GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREEN GRAM [*Vigna radiata* (L.) R. Wilczek]

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IN

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"GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREEN GRAM [*Vigna radiata* (L.) R. Wilczek]"

ABSTRACT

***Keywords*:** Genetic variability, heritability, genetic advance, correlation, path analysis, genetic divergence, *Vigna radiata* (L.) R. Wilczek.

The current empirical study on "Genetic variability, correlation, path analysis and genetic divergence in green gram (*Vigna radiata* (L.) R. Wilczek)" was conceded to assess variability, heritability, genetic advance, correlation, path analysis and genetic divergence in 72 genotypes of green gram. The experiment was conducted in randomized block design with three replications at the Pluses Research Station, Junagadh Agricultural University, Junagadh, during the period of the *kharif* season 2021-22. The observations were recorded on 11 traits *viz.*, days to 50 % flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seeds weight (g) and seed yield per plant (g).

The analysis of variance revealed that mean squares due to genotypes were highly significant for days to 50 % flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and seed yield per plant indicating the presence of sufficient amount of variability in the experimental material used. The present experimental material showed a wide range of phenotypic variation for seed yield per plant, number of clusters per plant, number of pods per plant, number of pods per cluster and number of primary branches per plant as revealed by high values of range coefficient. The magnitude of PCV was slightly greater than GCV which revealed that very little influence of environmental variation was observed on all the characters and stated that a sufficient amount of variability was noticed. Seed yield per plant show high phenotypic coefficient of variation and moderate genotypic coefficient of variation.

The estimates of high heritability coupled with high genetic advance expressed as per cent of mean was observed for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant. It indicates that most likely the heritability is due to additive gene action and selection may be effective for seed yield improvement.

Correlation analysis among the yield and its contributing characters revealed that the genotypic correlation coefficients in most of the cases were higher than their

phenotypic correlation coefficients indicating the association was largely due to genetic reasons. Seed yield per plant had a highly significant and positive correlation with the number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight at both genotypic and phenotypic levels indicating that these attributes were more influencing the seed yield and therefore these were important characters for bringing genetic improvement of seed yield. Moreover, seed yield per plant had significant and positive correlation with length of pod at both genotypic and phenotypic level.

The genotypic path coefficient analysis revealed that number of pods per plant, 100-seeds weight and number of seeds per pod expressed positive and higher direct effect on seed yield per plant. The residual effect was found to be 0.0755 at genotypic path coefficient analysis.

The phenotypic path coefficient analysis revealed that number of pods per plant, 100-seeds weight and number of seeds per pod exhibited high and positive direct effects on seed yield per plant. Whereas, negative direct effect on seed yield per plant were contributed through number of clusters per plant and plant height at phenotypic level. The residual effect was found to be 0.1321 at phenotypic path coefficient analysis.

Genetic diversity studies, using Mahalanobis's D^2 statistics, indicated existence of significant diversity among 72 green gram genotypes that were grouped into 12 clusters. Among 12 clusters formed, cluster II having largest number of genotypes (20) followed by cluster I (18) and cluster VI (12). On the other hand, cluster III, cluster IV, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters.The intra-cluster distance was highest in cluster X (7.81) and lowest in cluster I (5.55). The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81) which indicated that, crossing of genotypes among these clusters will give higher frequency of transgressive segregants or desirable combinations for high yield. It was also revealed that the seed yield per plant (26.49 %) contributed maximum towards the total divergence followed by 100-seeds weight (25.82 %), number of pods per plant (11.15 %), length of pod (9.04 %), plant height (8.33 %) and number of clusters per plant (7.71 %).

From the present investigation, it can be concluded that additive gene action was operating for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant as it showed high heritability coupled with high genetic advance as a per cent of mean. Study of correlation coefficient and path analysis clearly indicated that the number of pods per plant and 100-seeds weight was most important trait**.** The traits *viz*., seed yield per plant, 100-seeds weight, number of pods per plant, length of pod, plant height and number of clusters per plant had highest contribution towards total genetic divergence. Hence, emphasis must be given on the above-mentioned traits while imposing selection for genetic improvement in green gram.

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CERTIFICATE – I

This is to certify that the thesis entitled **"GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREEN GRAM [*Vigna radiata* (L.) R. Wilczek]"** submitted by **Mr. PATEL HARSH JITENDRAKUMAR (Reg. No. 2010120067)** in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** to the Junagadh Agricultural University is a record of bonafide research work carried out by him under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma or other similar title. The candidate had fulfilled all prescribed requirements. The assistance and help received during the course of the investigation have been fully acknowledged. He has successfully completed the comprehensive/preliminary examination held on 4th May, 2022 as required under the regulation for post-graduate studies. He has submitted kachcha bound thesis on, 30th June, 2022.

Place: Junagadh
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C E R T I F I C A T E – II

Date: 27/07/2022

This is to certify that the thesis entitled **"GENETIC VARIABILITY, CORRELATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREEN GRAM [*Vigna radiata* (L.) R. Wilczek]"** submitted by **Mr. PATEL HARSH JITENDRAKUMAR (Reg. No. 2010120067)** to the Junagadh Agricultural University, Junagadh in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **GENETICS AND PLANT BREEDING** after recommendation by the external examiners were defended by the candidate before the following members of the examination committee. The performance of the candidate in the oral examination was satisfactory. We, therefore, forward with recommendation.

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Now, as I carry this in my hand, I carry with me memories that will enrich my nostalgia.

Place: Junagadh

Date: 30/06/2022 (**Patel Harsh J.**)

CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF PLATE

LIST OF APPENDICES

CHAPTER I

INTRODUCTION

In Indian agriculture, pulse crops play an important role. Quality protein is higher in pulses nearly three times as compared to cereals. Thus, they are cheaper source of protein to overcome malnutrition among human beings. Pulses are the major source of protein for vegetarian diet. In fact, lysine is very well supplemented by the pulse protein, which is the most limiting essential amino acid in cereals. Pulses occupy a unique position almost in all cropping system as main, catch, cover, green manure, intercrop and its inclusion in crop rotation, thereby, kept the soil alive and productive, therefore, pulses are considered as life blood of agriculture. The soil fertility is enrich by them in terms of addition of organic matter and nitrogen through biological nitrogen fixation through *Rhizobium*. In addition, they also provide food and nutritious fodder for livestock. Due to their deep root and good ground cover, pulses are drought tolerant and prevent soil erosion.

Green gram [*Vigna radiata* (L.) R. Wilczek] is a legume cultivated for its edible seeds and sprouts across Asia. It belongs to family Fabaceae and sub family papilionaceae with diploid chromosome number 2n=2x=22. There are 3 subgroups of *Vigna radiata*: one is cultivated (*Vigna radiata subsp. radiata*) and two are wild (*Vigna radiata subsp. sublobata* and *Vigna radiata subsp. glabra*). India has a wide range of genetic diversity of cultivated, as well as of weedy wild types of green gram, it is considered as the region of its first domestication.

Pulses account for 32 per cent of world's production and 37.5 per cent of the world's area. At present the area under pulses in the world is 68.9 m. ha with a production of 69 m. t. with productivity of 999 kg/ha. In India, green gram productivity is 548 kg/ha which occupy 45.81 lakh ha area and total production of 2.51 lakh tons (Anon., 2019-20). Bengal gram, red gram, green gram, black gram, cowpea, lentil and pea are important pulses crops grown in India. Among, these an ancient and well-known leguminous crop of India is green gram (*Vigna radiata* (L.) R. Wilczek), known for its drought tolerance, early maturing, nutritional quality and suitability in cropping systems.

According to Vavilov (1939) green gram is native to India and Central Asia. Orissa, Maharashtra, Andhra Pradesh, Rajasthan, Madhya Pradesh, Bihar, Karnataka, Uttar Pradesh and Tamil Nadu are mainly confined states in India for the cultivation of green gram. It is cultivated in 1.35 lakh ha with annual production of 1.04 lakh metric tons leading to an average productivity of 772 kg/ha in Gujarat (Anon., 2019-20). Green gram is grown in Banaskantha, Kutch, Mehsana and Panchmahal districts of Gujarat in *kharif* season. Development of short duration as well as photo and thermo insensitive as well as yellow vein mosaic resistant varieties provided excellent opportunity for green gram cultivation both in *kharif* as well as in summer season, where adequate irrigation facilities are available.

Green gram [*Vigna radiata* (L.) R. Wilczek] contains about 24 per cent protein, this is being about two third of the protein content of soybean, twice that of wheat and thrice that of rice. This protein is comparatively rich in lysine, an amino acid that is deficient in cereal grains. So, green gram and cereal grains diet combining form a balanced amino acid diet. Every 100 g green gram seed contain 132 mg calcium, 2.251 mg niacin, 4.8 mg ascorbic acid, 0.621 mg thiamine, 0.233 mg riboflavin and 114 IU vitamin A (Haytowitz and Matthews, 1986). The calorific value of green gram is 334 calories per 100 g and it contains crude fat 1.3%, protein 24.0 % and carbohydrate 56.6 %.

Green gram is rich in protein, fibre and less in fat that's why ayurveda suggests green gram is the right choice in a condition wherein obesity and extra fat pose a problem in day-to-day life. It has also been proven that green gram can enhance heart health with its nutritional content of flavonoids, an antioxidant which improves heart protection capacity especially in the case of women. The phosphorus and calcium content in green gram make beneficial for bones. The manganese content in it helps in improving brain activity as well. Green gram also has zinc content which also helps skin protection and ayurveda proposes that it can be smeared on the skin after transforming it into cream form. Regular intake of green gram will also help protect the skin.

Green gram is an herbaceous annual plant with erect/ sub erect stem, sometime twinning in upper branches, furrowed & moderately/ sparsely haired usually 40 to 120 cm in height. The leaves are trifoliate, entire ovate and occasionally lobed with

long petiole. Roots are strong with a tap root system, provided with nodules for atmospheric nitrogen fixation. The inflorescence is axillary or terminal raceme with 10-20 flowers crowded on long peduncle. The flower is a typical papilionaceous, hermaphrodite, zygomorphic, either lighter yellowish/ olive yellow with 5 sepals, 5 petals, 10 stamens in diadelphous (9) + 1 condition and monocarpellary ovary with hairy style. Pods are 6-10 cm long, hairy and round having 7-10 seeds inside. Hilum is white and flat.

Green gram is a mandate crop at the Asian Vegetable Research and Development Centre (AVRDC). The world's largest green gram base collection is maintained at Asian Vegetable Research and Development Centre. A majority of the collections has been evaluated for agronomic characters, nutritional components and resistance or tolerance to the major pests and diseases. A pedigree method is commonly practiced to screen the segregating and advanced generations.

Due to green revolution, there has been a decrease in the production of pulses in our country. The major limiting factors for pulses production and productivity in our country is the non-availability of high yielding varieties that can tolerate environmental fluctuations to greater extent. Other limiting factors are poor management practices, lack of disease and pest resistant varieties *etc*. It is the reason the researches in this field are to be encouraged to make a quantum jump in the production and productivity of pulses.

In most developing countries people mainly use for food products which are rich in starch for example, rice, wheat, maize *etc*. These products are not rich in protein. The protein deficient nutrition of millions of people living in the region of hot climate has become one of today's most acute problems. Solving this problem largely depends on improvement of the yield and the further expansion of area under cultivation of legumes.

The basic rational in any crop improvement program is to increase the yield of the crops. The character, yield has a complex gene action and is the result of many factors. Different factors influencing the yield must be considered and evaluated with regard to their contribution towards the yield for a crop to study it properly. The knowledge of variability available in the breeding material due to genetic and nongenetic causes is a pre-requisite in the selection of superior plant type.

In exercising selection programs, the information on association of attributes with seed yield and among themselves is of considerable importance. Multiplicative end product of many factors is being a polygenic complex trait and sensitive to environmental variations in grain yield. There are also several component characters of yield. Therefore, a thorough understanding of yield contributing characters and a correlation study involving these characters and yield is necessary for an effective selection for higher yields. It is also necessary to examine whether the effects of different components of yield and other traits on yield are direct or indirect and to what extent? The path coefficient analysis provides an effective mean of finding direct and indirect causes of an association under such circumstances.

Genetic divergence is a useful technique in selecting diverse parents for purposeful hybridization programme. Multivariate analysis based on Mahalanobis D^2 statistic as well as principal component analysis is widely used for estimating the diversity. Genetic divergence coupled with information on genetic parameters and genetic gain obtained by selection and association analysis of yield and its components are the important pre-requisites for a systematic breeding programme.

Keeping all these facts in view, the present investigation was under taken using 72 diverse green gram genotypes during *kharif* 2021 with the following objectives;

1. To estimate genetic variability, heritability and genetic advance for seed yield and its contributing characters
2. To study the association among seed yield and contributing characters
3. To determine the direct and indirect effects of different character on seed yield using path coefficient analysis
4. To estimate the extent of genetic diversity present among the different green gram genotypes

CHAPTER II

REVIEW OF LITERATURE

In the present investigation an attempt has been made to study **"Genetic variability, correlation, path analysis and genetic divergence in green gram [*Vigna radiata* (L.) R. Wilczek]"**. The available literature pertaining to the various aspects of the present investigation has been reviewed under the following heads:

2.1 Genetic variability parameters
2.2 Correlation coefficient analysis
2.3 Path coefficient analysis
2.4 Genetic divergence

2.1 GENETIC VARIABILITY PARAMETERS

For successful breeding programme, amount of genetic variability present in the experimental material is a basic requirement. Therefore, it is essential for the plant breeders to measure the variability with the help of parameters like genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability (h^2 bs) and genetic advance. Hence, these parameters will give the information regarding the availability of genetic variability for different characters in the material to be used. The review of literature pertaining to variability parameters in green gram is presented in the subsequent paragraphs:

Makeen *et al.* (2007) evaluated twenty diverse green gram genotypes for the estimation of genetic variability, heritability and genetic advance for ten quantitative characters. The genotypes differed significantly for all characters studied. Results revealed that higher genotypic and phenotypic coefficient of variation was observed for seed yield and number of pods per plant. Maximum heritability values were recorded in seed protein content, plant height and test weight. High heritability coupled with high genetic advance was observed in pods per plant, plant height and test weight indicating the importance of additive gene effect for expression of these characters.

Kumar *et al.* (2010) conducted an experiment with 23 genotypes of *kharif* green gram for estimation of genetic variability and observed highly significant difference for all characters under study among the genotypes, indicating the presence of sufficient amount of variability in the varieties. The highest GCV and PCV were observed for harvest index and pods per plant, respectively. High value of GCV was recorded for harvest index (32.95), 100 seed weight (40.67) and cluster per plant (14.99) and low value of GCV was observed for number of seed per pod (5.26), days to 50 % flowering (5.99), cluster per branch (7.32) and days to maturity (9.04). High value of PCV was recorded for pods per plant (34.90) followed by harvest index (34.79) and primary branches per plant (20.82) while estimates of PCV were low for days to 50 % flowering (6.10) and number of seeds per pod (7.71). The study suggested ample scope for selection of different quantitative characters for crop improvement.

Tabasum *et al.* (2010) used 10 green gram genotypes to assess genetic variability. Primary and secondary branches, pods per cluster and pod length showed lesser variability while clusters per plant, 100-seed weight and harvest index exhibited intermediate range of variability. Sufficient genetic variability was observed for plant height, pods per plant, total plant weight and seed yield. The magnitude of PCV was higher than GCV for all the traits under study showing the pronounced effects of environment. Moderate to high heritability estimates were found for all traits. High heritability was manifested by number of secondary branches, plant height, clusters per plant, pods per plant, pods per cluster, pod length, 100-seed weight seed yield and harvest index. High genetic advance observed for pods per plant and lowest genetic advance was observed for primary branches followed by pod length. The study suggested high heritability and high genetic advance were indicating that these traits were controlled by additive genes and can easily be transferred to succeeding generations.

Narasimhulu *et al.* (2013) studied genetic variability in forty green gram genotypes for different quantitative characters. Results revealed that The PCV value was found higher than the GCV for all the characters and the differences between them were very less indicating less environmental influence on these characters except for number of branches per plant and number of clusters per plant where significant role of environment was observed. Highest GCV and PCV were observed for number of

branches per plant, pods per plant, biological yield per plant and harvest index. High estimates of genetic advance as per cent of mean were observed for 100 seed weight and harvest index. High heritability coupled with high genetic advance as per cent of mean was observed for plant height, pods per plant, pods per cluster, biological yield per plant, harvest index and seed yield per plant.

Twenty-three green gram genotypes were evaluated by Sarkar *et al.* (2014). Results revealed that phenotypic coefficient of variation was slightly higher than the genotypic coefficient of variation for all the characters suggesting the presence of environmental influence to some extent in the expression of these characters. They suggested that heritable portion of this variation is determined by the estimation of heritability. Therefore, heritability estimates give better idea about possible gain through selection. High heritability along with high genetic advance as per cent of mean was observed for the trait plant height, pods per plant and seed yield per plant indicating that these characters would be amenable for phenotypic selection.

Hemavathy *et al.* (2015) evaluated thirteen diverse green gram genotypes for the estimation of genetic variability, heritability and genetic advance. The genotypes differed significantly for all characters under study. Higher genotypic and phenotypic coefficient of variation was observed for seed yield, number of pods per plant and clusters per plant.

Katiyar *et al.* (2015) estimated genetic variability, heritability and genetic advance for seed yield per plant and its component traits in 45 genotypes of green gram. The maximum variability was observed for pods per plant followed by seed yield per plant, clusters per plant, 100-seed weight and branches per plant. Heritability estimates were observed to be high for all the traits except branches per plant and seeds per pod. High expected genetic advance coupled with high heritability estimates were observed for seed yield per plant, days to flowering and plant height indicating least influenced by the environmental variation.

Ruturi *et al.* (2015) conducted an experiment with 44 promising genotypes of green gram and performed genetic variability analysis. Results revealed that the estimates of PCV in all the traits were higher than the estimates on corresponding GCV. The higher estimates (>20 %) of GCV were recorded for seed yield (23.87 %)

followed by number of pods per plant (20.4 %). Whereas, higher PCV values (>25 %) were recorded for seed yield (30.16 %), number of secondary branches (29.64 %), number of pods per plant (26.15 %) and number of clusters per plant (25.64 %) indicate better chances for selection for these traits to be successful. The higher values of heritability in broad sense (>60 %) were recorded for days to 50 % flowering (66 %), seed yield (63 %), 1000-seed weight (62 %) and number of pods per plant (61 %). Higher estimates of genetic advance (>30 %) were recorded for seed yield and number of pods per plant.

Baisakh *et al*. (2016) analysed 30 genotypes of green gram for yield and component traits and found that both the GCV and PCV estimates were high (more than 10 %) for plant height, clusters per plant, seeds per pod, 100-seed weight, yield per plant in the mutant genotypes. Plant height and pods per plant showed high heritability with high genetic advance indicating additive gene action. Characters like 100-seed weight and seeds per pod showed preponderance of non-additive gene effect showing high-moderate heritability but low genetic advance.

Dangi *et al.* (2017) estimated genetic variability in 22 genotypes of green gram and found that the high range of variation were recorded for plant height and days to 50 % flowering indicating maximum scope for the selection of these characters for effective improvement. Maximum values of genotypic coefficient of variation was recorded for seed yield per plant (17.39), while it was lowest for days to 50 % flowering (2.54). The PCV for seed yield per plant (17.80) exhibited maximum and low for days to maturity (2.97). Heritability was found high for days to maturity (97 %) followed by plant height (95 %), number of primary branches per plant (95 %), pod length (72 %) and number of pods per plant (70 %). High heritability coupled with high genetic advance (as per cent of mean) was recorded for seed yield per plant while, high heritability coupled with moderate value of genetic advance was observed for plant height and pod length.

Thirty green gram genotypes were used by Garg *et al*. (2017a) to estimate genetic variability, heritability and genetic advance. They reported considerable amount of variability among all the characters under study. Character like seed yield per plant, harvest index, biological yield and number of pods per plant showed the highest GCV and PCV. They suggested that there is considerable possibility of further

improvement through intermating followed by appropriate selection for these characters. High genetic advance coupled with high heritability were observed for plant height, number of branches per plant, pod length, seeds per pod, 100-seeds weight, number of pods per plant, biological yield, seed yield and harvest index suggesting preponderance of additive gene action.

Kate *et al*. (2017) studied 30 green gram genotypes to estimate genetic variability, heritability, correlation and path analysis. Results revealed that higher GVC and PCV was observed for secondary branches per plant, primary branches per plant, pods per plant and grain yield per plant. Genetic advance was highest for plant height followed by days to maturity and pods per plant. High heritability coupled with moderate genetic advance was observed for plant height, days to maturity, pods per plant, days to 50 % flowering, secondary branches per plant, grain yield per plant and primary branches per plant.

Yadav *et al*. (2017) used 20 green gram genotypes to estimate genetic variability, heritability and genetic advance. They reported high GCV and PCV for number of branches per plant followed by number of clusters per plant, number of pods per plant, plant height, harvest index, seed yield per plant and seeds per pod. High heritability shown by the biological yield per plant followed by harvest index, seed yield per plant, plant height and 100 seeds weight indicating the impact of additive gene expression. They advocated that these traits can be improved through individual plant selection.

Fifty-eight exotic and indigenous diverse green gram genotypes were evaluated by Abbas *et al.* (2018) for seed yield and other related traits. Highly significant differences were observed among the genotypes for all the traits under study. The genetic analysis of green gram germplasm revealed high GCV and PCV for biological yield (GCV % = 31.70, PCV % = 33.58), harvest index (GCV % = 27.80, PCV % = 30.16) and seed yield (GCV % = 25.28, PCV % = 27.54). While heritability estimates were high for all the traits except days to maturity and clusters per plant. Biological yield, harvest index and seed yield depicted high estimates of heritability coupled with greater genetic advance indicating the involvement of additive type of genes and selection based on these traits may help to improve the germplasm. The trait days to maturity reveals low heritability and genetic advance indicating that the character is highly influenced by environmental effect.

Azam *et al.* (2018) evaluated 28 green gram genotypes for genetic variability and reported that all the traits showed highly significant difference among genotypes except seeds per pod. Pods per plant, plant height and 100 seed weight showed high genotypic coefficients of variation (GCV) and phenotypic coefficients of variation (PCV). They also reported high broadsense heritability coupled with moderate genetic advance as per cent of mean for 100 seed weight, days to flower and pods per plant suggesting preponderance of additive gene action for these characters and selection of such traits might be effective for the improvement of grain yield.

Ghimire *et al*. (2018) evaluated 7 green gram genotypes to estimate genetic variability and reported that high genotypic coefficient of variation was exhibited by secondary branches and seed yield per plant. Pod length, number of grains per pod and days to 50 % flowering expressed low genotypic coefficient of variation. Test weight, secondary branches and seed yield per plant showed high heritability estimates.

Sandhiya and Saravanan (2018) carried out an experiment during *kharif* 2016 to assess the genetic variability and correlation among yield and yield attributing characters of green gram. Thirty-six green gram germplasm were investigated for this study for 10 quantitative characters *viz.*, days to 50 % flowering, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length (cm), number of seeds per pod, 100 seed weight (g) and seed yield per plant (g). On the basis of genetic variability study all the characters exhibited high heritability coupled with high genetic advance, indicating the preponderance of additive gene action. Selection based on these traits will be fruitful.

Forty-four green gram genotypes were used by Asari *et al.* (2019) to assess the genetic variability parameters, heritability and genetic advance for yield and yield attributing traits. They reported that high genotypic and phenotypic coefficient of variation was observed for primary branches per plant, pods per plant, seed yield per plant and clusters per plant. Plant height, test weight, pods per cluster, seeds per pod and pod length had moderate genotypic and phenotypic coefficient of variation. Low values of genotypic and phenotypic coefficient of variation were noted for protein content, days to maturity and days to 50 % flowering. High heritability along with high genetic advance as per cent of mean was observed for plant height, primary branches

per plant, clusters per plant, pods per plant and seed yield indicating the preponderance of additive gene action. High heritability coupled with moderate genetic advance expressed as per cent of mean was observed for days to 50 % flowering, number of pods per cluster, number of seeds per pod and length of pod.

Muthuswamy *et al.* (2019) evaluated 100 germplasm accessions of green gram to assess the magnitude of genetic variability and to understand the heritable component of variation for seed yield and its component traits. Results revealed that the phenotypic coefficient of variation (PCV) was greater than that of genotypic coefficient of variation (GCV) for all the characters. The high estimates of GCV, heritability and genetic advance were exhibited by plant height, number of primary branches per plant, number of clusters per plant, number of pods per clusters, number of pods per plant and seed yield per plant. High heritability was observed for all the traits under study. High value of heritability coupled with high genetic advance as per cent of mean were recorded for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant indicating these characters were controlled by additive gene effects.

Abhisheka and Mogali (2020) evaluated 110 F_6 generations of green gram to estimate genetic variability, heritability and genetic advance for yield and yield attributing traits. High genotypic coefficient of variation and phenotypic coefficient of variation were recorded for number of pods per plant and seed yield per plant. It was moderate for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster and 100-seed weight. They suggested that characters expressed high GCV and PCV were less affected by environment. While, characters having moderate variability having reasonable scope of improvement through selection in advance generation. High heritability and high genetic advance recorded for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, hundred seed weight and seed yield per plant.

