100 seed weight, harvest index, plant height, number of seed per pod, number of pods per plant and number of branches per plant. Which attributed to the prevalence of additive gene action which is fixable for governing the character and acquired high selective value and thus, selection pressure could profitably be applied on these traits for their judicious improvement by following different breeding methods *viz.*, pedigree, bulk, single seed descent method, backcross and biparental mating design along with advance breeding method to speed up the improvement for yield and its contributing traits. The selection of these traits will be more effective in improvement. High heritability exhibited that larger portion of variation for the character in the material was due to additive gene action.

The values of genotypic correlation coefficient normally, higher as compared to the proportionate phenotypic correlation coefficient. This stipulated that though there was high degree of association between the two variables at genotypic and phenotypic level. The characters, seed yield per plant found to be highly significant and positive correlated with number of seed per pod (r_g = 0.5369** and r_p = 0.3534**), number of pod per plant (r_g = 0.6716** and r_p = 0.4692) and pod length (r_g = 0.5147** and r_p = 0.3332**) at both the genotypic and phenotypic levels. seed yield per plant found to be positive and non-significant correlation with number of branch per plant (r_g = 0.3259 and r_p = 0.2137*), days to flowering (r_g = 0.2706 and r_p = 0.1556*) and plant height (r_g = 0.2451 and r_p = 0.2088*) at the genotypic level while, significant and positively correlated at phenotypic levels. Seed yield per plant also recorded positively and non-significant correlation with days to maturity (r_g = 0.1994 and r_p = 0.1556), 100 seed weight (r_g = 0.0278 and r_p = 0.0083) and harvest index (r_g = 0.1535 and r_p = 0.084) at both the genotypic and phenotypic levels. Seed yield per plant also observed nagative and non-significant correlation with protein content (r_g = -0.0249 and r_p = -0.0053) both the genotypic and phenotypic levels. The yield components revealed varying tendency of association among themselves. The interrelationship among the yield constituents would help in increasing the yield levels and, consequently more importance should be given to yield components, while selecting better plant types in cowpea.

The genotypic path coefficient analysis estimated that pod length (1.1797), number of branch per plant (0.7733), number of seed per pod (0.4806) and number of pod per plant (0.3187) showed high and positive direct effect on seed yield per plant. Plant height exhibited low and positive direct effect (0.1372) on seed yield per plant while, 100 seed weight show negligible and positive direct (0.0708) effect on seed yield per plant. which exhibited to be the most important yield components. The character days to flowering (-0.2014) and protein content (-0.2013) showed moderate and negative direct effect on seed yield per plant while, days to maturity (-0.9825) and harvest index (-0.3664) showed high and negative direct effect on seed yield per plant. From the correlation and path coefficient analysis it is envisaged that pod length, number of branch per plant, number of seed per pod, and number of pod per plant were the most important traits which should be given more emphasis during selection programme for the improvement of seed yield in cowpea.

The genetic divergence was assessed by Mahalanobis D^2 statistics and grouped thirty genotypes of Cowpea into twelve clusters. The cluster II was the largest cluster having 9 genotypes followed by cluster I (6 genotypes), cluster III and V (3 genotypes), cluster VII (2 genotypes) and cluster IV, VI, VIII, IX, X, XI, XII (1 genotype). The perusal of intra- cluster and inter- cluster distance revealed that inter- cluster values were greater than intra- cluster distance values. The maximum inter- cluster distance (D^2 = 315.38) was found between cluster III and X followed by cluster XII and X (D^2 = 284.58). The minimum inter- cluster distance was observed between cluster I and II (D^2 = 72.10). The cluster IV, VI, VIII, IX, X, XI and XII contained single genotype therefore; its intra- cluster distance was Zero. Selections of parent based on large inter- cluster and intra- cluster distances for hybridization work gives a range of useful combination. Days to flowering followed by plant height, 100 seed weight, number of pod per plant and protein content contributed maximum toward to the total divergence in seed yield. Based on the cluster mean value, cluster VII with genotypes GC 2106, GC 2108 were having more number of pod per plant, pod length, harvest index and seed yield per plant. The genotypes belonging to the clusters separated by high stastical distance could be used in hybridization programme for obtaining a wide spectrum of variation among the genotypes and high heterosis. The genotypes with high value of any cluster can be used either for direct adoption for hybridization followed by selection.

An over view of the experimental results of present investigation indicated a wide spectrum of variation with respect to yield related traits among all the thirty genotypes of cowpea. From the foregoing discussion, it can be concluded that the characters coefficient of variation for GCV and PCV were found moderate for the following traits *i.e.,* 100 seed weight, harvest index, plant height, number of seed per pod, number of pod per plant and number of branch per plant. The high heritability coupled with high genetic advance was found for 100 seed weight, harvest index, plant height, number of seed per pod, number of pods per plant and number of branches per plant. This was due to less environmental influence and major effect of additive genes and therefore a selection of these traits will be more effective in improvement of crop. From the correlation and path coefficient analysis it is envisaged that number of pod per plant, number of seed per pod and pod length were most important traits which should be given more emphasis during selection programme for the improvement of seed yield in cowpea. Based on the relative magnitude of D^2 values, the thirty genotypes were grouped into twelve clusters. The cluster II exhibited maximum intera-cluster distance. Based on the genetic divergence studies, it was apprent that the maximum inter-cluster distance was observed between cluster X and III followed by X and XII indicating that the hybridization between the most diverse genotypes from these clusters would be desirable with the accumulation of favourable genes in the segregating generation. Days to flowering, plant height, 100 seed weight and number of pod per plant contributed maximum towards the total divergence in seed yield. Hence, selection for divergent parents, based on these characters would be useful for developing potential hybrids.