Majhi *et al.* (2020) conducted an experiment with the F_3 breeding lines derived from three crosses viz., DGGV-7 × V-02-709, DGGV-7 × V-02-802, DGGV-2 × SML-1815 along with their parents used as checks to estimate GCV, PCV, heritability

and genetic advance. Results revealed that the progeny lines derived from the cross DGGV-7 × V-02-709, recorded very high significant variation for the characters like the number of branches per plant (2.988), pod length (2.363) and seed yield per plant (13.007g). The 100 seed weight (4.7g) was observed in the cross derivative of DGGV-2 × SML-1815 with high heritability 73.26 per cent and moderate genetic advance under mean (19.65). The breeding lines of DGGV-7 × V-02-709 have recorded mean seed yield 3.7 g with the range of 3.22 to 4.65 g and the PCV (17.35 %), GCV (14.23 %) was moderate with high heritability (72.12 %) coupled with moderate genetic advance over mean (17.45 %). The progeny lines derived from DGGV-7 × V-02-709 showed higher heritability, more PCV and GCV for most of the characters, as compared to the other two cross derivatives.

Mohammed *et al.* (2020) conducted an experiment with 50 genotypes to estimate the genetic variability, heritability and genetic advance for twelve quantitative characters of green gram. Results revealed that the GCV for all the characters studied was less than the PCV indicating the interaction of genotype with the environment. Maximum estimate of phenotypic coefficient of variation was recorded for the number of branches per plant followed by seed yield per plant, number of pods per plant, plant height and number of clusters per plant. Low estimates of the phenotypic coefficient of variation was recorded for days to maturity. Highest heritability was recorded for the number of primary branches per plant (96.75 %) followed by days to 50 % flowering (96.08 %), days to maturity (93.05 %), 100 seed weight (85.51 %), plant height (83.17 %), pod length (82.80 %), seed yield per plant (74.59 %), number of pods per plant (73.83 %) and the number of seeds per pod (62.84 %). High heritability coupled with high genetic advance as per cent of mean was observed for number of primary branches per plant, seed yield per plant, plant height, number of pods per plant, 100 seed weight and days to 50 % flowering.

Talukdar *et al*. (2020) evaluated 38 green gram genotypes to determine the nature and extent of variation in the phenological traits related to synchronous maturity. A field trial was laid under a Randomized Block Design (RBD) with three replications. High GCV and PCV was observed for number of pods per plant followed by degree of indetermination of plant height from first pod maturity to 90 % pod maturity and number of branches per plant indicating the predominance of additive

gene action. A high heritability (h^2) in broad sense(bs) was recorded for all the traits except for degree of indetermination of plant height from first flower to first pod maturity which showed moderate heritability. The highest heritability was observed for plant height at 90 % pod maturity.

Wesly *et al*. (2020) evaluated 100 green gram genotypes to estimate genetic variability among genotypes for future breeding studies in RBD with three replications. Genetic analysis revealed that maximum genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for number of primary branches per plant followed by number of clusters per plant, while minimum genotypic variation was observed for days to 50 % flowering and days to maturity. High heritability was recorded for protein content followed by number of pods per plant and seed index. High estimates of genetic advance were noticed in character, plant height followed by harvest index and number of pods per plant whereas low estimates of genetic advance were observed for seed index and pod length. High heritability coupled with high genetic advance as per cent of mean was observed for number of primary branches per plant, pod length, number of clusters per plant, number of pods per plant, number of seeds per pod, 100-seeds weight and seed yield per plant.

Dhunde *et al*. (2021a) evaluated 35 F_2 genotypes of green gram along with ten parents and one local check with a view to study the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. The magnitude of PCV was found higher than that of GCV for all the traits indicating expression of genotype is affected by environmental factor. Highest and lowest coefficient of variation was noticed in the traits yield per plant and days to maturity, respectively. Plant height recorded high heritability coupled with high genetic advance as per cent of mean. which indicated that this character is governed by additive genes and selection will be rewarding for its improvement. While number of branches per plant, number of pods per plant and grain yield per plant exhibited moderate to high heritability coupled with moderate genetic advance as per cent of mean.

2.2 CORRELATION COEFFICIENT ANALYSIS

The concept of correlation was put forward by Galton (1889) and later the theory of correlation was developed by Pearson (1904). Correlation coefficient is a statistical measure which is used to find out the degree and direction of relationship between two and more variables. Direct selection for complex traits like yield is often not very effective. To determine the selection criteria for simultaneous improvement of various characters along with the seed yield is done by help of the information on nature and magnitude of correlation among various traits.

Various workers have extensively studied genotypic and phenotypic correlation of various yield attributes with seed yield as well among themselves in green gram are reviewed as under:

Begum *et al*. (2012) estimated genotypic association among yield and related attributes using 10 green gram genotypes. The result revealed significant variation among yield related traits *viz*.; number of branches per plant, number of pods per plant, pod length, number of seeds per pod, number of seeds per plant, seed yield per plant and 100-seed weight. Seed yield per plant revealed highly significant phenotypic correlation with pods per plant (0.65), seeds per plant (0.61) and with 100-seed weight. Seed yield per plant showed significant genotypic correlation with pods per plant (0.71) and with days to pods formation (0.70).

Narsimhulu *et al.* (2013) carried out correlation using 40 green gram genotypes for different quantitative characters during *rabi* 2012. Results revealed that seed yield had positive and significant correlation with number of pods per plant, clusters per plant, number of pods per cluster and biological yield per plant. All these traits had significant and positive association with branches per plant might play a vital role in indirect selection for yield.

Fifty green gram genotypes were evaluated by Prasanna *et al.* (2013). Results revealed that genotypic correlation were greater than the corresponding phenotypic correlations, indicating the preponderance of genetic variance in expression of different characters. Seed yield was positive and significant correlated with number of pods per plant, number of clusters per plant, number of primary branches and number of seeds per pod both at genotypic and phenotypic levels. Days to 50 % flowering

showed significant positive correlation with days to maturity and number of clusters per plant. Days to maturity exhibited significant positive correlation with number of clusters per plant and number of pods per plant. There was positive significant relationship of number of primary branches per plant with number of pods per plant and number of seeds per pod. Number of clusters per plant exhibited significant and positive association with number of seeds per plant. They suggested that strong inter correlation which paves way for the improvement of these attributes by a simple selection program.

Twenty-three green gram genotypes were evaluated by Sarkar *et al.* (2014). Genotypic correlation revealed that plant height at maturity was significantly and positively correlated with number of branches per plant, pods per plant, pod length, seeds per pod, 100-seed weight, final picking and seed yield per plant. Likewise, pods per plant, harvest index, final picking and seed yield per plant were positively correlated with number of branches per plant. The traits seeds per pod and harvest index were positively correlated with pods per plant and seeds per pod showed high level of significance. Phenotypic correlation revealed that number of branches per plant, pod length, seeds per pod, 100-seed weight and final picking were positively correlated with plant height. Likewise, number of branches per plant was positively correlated with pods per plant and harvest index.

Forty-five advance lines including four varieties of green gram were used by Katiyar *et al*. (2015) to study character association for seed yield per plant and its component traits. Results revealed that seed yield per plant exhibited positive and significant correlation with 100-seed weight, number of seeds per pod, number of pods per plant, and plant height; 100-seed weight with number of pods per plant and number of branches per plant; number of seeds per pod with pod length, number of clusters per plant and number of pods per plant; number of pods per plant with number of clusters per plant and number of branches per plant; plant height with days to maturity.

Muralidhara *et al*. (2015) evaluated F_2 population along with parents (BL 865 × Chinamung) and checks *viz* KKM-3. Results revealed that all the traits at phenotypic level showed highly significant and positive association with seed yield per plant. Hence, they suggested that these parameters may be considered as prime traits during the course of selection to have the higher potential of yield in green gram.

Raturi *et al.* (2015) conducted an experiment with 44 promising genotypes of green gram and performed correlation analysis. Results revealed that the seed yield had highly significant and positive correlation with number of pods per plant, 1000-seed weight, plant height, number of primary branches, number of clusters per plant, number of seeds per pod and pod length. Whereas, seed yield recorded highly significant negative correlation with days to 50 % flowering. Ironically number of secondary branches did not show any significant association with seed yield.

Baisakh *et al*. (2016) analysed 30 genotypes of green gram for yield and component traits to estimate correlation coefficient. Results revealed that plant height, number of clusters per plant, number of pods per plant and number of seeds per pod showed highly significant positive correlation with yield per plant both at genotypic and phenotypic level. Pod length showed significant and positive correlation with yield per plant both at genotypic and phenotypic level.

Dangi *et al*. (2017) estimated correlation coefficient in 22 genotypes of green gram and found that seed yield was non-significantly and positively correlated with days to 50 % flowering, pod length, seed index and negatively but non-significantly correlated with plant height, primary branches per plant, days to maturity and number of seeds per pod both at genotypic and phenotypic levels. They suggested that selection can be composed on those characters showing positive correlation with seed yield per plant.

Thirty green gram genotypes were used by Garg *et al*. (2017a) to estimate correlation coefficient. Correlation analysis reveals that seed yield per plant exhibited negative correlation with days to flowering and days to maturity suggesting the importance of short duration genotypes. On the other hand, seed yield per plant exhibited positive correlation with plant height, number of branches per plant, biological yield per plant, harvest index, number of pods per plant, pod length and number of seeds per pod indicating their importance in increasing yield. Number of pods per plant showed a positive and significant correlation with biological yield, harvest index and seeds per pod, but a negative and significant correlation with days to 50 % flowering and days to maturity. 100- seed weight had a positive and significant correlation with plant height and pod length.

Himabindu and Lavanya (2017) used 22 green gram genotypes to estimate correlation coefficient. Results revealed that the seed index, clusters per plant, biological yield and harvest index showed highly significant positive association with seed yield at both genotypic and phenotypic levels. Hence, they suggested that direct selection for these traits could be helpful in the improvement of green gram breeding.

Yadav *et al*. (2017) evaluated 20 green gram genotypes to estimate genotypic and phenotypic correlation coefficient. Results revealed that number of clusters per plant, number of pods per plant, pod length and harvest index had highly significant and positive correlations with seed yield at genotypic level. Thus, priority should be given to these characters for yield improvement in mungbean.

Fifty-eight exotic and indigenous diverse green gram genotypes were evaluated by Abbas *et al.* (2018) for seed yield and other related traits. Seed yield showed positive and significant genotypic and phenotypic correlations with clusters per plant, pods per plant, biological yield and harvest index. These traits also showed high positive direct effects on seed yield. Hence, they suggested that the indirect selection for these traits may facilitate for developing high yielding genotypes.

Kumar *et al*. (2018) evaluated 79 genotypes of green gram to estimate correlation coefficient. Results revealed that seed yield per plant had significant and positive correlation with number of pods per plant, biological yield per plant, harvest index, number of seeds per pod and pod length at phenotypic level. Seed yield per plant exhibited negative correlation with days to flowering and days to maturity.

Parihar *et al.* (2018) evaluated eight green gram genotypes along with two check varieties to estimate correlation coefficient. Results revealed that the seed yield recorded negative and significant correlation only with plant height and days to maturity, where as it showed non-significant correlation with remaining traits. The days to 50 % flowering has positive significant correlation with days to maturity, plant height and pods per plant. Pods per plant have positive significant correlation with plant height, secondary branches per plant and days to maturity. Plant height has positive significant correlation with days to maturity and secondary branches per plant. Seeds per pods have positive significant correlation with primary branches per plant. 100-seed weight has negative non-significant correlation with maturity, plant height while, significant correlation for pods per plant.

Sandhiya and Saravanan (2018) carried out an experiment during kharif 2016 to assess the genetic variability and correlation among yield and yield attributing characters of green gram. Thirty-six mungbean germplasm were investigated for this study for 10 quantitative characters. Results revealed that phenotypic correlation was higher than the genotypic correlation for all the characters under study. From the correlation studies, seed yield per plant showed positive and significant correlation with the traits *viz*., number of pods per plant, number of clusters per plant and number of pods per cluster. They suggested that selection for these traits will indirectly increase the seed yield per plant.

Kanavi *et al*. (2019) evaluated 200 germplasm lines of green gram to screen for drought tolerance using augmented design. The correlation coefficient analysis revealed that out of 17 independent variables studied, 15 variables showed positive correlation with dependent variable yield. Two variables namely, days to 50 % flowering and days to maturity did not show positive correlation with yield.

Twenty-one green gram hybrids were evaluated by Manivelan *et al.* (2019) in randomized block design with three replications for yield and its component traits for estimation of correlation coefficient and path coefficient analysis. Results revealed that both phenotypic and genotypic association, except plant height all other trait *viz*., number of clusters per plant, number of branches per plant, number of pods per plant, number of seed per pod, 100 seed weight and seed yield per plant exhibited positive and significant association with seed yield per plant. Number of clusters per plant showed significant and positive association both at genotypic and phenotypic levels with number of branches per plant, number of pods per plant and hundred grain weight. Whereas number of branches per plant showed significant and positive association with number of seed per pod and hundred grain weight.

Muthuswamy *et al*. (2019) evaluated 100 green gram genotypes to assess the correlation coefficient analysis for yield and yield attributing traits. Results revealed that seed yield per plant was highly significant and positively associated with plant height, number of branches per plant, number of clusters per plant, number of pods per cluster and number of pods per plant. They suggested that selection of these traits would offer scope for improvement of seed yield in green gram.

Abhisheka and Mogali (2020) evaluated 110 advanced breeding lines derived from 14 crosses in F_6 generations of green gram to estimate correlation coefficient for yield and yield attributing traits. Results revealed that number of pods per plant and 100-seed weight showed highest positive significant correlation with seed yield followed by number of branches per plant, number of clusters per plant, number of pods per plant and pod length. They suggested that these are the most important and reliable characters and it can be utilized in direct selection for improving the seed yield.

Ahmad and Belwal (2020) used 112 diverse genotypes of green gram, along with five high yielding checks. Correlation analysis indicated that seed yield showed positive and significant correlation with number of pods per plant, pod diameter, pod length, 100-seed weight, number of clusters, plant height, seed length, number of branches and seed density.

Majhi *et al*. (2020) conducted an experiment comprising F_3 breeding lines derived from three crosses *viz*., DGGV-7 × V-02-709, DGGV-7 × V-02-802 and DGGV-2 × SML-1815 along with their parents. All the three crosses shoewed positive and significant correlation between plant height, number of clusters per plant, number of pods per plant, number of branches per plant and seed yield per plant. Therefore, they suggested that these characters should give higher priority at the time of selection for improvement of yield in greengram.

Mohammed *et al*. (2020) evaluated 50 genotypes of green gram. Results revealed that number of pods per plant, number of clusters per plant, number of seeds per pod, number of primary branches per plant, plant height, days to maturity, pod length and 100 seed weight showed a positive and significant correlation both at genotypic and phenotypic levels with seed yield per plant. They recommended these characters can be utilized in indirect selection to improve the seed yield per plant.

Dhunde *et al*. (2021b) carried out correlation coefficients analysis among twelve quantitative traits in thirty-five green gram genotypes. The results of association study revealed that, grain yield per plant (g) showed highly significant and positive correlation at both genotypic and phenotypic levels with number of branches per plant, number of pods per cluster, number of clusters per plant, number of pods per plant and hundred seed weight (g). They suggested that due emphasis should be given on these

characters in the selection which would help in isolating high yielding genotypes from highly segregating population to improve yield potential of mungbean.

Goyal *et al.* (2021) evaluated twenty genotypes of advance generation along with five check varieties to determine association between yield and its contributing traits in green gram. The results of association study revealed that, majority of the cases have high genotypic correlation as compared to their phenotypic correlations for all the characters indicating little influence of environment. Seed yield per plant was found highly significant and positively correlated with plant height followed by pod length, number of pods per cluster and number of pods per plant. The days to 50 % flowering had a non-significant but negative correlation with seed yield per plant. 100-seed weight showed positive but non-significant association with seed yield per plant.

2.3 PATH COEFFICIENT ANALYSIS

A study on correlation alone is not enough to give an exact picture of relative importance of direct and indirect influence of each of component character on seed yield. In this context, the plant breeders may use the path coefficient analysis in partitioning the correlation coefficients into direct and indirect effects of independent variables on dependent variable. *i.e*., seed yield. Path co-efficient analysis is a standardized partial regression coefficient which splits genotypic correlation co-efficient into measures of direct and indirect effects. It measures the direct and indirect contribution of various independent characters on a dependent character. Selection based on yield alone cannot be relied upon as it is dependent upon other component characters. Thus, path analysis helps in selection of superior genotypes from diverse population. The concept of path coefficient analysis was originally developed by Wright (1921), but the technique was first used by Dewey and Lu (1959). A brief review of work related to path coefficient analysis in green gram is presented as under:

Tabasum *et al.* (2010) performed path analysis for different characters in ten mungbean genotypes and revealed that highest positive direct effects were exerted through pods per plant followed by total plant weight, harvest index, 100-seed weight, pod length and secondary branches; while, primary branches, plant height, clusters per plant and pods per cluster expressed negative direct effects on seed yield per plant.

Khanpara *et al*. (2012) studied path coefficient analysis in 58 genotypes of green gram. The results revealed that maximum direct effects as well as appreciable indirect influences were exerted by number of pods per plant, number of clusters per plant and number of pods per cluster towards seed yield per plant. They suggested that emphasis should be given to these traits in selection program for improvement of seed yield in green gram.

Ahmad *et al.* (2013) evaluated thirty-five green gram genotypes and results revealed that maximum positive direct contribution to seed yield per plant came from number of seeds per pod followed by 100 seed weight, number of pods per plant and number of primary branches per plant. Positive indirect contribution came from all the traits having maximum indirect effect of number of primary branches per plant *via* number of pods per plant and number of pods per plant *via* number of seeds per pod.

Prasanna *et al.* (2013) evaluated fifty green gram genotypes for path coefficient analysis. Results revealed that out of the 13 characters analyzed six characters showed positive direct effects on seed yield. Remaining six traits showed negative direct effect on seed yield. Number of pods per plant recorded maximum positive direct effect of 0.992 followed by harvest index, number of seeds per pod, days to maturity and 100-seeds weight. Plant height and test weight recorded low positive direct effect on seed yield. The high negative direct effect recorded through leaf area followed by number of clusters per plant while, number of primary branches per plant and pod length was moderate negative direct effect. Low negative direct effect was registered for protein content and days to flowering on seed yield. They suggested that maximum direct effect of number of pods per plant depicted a true relationship and selection based on this character would be highly desirable for improving seed yield of green gram.

Hemavathy *et al*. (2015) used thirteen diverse green gram genotypes for the estimation of path coefficient studies. Maximum direct effect on seed yield was observed through number of pods per plant, number of pods per cluster, number of clusters per plant and 100-seed weight. They suggested that number of pods per cluster, number of pods per plant, number of seed per pod and 100-seed weight should be given top most priority while formulating a selection strategy for improvement of yield in greengram.

Katiyar *et al.* (2015) studied forty-five advance lines including four varieties of green gram for path coefficient analysis. Results revealed that number of pods per plants had highest direct effect on grain yield per plant followed by number of seeds per pod, 100-seed weight, days to maturity and number of clusters per plant. The direct effect of days to 50 % flowering, plant height, number of primary branches per plant and pod length was found to be negative on grain yield per plant. The studies revealed that seed yield per plant is the product of seeds per plant and 100-seed weight, whereas seeds per plant, depends on pods per plant, seeds per pod, plant height, branching and pod length. Therefore, due emphasis need to be given on above mentioned traits for improving the productivity during selection.

Raturi *et al*. (2015) used 44 promising genotypes of green gram in their experiment to perform path analysis. Results revealed that number of pods per plant had the maximum direct effect followed by plant height and 1000-seed weight. It means a slight increase in any of these traits may directly contribute towards seed yield. They also reported positive direct effect of pods per plant on seed yield via indirect positive effect through 1000-seed weight, pod length, number of clusters per plant, number of seeds per pod, number of primary branches, number of secondary branches and plant height. The residual effect of 0.61 was observed in this study indicating the contribution of component characters was 39 % and the rest 61 % was the contribution of other factors.

Anand *et al*. (2016) evaluated 26 F_6 families of green gram for path coefficient analysis. Results revealed that the trait, number of clusters per plant had high positive direct effect on seed yield followed by number of pods per plant. Days to 50 % flowering and plant height had negative correlation and negative direct and indirect effects for grain yield indicating that dwarf and early maturing produces higher yield. Number of clusters per plant and number of pods per plant are the most important yield contributing components as they recorded high direct and indirect effects towards seed yield in green gram. The residual effect is low (0.375) indicating appropriateness of characters chosen.

Thirty green gram genotypes were used by Garg *et al*. (2017a) to perform path coefficient analysis. Results revealed that harvest index had the highest direct and positive effect on seed yield per plant followed by biological yield per plant, number

of pods per plant, pod length, 100-seed weight, days to maturity, number of branches per plant and days to flowering. The residual effect (0.157) indicates that the component characters under study were responsible for about 85 % of variability in seed yield per plant.

Kate *et al*. (2017) studied 30 green gram genotypes to estimate genetic variability, heritability, correlation and path analysis. Results revealed that positive direct effect was exhibited by 100 grain weight and plant height on grain yield per plant. The character grains per pod, 100 grain weight, days to 50 % flowering, plant height and days to maturity exhibited indirect effect on grain yield. They suggested that seed yield per plant could be improved through simultaneous selection of number of pods per plant and 100 grain weight. It is desirable to give more weightage to these characters in selection programme for both seed yield and green pod yield per plant.

Fifty-eight exotic and indigenous diverse green gram genotypes were evaluated by Abbas *et al.* (2018) for seed yield and other related traits. They observed positive direct effects of clusters per plant, pods per plant, 100-seed weight, biological yield and harvest index on seed yield. Days to maturity affected positively and indirectly through clusters per plant, pods per plant, 100-seed weight and biological yield. Likewise, positive indirect effect of plant height on seed yield had been observed through clusters per plant, pods per plant and biological yield. Clusters per plant affected positively and indirectly *via* pods per plant and biological yield. They also observed positive indirect effects of pods per plant through clusters per plant, biological yield and harvest index. They suggested that direct selection for traits like number of clusters per plant, pods per plant, biological yield and harvest index is effective for the improvement of seed yield in green gram. Indirect selection through clusters, pods, biological yield and harvest index may improve mungbean yield to evolve high yielding mungbean varieties.

Kumar *et al*. (2018) evaluated 79 genotypes of green gram to estimate correlation coefficient and path analysis. Results revealed that direct and positive effect on seed yield per plant was observed for characters like biological yield per plant followed by harvest index, number of pods per plant, pod length, number of seeds per pod, plant height, 100 seed weight, days to 50 % flowering. Days to maturity and number of branches per plant had negative direct effect on seed yield per plant. The

low value of residual effect at phenotypic (0.1723) and genotypic (0.1620) level indicated that characters studied in the present investigation had major contribution towards seed yield and therefore, other remaining characters have little contribution towards seed yield in mungbean.

Parihar *et al.* (2018) evaluated eight mungbean genotypes along with two check varieties to estimate direct and indirect effect of different characters on seed yield. Results revealed that days to 50 % flowering, primary branches per plant, secondary branches per plant, 100-seed weight and number of seeds per pod had positive direct effect on seed yield while, plant height, days to maturity and pods per plant had negative direct effects on seed yield. They observed that late flowering with numerous primary and secondary branches with more seed weight and more number of seeds per pod directly lead to increase in seed yield. Less pods per plant with high seeds per pods is more desirable trait for high seed yield.

Asari *et al*. (2019) used forty-four green gram genotypes to estimate direct and indirect effect of different characters on seed yield. Results revealed that days to 50 % flowering had high and positive direct effect on seed yield per plant followed by low and positive effect by test weight, clusters per plant, pods per plant and primary branches per plant. The direct effect of days to maturity on seed yield was very high and negative. They suggested that days to 50 % flowering, test weight, clusters per plant, pods per plant and primary branches per plant would be rewarding for yield improvement.

Twenty-one green gram hybrids were evaluated by Manivelan *et al.* (2019) in randomized block design with three replications for yield and its component traits for estimation of correlation coefficient and path coefficient analysis. Results revealed that plant height, clusters per plant, number of branches per plant, number of pods per plant, number of seed per pod will be effective to improve yield potential as they showed high direct positive effect in path analysis. The estimate of residual effects was high (0.5875) which indicated that the yield attributing characters considered in the present investigation only explained around 41 percentage of variability in seed yield, indicating possibilities of some other characters effecting seed yield per plant.

Muthuswamy *et al*. (2019) used 100 accessions of green gram to perform path coefficient analysis. Results revealed that number of pods per plant and hundred seed weight had positive direct effects on seed yield. The number of clusters per plant and number of pods per clusters exhibited positive and high indirect effects through number of pods per plant on seed yield per plant. They suggested that selection based on number of clusters per plant and number of pods per cluster would increase seed yield indirectly through the number of pods per plant.

Abhisheka and Mogali (2020) evaluated 110 F_6 generations of green gram to estimate genetic variability, correlation and path coefficient analysis for yield and yield attributing traits. Results revealed that the characters number of pods per plant and hundred seed weight had highest positive direct effect and also had high positive correlation with seed yield. Thus, these are the most important and reliable characters and it can be utilized in direct selection for improving the seed yield. The path diagram revealed a residual effect of 0.4367 which indicated that studied characters contribute 56.33 per cent to the yield.

Ahmad and Belwal (2020) carried out path analysis using 112 diverse genotypes of green gram, along with five high yielding checks. Results revealed that number of pods per plant and 100-seeds weight exerted a high magnitude of positive direct effect. Pod length showed moderate effect while number of cluster and seed density exerted positive but low magnitude of direct effect on seed yield. They suggested that selection strategy based on above traits would be rewarding for yield improvement.

Mohammed *et al*. (2020) performed path analysis using 50 green gram genotypes. Results revealed that the number of pods per plant had a positive and direct effect on seed yield per plant followed by pod length, 100 seed weight, plant height, number of primary branches per plant, harvest index and days to 50 % flowering both at the genotypic and phenotypic levels.