REFERENCES

Abadassi, J. (2015). Cowpea [*Vigna unguiculata* (L.) Walp] agronomic traits needed in tropical zone. *International Journal of Pure and Applied Biosciences*, **3** (4):158-165.

Adewale, B. D.; Okonji, C.; Oyekanmi, A. A.; Akintobi, D. A. C., and Aremu, C. O. (2010). Genotypic variability and stability of some grain yield components of Cowpea. *African Journal of Agricultural Research*, **5**(9), 874-880.

Ahamed, K. U.; Akhter, B.; Islam, M. R.; Alam, M. A. and Humauan, M. R. (2014). Assessment of genetic diversity in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm. *Bulletin of the Institute of Tropical Agriculture*, 37: 57-63.

Al-Jibouri, N. A.; Miller, P. A. and Robin, H. F. (1958). Genotypic and environmental variances, co-variances in an upland cotton cross of inter-specific origin. *Journal of Agron*, **50**: 633-637.

Allard, R. W. (1961). Relationship between genetic diversity and consistency performance in different environments. *Crop Science*, **1** (2): 127-133.

Anamika, N. and Tajane, P. A. (2014). Path analysis for seed yield in cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal of Plant Sciences* (Muzaffarnagar), **9**(1), 291-292.

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.

Animasaun, D. A., Oyedeji, S., Azeez, Y. K., Mustapha, O. T., and Azeez, M. A. (2015). Genetic variability study among ten cultivars of cowpea (*Vigna unguiculata* L. Walp) using morpho-agronomic traits and nutritional composition.

Anonymous (2019-20). Directorate of Agriculture Gujarat State, Gandhinagar.

Aswathi, C.; Devadas, V. S.; Francies, R. M. and Bastian, D. (2015). Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp] varieties for seed quality. *Journal of Tropical Agriculture*, 53(2): 197-199.

Aykroyd, W. R. (1963). ICMR Special Report, Series, No. 42.

Backlyaranl, S.; Nadarajan, N.; Rajendran, C. and Shanthi, S. (2000). Genetic divergence for physiological traits in cowpea [*Vigna unguiculata* (L.) Walp]. *Legume Research-An International Journal*, **23**(2): 114-111.

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

Benjamin, U.; Olamide, F.; Yusuf, D. O. A.; Abdulhakeem, A.; Dickson, N.; David, T. S. and Muhammad, L. (2018). Phenotypic variability studies in selected accessions of Nigerian wild cowpea [*Vigna unguiculata* (L.) Walp]. *GSC Biological and Pharmaceutical Sciences*, **3**(1): 19-27.

Bhagavati, P. P.; Kiran Patro, T. S. K. K.; Lakshmi Narayana Reddy, M.; Emmanuel, N.; Salomi Suneetha, D. R. and Vara Prasad, N. (2018). Studies on genetic variability, heritability and genetic advance in yardlong bean (*Vigna ungiculata* (L.) walp. ssp. sesquipedalis verdc.) *International Journal of Chemical Studies* 2018; **6**(4): 1135-1138.

Bhardu, D. and Navale, P. A. (2011). Correlation and path analysis studied in F_3 population of cowpea. (*Vigna unguiculata L.* Walp.). *Legume Research,* **34**(1): 65-69.

Bhardwaj, R.; Singh, D. P.; Upasana, R.; Tiwana, U. S. and Bajaj, R. K. (2014). Association studies in cowpea [*Vigna unguiculata* (L.) Walp]. *Journal of Food Legumes,* **27**(1): 74-73.

Bizeti, H. S.; Carvalho, C. G. P.; deSouza, J. R. P. and Destro, D. (2004). Path Analysis under Multi-collinearity in Soybean. *Brazilian Archives of Biology and Technology,* 47(5): 669-676.

Boukar, O.; Massawe, F.; Muranaka, S.; Franco, J.; Bussie, M. D.; Singh, B. and Fatokun, C. (2011). Evaluation of cowpea germplasm lines for protein and mineral concentrations in grains. *Plant genetic Resources,* **9**(4):515-522.

Bowely, A. L. (1920). Elements of Statistics. *Indian Journal of Agriculture Science,* **3**: 609-625.

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):107-111.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proceeding Sixth International Grassland Congress,* **1**: 277-283.

Chaudhary, A. R.; Solanki, S. D.; Rahevar, P. M. and Patel, D. A. (2020). Genetic variability, correlation and path coefficient analysis for yield and its attributing traits in cowpea [*Vigna unguiculata* (L.) Walp] accessions. *International Journal of Current Microbiology and Applied Science,* **9**(2): 1281-1293.

Chaudhary, R. R. and Joshi, B. K. (2005). correlation and path coefficient analyses in sugarcane. *Nepal Agriculture Research Journal,* 6 : 24-28.

Chandrakar, R.; Verma, A.; Singh, J. and Mehta, N. (2016). Genetic divergence in vegetable cowpea (*Vigna unguiculata* (L.) Walp.) *The Asian journal of horticulture* **11**(2): 323-328.

Cholin, S.; Uma, M. S.; Sangeeta, M.; Suma, B.; Salimath, P. M. (2010). Stability analysis for yield and yield components over seasons in cowpea [*Vigna unguiculata* (L.) Walp]. *Eletronic Journal of Plant Breeding,* **1**(16): 1392-1395.

Craufurd, P. Q.; Summerfield, R. J.; Ellis, R. H. and Roberts, E. H. (1997). Photoperiod, temperature and the growth and development of cowpea, *Vigna unguiculata* (L.) Walp. in Singh B. B. *et al.*, (eds). Advances in Cowpea Research. IITA-JIRCAS, Ibadan, Nigeria, pp. 75-86.

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.

Das, R. R.; Talukdar, P.; Kumar, P. and Neog, S. B. (2018). Relationship among different secondary traits and seed yield in Cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of Current Microbiology and Applied Sciences,* **7**(2): 1382-1396.

Davis, D. W.; Oelkae, E. A.; Oplinger, J.; Doll, J. D.; Hansan, C. V. and Putnam, D. H. (2000). *Alternative field crops manual*

Detroja, D. H.; Thakor, D. M.; Baldaniya, V. G.; Soni, N. V. and Patel, P. C. (2020). Association analysis of morpho-physiological traits in vegetable cowpea [*Vigna unguiculata* (L.) Walp]. *Electronic Journal of Plant Breeding*, **11**(3): 954-959.

Devi, M. S. and Jayamani, P. (2018). Genetic variability, heritability, genetic advance studies in cowpea germplasm [*Vigna unguiculata* (L.) Walp] *Electronic Journal of Plant Breeding*, **9**(2): 476-481.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path analysis of components of crested wheat grass seed production. *Agronomy Journal*, **51**: 515-518.

Dinesh, H. B.; Viswanatha, K. P.; Lohithaswa, H. C.; Pavan, R. and Singh, P. (2017). Variability, correlation and path analysis studies in F_3 generation of cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of current Microbiology Applied science*, **5**(5): 1389-1395.

Donald, C. M. and Hamblin, J. (1976). The biological yield and harvest index of cereals as agronomic and plant breeding criteria. *Advances in Agronomy*, **28**: 361-405

Duke, J. A. (1981). Handbook of legumes of world economic importance. Plenum Press, New York. 345 pp.

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-An International Journal*, **30** (1), 17-23.

Falconer, D. S. (1989). Introduction to Quantitative Genetics. 3rd Edn. Longman. New York. U.S.A.

Fatokun, C. A.; Tarawali, S.A.; Singh, B. B.; Kormawa, P. M. and Tamo, M. (2020). Challenges and opportunities for enhancing sustainable cowpea production. In Proceedings of the World Cowpea Conference III held at the International Institute of Tropical Agriculture (IITA), Ibadan, Nigeria,7-396

Fisher, R. A. and Yates, F. (1963). Statistical tables for biological agricultural and medical research. Oliver and Boyd, Edinberg, 6th Ed. Pp. – 63.

Food and Agriculture Organisation of United Nations (FAO) (2019) FAOSTAT Online Statistical Services: Crop Pro-duction Data. Rome, Italy. Available at http//www.fao.org/faostat/en/#data.

Get, S.; Shekhawat, S. S.; Gothwal, D. K.; Singh, J.; Yadav, M. and Choudhary, M. (2021). Heterosis for seed yield and associated traits in cowpea [*Vigna unguiculata* (L.) Walp] genotypes under rainfed condition of Rajasthan. *Pharma Innovation Journal*. **10**(7): 369-373.

Gerrano, A. S., Adebola, P. O., Jansen van Rensburg, W. S., and Laurie, S. M. (2015). Genetic variability in cowpea (*Vigna unguiculata* (L.) Walp.) genotypes. *South African Journal of Plant and Soil*, **32**(3), 165-174.

Goulden (1962). Methods of statistical analysis. *Asia Pulblication House*, NewDelhi.

Gupta, R. K.; Arya, M.; Kumar, A. and Kumari, P. (2019). Study on genetic variability in cowpea [*Vigna unguiculata* (L.) Walp]. *Current Journal of Applied Science and Technology*, 1-8.

Havaraddi, U. and Deshpande, S. K. (2018). Genetic variability studies in advanced stabilized lines of cowpea (*Vigna unguiculata* (L.) Walp.). *International Journal of Pure Applied Bioscience*, **6**(6), 221-226.

Horn, L. N.; Shimelis, H. (2020). Production constraints and breeding approaches for cowpea improvement for drought prone agro-ecologies in Sub-Saharan Africa. *Annals of Agricultural Sciences*. **65**(1):83-91.

Jat, S. R.; Patel, B. J.; Shrinivas, A. C.; Kuri, B. R and Jat, G. (2013). Effect of phosphorus and sulphur levels on growth and yield of cowpea under rainfed conditions. *Annals of Plant and Soil Research*, **15**((2):114-117.