Dhunde *et al*. (2021b) performed path analysis in 35 green gram genotypes. Results revealed that number of branches per plant, pod length, plant height, number of pods per cluster and number of pods per plant recorded the highest direct effect in desirable direction. Their association with grain yield was also significant and positive indicating true and perfect association between these traits. They suggested that due

emphasis should be given on these characters in the selection, which would help in isolating high yielding genotypes from highly segregating population to improve yield potential of mungbean.

Goyal *et al.* (2021) evaluated a set of twenty genotypes of advance generation along with five check varieties of green gram to determine path analysis. Results revealed that the traits like pod length, harvest index, primary branches per plant, 100 seed weight, pods per cluster, protein content and pods per plant exhibited high and positive direct effects on seed yield per plant. They suggested that direct selection for these characters can be carried out for the green gram improvement programs. A negative direct effect was observed on seed yield per plant with days to flowering, plant height and seeds per pod indicating the selection for these traits may have an undesirable impact on yield.

2.4 GENETIC DIVERGENCE

Genetic diversity plays an important role because hybrids between lines of diverse genetic background generally display a greater heterosis than those between closely related parents and may generate broad-spectrum genetic variability in segregating generation. A method proposed by Mahalanobis (1936) known as 'Mahalanobis' D^2 statistics is widely used to know genetic diversity in the available genotypes. The D^2 statistics measures the degree of diversification and determines the relative proportion of each component character to the total divergence. A brief review of work related to genetic divergence in green gram is presented as under:

Patel and Patel (2012) carried out diversity analysis using forty green gram genotypes. Results revealed that all genotypes grouped into 11 clusters and cluster V was the largest comprising seven genotypes followed by cluster VI with six and clusters X and XI with five genotypes. The maximum inter cluster distance was observed between cluster III and IX followed by cluster II and IX and cluster III and VI indicated wide divergence among these clusters. The minimum inter cluster distance (12.36) was observed between cluster IV and cluster V. They also observed that the genetic diversity was unrelated to geographical diversity.

Gadakh *et al.* (2013) studied the genetic divergence and clustering pattern among 50 genotypes of green gram. 50 genotypes were grouped into 7 clusters. Cluster

I have highest number of genotypes (22) followed by Cluster II (18), cluster III (5) and Cluster VII (2). The mono-genotypic cluster was cluster IV, V and VI. The maximum intra cluster distance was observed in the cluster II followed by cluster I, cluster VII and cluster III. Maximum inter-cluster distance was observed between the cluster III and IV followed by cluster III and V, cluster I and III and cluster III and VII indicating wide divergence among these clusters. Protein content contributed maximum towards divergence followed by biological yield per plant, number of primary branches per plant, plant height, length of pod and grain yield per plant.

Mehandi *et al.* (2015) performed multivariate analysis in green gram using 21 green gram genotypes. Results revealed that these genotypes were grouped into 10 and 5 clusters, following Tocher's and non-hierarchical Euclidian clustering methods, respectively. Based on the maximum diversity obtained in Tochers method genotype KM 10-1064 of cluster V and genotypes KM 10-1046, KM 10-1059 and KM 10-1070 of cluster VI were found suitable for improving the plant structure, whereas concerning high diversity along with high trait contribution towards total divergence, the genotype KM 10-1064 of cluster V and KM 10-1042 of cluster VIII were found to be appropriate for hybridization. The genotype KM 10-1068, which represents the mono genotypic cluster in case of both the clustering methods signifies that it could be the most diverse from other genotypes and it would be the suitable candidate for hybridization with genotypes present in other clusters to enhance the seed yield in green gram.

Sarkar and Kundagrami (2016) evaluated eleven agro-morphological traits in twenty-three genotypes of mungbean. Cluster analysis using UPGMA method grouped the genotypes into five clusters. The component of mungbean genotypes among different clusters was varied from two to nine genotypes. The maximum number of genotypes i.e., 9 is found in cluster III followed by cluster IV comprising of 6 genotypes. Cluster V showed the maximum mean value for plant height, branch per plant, pods per plant, seed per pod, seed yield per plant and lowest values for days to 50 % maturity, 1st picking and days to maturity. Principal component analysis revealed that the first five main PCAs amounted 71.11 % of the total variation among genotypes. PC1 accounts for maximum variability in the data with respect to succeeding components.

Garg *et al.* (2017b) estimated nature and magnitude of genetic divergence among 30 green gram genotypes using green gram using D^2 statistics. Genotypes were grouped into six clusters. The highest intra cluster distance was observed for cluster III (3.874) and the lowest was observed for cluster II (3.537). While, the highest inter cluster distance was observed between cluster I and VI (6.315). Cluster IV formed monogenotypic cluster. Cluster III showed the maximum mean value (35.407) for harvest index, plant height (31.85) and seed yield (2.51).

Jeeva and Saravanan (2017) estimated genetic divergence in green gram using D^2 statistics. The twenty genotypes were grouped into seven clusters based on hierarchical cluster analysis with cluster I containing the maximum of nine genotypes. The maximum intra cluster distance was observed in cluster I (16.62) and minimum of 0.00 in cluster VI and VII. The maximum inter cluster distance was between clusters III and cluster VII (118.43) followed by cluster II and cluster IV (112.07) indicating wide genetic diversity. The characters like days to first flowering, plant height, number of pods per plant and number of seeds per pod had contributed 77.32 per cent of total divergence. They suggested that plant height and days to first flowering contributed maximum towards divergence, so we go for direct selection for these traits for diversity purpose.

Rasal and Parhe (2017) estimated genetic divergence in green gram using D^2 statistics. The 50 genotypes were grouped into 10 clusters. Cluster III was largest with 18 genotypes followed by cluster I with 13 genotypes, cluster V with 8, cluster IV and VI with 3 genotypes. The clusters II, VII, VIII, IX and X were solitary. The highest intra cluster distance was observed for cluster V followed by cluster IV, cluster VI, cluster III and cluster I. The clusters II, VII, VIII, IX and X showed no intra cluster distance being monogenotypic. The maximum inter cluster distance was observed between cluster VII and VI followed cluster X and VI, cluster VII and II and cluster VII and IV. The inter cluster distance between cluster II and I followed by cluster IV and I and IX and II was comparatively low. Out of 11 characters, seed yield per plant (37.39 %) contributed the maximum for divergence among the genotypes studied followed by plant height (35.51 %).

Sen and De (2017) conducted a study to estimate nature and magnitude of genetic diversity among 30 green gram genotypes for yield traits using Mahalanobis's

D^2 statistics. Thirty genotypes were grouped in 6 clusters, among them cluster VI showed maximum intra-cluster distance while the highest inter-cluster distance was observed between cluster III and VI. Cluster II recorded highest means for seeds per pod, 100 seed weight, seed yield per plant and shelling %. The percent contribution towards genetic diversity was highest for shelling percentage (17.70) followed by seed yield per plant (16.55) and number of clusters per plant (14.71). From the divergence analysis, they suggested that the genotypes belonging to different clusters separated by high estimated statistical distance may be used in the hybridization programme for developing high yielding green gram varieties. Five genotypes *viz*., PDM-11, TARM-2, TM-98-50, PDM 54 and Basanti were identified as most useful in the future breeding programme.

Sofia *et al.* (2017) carried out multivariate analysis (D^2) in 35 green gram genotypes and grouped them into 7 clusters. They found that out of these seven clusters, cluster I contained maximum number of 13 genotypes, followed by cluster Il with 10 genotypes and cluster IV with 7 genotypes. The maximum intra-cluster distance was recorded by cluster IV, while the minimum distance was noted in the clusters V, VI and VIl as they included single genotype each. The maximum inter-cluster D^2 value was observed between cluster Ill and IV followed by II and IV and cluster IV and VII. While, the minimum D^2 value was found between cluster V and VI.

Fifty-eight exotic and indigenous diverse green gram genotypes were evaluated by Abbas *et al.* (2018) for seed yield and other related traits. The diversity analysis categorized fifty-eight genotypes into four clusters. Cluster-I with three genotypes and Cluster-II with seventeen genotypes showed the highest values for yield and yield contributing traits. Three distant genotypes were identified; a genotype, VC3012B was found high yielding, NIMB-101 had high biological yield and number of clusters per plant and VC 3404 had high 100-seed weight. They suggested that these genotypes may be used for the incorporation of genes for high seed yield, biological yield, clusters per plant and seed weight into well adapted germplasm.

Mahalingam *et al*. (2018) evaluated 445 genotypes of green gram for eight quantitative traits *viz*. plant height, number of branches per plant, number of clusters per plant, number of pods per clusters, number of pods per plant, pod length, 100-seed weight and seed yield per plant. The data was subjected to cluster analysis, and the

genotypes were grouped under three discrete clusters. This study concluded that an effective hybridization programme including the genotypes between the clusters I, II and III would produce wider segregation that might be used for development of improved green gram varieties.

Sixty-four green gram genotypes were evaluated by Sharma *et al*. (2018) to explore the extent of genetic diversity. On the basis of Tocher's method, genotypes were grouped into eight clusters. Cluster I was largest with maximum 29 genotypes, followed by Cluster III, II and V comprising 9, 8 and 8 genotypes, respectively. The maximum inter cluster D^2 value (20.56) was recorded between cluster VII and VI, while the minimum D^2 value (10.26) was found between cluster VIII and VII. The grain yield per plant was found to be maximum in cluster VI which indicated importance of this cluster in improvement of yield in green gram. Among all the traits studied 100-seed weight contributed maximum to the diversity followed by number of clusters per plant, days to 50 % flowering and days to maturity. They suggested that diverse parents should be used to produce desirable recombinants for developing new improved green gram varieties.

Kumar *et al.* (2019) studied genetic divergence in 79 green gram genotypes. On the basis of D^2 statistics genotypes were grouped into 15 clusters. The maximum intra cluster distance (145.87) was recorded for cluster IV followed by cluster II (105.50), cluster III (98.50), cluster XI (60.26) and cluster I (60.07). While, highest inter cluster distance was observed between cluster III and cluster IX (2356.28). Characters like days to 50 % flowering, 100-seed weight, biological yield per plant, number of branches per plant and number of pods per plant contributed 91.79 per cent towards total divergence. They advocated that genotype belonging to diversified clusters may be used in the hybridization programme for developing high yielding green gram varieties.

Tomar and Upadhyay (2019) studied genetic divergence in forty-five green gram genotypes. All the forty-five genotypes were grouped into seven different clusters using D^2 statistics. Cluster-I, II, III, IV, V, VI and VII had 8, 5, 4, 5, 13, 2 and 8 genotypes, respectively. Maximum intra cluster distance was observed in cluster IV. Maximum inter cluster distance was observed between cluster-II and cluster-V. 100-seed weight was ranked first, with a contribution of 60.61 % toward divergence

followed by grain yield per plant (11.11 %), plant height (9.49 %), days to 50 % flowering (7.88 %), number of pods per plant (3.74 %), pod length (3.64 %), number of clusters per plant (2.32 %), number of primary branches per plant (0.51 %), number of seeds per pod (0.40 %) and days to maturity (0.30 %).

Mathankumar *et al.* (2020) studied genetic divergence of 100 mungbean genotypes using Mahalanobis D^2 analysis. The genotypes were grouped into fifteen clusters, with cluster I having the maximum number of genotypes. Maximum intra cluster distance was recorded in cluster I indicating higher diversity among genotypes of this cluster. Cluster V and XV recorded maximum inter cluster distance indicating wider divergence between genotypes of these clusters. High mean performances for number of clusters per plant, number of pods per cluster, total number of pods per plant and seed yield per plant was observed in cluster XIII. They suggested that selecting genotypes from clusters with desirable mean value as parents could help in improving yield components in breeding program.

Nagda *et al*. (2020) evaluated 12 green gram genotypes to determine genetic divergence using D^2 statistics. The genotypes were grouped into four clusters. Cluster I and II with 5 genotypes and Cluster III and IV were solitary. Maximum differences among the genotypes within the same cluster were shown by cluster II (67.91) followed by cluster I (54.09). Solitary clusters III, IV showed zero intra-cluster distances. Cluster IV and III showed maximum inter cluster distance (733.47) followed by cluster IV and I (394.03), cluster III and II (337.00). The lower inter-cluster distance was noticed between cluster II and I (151.49) followed by that between cluster IV and III (131.01), cluster III and I (94.89). They suggested that inter-cluster distances were greater than intra-cluster distances revealing considerable amount of genetic diversity among the genotypes studied and hybridization between divergent clusters is likely to produce wide variability with desirable sergeants.

Talukdar *et al*. (2020) evaluated 38 green gram genotypes to determine genetic divergence using D^2 statistics. The genotypes were grouped into eight clusters. Results revealed that maximum intra cluster distance was observed in cluster IV with two genotypes AKM 8802 and KM 2241, indicating sufficient diversity between two genotypes within this cluster. Minimum inter-cluster distance between Cluster I and Cluster VII indicating close relationship among the genotypes and similarity for the

characters. Maximum inter-cluster distance observed between Cluster III and Cluster VI indicating diverse nature of the genotypes. They observed that higher inter cluster distance than intra cluster distance indicated existence of sufficient genetic variability among the genotypes.

Wesly *et al.* (2020) evaluated 100 green gram genotypes to estimate genetic variability and divergence for future breeding studies. The data were subjected to Mahalanobis D^2 statistics and grouped into ten clusters. Cluster II was largest with 18 genotypes followed by cluster IV and VI. The maximum inter cluster distance was observed between cluster III and IV (1128.22) followed by cluster I and IV (1106.89), while minimum inter cluster distance was observed between cluster III and X (39). Cluster IV showed highest mean value for seed yield per plant. They recommended that the genotypes present in cluster I, II, III and IV provide a broad spectrum of variability in segregating generations and may be used in hybridization program for yield improvement in green gram.

Goyal *et al.* (2021) evaluated twenty genotypes of advance generation along with five check varieties to determine genetic divergence in green gram. All the 25 accessions were grouped under four clusters based on Mahalanobis D^2 methods of clustering. Among all the clusters, cluster II had the highest accessions followed by cluster III, Cluster I and cluster IV. They suggested that selection of genotypes from cluster II and cluster IV will be effective for heterosis breeding as they are the most diverse groups. Protein content, 100 seed weight and seed yield per plant have high contribution towards total genetic divergence showing scope for selection criteria. Hence, selection for pod length, pods per cluster, protein content, 100 seed weight and seed yield per plant will lead to generate an improved population through a breeding programme enhancing the yield of green gram.

CHAPTER III
MATERIALS AND METHODS

The present investigation was carried out to assess the genetic variability, correlation, path analysis and genetic divergence in green gram [*Vigna radiata* (L.) R. Wilczek]. The study was conducted during *kharif* 2021 at the Pulses Research Station, Junagadh Agricultural University, Junagadh. Junagadh is situated in South Saurashtra Agro-climatic Zone of Gujarat state. Geographically Junagadh is situated at 21.5^0 N latitude and 70^0 E longitudes with an altitude of 107 meters above the mean sea level. The soil of experimental site was medium black and medium in organic matter. The climate of the area represents tropical and semiarid. The details of weather parameters recorded for the year 2020-2021 during which the experiment was conducted is presented in the Appendix I. The details of material used and the method adopted in the investigation are described under the following heads:

3.1 EXPERIMENTAL MATERIALS

The experimental material consisted of 72 genotypes (Table 3.1) of green gram from different origins were obtained from the Pulses Research Station, Junagadh Agricultural University, Junagadh.

3.2 EXPERIMENTAL DETAILS

Seventy-two genotypes of green gram were sown in a Randomized Block Design (RBD) with three replications during *kharif* 2021 at Pulses Research Station, Junagadh Agricultural University, Junagadh. Sowing was done on 1st July 2021. Each genotype was accommodated in a single row of 4 m length with a spacing of 45 cm × 10 cm. In order to obtain good crop, recommended package of practices and plant protection measures were timely and uniformly followed.

3.3 CHARACTERS STUDIED

The observations were recorded on five randomly selected competitive plants from each genotype in each replication for all the mentioned traits (except days to 50% flowering and days to maturity, which was recorded on plot basis) and mean values were used for statistical analysis. Procedure adopted to record the observations is described below:

Table 3.1 List of genotypes used in the experiment

Sr. No.	Genotype	Origin	Sr. No.	Genotype	Origin
1	GM 4	S. K. Nagar	37	EC 314286	IARI, New Delhi
2	K 851	Kanpur	38	EC 396523	IARI, New Delhi
3	BPMR 145	Kanpur	39	EC 450446	IARI, New Delhi
4	AKM 6802	Kanpur	40	EC 450450	IARI, New Delhi
5	Kopergaon	Kanpur	41	EC 482907	IARI, New Delhi
6	TARM 18	Akola / BARC	42	EC 482908	IARI, New Delhi
7	PM 2	Akola	43	EC 482909	IARI, New Delhi
8	Vaibhav	Rahuri	44	EC 486839	IARI, New Delhi
9	J 781	Akola	45	EC 496841	IARI, New Delhi
10	GM 1918	S. K. Nagar	46	EC 501566	IARI, New Delhi
11	GM 1924	S. K. Nagar	47	EC 501569	IARI, New Delhi
12	GM 1925	S. K. Nagar	48	IC 615-5	IARI, New Delhi
13	GM 1926	S. K. Nagar	49	IC 8917	IARI, New Delhi
14	GM 02-12	S. K. Nagar	50	IC 8961-5	IARI, New Delhi
15	GM 02-13	S. K. Nagar	51	IC 12434	IARI, New Delhi
16	GM 02-15	S. K. Nagar	52	IC 24789	IARI, New Delhi
17	GM 02-16	S. K. Nagar	53	IC 73536	IARI, New Delhi
18	GM 2K-3	S. K. Nagar	54	Local Collection 1	Junagadh
19	GM 2K-5	S. K. Nagar	55	Local Collection 2	Junagadh
20	RMG 62	Durgapur	56	Local Collection 3	Junagadh
21	RMG 268	Durgapur	57	GM 04-02	S. K. Nagar
22	OUM 11-5	Berhampur	58	GM 04-04	S. K. Nagar
23	GM 3	S. K. Nagar	59	GM 05-05	S. K. Nagar
24	CO 5	TNAU Coimbatore	60	GM 05-08	S. K. Nagar
25	CO 6	TNAU Coimbatore	61	GM 06-08	S. K. Nagar
26	COGG 912	TNAU Coimbatore	62	GM 02-16	S. K. Nagar

Sr. No.	Genotype	Origin	Sr. No.	Genotype	Origin
27	AKM 8803	Akola	63	GJM 1001	Junagadh
28	TARM 1	Akola	64	GJM 1002	Junagadh
29	TARM 2	Akola	65	GJM 1003	Junagadh
30	Asha	Haryana	66	GJM 1004	Junagadh
31	Pant M-2	Pantnagar	67	GJM 1005	Junagadh
32	Pant M-3	Pantnagar	68	GJM 1006	Junagadh
33	Pant M-4	Pantnagar	69	GJM 1007	Junagadh
34	Pant M-5	Pantnagar	70	GJM 1008	Junagadh
35	EC 251557-A	IARI, New Delhi	71	GJM 1009	Junagadh
36	EC 251810	IARI, New Delhi	72	GJM 1010	Junagadh

3.3.1 Days to 50 % flowering

The number of days from date of sowing to appearance of the flower on 50% plants on plot basis were recorded.

3.3.2 Days to maturity

The total number of days from the date of sowing to attain the physiological maturity were counted on plot basis.

3.3.3 Plant height (cm)

At maturity, plant height of selected plants were measured in centimeters from the ground level to the top of the main axis with the help of the meter rod.

3.3.4 Number of primary branches per plant

The number of pods bearing branches arising from the main stem were counted from each of the selected plant.

3.3.5 Number of clusters per plant

The peduncles possessing one or more pods were considered as cluster and total number of such clusters per plant were counted at the time of maturity.

3.3.6 Number of pods per cluster

All pods present in cluster, with full of seeds were counted from the selected plants.

3.3.7 Number of pods per plant

All pods present on the plant, with full of seeds were counted from the selected plant.

3.3.8 Number of seeds per pod

Total five pods from selected plants were used and average number of seeds per pod were worked out.

3.3.9 Length of pod (cm)

Length in centimeter of five pods from selected plants were measured and average value were worked out.

3.3.10 100-seeds weight (g)

Hundred seeds from selected plants were counted and weighed in grams on electronic balance.

3.3.11 Seed yield per plant (g)

At maturity, all the selected plants of each genotype in each replication were harvested separately and clean dried seeds of selected plants were weighed in grams on electronic balance.

3.4 STATASTICAL ANALYSIS

The replication wise mean value of each genotype was worked out. These values were used for the statistical analysis for 11 characters studied.

3.4.1 Analysis of variance

The data recorded for various characters were statistically analyzed at the Computer Cell, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh for various parameters *viz.*, genetic variability, heritability, genetic advance, genetic advance as per cent of mean, genotypic and phenotypic correlations, path coefficient analysis and genetic divergence.

The analysis of variance for RBD was done based on following linear model as suggested by Panse and Sukhatme (1985);

$$Y_{ij} = \mu + g_i + r_j + \in_{ij}$$

$i = 1, 2, 3, \ldots\ldots g$

$j = 1, 2, 3, \ldots\ldots r$

Where,

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

μ = General mean

g_i = Effect of i^{th}genotype

r_j = Effect of j^{th}replication

ϵ_{ij}= Uncontrolled variation associated with i^{th} genotype in j^{th} replication

The format of analysis of variance is given as under:

Table 3.2 Format for analysis of variance for experimental design

Source of Variation	**d.f.**	**Mean Squares**	**Expected mean squares**
Replications	(r-1)	M_r	$\hat{\sigma}^2 e + g\,\hat{\sigma}^2_r$
Genotypes	(g-1)	M_g	$\hat{\sigma}^2 e + r\,\hat{\sigma}^2_g$
Error	(r-1) (g-1)	M_e	$\hat{\sigma}^2 e$

Where,

r = Number of replications

g = Number of genotypes

M_r = Mean sum of square due to replications

M_g = Mean sum of square due to genotypes

M_e = Mean sum of square due to error

Significance of mean sum of square due to replications (M_r) and genotypes (M_g) was tested against error mean sum of square (M_e).

The standard error of mean (S.Em.) was calculated using following formula.

$$S.\,Em. \pm = \sqrt{\frac{M_e}{r}}$$

The critical difference (C.D.) to compare the mean of any two genotypes was calculated using following formula;

$$C.\,D. = S.\,Em. \times \sqrt{2} \times t_{0.05}$$

Where,

t = Table value of 't' at 5 % level of significance at error degree of freedom.

The coefficient of variation (C.V. %) was determined according to the following formula;

$$CV\% = \frac{\sqrt{M_e}}{\bar{X}} \times 100$$

Where,

M_e = Error mean square

$\bar{X}$ = General mean of a character

3.4.2 Estimation of components of variance

Total variation was partitioned into phenotypic ($\hat{\sigma}^2_p$), genotypic ($\hat{\sigma}^2_g$) and environmental ($\hat{\sigma}^2_e$) variance based on expectation of mean square for respective source of variation as described in ANOVA.

$\hat{\sigma}^2_e = Me$

$\hat{\sigma}^2_g = M_g - M_e/r$

$\hat{\sigma}^2_p = \hat{\sigma}^2_g + \hat{\sigma}^2_e$

Genotypic and phenotypic coefficients of variation were estimated as under:

(a) Genotypic coefficient of variation (GCV)

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

$$GCV\ (\%) = \frac{\sqrt{\hat{\sigma}^2_g}}{\bar{X}} \times 100$$

Where,

$\hat{\sigma}^2 g$ = Genotypic variance

$\bar{X}$ = Mean of the character

(b) Phenotypic coefficient of variation (PCV)

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

$$PCV\ (\%) = \frac{\sqrt{\hat{\sigma}^2_p}}{\bar{X}} \times 100$$

Where,

$\hat{\sigma}^2_p$ = Phenotypic variance

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

The GCV and PCV values were classified as per Subramanian and Menon (1973).

GCV and PCV Values (%)	Classification
0 – 10	Low
10 – 20	Medium
>20	High

(c) Phenotypic range and range coefficient

It is the difference between maximum and minimum value in a particular trait.

While comparing the range of different traits, it is necessary to make it unit less. Hence, range coefficient was calculated as per the following formula.

$$\text{Range Coefficient (\%)} = \frac{\text{Range}}{\text{Maximum value + Minimum value}} \text{ x } 100$$

Where ,

Range = Maximum value – Minimum value

(d) Heritability (h^2) in broad sense

It is the ratio of genotypic variance to the phenotypic variance, was calculated according to formula suggested by Allard (1960)

$$h^2 = \frac{\hat{\sigma}^2_g}{\hat{\sigma}^2_p} \times 100$$

Where,

$\hat{\sigma}^2_g$ = Genotypic variance

$\hat{\sigma}^2_p$ = Phenotypic variance

Heritability was categorized as low, moderate and high as suggested by Robinson *et al.* (1955) as follow

Heritability (%)	**Classification**
0 - 30 %	Low
30 - 60 %	Moderate
60 % or above	High

(e) Genetic advance (Gs)

The expected genetic advance under selection (Gs) was estimated as per the formula described by Allard (1960).

$$Gs = k \times \hat{\sigma}^2_p \times h^2$$

Where,

K = Selection differential (k) at 5% selection intensity = 2.06

$\hat{\sigma}^2_p$ = Phenotypic variance

h^2 = Heritability value of the character

(f) Genetic advance expressed as percentage of mean

The genetic advance expressed as percentage of mean was computed as under:

$$\text{GA as (\%) of mean} = \frac{\text{Genetic advance(GA)}}{\text{Mean of character}(\overline{X})} \times 100$$

Genetic advance as percentage of mean was categorised as low, moderate and high as given by Johnson *et al.* (1955) as follow

GA %	Classification
0-10	Low
10-20	Medium
20 and above	High

3.4.3 Correlation coefficients analysis

Correlation coefficient measures 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.