Johnson, H. W.; Robinson, H. E. and Comstock, R. E. (1955). Estimation of genetic and environmental variability in soyabean. *Agronomy Journal*. **47** (7): 314-318.

Kalambe, A. S.; Wankhade, M. P.; Bagade, A. B. and Shinde, A. V. (2019). Path analysis studies for quantitative traits in cowpea (*Vigna unguiculata* L.). *International Journal of Chemical Studies*, **7**(3): 475-478.

Khan, H., Viswanatha, K. P., and Sowmya, H. C. (2013). Genetic variability parameters and association studies in cowpea [*Vigna unguiculata* (L.) Walp]. *Journal of food legumes*, **26**(3&4), 42-45.

Khan, H., Viswanatha, K. P., and Sowmya, H. C. (2015). Study of genetic variability parameters in cowpea [*Vigna unguiculata* (L.) Walp] germplasm lines. *The bioscan*, **10**(2), 747-750.

Khanpara, S. V.; Jivani, L. L.;Vachhani, J. H. and Kachhadia, V. H. (2015). Genetic variability, heritability and genetic advance studies in vegetable cowpea [*Vigna unguiculata* (L.) Walp.]. *Electronic Journal of Plant Breeding*, **7**(2), 408-413.

Kumar P. K.; Kumar, R. N.; Muneeswari, T.; Nagaajothi, R. L. and Kumari, R. U. (2013). Morphological and genetic variation studies in cowpea genotypes [*Vigna unguiculata* (L.) Walp]. *Legume Research*, **36**(4):351-354.

Kumar, D., Golakia, B. A., & Parakhia, A. M. (2018). Characterization and genetic diversity of cowpea (*Vigna unguiculata* L.) genotypes linked to cowpea yellow mosaic virus. *Legume Research: An International Journal*, 41(1).

Kumar, V. E.; Thangaraj, K.; Kalaimagal, T.; Vanniarajan, C.; Senthil, N.; Kumar, J. P. and Souframanien, J. (2020). Inter relationship between yield and its attributing traits in cowpea [*Vigna unguiculata* (L.) Walp] germplasm accessions. *International Journal of Current microbiology and Applied Sciences*, **9**(5): 194-200.

Kumari, U. R.; Backiyarani, S. and Dhanakodi, C. V. (2000). Character contribution to diversity in cowpea (*Vigna unguiculata* L. Walp.) *Legume Research-An International Journal* **23(**2), 122-125.

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

Lenka, D. and Mishra, B. (1973). Path coefficient analysis of yield in rice varieties. *Indian Journal of Agricultural Science*, 43: 376-379.

Magashi, A. L.; Shawai, R. S.; Muhammad, A. and Ibrahim, M. B. (2019). Genetic variability studies of some quantative traits in cowpea [*Vigna unguiculata* (L.) Walp] under water stress. *African Journal of Plant Science*, **13**(2): 25-33.

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.

Manisha, R. P.; Vijay, S. K.; Madhavi, B. B. and Jadhav, R. D. (2018). Correlation and path analysis study in F_5 generation of cowpea. *International Journal of Current Microbiology and Applied Sciences*, **6**, 1529-1537.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceeding of national Academic of Science*, 2;49-55.

Meena, H. K.; Krishna, K. R. and Singh, B. (2015). Character association between seed yield and its components traits in cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of Agriculture Science and Research* (IJASR), **49**(6): 567-570.

Meenatchi, T.; Thangaraj, K.; Gnanamalar, R. P. and Pushpam, K. (2019). Genetic variability and heritability study on yield and its component traits in segregating population of cowpea [*Vigna unguiculata* (L.) Walp]. *Eletronic journal of Plant Breeding*, **10**(2): 736-741.

Miller, P. R.; Graves, W. L.; Williams, W. A. and Madson, B. A. (1989). Covercrops for California Agriculture. University of California Division of Agriculture and Natural Resources, Oakland, California. Leaflet 21471. 24 pp.

Mofokeng, M. A.; Mashilp, J.; Rantso, P. and Shimelis, H. (2020). Genetic variability and genetic advance in cowpea based on yield and yield-related traits. *Acta Agriculturae scandinavica, Section B- Soil & Plant Science*, DOI:10. 1-13.

Nagalakshmi, R. M.; Usha Kumari, R; Boranayaka, M. B.; (2010). Assessment of genetic diversity in cowpea (*Vigna unguiculata*). *Electronic Journal of Plant Breeding*, **1**(4): 453-461.

Nagalakshmi, R. M.; Kumari, U. R. and Kumar, A. R. (2020). Correlation and Path analysis in Cowpea [*Vigna unguiculata* (L.) Walp]. *An International Quarterly Journal of Life Science*, **15**(3): 397-401.

Nair, K. R.; Desai, S. S.; Sawardekar, S. V. and Burondkar, M. M. (2018). Study of genetic variability parameters in F_2 generation of interspecific hybrids in cowpea. *International Journal Pure Applied Bio science*, ***6***(1): 954-958.

Nancee; Rana, N. M. K.; Partap, P. S. and Ranjan, R. (2013). Study of genetic divergence on vegetable cowpea [*Vigna unguiculata* (L.) Walp]. *Vegetable science*, **40**(2): 182-184.

Nguyen, N. V.; Arya, R. K,; Panchta, R. and Tokas, J. (2017). Studied on genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp] by using D^2 satistics under semi- arid conditions. *Forage Research*, **43**(3): 197-201.

Nkoana, D. K.; Gerrano A. S. and Gwata. (2019). Agronomic performance and genetic variability of cowpea [*Vigna unguiculata* (L.) Walp] accessions. *Legume Research*, **42**(6): 757-762.

Nwofia, G. E.; Nwanebu M. and Agbo C. U. (2012). Variability and inter-relationships 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.

Nwosu, D. J.; Olatunbosun, B. D. and Adetiloye, I. S. (2013). Genetic variability, heritability and genetic advance in cowpea genotypes in two agro-ecological environments. *Greener Journal of Biological Sciences*, **3**(5), 202-207.

Panchta, R.; Arya, R. K.; Nguyen, N. V. and Behl, R. K. (2021). Genetic divergence in cowpea [*Vigna unguiculata* (L.) Walp.]- an Overview. *Journal of Crop Breeding and Genetics*, **7**(1): 1-20.

Pandey, P. K.; Lal, H. and Nath, V. (2014). Hierarchical clustering, genetic variability, correlation and path analysis studies in cowpea (*Vigna unguiculata* L. Walp). *Journal of Food Legumes*, **27**(2): 158-160.

Pandiyan, M.; Vaithilingan, M.; Krishnaveni, A.; Sivakumar, P.; Sivakumar, C.; Jamuna, E.; Sivakumar, B.; Sivaji, M.; Yuvaraj, M. and Kumar, S. P. (2020). Genetic variability studies on cowpea genotypes. *International Journal of Current Microbiology and Applied Sciences*, **9**(6): 3794-3797.

Panse and Sukhatme (1978). Statistical method for agricultural workers. *Indian council of Agricultural Research*, New Delhi. Pp.381.

Patil, S.; Pethe, U. B.; Mahadik, S. G.; Dalvi, V. V and Joshi, M. S. (2020). Correlation and path analysis study in F_3 generation of cowpea [*Vigna unguiculata* (L.) Walp] genotypes. *Journal of Pharmacognosy and Phytochemistry*,**10**(1):203-207.

Pasquet, R. S. (1993). Classification intraspecifique des formes spontanees de *Vigna unguiculata* (L.) Walp. (*Fabaceae*) a partir des donnees morphologiques. Bull. Jard. Bot. Nat. Belg. Bull. Nat. Plantention Belg. **62**: 127-173.

Pasquet, R. S. and Baudoin, J. P. (2001). Cowpea. In André, C. et al. (eds). Tropical plant Breeding. CIRAD and Science publishers, inc. pp. 177-198.

Patel, P. S.; Kumar, S.; Meena, R. K.; Kumar, P. and Rai, T. (2018). Correlation and Path analysis in Cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal of Pure and Aplied Bioscience*, **6**(5): 142-146. DOI: http://dx.doi.org/10.18782/2320-7051.6941.

Patel, U. V.; Parmar, V. K.; Patel, P. B. and Malviya, A. V. (2016). Correlation and path analysis study in cowpea (*Vigna unguiculata* L. Walp.). *International Journal of Science, Environment and Technology*, **5**(6), 3897-3904.

Patel, U. V.; Parmar, V. K.; Patel, P. B. and Malviya, A. V. (2017). Genetic divergence in cowpea [*Vigna unguiculata* (L.) walp.] for yield components parameters. *Electronic journal of Plant Breeding*, **8**(1): 331-335.

Purohit, P.; Nautiyal, M. K.; Bhatt, L.; Massey, P. and Pal, K. (2020). Estimation of genetic advance, heritability, genetic gain and genetic diversity of elite genotypes of grain cowpea [*Vigna unguiculata* (L.) walp.]. *International Journal of Chemical Studies*, **8**(2): 631-637.

Rao, C. R. (1952). Advanced Statistical Methods in Biometrical Research, John Willey and Sons, Inc., New York,: 357-363

Robinson, H. F. (1966). Breeding on the centennial of Mendelism. *Environment and Ecology*, **8** (1A): 236-238.

Rocha, M. M.; Campelo, R. E.; Freire.; Filho, F. R.; Ribeiro, V. O.; Lopes, C.; (2003). Estimates of genetic parameters in white coat cowpea genotypes. *Revista Cientifica Rural*, 8(**1**): 135-141.

Rai, N. K.; Sharma, A. K.; Parihar, A. K.; Pal, S. and Beniwal, R. (2020). Genetic divergence analysis in cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal of Current Microbiology and Applied Science*, **9**(12): 2241-2244.

Roquib, M. A. and Patnaik, P. K. (1990). Genetic variability in forage yield and its component in cowpea (*Vigna unguiculata* L. Walp.). *Indian journal of genetics*, **26**(A): 126-172.

Sabale, G. R.; Bhave, S. G.; Desai, S. S.; Dalvi, M. B. and Pawar, P. R. (2018). Variability, heritability and genetic advance studies in F_2 generation of cowpea (*Vigna unguiculata* sub sp. *unguiculata*). *Int. J Curr. Microbiol. App. Sci*, **7**(9), 3314-3320.