The genotypic and phenotypic correlation coefficients of all the characters were worked-out as per Al-Jibouri *et al.* (1958). The data were subjected to covariance analysis.

Table 3.3 Format for analysis of covariance between two characters

Source of Variation	d.f.	Mean sum of products	Expectation of mean sum of products
Replications	(r-1)	M_r	-
Genotypes	(g-1)	M_g	$Cov_{exy} + r\, Cov_{gxy}$
Error	(r-1) (g-1)	M_e	Cov_{exy}

Where,

r = Number of replications

g = Number of genotypes

Cov_{gxy} = Genotypic covariance between x and y characters.

Cov_{exy} = Environmental (error) covariance between x and y characters.

1. Genotypic covariance (Cov_{gxy})

Formula for calculating genotypic covariance is described as below:

$$Cov_{gxy} = \frac{M_g - M_e}{r}$$

Where,

M_g = Mean sum of products due to genotypes between two characters x and y

M_e = Mean sum of products due to error between two characters x and y

r = Number of replications

2. Phenotypic covariance (Cov_{pxy})

The formula for calculating phenotypic covariance is explained as under:

$$Cov_{pxy} = Cov_{gxy} + M_e$$

Where,

Cov_{gxy} = Genotypic covariance

M_e = Mean sum of products due to error between two characters x and y

3. Error covariance (Cov_{exy})

$Cov_{exy} = Me$

Where,

M_e = Mean sum of products due to error between two characters x and y

Now, genotypic and phenotypic correlation coefficients were worked out according to formula described below;

a. Genotypic correlation coefficient (r_{gxy}**)**

$$r_{gxy} = \frac{Cov_{gxy}}{\sqrt{\hat{\sigma}^2_{gx}.\hat{\sigma}^2_{gy}}}$$

Where,

Cov_{gxy} = Genotypic covariance between two characters x and y

$\hat{\sigma}^2_{gx}$ = Genotypic variance for character x

$\hat{\sigma}^2_{gy}$ = Genotypic variance for character y

b. Phenotypic correlation coefficient (r_{pxy})

$$r_{pxy} = \frac{Cov_{pxy}}{\sqrt{\hat{\sigma}^2_{px}.\hat{\sigma}^2_{py}}}$$

Where,

Cov_{pxy}= Phenotypic covariance between two characters x and y

$\hat{\sigma}^2_{px}$ = Phenotypic variance for character x

$\hat{\sigma}^2_{py}$ = Phenotypic variance for character y

c. Test of significance

The test of significance of the correlation coefficient was done by calculating 't' value using following formula suggested by Panse and Sukhatme (1985).

$$t = \frac{r}{\sqrt{1-r^2}} \times \sqrt{(n-2)}$$

Where,

r = Correlation coefficient

n = Total number of observations

The calculated 't' value was compared with table 't' value at (n-2) degree of freedom to test the significance of correlation coefficient.

3.4.4 Path coefficient analysis

Path coefficient is a standardized partial regression coefficient and measures the direct and indirect effects of one variable upon another and permits the separation of correlation coefficient into the component of direct and indirect effects. The genotypic as well as phenotypic path coefficient analysis was done as per the method suggested by Dewey and Lu (1959).

Genotypic as well as phenotypic correlation coefficients of ten variables with seed yield were used to estimate the genotypic path coefficient and phenotypic path coefficient for the direct effects of various independent characters on seed yield.

The path coefficients were obtained by solving simultaneous equation which represents the basic relationship between correlation and path coefficients as given below;

$$r_{1y} = P_{1y} + P_{2y}r_{1.2} + ...,\ldots+P_{10y}\, r_{1.10}$$
$$r_{2y} = P_{1y}\, r_{1.2} + P_{2y} +...,\ldots+P_{10y}\, r_{2.10}$$
$$,\quad ,\quad ,\quad ,\quad ,$$
$$,\quad ,\quad ,\quad ,\quad ,$$
$$,\quad ,\quad ,\quad ,\quad ,$$
$$r_{10y} = P_{1y}\, r_{1.10} + P_{2y}\, r_{2.10} + ..., +P_{10y}$$

Where,

r_{1y}, r_{2y}, r_{3y},…,..., r_{10y} are the genotypic correlations of days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusret per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod(cm) and 100-seeds weight (g), respectively.

P_{1y}, P_{2y}, P_{3y},…,…,…,..,P_{10y} are the direct effects of characters *viz*., days to 50% flowering, days to maturity, plant height (cm), number of primary branches per plant, number of cluster per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod(cm) and 100-seeds weight (g), respectively.

The coefficient of determination was calculated by using the following relationship.

$$1 = P^2_{1.y} + 2P_{1.y}\, r_{1.2}P_{2.y} + 2P_{1.y}\, r_{1.3}P_{3.y} + 2P_{1.y}\, r_{1.4}P_{4.y} + 2P_{1.y}\, r_{1.5}P_{5.y} + 2P_{1.y}\, r_{1.6}P_{6.y} + 2P_{1.y}\, r_{1.7}P_{7.y} + 2P_{1.y}\, r_{1.8}P_{8.y} + 2P_{1.y}\, r_{1.9}P_{9.y} + 2P_{1.y}\, r_{1.10}P_{10.y}\ldots\ldots\ldots..+ P^2_{9.y} + 2P_{9.y}\, r_{9.10}P_{10.y} + P^2_{10.y} + R$$

The residual variation was computed using the following formula:

Residual variation (X) = 1- R^2

Where,

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

3.4.5 Genetic Divergence

Genetic diversity between genotypes can be better estimated using D^2 statistics given by Mahalanobis (1936). Transformation of original means of various charecters (X_1`S) to uncorrelated variates ($Y_1$`S) was carried out by pivotal condensation method

as the common dispersion matrix by using the computer. This made D^2 values as simple sum of squares of difference in transformed values for various characters. The generalized distance between any two-population defined as,

$$D^2p = b_1d_1 + b_2d_2 + \ldots + b_pd_p$$

Where,

$X_1, X_2, X_3, \ldots, X_p$ as the multiple measurements available on each individual and $d_1, d_2, \ldots, d_p$ as $X_1^{-1} - X_1^{-2}$, $X_2^{-1} - X_2^{-2}$, …., $X_p^{-1} - X_p^{-2}$, respectively being the differences in the means of two populations.

In terms of variances and covariance, the D^2 value is obtained as follow:

$$D^2p = W_{ij} (\bar{X}_i^{-1} - \bar{X}_i^{-2}) (\bar{X}_j^{-1} - \bar{X}_j^{-2})$$

Where,

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

Grouping of the genotypes into different clusters was done by using Tocher's method as described by (Rao, 1952). The criteria for clustering were that, any two populations in the same cluster should show a smaller D^2-value than those belonging to different clusters. The first step of grouping the genotypes into distinct clusters was to arrange them in order of their relative distance from each other. After arranging the D^2-values in this manner, the two populations having the smallest distance from each other were considered first, to which a third population was added having a smallest average D^2-value but higher than the previous two. Similarly, the next population was added and the process continued till the average D^2-value increased considerably with the next addition. Generally, this level should be approximately near to the maximum D^2-value shown by a population to the nearest population. At certain stage, when it was felt that after adding a particular population, if there was an abrupt increase in the average D^2, this population was not added in that cluster. Similarly, a second cluster was formed and this process was continued till all the populations were included into one or the other clusters. After formation of clusters, average inter- and intra-cluster distance values were calculated.

Average intra-cluster and inter-cluster distances were measured as under:

1. Average intra-cluster distance ($D=\sqrt{D^2}$)

$$D^2 = \frac{\sum D_i^2}{n}$$

Where,

ΣD_i^2 = Sum of distances between all possible combinations of the populations included cluster

n = Number of populations in the cluster

2. Average inter-cluster distance ($D=\sqrt{D^2}$)

$$D^2 = \frac{\sum D_{ij}^2}{n_i \times n_j}$$

Where,

ΣD_{ij}^2 = Sum of distance between all possible combinations of the two clusters

n_i= Number of populations in i^{th} cluster

n_j= Number of populations in j^{th} cluster

The inter-cluster distance was calculated by measuring the distance between cluster I and II, between I and III, between I and IV and so on. Likewise, one by one cluster was taken and their distances from each other were calculated.

The cluster means for all the 11 characters were computed using character means for the genotypes included in the clusters. Finally, per cent contribution of each character toward total genetic divergence was calculated taking into account number of time that character ranked first and expressed in percentage.

Plate no. 3.1 General view of field experiment

CHAPTER IV

EXPERIMENTAL RESULTS

The results obtained in the present investigation entitled **"Genetic variability, correlation, path analysis and genetic divergence in green gram [*Vigna radiata* (L.) R. Wilczek]"** conducted at, Pulses Research Station, Junagadh Agricultural University, Junagadh during *kharif* – 2021 are presented here under the following subheads:

4.1 ANALYSIS OF VARIANCE

The analysis of variance for all the eleven characters studied is presented in Table 4.1. The analysis of variance revealed that mean squares due to genotypes were highly significant for days to 50 % flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and seed yield per plant indicating the presence of sufficient amount of variability in the experimental material used. This indicated that there is enough scope for identifying genotypes with desirable character to improve yield.

4.2 GENETIC VARIABILITY PARAMETER

Presence of genetic variability is prerequisites for any crop improvement programme as it gives wider scope for selection. The assessment of extent of variation present in the genetic material becomes an essential step to know the magnitude of improvement that can be attained for various characters and to decide the ways to achieve it. The results of variability analysis are presented as under.

Table 4.1 Analysis of variance for eleven characters in 72 genotypes of green gram

Source of variation	d.f	Days to 50 % flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster
Replications	2	7.03	4.12*	2.48	0.31	0.15	0.03
Genotypes	71	6.07**	10.03**	120.35**	0.61	0.89	1.05
Error	142	2.36	4.59	14.18	0.11	0.08	0.10

Source of variation	d.f	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100-seeds weight (g)	Seed yield per plant (g)
Replications	2	8.18**	2.18	0.27	0.12	1.93
Genotypes	71	38.38**	3.68**	0.74	1.25	7.72**
Error	142	2.88	0.72	0.09	0.04	0.70

*, ** Significant at 5 and 1 % levels, respectively

Table 4.2 Phenotypic range, mean, range coefficient (%), genotypic coefficient of variation (%), phenotypic coefficient of variation (%), heritability, genetic advance and genetic advance as per cent of mean for eleven characters in green gram

Characters	Phenotypic range	Mean	Range coefficient (%)	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability in broad sense (%)	Genetic advance	Genetic Advance expresses as % of mean
Days to 50% flowering	35.33-41.67	38.37	8.23	2.90	3.71	61.10	1.79	4.67
Days to maturity	66.33-75.33	71.27	6.35	1.89	2.57	54.20	2.04	2.86
Plant height (cm)	48.93-73.67	59.24	20.18	10.04	10.69	88.20	11.51	19.43
Number of primary branches per plant	1.93-3.73	2.72	31.80	15.02	16.63	81.50	0.76	27.93
Number of clusters per plant	2.00-4.33	2.90	36.81	17.91	18.80	90.80	1.02	35.16
Number of pods per cluster	2.53-4.93	3.56	32.17	15.75	16.59	90.10	1.10	30.79
Number of pods per plant	13.20-28.20	17.99	36.23	19.11	19.88	92.50	6.81	37.87
Number of seeds per pod	7.67-12.60	9.86	24.32	10.09	11.24	80.50	1.84	18.65
Length of pod (cm)	6.60-8.73	7.53	13.89	6.20	6.62	87.90	0.90	11.98
100-seeds weight (g)	3.56-5.96	4.50	25.21	14.11	14.35	96.70	1.29	28.60
Seed yield per plant (g)	4.90-12.03	7.82	42.11	19.56	20.51	90.90	3.01	38.42

4.2.1 Mean performance and range

The mean value of 72 genotypes of green gram for 11 characters along with the standard error of mean (S.Em), critical difference (CD) and coefficient of variance (CV %) are given in Appendix II, the summary which is also presented in Table 4.2.

4.2.1.1 Days to 50 % flowering

The range of days to 50 % flowering in green gram was 35.33 to 41.67 days. The genotype GM 02-16 found the earliest (35.33 days) followed RMG 62 (35.67 days), GJM 1002, (35.67 days), GM 4 (36 days), GJM 1001 (36 days), GJM 1003 (36 days) and GJM 1005 (36 days). Whereas, the genotype IC 12434 took the maximum days to 50 % flowering (41.67). Out of 72 genotypes, thirty-nine genotypes were early and thirty-three genotypes were late than the mean days to 50 % flowering (38.37). The range coefficient for days to 50 % flowering was low (8.23 %).

4.2.1.2 Days to maturity

With respect to days to maturity, mean values ranged from 66.33 to 75.33 days. The genotype GJM 1001 (66.33 days) was the earliest to mature which was followed by GM 02-16 (67 days), EC 450450 (67.33), GM 4 (67.67 days) and GJM 1002 (67.67 days). The genotype IC 8917 took maximum days for maturity (75.33). Out of 72 genotypes, twenty-four genotypes were earlier and forty-eight genotypes were late than mean values (71.27). The range coefficient for days to maturity was low (6.35 %).

4.2.1.3 Plant height (cm)

The phenotypic range for plant height in material was 48.93 to 73.67 cm. The genotype GM 02-13 (48.93 cm) found the shortest followed by PANT M-5 (50.23), AKM 6802 (50.97 cm), EC 314286 (51.33 cm) and LOCAL COLLECTION 3 (51.33 cm). whereas, EC 496841 (73.67 cm) had the highest plant height. Forty, out of 72 genotypes remained above the mean value (59.24) and remaining Thirty-two genotypes below the mean value. The range coefficient for plant height was medium (20.18 %).

4.2.1.4 Number of primary branches per plant

The range for number of primary branches per plant was 1.93 to 3.73. The number of primary branches per plant was highest in GM 05-05 (3.73) followed by GJM 1004 (3.67), EC 501569 (3.47) and IC 615-5 (3.47). Whereas, minimum number of primary branches per plant was observed in K 815 (1.93). The overall mean for

number of primary branches per plant was 2.72. The range coefficient for number of primary branches per plant was high (31.80) %.

4.2.1.5 Number of clusters per plant

Among 72 genotypes, GJM 1002 possessed the maximum number of clusters per plant (4.33) followed by EC 251810 (4.20), GM 06-08 (4.07) and AKM 8803 (4.00). The number of clusters per plant ranged from 2.00 to 4.33. The mean value for number of clusters per plant was noted 2.90. The range coefficient for number of pods per plant was high (36.81 %).

4.2.1.6 Number of pods per cluster

The mean value for number of pods per cluster ranged from 2.53 to 4.93. The genotype GM 05-05 exhibited the maximum number of pods per cluster (4.93) followed by EC 251810 (4.67), GJM 1001 (4.67), GJM 1002 (4.60) and GJM 1005 (4.47). The overall mean for this character was 3.56. Out of 72 genotypes, 36 genotypes remained above the mean value while, 36 genotypes remained below the mean value. The range coefficient for number of pods per cluster was high (32.17 %).

4.2.1.7 Number of pods per plant

Number of pods per plant ranged from 13.20 to 28.20. The genotype GJM 1002 (28.20) expressed maximum number of pods per plant followed by PANT M-5 (26.27), EC 251557-A (26.27) and GM 05-05 (25.93). The mean value for Number of pods per plant was noted 17.99. The range coefficient for length of pod was high (36.23 %).

4.2.1.8 Number of seeds per pod

The mean value for number of seeds per pod ranged from 7.67 to 12.60. The genotype GJM 1005 (12.60) exhibited the maximum number of seeds per pod followed by PM 2 (12.53), LOCAL COLLECTION 2 (12.33) and IC 615-5 (12.00). The overall mean for this character was 9.86. Out of 72 genotypes, 36 genotypes remained above the mean value while, 36 genotypes remained below the mean value. The range coefficient for number of pods per cluster was medium (24.32 %).

4.2.1.9 Length of pod (cm)

Length of pod (cm) ranged from 6.60-8.73. The genotype IC 73536 (8.73) expressed maximum length of pod followed by GM 05-05 (8.57), EC 482909 (8.47), ASHA (8.40), IC 615-5 (8.40) and PANT M-4 (8.40). The genotype GM 02-16 (6.60)

and IC 8961-5 (6.60) expressed minimum length of pod. The mean value for length of pod was noted 7.52. The range coefficient for length of pod was medium (13.89 %).

4.2.1.10 100-seeds weight (g)

The range of this character was 3.56 to 5.96 g. Mean value was registered to be 4.50 g. The genotype EC 396523 (5.96 g) had the maximum 100-seeds weight followed by TARM 2 (5.85 g), EC 482907 (5.77 g) and GJM 1004 (5.76 g). On the contrary, minimum weight of 100-seedss was found in IC 24789 genotype (3.56 g). Out of 72 genotypes of green gram, 33 genotypes observed more 100-seeds weight over its mean value (4.50 g), while 39 genotypes observed less 100-seeds weight. The range coefficient for 100-seeds weight was medium (25.21 %).

4.2.1.11 Seed yield per plant (g)

The range for seed yield per plant exhibited from 4.90 to 12.03 g. The genotype GM 05-05 gave the maximum seed yield (12.03 g) followed by EC 251557-A (11.58 g), GJM 1005 (11.44 g) and PANT M-5 (11.21 g) whereas, the minimum seed yield per plant was noted by the genotype PANT M-4 (4.90). Out of 72 genotypes, 36 noticed seed yield per plant above the mean value (7.82). The range coefficient for seed yield per plant was high (42.11 %).

4.2.2 Genotypic coefficient of variation (GCV)

Genotypic coefficient of variation for all eleven characters of green gram are furnished in Table 4.2. It is also graphically presented in Figure 4.1. The highest GCV was observed for seed yield per plant (19.56 %). Seed yield per plant (19.56 %), number of pods per plant (19.11 %), number of clusters per plant (17.91 %), number of pods per cluster (15.75 %), number of primary branches per plant (15.02 %), 100-seeds weight (14.11 %), number of seeds per pod (10.09 %) and plant height (10.04 %) exhibited moderate values for GCV. Length of pod (6.20 %), days to 50 % flowering (2.89 %) and days to maturity (1.89 %) had low GCV.

4.2.3 Phenotypic coefficient of variation (PCV)

Phenotypic coefficients of variation for all eleven characters of green grem are furnished in Table 4.2. and in Figure 4.1. The highest phenotypic coefficient of variation was observed for seed yield per plant (20.51 %). Number of pods per plant (19.88 %), number of clusters per plant (18.80 %), number of primary branches per plant (16.63 %), number of pods per cluster (16.59 %), 100-seeds weight (14.35 %),

number of seeds per pod (11.24 %) and plant height (10.69 %) exhibited moderate values for PCV. Length of pod (6.62 %), days to 50 % flowering (3.71 %) and days to maturity (2.57 %) had low PCV. PCV was higher than that of GCV for all the character.

4.2.4 Heritability (broad sense)

The ratio of genotypic variance to total variance or the phenotypic variance is known as 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 character from parents to offspring. The broad sense heritability estimates for eleven characters of green gram are given in Table 4.2 as well as presented in graphical form in Figure 4.2. High heritability estimates were observed for 100-seeds weight (96.70), number of pods per plant (92.50), seed yield per plant (90.90), number of clusters per plant (90.80), number of pods per cluster (90.10), plant height (88.20), length of pod (87.90), number of primary branches per plant (81.50), number of seed per pod (80.50) and days to 50 % flowering (61.10). Days to maturity (54.20) expressed moderate heritability.

4.2.5 Genetic advance

The values of genetic advance estimated for different characters in green gram are summarized in Table 4.2. Genetic advance at 5 % selection intensity (k=2.06) was estimated for different characters. The highest genetic advance was observed for plant height (11.51). The value was moderate for number of pods per plant (6.81). Low value of genetic advance was observed for seed yield per plant (3.01), days to maturity (2.04), number of seeds per pod (1.84), days to 50 % flowering (1.79), 100-seeds weight (1.29), number of pods per cluster (1.10), number of clusters per plant (1.02), length of pod (0.90) and number of primary branches per plant (0.76).

4.2.6 Genetic advance expressed as percentage of mean

Genetic advance expressed as percentage of mean is presented in Table 4.2 as well as presented in Figure 4.2 found high for seed yield per plant (38.42 %) followed by number of pods per plant (37.87 %), number of clusters per plant (35.16 %), number of pods per cluster (30.79 %), 100-seeds weight (28.60 %) and number of primary branches per plant (27.93 %). It was moderate for plant height (19.43 %), number of seeds per pod (18.65 %) and length of pod (11.98 %). The values were low for days to 50 % flowering (4.67 %) and days to maturity (2.86 %).

4.3 CORRELATION COEFFICIENT ANALYSIS

The correlation coefficient was estimated for all the combination of eleven characters under study at genotypic level (r_g) as well as phenotypic level (r_p). The genotypic correlation coefficient was higher than that of phenotypic one for most of the traits which indicates presence of environmental influence. The data of correlation are given in Table 4.3. The results of correlation coefficient between different pairs of characters are described as under:

4.3.1 Days to 50 % flowering

Days to 50 % flowering had highly significant and positive correlation with days to maturity (r_g = 0.893) while, there was significand positive correlation with 100-seeds weight. This trait expressed highly significant and negative correlation with number of pods per cluster (r_g = -0.567), number of pods per plant (r_g = -0.502), numbers of cluster per plant (r_g = -0.456) and seed yield per plant (r_g = -0.334) at genotypic level. Positive and non- significant correlation was observed with plant height (r_g = 0.181) and negatively and non- significant correlated with number of seeds per pod (r_g = -0.171), length of pod (r_g = -0.061) and number of primary branches per plant (r_g = -0.016) at genotypic level.

Days to 50 % flowering showed positive and highly significant correlation only with days to maturity (r_p = 0.618) while, it showed negative and highly significant correlation with number of pods per cluster (r_p = -0.441), number of pods per plant (r_p = -0.396) and number of clusters per plant (r_p = -0.339) at phenotypic level. It had negative and non-significant correlation with 100-seeds weight (r_p = -0.227), number of seeds per pod (r_p = -0.087) and length of pod (r_p = -0.032) while, it showed negative and significant correlation with seed yield per plant (r_p = -0.249) at phenotypic level. For remaining characters, this trait expressed positive and non-significant correlation.

4.3.2 Days to maturity

Days to maturity had a highly significant and positive correlation with 100-seeds weight (r_g = 0.539) and plant height (r_g = 0.372) at genotypic level. This trait showed positive and significant correlation with number of seeds per pods (r_g = 0.263) while, it showed negative and highly significant correlation with number of pods per plant (r_g = -0.835), number of pods per cluster (r_g = -0.712) and number of clusters per plant (r_g = -0.673) at genotypic level. It was negatively and significant correlation with

Table 4.3 Genotypic (r_g) and phenotypic (r_p) correlation coefficients among eleven characters in green gram

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100-seed weight (g)	Seed yield per plant (g)
Days to 50% flowering	r_g	1.000	0.893**	0.181	0.016	-0.456**	-0.567**	-0.502**	-0.171	-0.061	0.289*	-0.334**
	r_p	1.000	0.618**	0.145	0.036	-0.339**	-0.441**	-0.396**	-0.087	-0.032	0.227	-0.249*
Days to maturity	r_g		1.000	0.372**	0.104	-0.673**	-0.712**	-0.835**	0.263*	0.080	0.539**	-0.267*
	r_p		1.000	0.277*	0.060	-0.515**	-0.549**	-0.593**	0.174	0.078	0.381**	-0.192
Plant height (cm)	r_g			1.000	0.191	-0.092	-0.111	-0.127	0.302**	0.336**	0.165	0.135
	r_p			1.000	0.156	-0.085	-0.107	-0.122	0.258*	0.284*	0.159	0.117
Number of primary branches per plant	r_g				1.000	0.323**	0.218	0.304**	0.118	0.165	0.201	0.458**
	r_p				1.000	0.305**	0.202	0.261*	0.101	0.133	0.196	0.395**
Number of clusters per plant	r_g					1.000	0.660**	0.818**	-0.139	0.134	-0.254*	0.469**
	r_p					1.000	0.617**	0.750**	-0.121	0.100	-0.231	0.424**
Number of pods per cluster	r_g						1.000	0.809**	-0.020	0.063	-0.290*	0.539**
	r_p						1.000	0.738**	-0.021	0.060	-0.273*	0.482**
Number of pods per plant	r_g							1.000	-0.093	0.082	-0.339**	0.612**
	r_p							1.000	-0.084	0.084	-0.320**	0.619**
Number of seeds per pod	r_g								1.000	0.341**	0.116	0.473**
	r_p								1.000	0.293*	0.099	0.486**
Length of pod (cm)	r_g									1.000	-0.026	0.250*
	r_p									1.000	-0.014	0.235*
100- seeds weight (g)	r_g										1.000	0.387**
	r_p										1.000	0.363**

*, ** Significant at 5 and 1 % levels, respectively

seed yield per plant (r_g = -0.267) at genotypic level. For remaining characters, this trait expressed positive and non-significant correlation.

Days to maturity expressed highly significant and positive correlation with 100-seeds weight (r_p = 0.381) while, it showed negative and highly significant correlation with number of pods per plant (r_p = -0.593), number of pods per cluster (r_p = -0.549) and number of clusters per plant (r_p = -0.515) at phenotypic level. Days to maturity had positive and significant correlation with plant height (r_p = 0.277). For remaining characters, this trait expressed positive and non-significant correlation.