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

Santos, A. D.; Ceccon, G.; Davide, L. M. C.; Correa, A. M. and Alves, V. B. (2014). Correlations and path analysis of yield components in cowpea. *Crop Breeding and Applied Biotechnology*, **14**(2), 82-87.

Sapara, G. K. and Javiya, R. M. (2014). Correlation and path analysis in vegetable cowpea (*Vigna unguiculata* L.). *International J. Pl. Sciences*, **9**(1): 138-141.

Sarath, P. S. and Reshma, T. (2017). Genetic variability studies in cowpea (*Vigna unguiculata* L. Walp). *International Journal of Agriculture Science and Research* (IJASR), **7**(3):129-132.

Sandeep, V.; Hemalatha,V.; Bushan, D. S. and Swarnalatha, V. (2014). Studies on genetic diversity in indian cowpea [*Vigna unguiculata* (L.) Walp] germplasm. *International Journal of Plant, Animal and Environmental Science*, **4**(3): 177-180.

Shahid, A.; Zargar, M. A. and Tahir, A. (2005). Genetic variability, heritability, genetic advance for seed yield and component traits in cowpea. *National Journal of Plant Improvement*, ***7***(2): 85-87.

Shanko, D., Andargie, M., & Zelleke, H. (2014). Interrelationship and path coefficient analysis of some growth and yield characteristics in cowpea (*Vigna unguiculata* L. Walp.) genotypes. *Journal of Plant Sciences*, **2**(2): 97-101.

Sharma, A.; Mishra, S. P. and Gour L.(2019). Heritability and variability of yield and yield determinants in cowpea [*Vigna unguiculata* (L.) Walp.] *International journal of chemical studies,* **7**(3): 3605-3611.

Sharma, M.; Sharma, P. P.; Meghawal, D. and Sharma, H. (2017_a). Genetic variability in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm lines. *Journal of pharmacognosy and phytochemistry,* **6**(4): 1384-1387.

Sharma, M.; Sharma, P. P.; Upadhyay, B. and Bairwa, H. L. (2016). Study the correlation coefficient and path analysis in cowpea [*Vigna unguiculata* (L.) Walp germplasm line.*International journal of development research*, **6**(8): 9011-9016.

Sharma, P. P.; Baranda, B.; Haritwal, S. and Sharma, M. (2017_b). Character association for seed yield and its components in cowpea [*Vigna unguiculata* (L.) Walp.] *International Journal Pure Applied Biosci*ence, ***6***(9): 967-975.

Shimelis, H. and Shiringani, R. (2010). Variance components and heritabilities of yield and agronomic traits among cowpea [*Vigna unguiculata* (L.) Walp.] genotypes. *Euphytica*, 176: 386-389.

Shivasubramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agriculture Journal*, 60: 1139.

Shrinivas, J.; Kale, V. S.; Nagre, P. K. and Meshram, S. (2016). Genetic divergence studies in cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal of Agricultural Science and Research*, **6**(3): 97-104.

Singh A.; Shweta and Singh, V. (2018_a). Estimates of genetic variability, heritability and genetic advance for yield and yield component traits in Indian cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal Pure Applied Biosci*ence, **6**(1): 1142-1147.

Singh, O. V.; Shekhawat, N.; Singh, K. and Gowthami, R. (2018_b). Genetic divergence studies in cowpea [*Vigna unguiculata* (L.) Walp.] germplasm using Mahalanobis D^2 analysis. *International Journal Currnt Microbiology Applied Science,* **7**(3): 2616-2624

Srinivas, J; Kale, V. S. and Nagre, P. K. (2017). Study of genetic variability, heritability and genetic advance in cowpea [*Vigna unguiculata* (L.) Walp.]. *International Journal of Current Microbiology and Applied Sciences*, **6**(6): 3314-3318.

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

Thapa, B.; Adhikari, N. V.; Darai, R. and Kandel, B. P. (2021). Genetic variability of exotic cowpea genotypes for agro-morphological traits in mid-western region of Nepal. *Alinteri Journal of Agriculture sciences,* **36**(1): 47-54.

Thouseem, N.; Thomas, B. and Elizabeth, N. (2018). Genetic parameters in seed yield components of cowpea [*Vigna unguiculata* (L.) Walp.] *International Journal of Current Microbiology and Applied Sciences,* **7** (2): 2268-2274.

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.

Timko, M. P.; Ehlers, J. D. and Roberts, P. A. (2007). “Cowpea”, in: Kole, C., (ed.), *Pulses, Sugar and Tuber Crops, Genome Mapping and Molecular Breeding in Plants*, Vol. 3, Springer-Verlag, Berlin Heidelberg, pp. 49-67.

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-An International Journal*, **23**(2), 92-96.

Udensi, O. and Ikpeme, E. V. (2012). Relationship studies in cowpea (*Vigna unguiculata* L. Walp.) landraces grown under humid low land condition. *International Journal of Agriculture Research*, **7**(1): 3-45.

Ugale, P. N; Wankhade, M. P. and Bagade, A. B. (2020). Genetic variability study in cowpea [*Vigna unguiculata* (L.) Walp.]. *Journal of pharmacognosy and phytochemistry*, **9**(6), 476-479.

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.

Vavilov, N. I. 19. (1951). The origin, variation, immunity and breeding of cultivated plants. *Chronica Botanical,* **13**: 1-54.

Vedcourt, B. (1970). Studies in leguminosepapillonoidae flora of tropicalist. Africa Kew Bulletin. 24: 556-569.

Verma, A. K.; Mehta, A. K.; Gontia, A. S.; Sharma, D.; Singh, R. P. and Singh, P. (2019). Genetic variability, heritability and genetic advance studies for yield components in F_2 generation of cowpea (*Vigna unguiculata* L. Walp). *International Journal of Chemical Studies,* **7**(6): 3084-3088

Vir, O. and Singh, A. K. (2014). Genetic variability and inter-characters associations studies in the germplasm of cowpea (*Vigna unguiculata* L. Walp.) in fragile climate of western Rajasthan. *Indian Legume Research,* **37**(2): 126-132.

Viswanatha, K. P. and Yogeesh, L. N. (2017). Genetic variation and morphological diversity in cowpea [*Vigna unguiculata* (L.) walp.]. *Archives of Agriculture and Environmental Science*, 2(3): 176-180.

Waghmare, P. D.; Pethe, U. B. and Sabale, G. R. (2019). Study on correlation and path analysis for yield and yield components in cowpea [*Vigna unguiculata* (L.) Walp]. *Int.J.Curr.Microbiol.App.Sci*, **8**(12): 296-303.

Walle, T.; Mekbib, F.; Amsalu, B. and Gedil, M. (2018). Correlation and path coefficient analyses of cowpea (*Vigna unguiculata* L.) landraces in Ethiopia. *American Journal of Plant Sciences*, **9**: 2794-2812.

Wilk’s, S. S. (1932). Criterion of generalization in the analysis of variance. *Biometrics*, 24: 471-484.

Wright, S. J. (1921). Correlation and causation. *Journal of Agriculture Research*, **20:** 557-585.

Yadav, N. B. and Duddukur, R. (2019). Genetic variability, trait association and path analysis in cowpea [*Vigna unguiculata* (L.) Walp]. *International Journal of Current Microbiology and Applied Sciences*, **8**(12):1979-1986.

Yasin, G.; Elias, U.; Walelign, W. and Hussein, M. (2021). Assessment of genetic diversity in cowpea genotypes in southern Ethiopia based on morpho-agronomic traits. *International Journal of Agricultural Technology*, **17**(4): 1631-1650.

APPENDICES

Appendix-A: Weekly meteorological data recorded during the crop season (July-2021 to October-2021)

Month and year	Std. Weeks	Temperature (°C)		Relative Humidity (%)		Rain fall (mm)	Bright sunshine (hrs./ day)	Wind velocity (km/ hr)	Pan Evaporation (mm/ day)
		Max.	Min.	Morn.	Even.				
July 2021	26	37.2	25.6	79	65	9.0	6.0	7.9	6.0
	27	38.0	26.8	76	65	0.0	8.4	11.1	7.3
	28	39.1	26.0	81	63	47.0	5.7	6.7	7.1
	29	36.1	26.2	82	75	8.0	3.8	7.4	7.0
	30	31.6	24.8	85	90	65.5	0.7	10.2	4.6
	31	29.0	24.3	84	85	17.5	0.0	8.6	3.5
August 2021	32	33.5	25.9	80	74	0.0	6.8	5.4	6.1
	33	36.5	25.7	73	68	0.0	9.5	5.9	7.5
	34	36.9	26.0	76	67	2.0	7.6	4.9	7.3
	35	35.6	24.7	82	66	36.5	6.6	5.3	6.0
September 2021	36	34.4	24.9	88	83	41.0	4.1	5.7	5.5
	37	32.9	24.2	85	83	109.5	3.6	3.3	4.4
	38	33.5	23.6	80	77	6.0	5.2	4.7	5.6
	39	33.1	24.9	81	77	87.5	4.4	5.1	5.8
October 2021	40	34.7	25.0	78	70	0.0	7.7	3.9	7.0
	41	37.4	25.8	77	62	0.0	9.8	2.1	7.9
	42	36.9	21.1	69	62	0.0	9.7	2.2	7.3
	43	36.2	18.0	66	59	0.0	9.9	4.7	6.8
	44	33.3	15.9	69	50	0.0	9.7	2.3	5.8