4.3.3 Plant height

In case of plant height, highly significant positive relationship was observed with length of pod (r_g = 0.336) and number of seed per pod (r_g = 0.302) at genotypic level. But non-significant positive correlation was observed with number of primary branches (r_g = 0.191), 100-seeds weight (r_g = 0.165) and seed yield per plant (r_g = 0.135) at genotypic level. It was negatively correlated with number of pods per plant (r_g = -0.127), number of pods per cluster (r_g = -0.111) and number of clusters per plant (r_g = -0.092) at genotypic level.

Plant height showed significant and positive correlation with number of seeds per pod (r_p = 0.258) and length of pod (r_p = 0.284) at phenotypic level. This trait showed positive and non-significant correlation with 100-seeds weight (r_p = 0.159), number of primary branches (r_p = 0.156) and seed yield per plant (r_p = 0.117) at phenotypic level. It was negatively correlated with number of pods per plant (r_p = -0.122), number of pods per cluster (r_p = -0.107) and number of clusters per plant (r_p = -0.085) at phenotypic level.

4.3.4 Number of primary branches per plant

Highly significant and positive association of number of primary branches per plant was observed with seed yield per plant (r_g = 0.458), number of clusters per plant (r_g = 0.323) and number of pods per plant (r_g = 0.304) while, other trait had positive and non-significant correlation with number of primary branches per plant at genotypic level.

Positive and highly significant correlation of number of primary branches per plant was observed with seed yield per plant (r_p = 0.395) and number of clusters per plant (r_p = 0.305) while, positive and significant correlation was observed with number

of pods per plant (r_p = 0.261). Association of this trait at phenotypic level was positive and non-significant with number of pods per cluster (r_p = 0.202), 100-seeds weight (r_p = 0.196), length of pod (r_p = 0.133) and number of seeds per pod (r_p = 0.101).

4.3.5 Number of clusters per plant

The characters, number of pods per plant (r_g = 0.818), number of pods per cluster (r_g = 0.660) and seed yield per plant (r_g = 0.469) were found to be highly significant and positively associated with number of clusters per plant while, it shows negative and significant correlation with 100-seeds weight (r_g = -0.254) at genotypic level. Association of this trait was non-significant with number of seeds per pod (r_g = -0.139) and length of pod (r_g = 0.134).

At phenotypic level, number of clusters per plant had positive and highly significant correlation with number of pods per plant (r_p = 0.750), number of pods per cluster (r_p = 0.617) and seed yield per plant (r_p = 0.424) while positive and non-significant correlation was observed with length of pod (r_p = 0.100). Association of this trait was negative and non-significant with 100-seeds weight (r_p = -0.213) and number of seeds per pod (r_p = -0.121).

4.3.6 Number of pods per cluster

Number of pods per cluster had positive and highly significant correlation with number of pods per plant (r_g = 0.809) and seed yield per plant (r_g = 0.539) while, it showed negative and significant correlation with 100-seeds weigh (r_g = -0.290) at genotypic level. Other traits were non-significantly correlated with number of pods per cluster at genotypic level.

At phenotypic level, number of pods per cluster showed positive and highly significant correlation with number of pods per plant (r_p = 0.738) and seed yield per plant (r_p = 0.482) while, it showed negative and significant correlation with 100-seeds weight (r_p = -0.273). Association of this trait was non-significant with number of seeds per pod and length of pod.

4.3.7 Number of pods per plant

At genotypic level, number of pods per plant showed positive and highly significant association with seed yield per plant (r_g = 0.612). It had negative and highly significant correlation with 100-seeds weight (r_g = -0.339) at genotypic level. For remaining characters association was non-significant.

The correlation of number of pods per plant had positive and highly significant with seed yield per plant (r_p = 0.619) at phenotypic level. This character showed negative and highly significant correlation with 100-seeds weight (r_p = -0.320) at phenotypic level. For remaining characters, this trait expressed non-significant correlation.

4.3.8 Number of seeds per pod

Number of seeds per pod expressed highly significant and positive correlation with seed yield per plant (r_g = 0.473) and length of pod (r_g = 0.341) while this trait had positive and non-significant correlation with 100-seeds weight (r_g = 0.116) at genotypic level.

Positive and highly significant correlation of number of seeds per pod with seed yield per plant (r_p = 0.486) while, there was positive and significant correlation with length of pod (r_p = 0.293). It had positive and non-significant correlation with 100-seeds weight (r_p = 0.099) at phenotypic level.

4.3.9 Length of pod

This trait showed genotypically and phenotypically significant positive correlation with only one trait i.e. seed yield per plant (r_g = 0.250, r_p = 0.235). Where there was negative and non-significant correlation with 100-seeds weight (r_g = -0.026, r_p = -0.014) at both genotypic and phenotypic levels.

4.3.10 100-seeds weight

Interrelationship between 100-seeds weight and seed yield was found positive and highly significant (r_g = 0.387, r_p= 0.363) at both genotypic and phenotypic levels, respectively.

4.3.11 Seed yield per plant (g)

The characters, number of primary branches per plant (r_g = 0.458, r_p = 0.395), number of clusters per plant (r_g = 0.469, r_p = 0.424), number of pods per cluster (r_g = 0.539, r_p = 0.482), number of pods per plant (r_g = 0.612, r_p = 0.619), number of seeds per pod (r_g = 0.473, r_p = 0.486) and 100-seeds weight (r_g = 0.387, r_p = 0.363) were found to be highly significant and positively associated with Seed yield per plant while, Seed yield per plant showed positive and significant correlation with length of pod (r_g = 0.250, r_p = 0.235) at both genotypic and phenotypic levels. This trait had negative

and highly significant correlation with days to 50 % flowering (r_g = -0.334) at genotypic level and negative and significant at phenotypic level (r_p = -0.249). Days to maturity (r_g = -0.267) was significantly and negatively correlated with seed yield at genotypic level only. For remaining characters, this trait expressed non-significant association.

4.4 PATH COEFFICIENT ANALYSIS

Path analysis was carried out at genotypic and phenotypic level considering seed yield per plant as dependent variable and its attributes *viz*., days to 50 % flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod and 100-seeds weight as independent variables. Each component has two path actions *viz*., direct effect on seed yield and indirect effect through other components which are not revealed by correlation studies. The results of genotypic and phenotypic path coefficient analysis are presented in Table 4.4. The path coefficient analysis revealed the cause and effect relationship which is shown at genotypic level in Figure 4.3 and phenotypic level in Figure 4.4.

4.4.1 Genotypic path coefficient analysis

The genotypic correlation coefficients calculated for different pairs of characters were subjected to path coefficient analysis for partitioning these values into direct and indirect effects. The results obtained for direct and indirect effects of different characters on seed yield are presented in Table 4.4 and Figure 4.3.

The genotypic path coefficient analysis revealed that number of pods per plant (0.8948), 100-seeds weight (0.6174) and number of seeds per pod (0.4402) expressed positive and higher direct effect on seed yield. While, number of pods per cluster (0.0770) followed by days to maturity (0.0754), length of pod (0.0460) and number of primary branches per plant (0.0053) had moderate to low and positive direct effect on seed yield. However, negative direct effect on seed yield per plant were contributed through number of clusters per plant (-0.0723), days to 50 % flowering (-0.0380) and plant height (-0.0221) at genotypic level.

The characters which had shown significant genotypic correlation with seed yield per plant were considered for results.

Table 4.4 Genotypic and Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 72 genotypes of green gram

Characters		Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100- seeds weight (g)
Days to 50% flowering	**G**	**-0.0380**	-0.0339	-0.0069	0.0006	0.0173	0.0215	0.0191	0.0065	0.0023	-0.0110
	P	**0.0018**	0.0011	0.0003	0.0001	-0.0006	-0.0008	-0.0007	-0.0002	-0.0001	0.0004
Days to maturity	**G**	0.0674	**0.0754**	0.0280	0.0078	-0.0507	-00537	-0.0629	0.0198	0.0060	0.0406
	P	0.0006	**0.0010**	0.0003	0.0001	-0.0005	-0.0006	-0.0006	0.0002	0.0001	0.0004
Plant height (cm)	**G**	-0.0040	-0.0082	**-0.0221**	-0.0042	0.0020	0.0025	0.0028	-0.0067	-0.0074	-0.0036
	P	-0.0014	-0.0026	**-0.0095**	-0.0015	0.0008	0.0010	0.0012	-0.0024	-0.0027	-0.0015
Number of primary branches per plant	**G**	-0.0001	0.0005	0.0010	**0.0053**	0.0017	0.0012	0.0016	0.0006	0.0009	0.0011
	P	0.0005	0.0009	0.0023	**0.0147**	0.0045	0.0030	0.0038	0.0015	0.0020	0.0029
Number of clusters per plant	**G**	0.0329	0.0486	0.0067	-0.0233	**-0.0723**	-0.0477	-0.0591	0.0100	-0.0097	0.0183
	P	0.0184	0.0280	0.0046	-0.0166	**-0.0544**	-0.0336	-0.0408	0.0066	-0.0055	0.0126
Number of pods per cluster	**G**	-0.0436	-0.0548	0.0085	0.0168	0.0508	**0.0770**	0.0622	-0.0016	0.0049	-0.0224
	P	-0.0300	-0.0382	-0.0074	0.0140	0.0429	**0.0696**	0.0513	-0.0015	0.0042	-0.0190
Number of pods per plant	**G**	-0.4492	-0.7468	-0.1136	0.2720	0.7320	0.7234	**0.8948**	-0.0834	0.0732	-0.3031
	P	-0.3284	-0.4914	-0.1014	0.2161	0.6216	0.6114	**0.8290**	-0.0696	0.0693	-0.2649
Number of seeds per pod	**G**	-0.0754	0.1157	0.1330	0.0520	-0.0610	-0.0089	-0.0410	**0.4402**	0.1501	0.0510
	P	-0.0418	0.0843	0.1246	0.0488	-0.0584	-0.0103	-0.0406	**0.4837**	0.1419	0.0480
Length of pod (cm)	**G**	-0.0028	0.0037	0.0155	0.0076	0.0062	0.0029	0.0038	0.0157	**0.0460**	-0.0012
	P	-0.0011	0.0027	0.0098	0.0046	0.0034	0.0021	0.0029	0.0101	**0.0343**	-0.0005
100- seeds weight (g)	**G**	0.1787	0.3324	0.1017	0.1238	-0.1565	-0.1793	-0.2091	0.0715	-0.0158	**0.6174**
	P	0.1327	0.2226	0.0931	0.1146	-0.1352	-0.1596	-0.1867	0.0579	-0.0083	**0.5842**
Genotypic correlation with Seed yield per plant (g)	**G**	-0.334**	-0.267*	0.135	0.458**	0.469**	0.539**	0.612**	0.473**	0.250*	0.387**
Phenotypic correlation with Seed yield per plant (g)	**P**	-0.249*	-0.192	0.117	0.395**	0.424**	0.482**	0.619**	0.486**	0.235*	0.363**

*, ** Significant at 5 and 1 % levels, respectively Genotypic residual effect = 0.0755 Phenotypic residual effect = 0.1321

4.4.1.1 Days to 50% flowering Vs. seed yield per plant

Days to 50% flowering showed negative and highly significant association with seed yield per plant (r_g = -0.334) and direct effect was negative in magnitude (-0.0380). Days to 50% flowering had positive and moderate indirect effect *via* 100-seeds weight (0.1787). Days to 50% flowering had positive and low indirect effect *via* days to maturity (0.0674) and number of clusters per plant (0.0329)**,** while negative indirect effect *via* number of pods per plant (-0.4492), number of seeds per pod (-0.0754), number of pods per cluster (-0.0436), plant height (-0.0040), length of pod (-0.0028) and number of primary branches per plant (-0.0001).

4.4.1.2 Days to maturity Vs. seed yield per plant

Days to maturity exhibited negative and significant association with seed yield per plant (r_g = -0.267) and direct effect was positive and lower in magnitude (0.0754). Days to maturity had positive indirect effect *via* 100-seeds weight (0.3324), number of seeds per pod (0.1157), number of clusters per plant (0.0486), length of pod (0.0037) and number of primary branches per plant (0.0005). This trait shows negative indirect effect *via* number of pods per plant (-0.7468), number of pods per cluster (-0.0548), days to 50% flowering (-0.0339) and plant height (-0.0082).

4.4.1.3 Number of primary branches per plant Vs. seed yield per plant

This character showed positive and highly significant association with seed yield per plant (r_g = 0.458) and direct effect was positive in magnitude (0.0053). This trait shows positive indirect effect *via* number of pods per plant (0.2720), 100-seeds weight (0.1238), number of seeds per pod (0.0520), number of pods per cluster (0.0168), days to maturity (0.0078), length of pod (0.0076), and days to 50 % flowering (0.0006). Number of primary branches per plant had negative indirect effect *via* number of clusters per plant (-0.0233) and plant height (-0.0042).

4.4.1.4 Number of clusters per plant Vs. seed yield per plant

Positive and highly significant association with seed yield per plant (r_g = 0.9200) exhibited by number of clusters per plant and direct effect was negative in magnitude (-0.0723). Number of clusters per plant had positive indirect effect *via* number of pods per plant (0.7320), number of pods per cluster (0.0508), day to 50 % flowering (0.0173), length of pod (0.0062), plant height (0.0020) and number of primary branches per plant (0.0017). Number of clusters per plant had negative indirect effect *via* 100-seeds weight (-0.1565), number of seeds per pod (-0.0610) and days to maturity (-0.0507).

4.4.1.5 Number of pods per cluster Vs. seed yield per plant

Association of number of pods per cluster was positive and highly significant with seed yield per plant (r_g = 0.539) and direct effect was positive in magnitude (0.0770). Number of pods per cluster had positive indirect effect *via* number of pods per plant (0.7234), days to 50 % flowering (0.0215), length of pod (0.0029), plant height (0.0025) and number of primary branches per plant (0.0012). Number of pods per cluster had negative indirect effect *via* 100-seeds weight (-0.1793), days to maturity (-0.0537), number of clusters per plant (-0.0477) and number of seeds per pod (-0.0089).

4.4.1.6 Number of pods per plant Vs. seed yield per plant

The genotypic correlation between number of pods per plant and seed yield per plant was positive and highly significant (r_g = 0.612) and direct effect was positive in magnitude (0.8948). Number of pods per plant had positive indirect effect *via* number of pods per cluster (0.0622), days to 50 % flowering (0.0191), length of pod (0.0038), plant height (0.0028) and number of primary branches per plant (0.0016). This trait shows negative indirect effect *via* 100-seeds weight (-0.2091), days to maturity (-0.0629), number of clusters per plant (-0.0591), number of seeds per pod (-0.0410).

4.4.1.7 Number of seeds per pod Vs. seed yield per plant

Number of seeds per pod had highly significant and positive genotypic correlation with seed yield per plant (r_g = 0.473) and direct effect was positive in magnitude (0.4402). It exhibited positive indirect effect *via* 100-seeds weight (0.0715), days to maturity (0.0198), length of pod (0.0157), number of clusters per plant (0.0100), days to 50% flowering (0.0065) and number of primary branches per plant (0.0006), while negative indirect effect *via* number of pods per plant (-0.0834), plant height (-0.0067) and number of pods per cluster (-0.0016).

4.4.1.8 Length of pod Vs. seed yield per plant

Length of pod displayed positive and highly significant association with seed yield per plant (r_g = 0.250) direct effect was positive in magnitude (0.0460). This trait had positive indirect effect *via* number of seeds per pod (0.1501), number of pods per plant (0.0732), days to maturity (0.0060), number of pods per cluster (0.0049), days to 50 % flowering (0.0023) and number of primary branches per plant (0.0009). It showed negative indirect effect *via* 100-seeds weight (-0.0158), number of clusters per plant (-0.0097) and plant height (-0.0074).

4.4.1.9 100-seed weight Vs. seed yield per plant

100-seed weight exhibited positive and highly significant association with seed yield per plant (r_g = 0.387) and direct effect was positive in magnitude (0.6174). This trait had positive indirect effect *via* number of seeds per pod (0.0510), days to maturity (0.0406), number of clusters per plant (0.0183) and number of primary branches per plant (0.0011). It exhibited negative indirect effect *via* number of pods per plant (-0.3031), number of pods per cluster (-0.0224), days to 50 % flowering (-0.0110), plant height (-0.0036) and length of pod (-0.0012).

The residual effect was found to be 0.0755 at genotypic path coefficient analysis.

4.4.2 Phenotypic path coefficient analysis

The phenotypic path coefficient analysis (Table 4.4) revealed that number of pods per plant (0.8290), 100-seeds weight (0.5842) and number of seeds per pod (0.4837) expressed positive and higher direct effect on seed yield. While, number of pods per cluster (0.0696) followed by length of pod (0.0343), number ofbranches per plant (0.0147) days to 50 % flowering (0.0018) and days to maturity (0.0010) had moderate to low and positive direct effect on seed yield. However, negative direct effect on seed yield per plant were contributed through number of clusters per plant (-0.0544) and plant height (-0.0095) at phenotypic level.

The characters which had shown significant phenotypic correlation with seed yield per plant were considered for results and discussion.

4.4.2.1 Days to 50 % flowering *vs* seed yield per plant

Days to 50 % flowering had negative and significant association with seed yield per plant (r_p = -0.249). This trait also exhibited positive and low (0.0018) direct effect on seed yield in phenotypic path coefficient analysis. Positive indirect effect on seed yield per plant was contributed *via* 100-seeds weight (0.1327), number of clusters per plant (0.0184), days to maturity (0.0006), number of primary branches per plant (0.0005). This trait had negative indirect effects *via* number of pods per plant (-0.3284), number of seeds per pod (-0.0418), number of pods per cluster (-0.0300), plant height (-0.0014) and length of pod (-0.0011).

4.4.2.2 Number of primary branches per plant *vs* seed yield per plant

Number of primary branches per plant had positive and highly significant association with seed yield per plant (r_p= 0.395). This trait also exhibited positive direct effect (0.0147) on seed yield per plant. Number of primary branches per plant had positive indirect effect on seed yield per plant *via* number of pods per plant (0.2161), 100-seeds weight (0.1146), number of seeds per pod (0.0488), number of pods per cluster (0.0140), length of pod (0.0046), days to 50 % flowering (0.0001) and days to maturity (0.0001). However negative and negligible indirect effect was observed *via* number of clusters per plant (-0.0166) and plant height (-0.0015).

4.4.2.3 Number of clusters per plant *vs* seed yield per plant

Number of clusters per plant had positive and highly significant association with seed yield per plant (r_p= 0.424). This trait also exhibited negative direct effect (-0.0544) on seed yield per plant. Number of clusters per plant had positive indirect effect on seed yield per plant *via* number of pods per plant (0.6216), number of pods per cluster (0.0429), number of primary branches per plant (0.0045), length of pod (0.0034) and plant height (0.0008). However, negative and negligible indirect effect was observed *via* 100-seeds weight (-0.1352) followed by number of seeds per pod (-0.0584), days to 50 % flowering (-0.0006) and days to maturity (-0.0005).

4.4.2.4 Number of pods per cluster *vs* seed yield per plant

Number of pods per plant exhibited positive and highly significant association with seed yield per plant (r_p= 0.482). This trait also exhibited positive direct effect (0.0696) on seed yield per plant. This trait showed positive and high indirect effect *via* number of pods per plant (0.6114). Number of pods per cluster showed positive and negligible indirect effect *via* number of primary branches per plant (0.0030), length of pod (0.0021) and plant height (0.0010) while, it showed negative indirect effect *via* 100-seeds weight (-0.1596), number of clusters per plant (-0.0336), number of seeds per pod (-0.0103), days to 50 % flowering (-0.0008) and days to maturity (-0.0006).

4.4.2.5 Number of pods per plant *vs* seed yield per plant

Number of pods per plant showed positive and highly significant association with seed yield per plant (r_p= 0.619) and direct effect was positive and higher in magnitude (0.8290). Number of pods per plant had positive indirect effect *via* number of pods per cluster (0.0513), number of primary branches per plant (0.0038), length of

pod (0.0029) and plant height (0.0012). While negative and negligible indirect effect *via* number of clusters per plant (-0.0408), number of seeds per pod (-0.0406), days to 50 % flowering (-0.0007) and days to maturity (-0.0006). Number of pods per plant showed negative and moderate indirect effect on seed yield *via* 100-seeds weight (-0.1867).

4.4.2.6 Number of seeds per pod *vs* seed yield per plant

Number of seeds per pod exhibited positive and highly significant association with seed yield per plant (r_p= 0.486) and direct effect was positive and higher in magnitude (0.4837). This trait shows positive and low indirect effect *via* 100-seeds weight (0.0579), length of pod (0.0101), number of clusters per plant (0.0066), number of primary branches per plant (0.0015) and days to maturity (0.0002). Number of seeds per pod showd negative indirect effect *via* number of pods per plant (-0.0696) while, it was negative and negligible for plant height (-0.0024), number of pods per cluster (-0.0015) and days to 50 % flowering (-0.0002).

4.4.2.7 Length of pod *vs* seed yield per plant

Length of pod exhibited positive and significant association with seed yield per plant (r_p = 0.235) and it also exhibited positive direct effect (0.0343) on seed yield per plant. It expressed positive and low indirect effect *via* number of seeds per pod (0.1419), while it exerted positive and negligible indirect effect *via* number of pods per plant (0.0693), number of pods per cluster (0.0042), number of primary branches per plant (0.0020) and days to maturity (0.0001). Length of pod showed negative and negligible indirect effect *via* 100-seeds weight (-0.0083), number of clusters per plant (-0.0055), plant height (-0.0027) and days to 50 % flowering (-0.0001).

4.4.2.8 100-seeds weight *vs* seed yield per plant

100-seeds weight exhibited positive and highly significant association with seed yield per plant (r_p= 0.363) and direct effect was positive and higher in magnitude (0.5842). 100-seeds weight had positive indirect effect *via* number of seeds per pod (0.0480), number of clusters per plant (0.0126), number of primary branches per plant (0.0029), days to maturity (0.0004) and days to 50 % flowering (0.0004). While, it expressed negative indirect effect *via* number of pods per plant (-0.2649), number of pods per cluster (-0.0190), plant height (-0.0015) and length of pod (-0.0005) on seed yield per plant.

The residual effect was found to be 0.1321 at phenotypic path coefficient analysis.

4.5 GENETIC DIVERGENCE

The analysis of variance revealed that the differences among the mean square due to genotypes were highly significant for all the characters indicating the presence of high amount of genetic variability for all the 11 characters studied. The D^2 values between all possible pairs indicated the presence of greater diversity among the genotypes for all the traits. Genetic divergence along with genetic variability is of the greatest interest to the plant breeder as they play a vital role in forming a successful breeding programme. In the present investigation genetic divergence has been studied according to the suggested by Mahalanobis D^2 statistics.

4.5.1 Composition of clusters

Grouping of the genotypes into different clusters was done by using Tocher's method as described by Rao (1952) with the assumption that the genotypes within cluster have smaller D^2 values among themselves than those from groups belonging to different clusters.

In the present investigation, 12 different clusters are made from 72 genotypes which are given in Table 4.5. Cluster diagram showing inter and intra cluster distance among 12 clusters in Figure 4.5. The cluster II having highest number of genotypes (20) followed by cluster I (18) cluster VI (12) and cluster V (11). On the other hand, cluster III, cluster IV, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters.

Table 4.5: Grouping of 72 green gram genotypes with clustering pattern in various clusters on the basis of D^2 statistics

Cluster	Total number of genotypes	Name of the genotypes
I	18	GM 4, AKM 6802, Kopergaon, TARM 18, VAIBHAV, GM 1918, GM 1925, GM 1926, GM 02-13, GM 2K-5, RMG 268, GM 3, EC 450446, EC 501566, IC 8961-5, LOCAL COLLECTION-3, GJM 1007 and GJM 1009

II	20	K 851, BPMR 145, TARM 1, GM 1924, GM 02-16, GM 2K-3, RMG 62, OUM 11-5, CO 5, CO 6, PANT M-2, EC 314286, EC 450450, IC 24789, LOCAL COLLECTION-1, LOCAL COLLECTION - 2, GM 04-02, GM 04-04, GM 05-08 and GJM 1003
III	1	GM 02-16
IV	1	ASHA
V	11	J 781, GM 02-12, GM 02-15, TARM 2, EC 396523, EC 482907, EC 482908, EC 486839, IC8917, GJM 1004 and GJM 1010
VI	12	COGG 912, AKM 8803, PANT M-3, EC 251810, EC 496841, EC 501569, IC 12434, IC 73536, GM 05-05, GM 06-08, GJM 1001 and GJM 1002
VII	1	PM 2
VIII	1	GJM 1006
IX	1	GJM 1008
X	4	PANT M-5, EC 251557-A, EC 482909 and IC 615-5
XI	1	PANT M-4
XII	1	GJM 1005

4.5.2 Average intra and inter-cluster distances among 12 clusters in green gram

The intra and inter-cluster distances are shown in Table 4.6. The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81). The minimum inter-cluster distance was observed between cluster VIII and IX (D = 4.36) followed by cluster IV and XI (D = 5.88), cluster III and VI (D = 5.92), cluster VII and IX (D = 6.15), cluster I and VII (D = 6.43) and cluster I and VIII (D = 6.44). The intra-cluster distance (D) ranged from 5.55 (cluster I) to 7.81 (cluster X). The clusters III, IV, VII, VIII, IX, XI and XII contained only single genotype and therefore, their intra-cluster distance was zero.

Table 4.6: Average inter and intra-cluster (diagonal and bold) distance ($D = \sqrt{D^2}$) values for 72 genotypes of green gram

Cluster	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII
I	**5.55**	8.58	10.24	11.33	8.51	10.19	6.43	6.44	7.37	8.32	10.35	11.41
II		**5.92**	7.07	7.05	13.48	7.99	8.08	8.13	9.59	10.16	7.65	16.22
III			**0.00**	7.25	14.04	5.92	9.19	9.83	11.23	9.35	10.08	16.59
IV				**0.00**	15.89	9.33	9.89	9.89	10.16	12.29	5.88	19.16
V					**6.69**	13.72	9.32	9.72	9.11	9.30	14.85	8.30
VI						**7.40**	9.63	9.91	11.42	9.39	10.68	15.81
VII							**0.00**	6.69	6.15	8.06	10.58	11.20
VIII								**0.00**	4.36	8.54	8.92	12.45
IX									**0.00**	8.81	8.96	11.91
X										**7.81**	11.98	10.63
XI											**0.00**	18.01
XII												**0.00**

4.5.3 Cluster means of various characters

The cluster means for 11 characters are presented in Table 4.7. The coefficient of variation (CV %) was calculated for of all the attributes. High coefficient of variation was recorded for number of primary branches per plant (12.38 %) followed by seed yield per plant (10.70 %), number of clusters per plant (9.89 %), number of pods per plant (9.44 %), number of pods per cluster (9.05 %), number of seeds per pod (8.59 %), plant height (6.36 %), 100-seeds weight (4.48 %), days to 50% flowering (4.00 %), length of pod (3.98 %) and days to maturity (3.01 %). Greater range of mean values among the clusters was recorded for different traits.

Days to 50% flowering had the minimum cluster mean in cluster III (35.33) followed by cluster XII (36.00), Cluster IV (37.00), cluster VII (37.67) and cluster VI (38.03). Days to maturity had the minimum cluster mean in cluster III (67.00) followed by cluster VI (70.31), cluster II (70.68), cluster X (71.17) and I (71.63). Plant height had the minimum cluster mean (54.23) in cluster VII followed by cluster I (56.10), cluster II (56.85) and cluster XI (59.63). Number of primary branches per plant had the maximum cluster mean (3.13) in cluster XI followed by cluster XII (3.07), cluster X (2.97), cluster VI (2.96) and cluster V (2.79). Number of clusters per plant had the maximum cluster mean (3.93) in cluster III followed by cluster VI (3.54), cluster IV (3.07), cluster VII (3.00) and cluster X (2.97). Number of pods per cluster had the maximum cluster mean (4.47) in cluster XII followed by cluster VI (4.16), cluster III (3.87), cluster X (3.78) and cluster II (3.62). Number of pods per plant had the maximum cluster mean (22.73) in cluster III followed by cluster VI (22.42), cluster X (21.67), cluster II (17.48) and cluster XII (16.87). Number of seeds per pod had the maximum cluster mean (12.60) in cluster XII followed by cluster VII (12.53), cluster IX (11.60), cluster X (10.72) and cluster VIII (10.67). Length of pod had the maximum cluster mean (8.40) in cluster IV and XI followed by cluster IX (8.27), cluster X (7.98), cluster VII (7.73) and cluster XII (7.73). 100-seeds weight had the maximum cluster mean (5.57) in cluster V followed by cluster XII (5.45), cluster IX (4.87), cluster X (4.78) and cluster I (4.75). Seed yield per plant had the maximum cluster mean (11.44) in cluster XII followed by cluster X (10.40), cluster VI (8.83), cluster VII (8.79) and cluster III (8.68).

Table 4.7: Cluster mean for 11 different characters in 72 genotypes of green gram

Clusters	Days to 50% flowering	Days to maturity	Plant height (cm)	Number of primary branches per plant	Number of clusters per plant	Number of pods per cluster	Number of pods per plant	Number of seeds per pod	Length of pod (cm)	100-seeds weight (g)	Seed yield per plant (g)
I	38.57	71.63	56.10	2.71	2.66	3.32	16.14	9.59	7.18	4.75	7.28
II	38.18	70.68	56.85	2.56	2.87	3.62	17.48	9.68	7.50	3.92	6.75
III	35.33	67.00	64.00	2.67	3.93	3.87	22.73	9.60	7.63	3.99	8.68
IV	37.00	73.00	60.83	2.27	3.07	2.87	15.87	9.20	8.40	3.64	5.45
V	38.85	72.33	60.52	2.79	2.78	3.35	16.45	9.76	7.64	5.57	8.67
VI	38.03	70.31	63.40	2.96	3.54	4.16	22.42	9.86	7.61	4.09	8.83
VII	37.67	72.67	54.23	2.00	3.00	3.47	15.60	12.53	7.73	4.51	8.79
VIII	39.33	74.00	71.90	2.20	2.13	2.80	15.07	10.67	7.23	4.55	7.32
IX	39.67	73.67	67.60	2.13	2.07	2.53	13.47	11.60	8.27	4.87	7.61
X	38.75	71.17	63.10	2.97	2.97	3.78	21.67	10.72	7.98	4.78	10.40
XI	41.00	71.67	59.63	3.13	2.13	2.73	13.20	9.00	8.40	3.80	4.90
XII	36.00	72.67	61.47	3.07	2.33	4.47	16.87	12.60	7.73	5.45	11.44
Mean	38.37	71.27	59.24	2.72	2.90	3.56	17.99	9.86	7.52	4.50	7.82
SEm ±	0.88	1.24	2.17	0.19	0.17	0.19	0.98	0.49	0.17	0.12	0.48
CV %	4.00	3.01	6.36	12.38	9.89	9.05	9.44	8.59	3.98	4.48	10.70
Per cent contribution of characters towards total genetic divergence											
No. of times ranked first	10	3	213	84	197	99	285	97	231	660	677
Contribution (%)	0.39	0.12	8.33	3.29	7.71	3.87	11.15	3.79	9.04	25.82	26.49

The analysis of per cent contribution of various characters towards the expression of total genetic divergence (Table 4.7 and Figure 4.6) indicated that seed yield per plant contributed the maximum (26.49 %) towards total divergence followed by 100-seeds weight (25.82 %), number of pods per plant (11.15 %), length of pod (9.04 %), plant height (8.33 %), number of clusters per plant (7.71 %), number of pods per cluster (3.87 %), number of seeds per pod (3.79 %) and number of primary branches per plant (3.29 %). These nine characters accounted for more than 99% of total divergence in the material studied. Days to 50 % flowering (0.39 %) and days to maturity (0.12 %) had very little contribution towards total divergence.

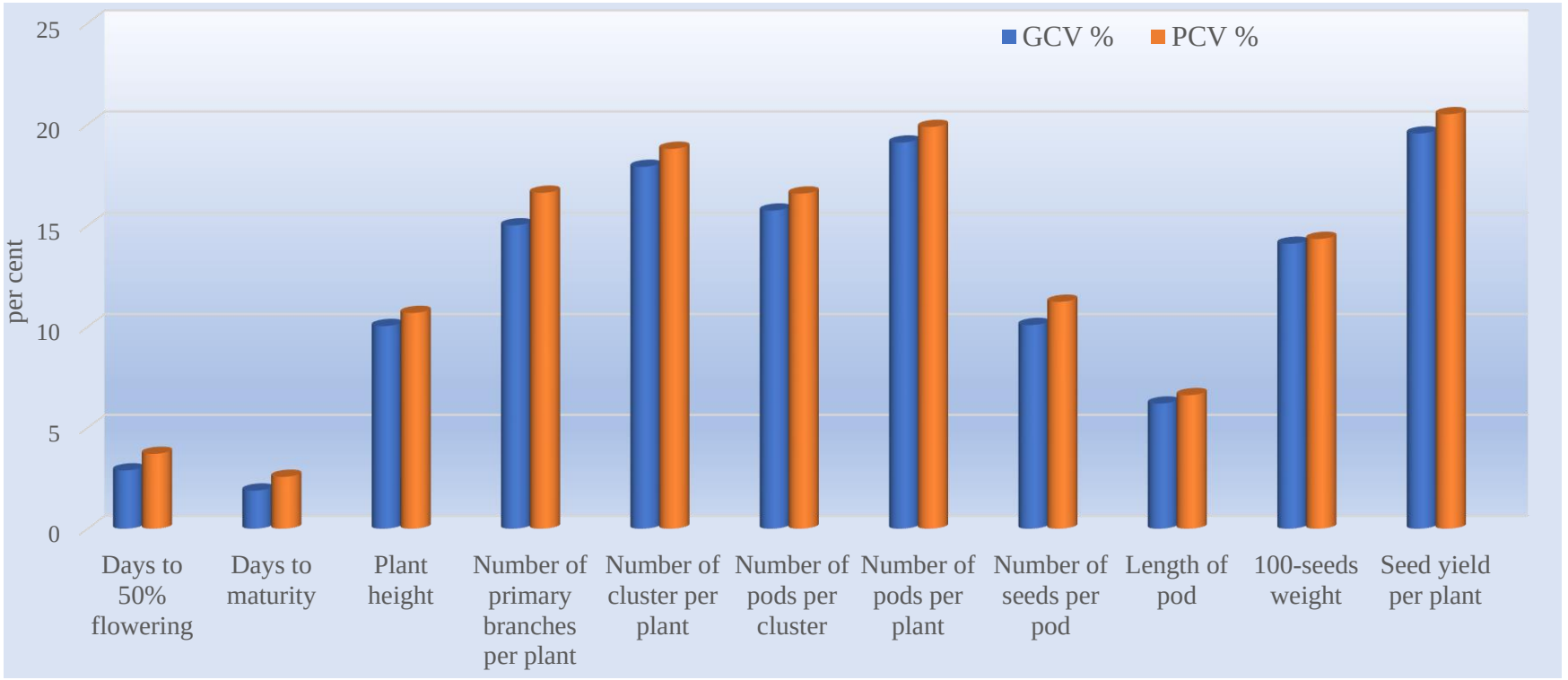

Figure 4.1: Graphical representation of genotypic and phenotypic coefficients of variation for various characters in green gram

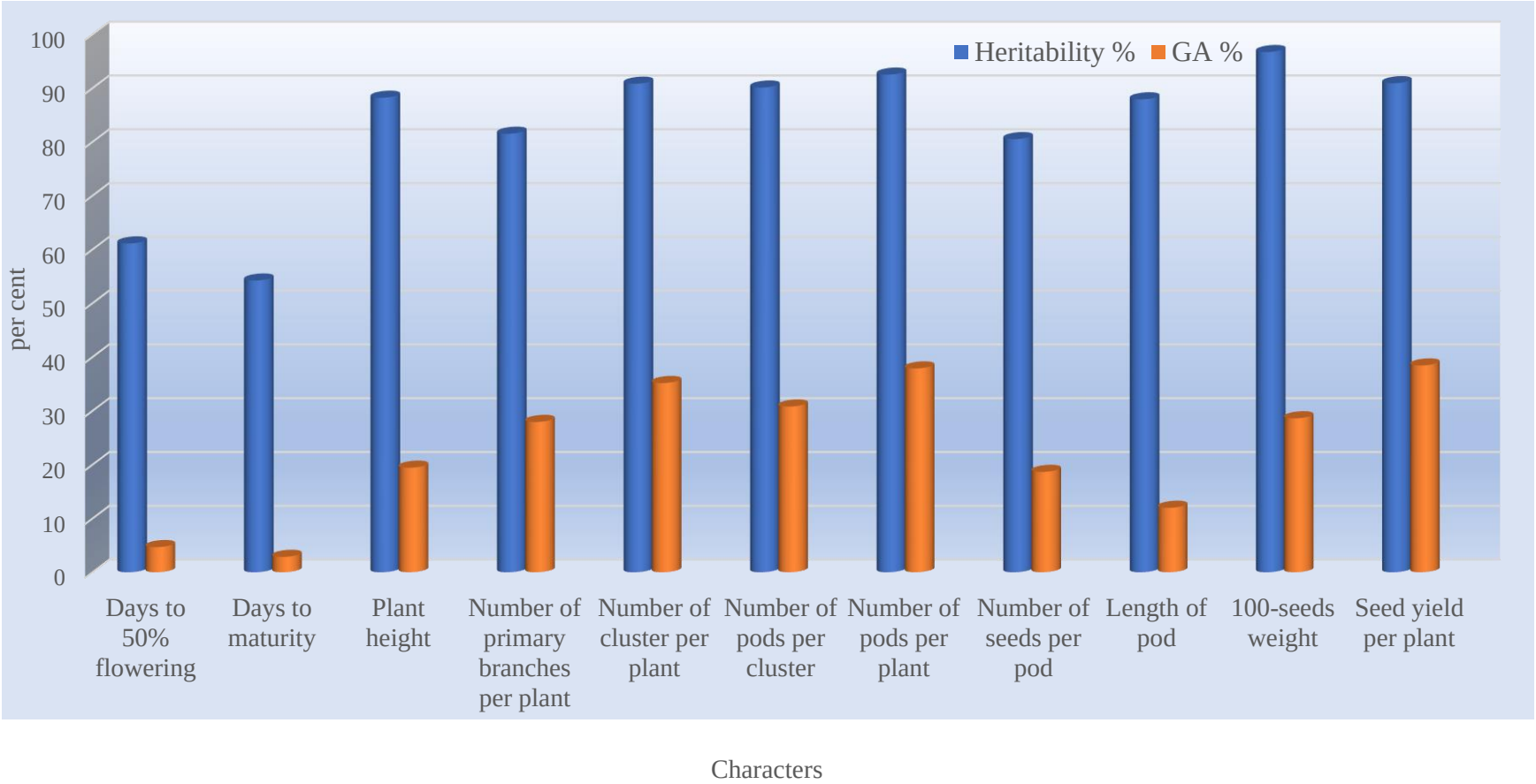

Figure 4.2: Graphical representation of heritability (broad sense) and genetic advance expressed as per cent of mean for various characters in green gram

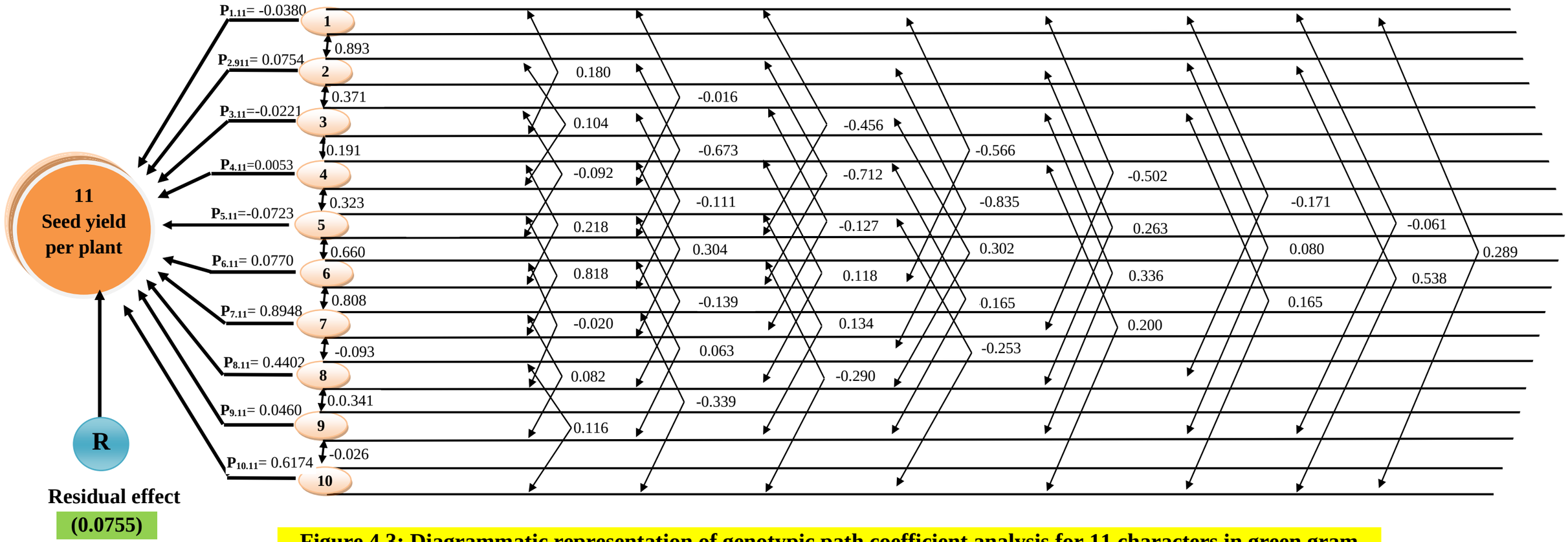

Figure 4.3: Diagrammatic representation of genotypic path coefficient analysis for 11 characters in green gram

Characters

1. **Days to 50% flowering**
2. **Days to maturity**
3. **Plant height (cm)**
4. **Number of primary branches per plant**
5. **Number of clusters per plant**
6. **Number of pods per cluster**
7. **Number of pods per plant**
8. **Number of seeds per pod**
9. **Length of pod (cm)**
10. **100-seeds weight (g)**
11. **Seed yield per plant (g)**

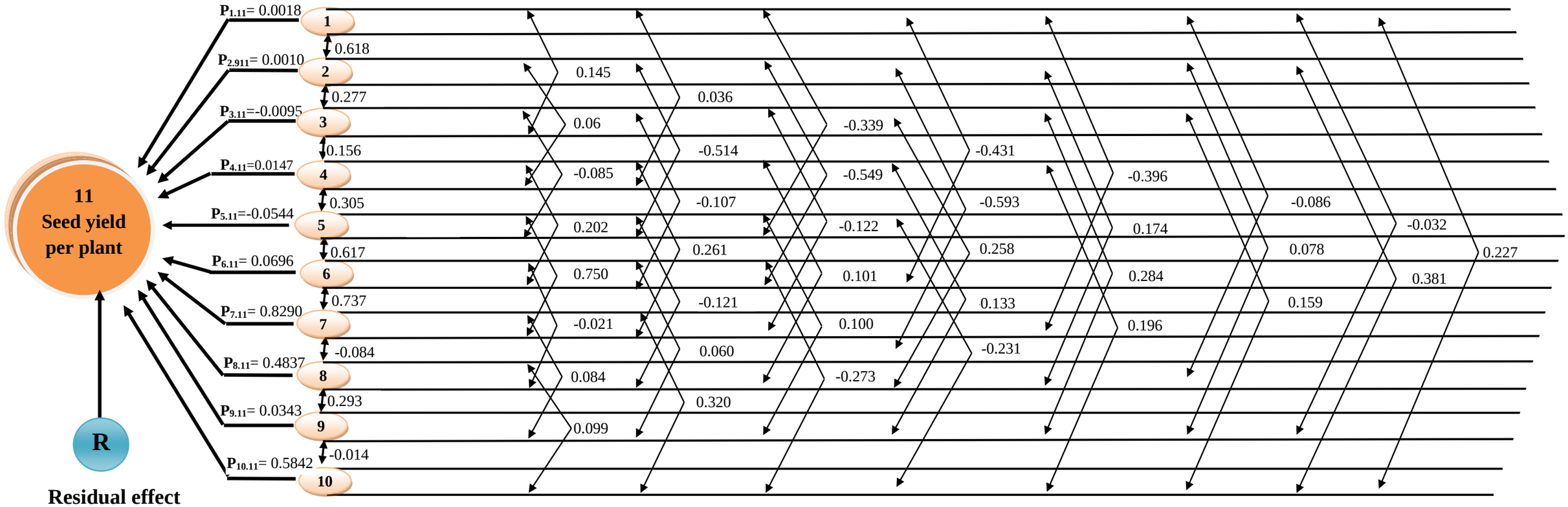

Figure 4.4: Diagrammatic representation of phenotypic path coefficient analysis for 11 characters in green gram

Characters

1. **Days to 50% flowering**
2. **Days to maturity**
3. **Plant height (cm)**
4. **Number of primary branches per plant**
5. **Number of clusters per plant**
6. **Number of pods per cluster**
7. **Number of pods per plant**
8. **Number of seeds per pod**
9. **Length of pod (cm)**
10. **100-seeds weight (g)**
11. **Seed yield per plant (g)**

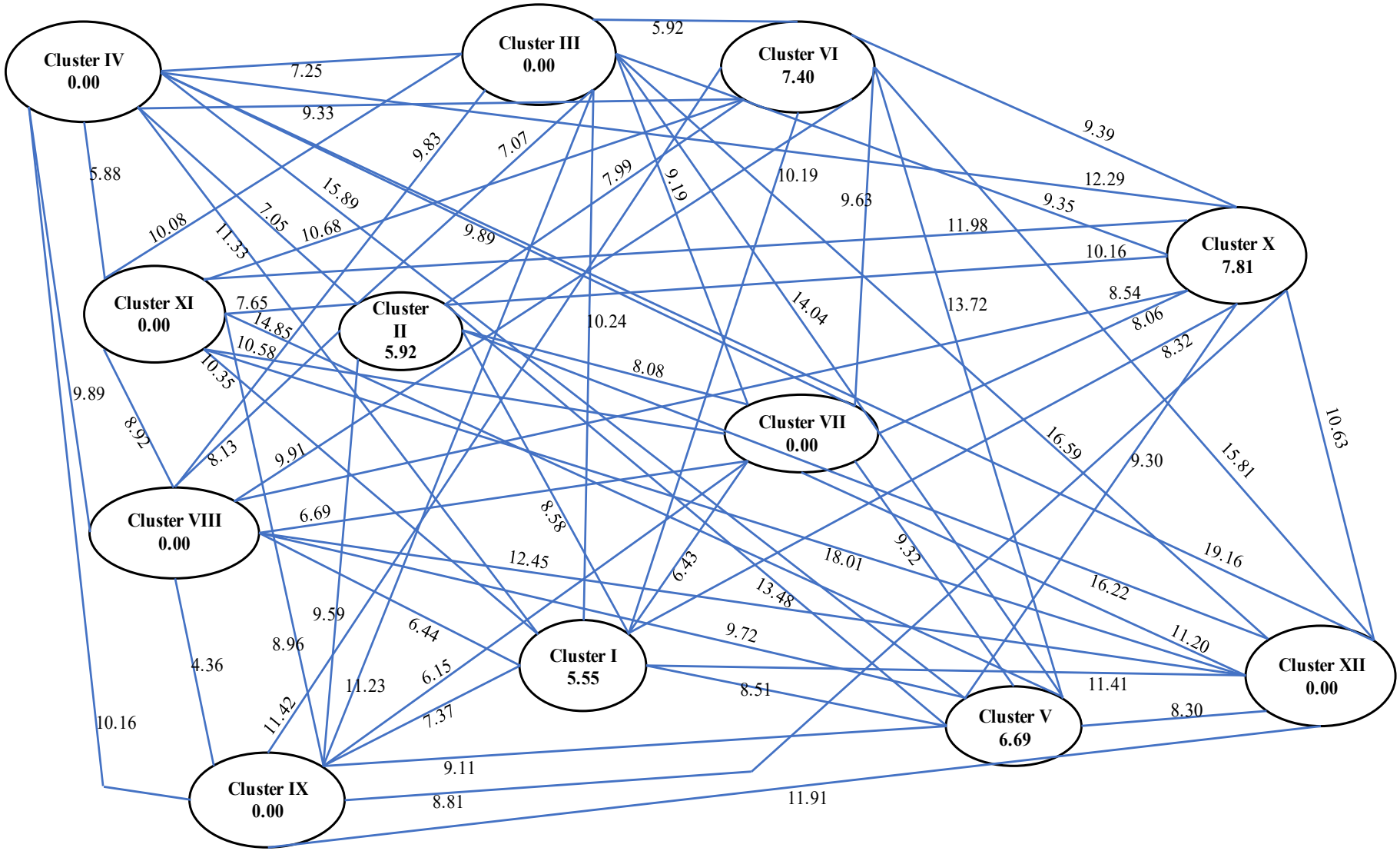

Figure 4.5: Cluster diagram showing inter and intra cluster distance in green gram

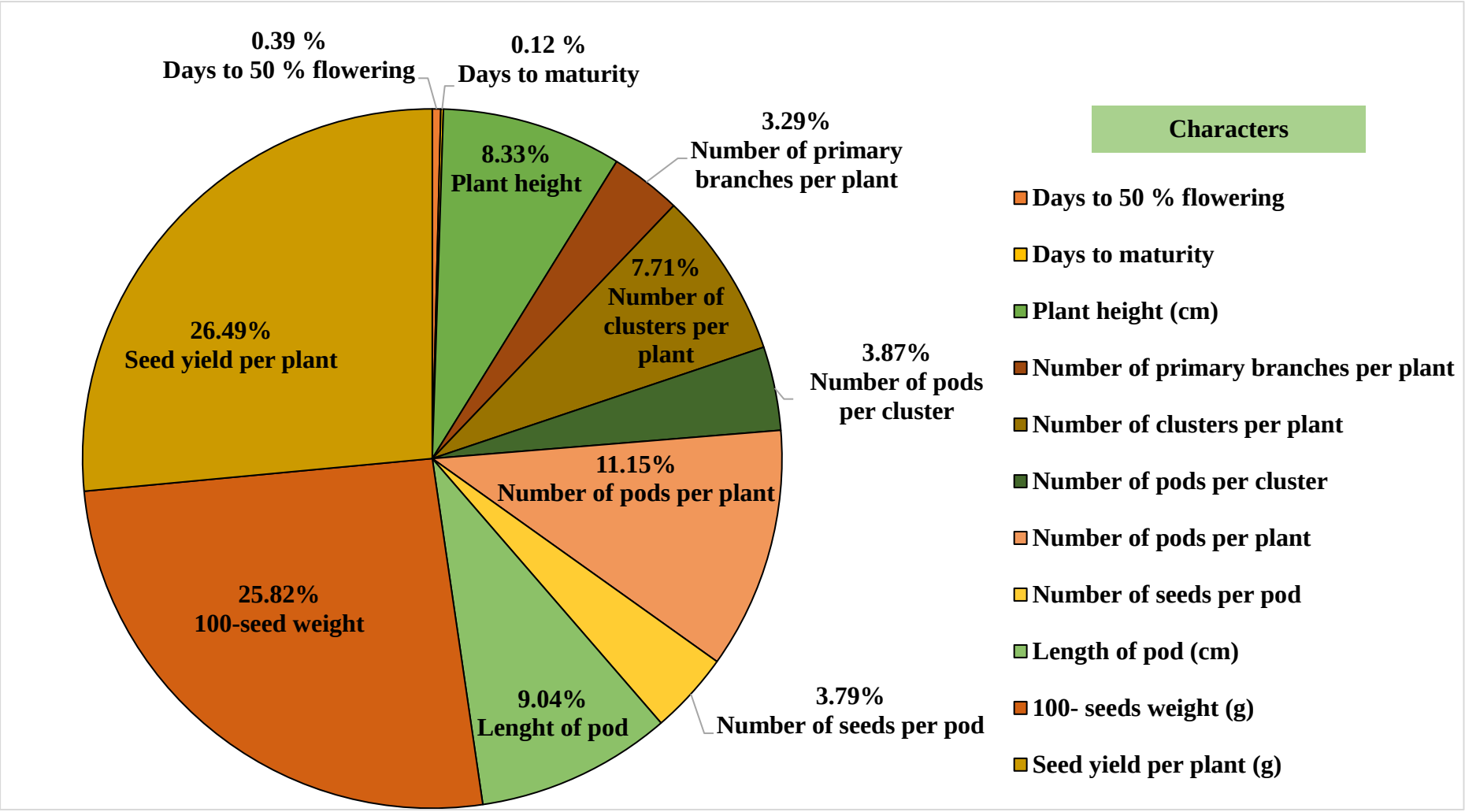

Figure 4.6: Graphical representation of per cent contribution of different characters towards total genetic divergence

CHAPTER V
DISCUSSION

Towards increasing sustainable agricultural growth and enhancing agricultural productivity, food legumes deserve special attention, as they are the third largest family of higher plants and second to cereal crops in agricultural importance. Despite the fact that grain legumes possess the outstanding features such as high protein almost twice than wheat and thrice than rice and mineral content and serve as an important source of nitrogen for the soil. Global population explosion is triggering the serious problem of malnutrition. Pulses are one of the reliable options to overcome malnutrition. They are major sources of inexpensive plant-based proteins, vitamins, minerals and dietary fibers, besides having low fat content, zero cholesterol and gluten and consequently have got significant place in the human meal where vegetarian diet is predominant.