Source: Agricultural Meteorology Department, C. P. C. A., Sardarkrushinagar

Appendix- B: Mean values of different characters in cowpea

Genotype	Days to flowering	Days to maturity	Plant Height (cm)	Number of branch per plant	Number of pod per plant	Number of seed per pod
GC 3	44.25	63.75	44.21	7.31	14.40	14.44
GC 4	43.75	64.00	52.25	6.95	13.35	11.14
GC 5	44.50	63.00	53.84	7.65	15.14	12.49
GC 6	41.50	62.75	52.70	7.70	13.29	11.54
GC 1501	41.50	60.25	49.98	6.86	17.17	10.19
GC 2101	43.25	62.50	39.89	8.00	13.69	7.34
GC 2102	42.25	63.50	50.83	8.11	11.09	10.39
GC 2103	42.50	63.50	50.27	7.15	13.14	14.34
GC 2104	42.25	63.50	50.78	7.96	15.24	12.84
GC 2105	41.50	62.75	41.66	7.94	14.55	9.64
GC 2106	43.50	63.75	69.22	7.30	18.19	11.64
GC 2107	43.75	63.25	61.83	8.80	15.04	10.89
GC 2108	45.00	65.75	60.90	9.00	17.74	11.98
GC 2109	45.75	66.00	51.81	10.45	15.95	13.40
GC 2110	44.75	65.75	47.77	8.37	14.09	10.99
GC 2111	43.50	65.25	68.89	7.85	11.34	10.59
GC 2112	39.50	65.25	54.12	8.40	14.69	9.27
GC 2113	42.75	65.25	63.66	8.90	14.04	10.20
GC 2114	44.25	63.50	56.77	8.00	13.74	9.75
GC 2115	43.00	64.25	54.49	9.15	12.06	11.90
GC 2116	43.75	63.50	57.14	9.40	12.24	10.19
GC 2117	42.25	63.75	48.39	6.45	13.59	11.29
GC 2118	40.50	64.25	39.19	7.36	12.44	14.59
GC 2119	41.75	63.00	61.42	7.45	13.04	10.14
GC 2120	39.75	62.25	59.12	7.95	12.64	13.44
GC 2121	42.25	63.00	35.97	7.30	13.14	9.19
GC 2002	39.25	61.50	52.42	7.90	13.09	11.74
GC 2006	41.75	61.50	56.95	8.30	16.24	13.39
GC 2007	39.50	62.00	52.07	6.50	15.49	11.14
GC 1905	40.75	63.50	48.13	5.95	13.39	11.34
General mean	**42.48**	**63.53**	**52.89**	**7.88**	**14.11**	**11.38**
Range	**39.25 – 45.75**	**60.25 – 66.00**	**35.97 – 69.22**	**5.95 – 10.45**	**11.09 – 18.19**	**7.34 – 14.59**
S. Em. ±	**0.29**	**0.44**	**1.35**	**0.24**	**0.33**	**0.45**
C.D. at 5%	**0.80**	**1.25**	**3.79**	**0.67**	**0.92**	**1.27**
C.V. %	**1.34**	**1.73**	**5.10**	**6.05**	**4.64**	**7.93**

Genotype	Pod length (cm)	100 seed weight (g)	Harvest Index	Protein content	Seed yield per plant
GC 3	13.80	11.38	69.26	21.92	19.58
GC 4	12.16	15.17	66.88	21.89	17.71
GC 5	12.69	10.09	59.69	22.00	18.78
GC 6	12.05	12.94	52.21	20.89	17.67
GC 1501	11.09	10.29	65.46	22.00	18.93
GC 2101	14.45	11.37	40.38	23.53	18.70
GC 2102	11.61	14.12	63.29	22.54	15.70
GC 2103	12.13	15.27	55.75	22.23	19.58
GC 2104	12.47	14.42	54.95	22.36	18.79
GC 2105	11.11	11.49	33.63	22.49	19.57
GC 2106	15.27	14.47	69.51	21.51	**20.23**
GC 2107	11.16	10.04	55.22	23.07	19.06
GC 2108	15.29	14.29	73.17	21.73	21.70
GC 2109	14.09	15.37	70.43	22.58	20.35
GC 2110	13.85	14.22	58.43	21.50	18.99
GC 2111	13.98	16.14	65.58	20.77	17.92
GC 2112	12.25	16.17	66.84	20.74	18.02
GC 2113	12.49	15.44	42.61	21.54	19.07
GC 2114	13.08	9.22	65.90	22.73	18.12
GC 2115	12.77	12.47	65.88	21.48	**18.86**
GC 2116	12.19	11.34	57.04	22.52	18.98
GC 2117	14.05	10.52	67.93	22.56	18.25
GC 2118	14.53	12.12	70.37	22.33	19.60
GC 2119	11.96	11.57	66.68	23.72	17.12
GC 2120	11.82	9.19	68.65	21.37	18.79
GC 2121	11.60	11.60	53.80	22.24	**14.96**
GC 2002	11.44	12.64	33.50	24.19	18.83
GC 2006	11.88	8.59	70.08	23.32	19.98
GC 2007	11.74	9.64	62.71	23.75	18.76
GC 1905	14.09	9.02	55.89	22.38	18.77
General mean	**12.77**	**12.35**	**60.06**	**22.26**	**18.71**
Range	**11.09 – 15.29**	**8.59 – 16.17**	**33.50 – 73.17**	**20.74 – 24.19**	**14.96– 21.70**
S. Em. ±	**0.56**	**0.48**	**2.79**	**0.17**	**0.54**
C.D. at 5%	**1.57**	**1.35**	**7.85**	**0.47**	**1.52**
C.V. %	**8.76**	**7.80**	**9.30**	**1.51**	**5.79**

CERTIFICATE

This is to certify that I have no objection for supplying to any scientist only one copy or any part of this thesis at a time through reprographic process, if necessary for rendering reference service in a library or documentation centre.

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