A logical way to start any new comprehensive breeding programme is to survey the kind of variation present in the available germplasm. For effective selection, genetic variability must be present in the material. Thus, the success of breeding programme depends upon choosing breeding stocks that have sufficient variability. Classification of total variability into its heritable and nonheritable components such as phenotypic and genotypic coefficient of variations, heritability estimates and expected genetic advance are of paramount importance in understanding the genetic makeup of any breeding material under improvement.

The information on genetic variability and character association contributes with grain yield and among itself is of considerable importance in selection for elite genotype as well as exploitation of heterosis breeding programme. A study on genetic variability and correlation alone are not enough to give an exact figure of relative importance of direct and indirect influence of each of the component traits on seed yield. In such case, path coefficient analysis is an important technique for partitioning the correlation coefficient in to direct and indirect effect of independent variables on dependent variable. The information on genetic variability, correlation and path analysis may be helpful to the breeder for planning suitable selection criteria for enhancing the genetic yield potential of the green gram. Genetic diversity plays an important role because hybrids between lines of diverse genetic background generally

display a greater heterosis than those between closely related parents and may generate broad-spectrum genetic variability in segregating generation. Estimate of the genetic divergence helps in identification of genotypes as potential parents for hybridization programme.

The present study was conducted to assess genetic variability, heritability along with genetic advance, correlation coefficient, path coefficient analysis and genetic divergence on yield and its component characters to provide necessary information that could be useful in green gram improvement programs aimed at improving seed yield.

5.1 ANALYSIS OF VARIANCE

In the present experiment, 72 green gram genotypes were studied to assess their performance in terms of traits implicated to seed yield. The analysis of variance (Table 4.1) revealed that mean squares due to genotypes were highly significant for days to 50 % flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and seed yield per plant indicating the presence of sufficient amount of variability in the experimental material used. These findings are in accordance with the findings of Makeen *et al.* (2007); Kumar *et al.* (2010) and Garg *et al.*(2017a) indicating adequate genetic variability among the genotype which provide ample scope for identifying genotypes with desirable character to improve yield, provided the material be subjected to sensible pressure. It reveals that the selection of superior genotypes for development of new varieties may be helpful.

5.2 GENETIC VARIBILITY PARAMETER

Genetic variability is basic tool for crop improvement due to its wider scope for selection. Therefore, the effectiveness of selection depends upon the nature and magnitude of genetic variability present in the experiment material and the extent of its heritability. The only phenotypic variation is not the precise criterion to estimate the amount of genetic variability present in breeding population and is not comparable among various traits. The other parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance as expressed as percentage of mean are important to study the extent genetic variability parameter more precisely.

5.2.1 Genotypic and phenotypic coefficients of variation

The better index for measuring the genetic variation is genetic coefficient of variation (GCV) as described by Burton (1952) for comparing the genetic variability

present in different traits. Close relationship between genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for all the characters in present study (Table 4.2). The magnitude of PCV was slightly greater than GCV for all the traits, revealed a very little influence of environmental variation for their expression. This indicated that phenotypic variability may be considered as reliable measure of genotypic variability. The range of GCV was 1.89 % to 19.56 % whereas, it was 2.57 % to 20.51 % for phenotypic coefficient of variation indicating extent of GCV and PCV in the material studied. This finding are in agreement with earlier reports of Tabasum *et al*. (2010), Ruturi *et al*. (2015), Mathuswamy *et al*. (2019), Mohammed *et al*. (2020) and Dhunde *et al*. (2021a).

The high phenotypic coefficient of variation was observed for seed yield per plant (20.51 %). High value of phenotypic coefficient of variation for seed yield per plant was also reported by Makeen *et al*. (2007), Ruturi *et al*. (2015), Kate *et al*. (2017), Yadav *et al*. (2017), Abbas *et al*. (2018), Asari *et al*. (2019) and Abhisheka and Mogali (2020).

In the present study moderate value for genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) was observed for plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight. In addition to this, the characters seed yield per plant also exhibited moderate value for genotypic coefficient of variation only. The moderate GCV and PCV for plant height, 100-seeds weight, number of pods per cluster, number of seeds per pod was reported by Asari *et al*. (2019). Moderate GCV and PCV for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster and 100-seeds weight were in agreement of Abhisheka and Mogali (2020). While Tabasum *et al*. (2010) reported moderate GCV and PCV for number of pods per plant and moderated GCV for seed yield per plant.

Low value for phenotypic and genotypic coefficient of variation was observed for days to 50% flowering, days to maturity and length of pod. This findings are in accordance with Dangi *et al*. (2017), Yadav *et al*. (2017) and Dhunde *et al*. (2021a). Kumar *et al*. (2010) and Asari *et al*. (2019) reported low values for days to 50 % flowering and days to maturity.

The characters showed moderate genotypic and phenotypic coefficient of variation indicated that selection would be effective based on the heritable nature of these traits. Low values of genotypic and phenotypic coefficient of variation indicated low range of variation for characters in the genotypes, thus offering little scope for further improvement of these characters through simple selection.

5.2.2 Heritability

The genotypic coefficient of variation (GCV %) does not reflect the amount of heritable variation. Thus, the knowledge of heritability of a character helps the plant breeders in predicting the genetic advance for any quantitative characters and aids in exercising necessary selection procedure. Burton (1952) suggested that genotypic coefficient of variation together with heritability estimate would give the best picture expected for selection.

In present study, high heritability (>60 %) in broad sense estimates (Table 4.2) were observed for 100-seeds weight followed by number of pods per plant, seed yield per plant, number of clusters per plant, number of pods per cluster, plant height, length of pod, number of primary branches per plant, number of seeds per pod and days to 50 % flowering. Similar conclusion is derived by Muthuswamy *et al*. (2019). Abbas *et al*. (2018) for plant height, number of clusters per plant, number of pods per plant, 100-seeds weight and seed yield per plant; Mohammed *et al*. (2020) for number of branches per plant, days to 50 % flowering, 100-seeds weight, plant height, pod length, seed yield per plant, number of pods per plant and number of seeds per pod.

Moderate heritability in broad sense estimates was observed for days to maturity. This finding in agreement with earlier report of Abbas *et al.* (2018). Moderate heritability indicated that this trait is more affected by environment and under the control of non-additive gene action.

Heritability of a metric character is a parameter of particular significance to the breeder as it measures the degree of resemblance between the parents and the off-springs and its magnitude indicates the efficacy with which a genotype can be identified by its phenotypic expression. The characters which exhibited high heritability suggests that the selection would be more effective, whereas the traits showing low heritability indicates that the selection would be influenced by the environmental factors.

5.2.3 Genetic advance expressed as per cent of mean

The genetic advance expressed as per cent of mean was high (>20 %) for seed yield per plant (38.42 %) followed by number of pods per plant (37.87 %), number of clusters per plant (35.16 %), number of pods per cluster (30.79 %), 100-seeds weight (28.60 %) and number of primary branches per plant (27.93 %). Similar finding also reported by Muthuswamy *et al.* (2019). Garg *et al*. (2017a) for number of branches per plant, 100-seeds weight and seed yield per plant. The similar results were corroborated by Ruturi *et al*. (2015) for seed yield per plant and number of pods per plant. The highest values of genetic advance expressed as per cent of mean have been reported in green gram for seed yield per plant by Makeen *et al*. (2007), Katiyar *et al*. (2015) and Dangi *et al*. (2017).

The moderate estimate of genetic advance as per cent of mean (10-20 %) was observed for the plant height (19.43 %), number of seeds per pod (18.65 %) and length of pod (11.98 %). Result are in conformity of Mohammed *et al*. (2020) for number of seeds per pod and length of pod; Katiyar *et al*. (2015) and Dangi *et al*. (2017) for plant height and length of pod.

The lower genetic advance as per cent of mean (< 10 %) was observed for the days to 50% flowering (4.67 %) and days to maturity (2.86 %). The similar finding was also reported by Dangi *et al*. (2017). Baisakh *et al*. (2016) for days to 50% flowering. Katiyar *et al*. (2015) and Abbas *et al*. (2018) for days to maturity.

In the present investigation, the estimates of high heritability coupled with high genetic advance expressed as per cent of mean (Fig-4.2) was observed for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant. These characters may have contributed to preponderance of additive gene action and selection pressure could profitably be applied on these characters for their rationale improvement. Similar result are reported by Muthuswamy *et al.* (2019), Abhisheka and Mogali (2020). Wesly *et al*. (2020) for number of primary branches per plant, number of clusters per plant, number of pods per plant, 100-seeds weight and seed yield per plant. While, Garg *et al*. (2017a) for number of primary branches per plant, number of pods per plant, 100-seeds weight and seed yield per plant. Mohammed *et al.* (2020) for number of primary branches per plant, seed yield per plant, number of pods per plant and 100 seed weight.

The high heritability coupled with moderate genetic advance expressed as per cent of mean was observed for plant height, number of seeds per pod and length of pod. These results are in agreement of Dangi *et al*. (2017) for plant height and length of pod, Asari *et al*. (2019) for number of seeds per pod and length of pod. The high heritability coupled with low genetic advance as per cent of mean was found for days to 50 % flowering indicating the presence of additive as well as non-additive gene action. For these traits improvement can be made opting the two to three cycles of recurrent selection followed by pedigree or single seed descent methods of breeding as also recommended by Makeen *et al*. (2007) and Abhisheka and Mogali (2020). Moderate estimates of heritability coupled with low genetic advance as per cent of mean was expressed by days to maturity. Similar result are reported by Katiyar *et al*. (2015) and Abbas *et al*. (2018).

5.3 CORRELATION COEFFICIENT ANALYSIS

In plant breeding programme, where the aim is for improving seed yield, it becomes necessary to gather the detailed information regarding the association of various components with seed yield and among themselves. Seed yield is a complex trait and is determined by the interactive effects of many component traits, which are in turn influenced by their genetic structures and the environment where the plant is grown. The estimation of correlation coefficient can be done at both genotypic and phenotypic levels. The simple correlation is an important tool for this purpose as knowledge of correlation is essential when selection is to be made on several characters at a time through some simultaneous selection model. True association can only be known through genotypic correlation since phenotypic correlation includes the interaction between genotype and environment.

Correlation among traits may result from pleiotropy, linkage or physiological associations among characters. The linkage is a cause of transit correlations particularly in a population derived from crosses between divergent strains. The correlation is the overall or net effect of the segregating genes; some of the genes may increase both the characters causing the positive correlation, while the others may increase the one and decrease the other causing the negative correlation (Falconer, 1981). Thus, to accumulate optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the interrelationship of various characters. The

study of genotypic correlation gives an idea of the extent of relationship between different variables. This relationship among yield contributing characters as well as their association with seed yield provides information for exercising selection pressure for bringing genetic improvement in seed yield. In general, the values of genotypic correlations were higher than their corresponding phenotypic correlations. This indicated that there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environment.

In the present investigation magnitude of genotypic correlation was found slightly higher than phenotypic correlation for most of the traits. This indicated a greater role of genetic factors in determining these associations which reflected that the environment could not deviate the expression of phenotypic association (Table 4.3). The difference between genotypic and phenotypic correlation was found very less. The occurrence of higher estimates of genotypic correlation than the corresponding phenotypic correlation between seed yield and yield components in green gram has also been reported by Prasanna *et al*. (2013), Abbas *et al*. (2018) and Dhunde *et al*. (2021b).

In the present investigation, seed yield per plant had highly significant and positive correlation with number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight at both genotypic and phenotypic level indicating any improvement in these traits with positive correlation with seed yield will results in a substantial increment of seed yield. Such result also reported by Prasanna *et al*. (2013) for number of primary branches per plant, number of clusters per plant and number of pods per plant; Baisakh *et al.* (2016) for number of clusters per plant, number of pods per plant and number of seeds per pod; Mohammed *et al.* (2020) for number of branches per plant, number of clusters per plant, number of seeds per pod and number of pods per plant; Sarkar *et al*. (2014) for number of seeds per pod and 100-seeds weight at genotypic level; Garg *et al*. (2017a) for number of primary branches per plant, number of pods per plant and number of seeds per pod at phenotypic level; Abhisheka and Mogali (2020) and Dhunde *et al*. (2021b) for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight at phenotypic level. Seed yield per plant had significant and positive correlation with length of pod at both genotypic and phenotypic level. Similar relationship has been reported by Baisakh *et al.* (2016).

Significant and positive relationship among these pair of characters indicated that the improvement in one will bring the improvement in another which, in turn automatically leads to increase in seed yield.

Days to 50 % flowering had a positive and highly significant association at both genotypic and phenotypic levels with days to maturity. Similar relationship among days to 50% flowering and days to maturity has been reported by Prasanna *et al.* (2013) and Mohammed *et al.* (2020). Days to maturity had a positive and highly significant association at both genotypic and phenotypic levels with 100-seeds weight. Similar relationship has been reported by Yadav *et al*. (2017) at genotypic level and Abhisheka and Mogali (2020) at phenotypic level.

Plant height exhibited highly significant and positive correlation with number of seeds per pod and length of pod at genotypic levels. Similar findings were reported by Narsimhulu *et al.* (2013), Himabindu and Lavanya (2017) and Mohammed *et al.* (2020) for number of seeds per pod and Garg *et al.* (2017a) for length of pod. Number of primary branches per plant showed positive and highly significant correlation with number of clusters per plant and number of pods per plant at genotypic level. Similar finding confounded by Mohmmed *et al*. (2020) and Narsimhulu *et al*. (2013). Number of primary branches per plant showed positive and significant correlation with number of clusters per plant and number of pods per plant at phenotypic level. Similar results were obtained by Narsimhulu *et al*. (2013) for number of clusters per plant and Goyal *et al*. (2021) for number of pods per plant. Number of clusters per plant had a positive and highly significant association at with number of pods per cluster and number of pods per plant at both genotypic and phenotypic levels. Similar results were obtained by Mathuswamy *et al*. (2019) and Dhunde *et al*. (2021b) for number of pods per cluster and number of pods per plant and Prasana *et al*. (2013) and Mohammed *et al*. (2020) for number of pods per plant. Number of pods per cluster showed positive and highly significant correlation with number of pods per plant at both genotypic and phenotypic levels confirming earlier report of Narsimhulu *et al*. (2013) and Dhunde *et al*. (2021b).

The present results on correlation coefficients revealed that number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight were the most important traits and may contribute considerably towards higher seed yield. The interrelationship

among yield components would help in increasing the yield levels and therefore, more emphasis should be given to these components while implementing selection criteria for seed yield improvement programme.

5.4 PATH COEFFICIENT ANALYSIS

In selection programme when inter- relationship of large number of variables with seed yield and among themselves is studied, the situation become very complex to understand the actual role of a variable for increasing yield. In such a situation, the information of correlation coefficient coupled with the information on path coefficient greatly helps in identification of suitable characters for giving due weightage during selection.

The path coefficient analysis was done for yield and yield attributes to estimate the direct and indirect effects of various characters on seed yield. Path coefficient analysis considers direct as well as indirect effects of the variables by partitioning the correlation coefficients.

In order to understand these effects, genotypic and phenotypic correlation coefficient of different characters with seed yield was portioned into their direct and indirect effects (Table 4.4). This facilitates the selection of genotypes on the basis of those traits which will eventually contribute more towards seeds yield.

5.4.1 Genotypic path coefficient analysis

The genotypic path coefficient analysis (Table 4.4) revealed that number of pods per plant, 100-seeds weight and number of seeds per pod expressed positive and higher direct effect on seed yield per plant. These results were in conformity with earlier report of Ahmad *et al.* (2013). Goyal *et al.* (2021) for 100-seeds weight and number of pods per plant; Kate *et al.* (2017) for 100-seeds weight; Azam *et al.* (2018) for number of pods per plant, 100-seeds weight and Kumar *et al.* (2018) for number of pods per plant.

While, negative direct effect on seed yield per plant were contributed through number of clusters per plant, days to 50 % flowering and plant height at genotypic level, indicating that the selection for these traits may have an undesirable impact on seed yield. These results are in accordance with the reports of Prasanna *et al.* (2013) and Mohammed *et al.* (2020) for number of clusters per plant and days to 50 % flowering.

Garg *et al.* (2017a), Abbas *et al.* (2018) and Asari *et al.* (2019) for plant height; Kate *et al.* (2017) and Azam *et al.* (2018) for days to 50 % flowering.

5.4.2 Phenotypic path coefficient analysis

The phenotypic path coefficient analysis (Table 4.4) revealed that highest positive direct effect on seed yield were exerted through number of pods per plant followed by 100-seeds weight and number of seeds per pod. So, emphasis should be given to these traits in selection program for improvement of seed yield in green gram. Which coincides earlier reported by Parihar *et al.* (2018) for 100-seeds weight and number of seeds per pod; Ahmad *et al.* (2013) and Prasanna *et al*. (2013) for number of seeds per pod, 100-seeds weight and number of pods per plant; Tabasum *et al*. (2010) for number of pods per plant and 100-seed weight; Khanpara *et al*. (2012) for number of pods per plant.

However, negative direct effect on seed yield per plant were contributed through number of clusters per plant and plant height at phenotypic level, indicating that the selection for these traits may have an undesirable impact on seed yield. Similar outcome were also reported by Abhisheka and Mogali (2020) and Mohammed *et al*. (2020) for number of clusters per plant; Goyal *et al*. (2021) and Abbas *et al.* (2018) for plant height.

It was apparent from the phenotypic path analysis that higher direct effects as well as appreciable indirect influences were exerted by number of pods per plant, 100-seeds weight and number of seeds per pod towards seed yield per plant. These three characters also exhibited highly significant and positive association with seed yield per plant. Hence, these may be considered as most important yield contributing characters and due emphasis should be placed on this component while breeding for high seed yield in green gram.

The residual effect was found to be 0.0755 at genotypic path coefficient analysis, while it was 0.1321 at phenotypic path coefficient analysis. The results of residual effect indicated that the majority of the yield attributes have been included in the study of path analysis. It can also be concluded that the characters which are most important for correlation studies are also important for path analysis. Thus, it can be suggested that correlation and path analysis study should be considered together for

rapid gain of final genetic improvement for seed yield in green gram. These results are in accordance with the reports of Manivelan *et al.* (2019), Kumar *et al*. (2018) and Garg *et al*. (2017a).

5.5 GENETIC DIVERGENCE ANALYSIS

Success of any breeding programme depends upon the amount of genetic variability present in the population. The use of Mahalanobis's D^2 statistic for estimating genetic divergence have been emphasized by many workers, because it permits precise comparison among all the population given in any group before effecting actual crosses. Earlier, geographic diversity among the parents was generally taken as an index of genetic divergence.

To a plant breeder, single character is of not much importance as the combined merit of number of desirable traits and it becomes more important when they are concerned with a complex trait like seed yield. Therefore, while improving seed yield, selection of parents based on number of characters having quantitative divergence is required that can be assessed by D^2 statistics developed by Mahalanobis (1936).

5.5.1 Clustering pattern

With the help of Tocher's method, 12 clusters were formed from 72 genotypes of green gram. The composition of clusters is given in Table 4.6. The result revealed that cluster II having largest number of genotypes (20) followed by cluster I (18) and cluster VI (12). On the other hand, cluster III, cluster IV, cluster VII, cluster VIII, cluster IX, cluster XI and cluster XII are solitary clusters.

The intra-cluster distance (D) ranged from 5.55 (cluster I) to 7.81 (cluster X). The clusters III, IV, VII, VIIII, IX, XI and XII contained single genotype and therefore, their intra-cluster distance was zero. High intra-cluster distance indicated about the wider genetic diversity among the genotypes which could be used in yield improvement of green gram. Thus, the genotypes included within a cluster tended to less diverse from one another. The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81). The minimum inter-cluster distance was observed between cluster VIII and IX (D = 4.36). The genotypes belonging to the clusters separated by high statistical

distance could be used in hybridization programme for obtaining a wide spectrum of variation among the segregates or to exploit maximum level of hybrid vigour in green gram.

The clustering pattern indicated that geographic diversity was not associated with genetic diversity as the genotypes from same origin are distributed across the different clusters. The clustering pattern could be utilized in selection of parents for crossing and deciding the best cross combinations which may generate the highest possible variability for various traits. The genotypes with high values of any cluster can be used either for direct adoption as improved varieties or for hybridization to exploit heterosis breeding. In the present study, desirable rating in respect of earliness for days to 50 % flowering and days to maturity were observed in cluster III. Cluster VI had maximum mean value for number of clusters per plant. Cluster XII had maximum mean value for number of pods per cluster, number of seeds per pod and seed yield per plant. Cluster III had maximum mean value for number of pods per plant. Cluster V had maximum mean value for 100-seeds weight.

5.5.2 Contribution of various characters towards total genetic divergence

A wide range of variation for several characters among multi-genotypic clusters was observed. However, the most important trait causing maximum genetic divergence was observed in seed yield per plant (26.49 %) and was responsible for differentiating the genotypes studied. 100-seeds weight (25.82 %), number of pods per plant (11.15 %), length of pod (9.04 %), plant height (8.33 %) and number of clusters per plant (7.71 %) were the next important traits contributed to total genetic divergence. A considerable diversity of 88.54 % was observed due to these six characters. Hence selection for divergent parents based on these six characters would be useful for heterosis breeding in green gram. Seed yield per plant contributed maximum to genetic divergence and similar result was reported by Rasal and Parhe (2017) and Nagda *et al.* (2020).

On the other hand, characters like days to 50% flowering, days to maturity, number of primary branches per plant, number of pods per cluster and number of seeds per pod contributed negligible genetic divergence towards total divergence. Low genetic diversity for these traits in such diverse group of genotypes may also suggest high degree of consistency and moderate to low heritability of these traits. Similar result was reported by Rasal and Parhe (2017) for days to 50% flowering, days to maturity,

number of primary branches per plant and number of seeds per pod. Nagda *et al.* (2020) for days to 50% flowering, number of primary branches per plant and number of seeds per pod. Manthankumar *et al.* (2020) for number of pods per cluster and number of seeds per pod.

5.5.3 Cluster means for various characters

The comparison of cluster means for the different characters indicated that considerable differences exist between clusters of all the characters. The average intra and inter cluster distances were calculated from the D^2 values of the respective accessions within and between clusters.

Days to 50% flowering ranged from 35.33 days (cluster III) to 41.00 days (cluster XI), days to maturity ranged from 67.00 days (cluster III) to 74.00 days (cluster VIII), plant height ranged from 54.23 cm (cluster VII) to 71.90 cm (cluster VIII), number of primary branches per plant ranged from 2.00 (cluster VII) to 3.13 (cluster XI), number of cluster per plant ranged from 2.07 (cluster IX) to 3.93 (cluster III), number of pods per cluster ranged from 2.53 (cluster IX) to 4.47 (cluster XII), number of pods per plant ranged from 13.47 (cluster IX) to 22.42 cm (cluster VI), number of seeds per pod ranged from 9 (cluster XI) to 12.60 (cluster XII), length of pod ranged from 7.18 cm (cluster I) to 8.40 cm (cluster IV and XI), 100-seeds weight ranged from 3.64 g (cluster IV) to 5.57 g (cluster V) and seed yield per plant ranged from 4.91 g (cluster XI) to 11.44 g (cluster XII).

It has been well-established fact that more the genetically diverse parents used in hybridization programme, greater will be the chances of obtaining high heterotic hybrids and broad-spectrum variability in segregating generations (Arunachalam, 1981). It has also been observed that most productive hybrids may come from high yielding parents with a high genetic diversity.

In this context, genotype from cluster V (EC 396523, TARM-2, EC 482907 and GJM 1004); cluster VI (GM 05-05, GJM 1002 and EC 251810); cluster X (EC 251557-A, PANT M-5 and IC 615-5) and cluster XII (GJM 1005) should be selected as parent in hybridization programme for yield improvement in green gram, while for developing early maturing variety of green gram, parents will be selected from cluster I (GM 4); cluster II (RMG 62); cluster III (GM 02-16) and cluster VI (GJM 1002 and GJM 1001).

CHAPTER VI

SUMMARY AND CONCLUSIONS

Present investigation entitled “Genetic variability, correlation, path analysis and genetic divergence in green gram [*Vigna radiata* (L.) R. Wilczek]” was conducted at, Pulses Research Station, Junagadh Agricultural University, Junagadh during *kharif* – 2021. The material consisted of 72 green gram genotypes obtain from Pulses Research Station, Junagadh Agricultural University, Junagadh. The material was evaluated in the field in a randomized block design with three replications. The observations were recorded for 11 characters *viz*., days to 50 % flowering, days to maturity, plant height (cm), number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod, length of pod (cm), 100-seeds weight (g) and seed yield per plant (g). The data were analysed at the Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh. An attempt was also made to know the amount of genetic variability, heritability and genetic advance present for the seed yield and important yield component traits. In addition, an emphasis was also given to understand the nature of association between the component traits with the yield as well as direct and indirect effect of various characters on yield per plant. The results obtained in the present study are summarized below:

The salient features of the findings are as under:

1. The analysis of variance revealed that mean squares due to genotypes were highly significant for days to 50 % flowering, days to maturity, plant height, number of pods per plant, number of seeds per pod and seed yield per plant indicating the presence of sufficient amount of variability in the experimental material used.

2. Maximum phenotypic range of variation was recorded for seed yield per plant followed by number of clusters per plant, number of pods per plant, number of pods per cluster, number of primary branches per plant, 100-seeds weight, number of seeds per pod, plant height, length of pod, days to 50 % flowering and days to maturity.

3. The genotype GM 05-05 gave the maximum seed yield per plant (12.03 g) followed by EC 251557-A (11.59 g), GJM 1005 (11.44 g) and PANT M-5 (11.21 g) while, genotype EC 396523 (5.96 g) had the maximum 100-seeds weight followed by TARM 2 (5.85 g), EC 482907 (5.77 g) and GJM 1004 (5.76 g). The genotype GJM 1002 (28.20), PANT M-5 (26.27), EC 251557-A (26.27) and GM 05-05 (25.93) were the best genotypes with respect to number of pods per plant. The genotype GJM 1005 (12.60) exhibited the maximum number of seeds per pod followed by PM 2 (12.53), LOCAL COLLECTION 2 (12.33) and IC 615-5 (12.00). Among 72 genotypes, GJM 1002 possessed the maximum number of clusters per plant (4.33) followed by EC 251810 (4.20), GM 06-08 (4.07) and AKM 8803 (4.00). Therefore, these genotypes could be utilized in further breeding programme for the yield improvement in green gram.

4. The values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the traits studied, indicating less effect of environment on the expression of characters studied.

5. The maximum GCV was observed for seed yield per plant. Seed yield per plant, plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight also exhibited moderate values of GCV. This indicated the presence of genetic variation for these traits. Low value of GCV observed for length of pod, days to 50 % flowering and days to maturity.

6. The maximum and high PCV was observed for seed yield per plant. The trait plant height, number of primary branches per plant number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight exhibited moderate values for PCV. Length of pod, days to 50 % flowering and days to maturity had low PCV.

7. High heritability (broad sense) estimates were observed for 100-seeds weight followed by number of pods per plant, seed yield per plant, number of clusters per plant, number of pods per cluster, plant height, length of pod, number of primary branches per plant, number of seeds per pod and days to 50 % flowering

while, days to maturity expressed moderate heritability. High heritability values suggested presence of sufficient amount of heritable variation in these characters.

8. High estimates of genetic advance as per cent of mean were found for seed yield per plant (38.42 %) followed by number of pods per plant (37.87 %), number of clusters per plant (35.16 %), number of pods per cluster (30.79 %), 100-seeds weight (28.60 %) and number of primary branches per plant (27.93 %). Moderate values of genetic advance as per cent of mean were observed for plant height (19.43 %), number of seeds per pod (18.65 %) and length of pod (11.98 %). On the other hand, low values of genetic advance as per cent of mean was observed for days to 50% flowering (4.67 %) and days to maturity (2.86 %).

9. High heritability coupled with high genetic advance expressed as per cent of mean were observed for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant suggesting the role of additive gene action in inheritance of these character and in breeding program selection of parents based on this character will be effective for seed yield improvement.

10. Higher values of genotypic correlations than their corresponding phenotypic correlations were recorded by most of the character pairs. This indicated that there was high degree of association between two variables at genotypic level, its phenotypic expression was deflated by the influence of environmental factors.

11. Seed yield per plant was found highly significant and positively correlated with number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, number of seeds per pod and 100-seeds weight at both genotypic and phenotypic levels. Thus, these characters were the most important traits and may contribute considerably towards higher seed yield. Seed yield per plant also registered positive and significant correlation with length of pod. The yield components exhibited varying trends of association among themselves. The interrelationship among yield components would help in increasing the yield levels and therefore, more emphasis should be given to above mentioned yield components while selecting better plant types in green gram.

12. The genotypic path analysis revealed that number of pods per plant, 100-seeds weight and number of seeds per pod expressed positive and higher direct effect on seed yield per plant.

13. The phenotypic path analysis revealed that number of pods per plant, 100-seeds weight and number of seeds per pod had high and positive direct effect on seed yield per plant and that was found to be the most important yield components.

14. The residual effect was of low magnitude suggesting that the majority of the yield attributes have been included in the study of path analysis.

15. D^2 analysis indicated wider genetic diversity among 72 genotypes of green gram which were grouped into 12 clusters. The clustering pattern indicated that geographic diversity was not associated with genetic diversity. The maximum inter-cluster distance was found between cluster IV and XII (D = 19.16) followed by cluster XI and XII (D = 18.01), cluster III and XII (D = 16.59), cluster II and XII (D = 16.22), cluster IV and V (D = 15.89) and cluster VI and XII (D = 15.81). Therefore, in the present investigation, based upon high yielding genotypes and large inter-cluster distances, it is advisable to attempt crossing of the genotypes from cluster XII, II, V and VI which may lead to broad spectrum of favorable genetic variability for seed yield improvement in green gram.

16. The traits *viz*., seed yield per plant (26.49 %), 100-seeds weight (25.82 %), number of pods per plant (11.15 %), length of pod (9.04 %), plant height (8.33 %) and number of clusters per plant (7.71 %) had higher contribution towards total genetic divergence. These six characters accounted for 88.54% of the total genetic divergence in the material studied. Hence, selection for divergent parents based on these six characters would be useful for yield improvement in green gram.

17. On the basis of cluster means, desirable rating in respect of earliness for days to 50% flowering (35.33 days) and days to maturity (67.00 days) were observed in cluster III. Cluster III also showed desirable mean values for number of clusters per plant and number of pods per plant. Cluster XII showed desirable mean

values for seed yield per plant, number of seeds per pod and number of pods per cluster.

From the present investigation, it can be concluded that additive gene action was operating for number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, 100-seeds weight and seed yield per plant as it showed high heritability coupled with high genetic advance as a per cent of mean. Study of correlation coefficient and path analysis clearly indicated that the number of pods per plant and 100-seeds weight was most important trait**.** The traits *viz*., seed yield per plant, 100-seeds weight, number of pods per plant, length of pod, plant height and number of clusters per plant had highest contribution towards total genetic divergence. Hence, emphasis must be given on the above mentioned traits while imposing selection for genetic improvement in green gram.

BIBLIOGRAPHY

Abhisheka, L. S. and Mogali, S. C. (2020). Genetic variability, correlation and path coefficient analysis for yield and yield attributing traits in advanced breeding lines (ABLs) of green gram [*Vigna radiata* (L.) Wilczek] in F_6 generation. *Int. J. Curr. Microbiol. App. Sci.*, **9**(6): 314-321.

Abbas G.; Asghar, M. J.; Rizwan M.; Akram M.; Hussain, J. and Ahmad, F. (2018). Genetic analysis of yield and yield components for the improvement of mungbean germplasm. *Pak. J. Agric. Res.*, **31**(2): 158-165.

Ahmad, A.; Razvi, S. M.; Rather, M. A.; Gulzafar; Dar, M. A. and Ganie, S. A. (2013). Association and inter-relationship among yield and yield contributing characters and screening against cercospora leaf spot in mung bean (*Vigna radiata* L.). *Academic journals*, **8**(41)**:** 2008-2014.

Ahmad, S. and Belwal, V. (2020). Study of correlation and path analysis for yield and yield attributing traits in mung bean [*Vigna radiata* (L.) Wilczek]. *Int. J. Chem. Stud*., **8**(1): 2140-2143.

Al-Jibouri, H. A.; Miller, P. A. and Robinson, H. F. (1958). Genotypic and environmental variances and co-variances in an upland cotton cross of inter-specific origin. *Agron. J.*, **50**(10): 633-637.

Allard, R. W. (1960). *Principles of Plant Breeding*. John Wiley and Sons, New York.

Anand, G.; Anandhi, K. and Paulpandi, V. K. (2016). Genetic variability, correlation and path analysis for yield and yield components in F_6 families of greengram (*Vigna radiata* (L.) Wilczek) under rainfed condition. *Electron. J. Plant Breed.*, **7**(2): 434-437.

Anonymous, (2019-20). Directorate of Economics and Statistics, Department of Agriculture, Co- operation and Farmers Welfare, New Delhi.

Arunachalam, V. (1981). Genetic distances in plant breeding. *Indian J. Genet*., **41**: 226-236

Asari, T.; Patel, B. N.; Patel, R.; Patil, G. B. and Solanki, C. (2019). Genetic variability, correlation and path coefficient analysis of yield and yield contributing characters in mung bean [*Vigna radiata* (L.) Wilczek]. *Int. J. Chem. Stud*., **7**(4): 383-387.

Azam, M. G.; Hossain M. A.; Alam M. S.; Rahman K. S. and Hossain M. (2018). Genetic variability, heritability and correlation path analysis in mung bean (*Vigna radiata* L.). *Bangladesh J. Agril. Res.*, **43**(3): 407-416.

Baisakh, B.; Swain, S. C.; Panigrahi, K. K.; Das, T. R. and Mohanty, A. (2016). Estimation of genetic variability and character association in micro mutant lines of green gram [*Vigna radiata* (L.) Wilczek] for yield attributes and cold tolerance. *Legume Genomics Genet*., **7**(2): 1-9.

Begum, S.; Noor, M.; Hassan, G.; Rahman, H; Durrishwar; Ullah, H. and Jan, M. (2012). Genotypic association among yield and related attributes in green gram genotypes. *Int. Res. J. Agric. Sci. Soil Sci*., **2**(5): 188-193.

Burton, G. W. (1952). Quantitative inheritance in grasses. *Proc. 6th Int. Grassland Cong*., held at Pennsylvania State College, **1**: 277-283.

Dangi, R.K.; Gurjar, D.; Singh P. B. and Lavanya, G. R. (2017). Correlation studies on morphological and yield characters of mungbean (*Vigna radiata* L. Wilczek). *J. Multidiscip. Adv. Res*., **6**(1): 6-9.

Dewey, D. R. and Lu, K. H. (1959). A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agron. J.,* **51**(9): 515-518.

Dhunde, B. B.; Devmore, J. P.; Mahadik, S. G.; Palshetkar, M. G.; Vanve, P. B.; Bhave, S. G. and Thorat, B. S. (2021b). Correlation and path analysis studies on yield and its components in green gram (*Vigna radiata* L. Wilczek). *the Pharm. Innov. J.*, **10**(1): 727-730.

Dhunde, B. B.; Devmore, J. P.; Palshetkar, M. G.; Jagtap, D. N.; Dhekale, J. S. and Burondkar, M. M. (2021a). Genetic variability studies in F_2 generation for yield and yield component traits in green gram (*Vigna radiata* L. Wilczek). *Int. J. Curr. Microbiol. App. Sci.*, **10**(1): 321-327.

Falconer, D. S. (1981). *An introduction to quantitative genetics.* Longman, New York.

Gadakh S. S.; Dethe A. M.; Kathale M. N. and N. S. Kahate (2013). Genetic diversity for yield and its component traits in green gram [*Vigna radiata* (L.) Wilczek]. *J. Crop Weed*, **9**(1): 106-109.

*****Galton, F. (1889). Correlations and their measurement, chiefly from anthropometric data. *Proceedings of the Royal Society of London*, 45(273-279): 135-145.

Garg, G. K.; Verma, P. K. and Kesh, H. (2017a). Genetic variability, correlation and path analysis in mungbean (*Vigna radiata* L. Wilczek). *Int. J. Curr. Microbiol. App. Sci*., **6**(11): 2166-2173.

Garg, G. K.; Verma, P. K. and Kesh, H. (2017b). Multivariate analysis in mungbean (*Vigna radiata)* for genetic diversity under rainfed condition. *Forage Res.*, **43**(2): 156-159.

Ghimire, S.; Khanal, A.; Kohar, G. R.; Acharya, B.; Basnet, A.; Kandel, P.; Subedi, B.; Shrestha, J. and Dhakal, K. (2018). Variability and path coefficient analysis for yield attributing traits of mungbean (*Vigna radiata* L.). *Azarian J. Agric*., **5**(1): 7-11.

Goyal, L. Intwala C. G.; Modha K. G. and Acharya V. R. (2021). Association and diversity analysis for yield attributing traits in advance generation of green gram [Vigna radiata (L.) Wilczek]. *Int. J. Chem. Stud*., **9**(1): 1934-1939.

Haytowitz, O. B. and Matthews, R. H. (1986). Composition of foods: Legumes and legume products. United States of Agriculture. Agril. Hand Book, pp.8-16.

Hemavathy, A. T.; Shunmugavalli, N. and Anand, G. (2015). Genetic variability, correlation and path co-efficient studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *Legum. Res.: Inter. J.*, **38**(4): 442-446.

Himabindu Ch. and Lavanya G. R. (2017). Character association among yield component characters and with seed yield in greengram (*Vigna radiata* (L.) Wilczek). *J. pharmacogn. phytochem*., **6**(5): 119-122.

Jeeva, G. and Saravanan, K. (2017). Genetic divergence of green gram [*Vigna radiata* (L.) Wilczek] grown in coastal saline low land of Tamilnadu, India. *Plant Arch*., **17**(2): 1617-1620.

Johnson, H. W.; Robinson, H. F. and Comstock, R. E. (1955). Genotypic correlation in soyabean and their implication in selection. *Agron. J.,* **47**(10): 477- 483.

Kanavi M. S. P.; Rangaiah, S and Shashidhara K. S. (2019). Correlation coefficient studies among physiological and yield attributing traits in germplasm accessions of green gram [*Vigna radiata* (L.)] under drought condition. *J. Pharmacogn. Phytochem*., **8**(6): 965-969.

Kate, A. M.; Dahat, D. V. and Chavan, B. H. (2017). Genetic variability, heritability, correlation and path analysis studies in green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Dev. Res***.,** **7**(11): 16704-16707.

Katiyar, M.; Kumar, S. and Kumar, N. (2015). Path analysis, association and variation of grain yield attributes in mungbean (*Vigna radiata* L. Wilczek). *Int. J. Adv. Res*., **3**(6): 2410-2413.

Khanpara, M. D.; Vachhani, J. H.; Jivani, L. L.; Jethava, A. S. and Vaghasia, P. M. (2012). Correlation and path coefficient analysis in green gram [*Vigna radiata* (L.) R. Wilczek]. *Asian J. Bio. Sci*., **7**(l): 34 - 38.

Kumar, A.; Sharma, N. K.; Kumar, R.; Chandel, D. and Yadav, M. K. (2019). Genetic divergence studies in mungbean germplasm under arid environment. *Int. J. Chem. Stud*., **7**(2): 1617-1619.

Kumar, A.; Sharma, N. K.; Kumar, R.; Sanadya, S. K. and Sahoo, S. (2018). Correlation and path analysis for seed yield and components traits in mungbean under arid environment. *Int. J. Chem. Stud.*, **6**(4): 1679-1681.

Kumar, N. V.; Lavanga G. R.; Singh, S. K. and Pandey, P. (2010). Genetic association and path coefficient analysis in mung bean *Vigna radiata* (L.) Wilczek. *Advances in Agril. and Botanics*., **2**(3): 251-258.

Mahalanobis, P. C. (1936). *On the generalized distance in statistics*. National Institute of Science of India, **2**: 49-55.

Mahalingam, A.; Manivannan, N.; Ragul, S. and Lakshmi N. S. (2018). Genetic divergence among green gram [*Vigna radiata* (L.) Wilczek] germplasm collections. *Electron. J. Plant Breed*., **9**(1): 350-354.

Majhi, P. K.; Mogali, S. C. and Abhisheka, L. S. (2020). Genetic variability, heritability, genetic advance and correlation studies for seed yield and yield components in early segregating lines (F_3) of greengram [*Vigna radiata* (L.) Wilczek]. *Int. J. Chem. Stud*., **8**(4): 1283-1288.

Makeen, K.; Abrahim, G.; Jan, A. and Singh A. K. (2007). Genetic variability and correlation studies on yield and its components in mungbean [*Vigna radiata* (L.) Wilczek]. *J. Agron*., **6**(1): 216-218.

Manivelan, K.; Karthikeyan, M.; Blessy, V.; Priyanka, AR.; Palaniyappan, S. and Thangavel, P. (2019). Studies on correlation and path analysis for yield and yield related traits in green gram [*Vigna radiata* (L.) Wilczek]. *The. Pharm. Innov. J.*, **8**(9): 165-167.

Mathankumar, P.; Manivannan, N.; Subramanian, A.; Shanthi, P. and Prasad, V. B. R. (2020). Genetic divergence in advanced breeding lines and varieties of mungbean. *Electron. J. Plant Breed*., **11**(1): 263-266.

Mehandi, S.; Singh I. P.; Bohra A. and Singh C. M. (2015). Multivariate analysis in green gram [*Vigna radiata (L.) Wilczek*]. *Legume Res*., **38**(6): 758-762.

Mohammed, R. J.; Prasanthi, L.; Vemireddy, L. R. and Latha, P. (2020). Studies on genetic variability and character association for yield and its attributes in greengram [*Vigna radiata* (L.) Wilczek]. *Electron. J. Plant Breed.*, **11**(02): 392-398.

Muralidhara, Y. S.; Lokesh Kumar, B. M.; Uday, G. and Shanthala, J. (2015). Studies on genetic variability, correlation and path analysis of seed yield and related traits in green gram [*Vigna radiata* L. Wilczek]. *Int. J. Agric. Sci. Res.*, **5**(3): 125-132.

Muthuswamy, A.; Jamunarani M. and Ramakrishnan, P. (2019). Genetic variability, character association and path analysis studies in green gram [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.,* **8**(4): 1136-1146.

Nagda R.; Gopal K. and Kumar B. (2020). Genetic diversity estimation among the cultivated green gram genotypes [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci.,* **11**: 2540-2547.

Narasimhulu R.; Naidu N.V.; Shanthi Priya M.; Rajarajeswari V. and Reddy K. H. P. (2013). Genetic variability and association studies for yield attributes in mungbean (*Vigna radiata* L. Wilczek). *Indian J. Plant Sci.*, **2**(3): 82-86.

Panse, V. G. and Sukhatme, P. V. (1985). *Statistical Methods for Agricultural Workers*. (3rd Revised eds.) I.C.A.R., New Delhi.

Parihar, R.; Agrawal, A. P.; Sharma, D. J. and Minz, M. G. (2018). Character association and path analysis studies on seed yield and its yield attributing traits in mungbean [*Vigna radiata* (L.) Wilczek]. *J. pharmacogn. phytochem.*, **7**(1): 2148-2150.

Patel, J. N. and Patel, N. K. (2012). Genetic divergence in *Vigna radiata* (L.) Wilczek. *Life sci. leafl.,* **11**: 53-56.

*Pearson, K. (1904). *On the theory of contingency and its relation to association and normal correlation*. Dulau and Company.

Prasanna B. L.; Rao P. J. M.; Murthy K. G. K.; and Prakash K. K. (2013). Genetic variability, correlation and path coefficient analysis in mungbean. *Environ. Ecol*., **31**(4): 1782—1788.

Rao, C. R. (1952). *Advanced ststistical methods in biometrical research*. John willey and Sons. Inc., New York, pp. 337-363.

Rasal M. M. and Parhe S. D. (2017). Genetic diversity studies in mungbean (*Vigna radiata* L. Wilczek) germplasm. *Trends Biosci.,* **10**(2): 868-872.

Raturi, A.; Singh, S. K.; Sharma, V. and Pathak, R. (2015). Genetic variability, heritability, genetic advance and path analysis in mungbean [*Vigna radiata* (L.) Wilczek]. *Legume Res*., **38**(2): 157-163.

Robinson, H. F.; Comstock, R. E. and Harvery, V. H. (1955). Estimates of heritability and degree of dominance in corn. *Agron. J*., **41**(4): 353-359.

Sandhiya, V. and Saravanan, S. (2018). Genetic variability and correlation studies in green gram (*Vigna radiata* L.). *Electron. J. Plant Breed.*, **9**(3): 1094-1099.

Sarkar, M.; Ghosh, S. and Kundagrami S. (2014). Genetic variability and character association of yield and yield components in mungbean [*Vigna radiata* (L.) R. Wilczek]. *J. Agroecol. & Nat. Resour. Manage.*, **1**(3): 161-165.

Sarkar, M. and Kundagrami S. (2016). Multivariate analysis in some genotypes of mungbean [*Vigna radiata (L.) Wilczek*] on the basis of agronomic traits of two consecutive growing cycles. *Legume Res*., **39**(4): 523-527.

Sen M. and De, D. K. (2017). Genetic divergence in mung bean. *Legume Res*., **40** (1): 16-21.

Sharma, S. R.; Singh D.; Pawan K.; Khedar O.P. and Varshnay N. (2018). Assessment of genetic diversity in mungbean [*Vigna radiata* L. Wilczek] genotypes. *Int. J. Genet.,* **10**(7): 471-474.

Sofia, S.; Reddy, D. M.; Shanti Priya, M. and Latha P. (2017). Parental selection for varietal improvement through genetic divergence analysis in mungbean [*Vigna radiata* (L.) Wilczek]. Int. J. Curr. Microbio., **6**(10): 1592-1599.

Subramanian, S. and Menon, M. (1973). Heterosis and inbreeding depression in rice. *Madras Agri. J.*, **6**: 1139-1140.

Tabasum, A.; Saleem, M. and Aziz, I. (2010). Genetic variability, trait association and path analysis of yield and yield components in mungbean [*Vigna radiata* (L.) Wilczek]. *Pak. J. Bot.,* **42**(6): 3915-3924.

Talukdar, N.; Borah, H. K. and Sarma, R. N. (2020). Genetic variability of traits related to synchronous maturity in greengram [*Vigna radiata* (L.) Wilczek]. *Int. J. Curr. Microbiol. App. Sci*., **9**(1): 1120-1133.

Tomar, A. and Upadhyay, D. K. (2019). Genetic divergence analysis in mungbean (*Vigna radiata* L. Wilczek). *Int. j. agri. invent*., **4**(1): 106-109.

*Vavilov, N. I. (1939). The origin, variation, immunity and breeding of cultivated plants. *Chronica botanica.* B. Walthum, mass, USA.

Wesly, K. C.; Nagaraju, M. and Lavanya, G. R. (2020). Estimation of genetic variability and divergence in green gram *Vigna radiata* (L.) germplasm. *J. pharmacogn. phytochem.*, **9**(2): 1890-1893.

Wright, S. (1921). Correlation and causation. *J. Agric. Res.,* **20**(7): 557-585.

Yadav, R.; Ram, B. L.; Suresh, B. G. and Lavanya, G. R. (2017). Studies on genetic variability, character association for yield and yield components in green gram (*Vigna radiata* L. Wilczek). *J. Pharmaco. & Phytochem*., **6**(4): 1988-1991.

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*Original not seen

Appendix- I.

Mean weekly meteorological data recorded during the crop season *kharif*- 2021 at Meteorological laboratory, College of Agriculture, Junagadh Agricultural University, Junagadh.

Month	Std. weak No.	Temperature (C°)		Relative Humidity (%)		Rainfall (mm)	Rainy Days
		Max.	Min.	Max.	Min.		
June	23	38.2	27.3	77	50	0.0	0
	24	37.8	28.0	79	45	1.2	0
	25	34.0	25.1	85	67	61.8	4
	26	35.1	26.2	82	56	18.0	1
July	27	36.5	26.0	78	46	0.0	0
	28	33.6	25.3	87	72	87.3	3
	29	31.4	25.0	76	81	49.1	3
	30	30.3	24.6	92	82	123.8	2
	31	30.5	24.8	85	71	2.0	0
August	32	32.5	24.3	88	65	7.6	1
	33	32.9	24.3	84	57	8.1	1
	34	31.8	23.8	90	73	14.4	1
	35	32.3	23.4	89	69	69.2	3
September	36	30.1	23.7	94	83	179.3	6
	37	29.3	24.5	96	88	393.4	4
	38	30.4	25.0	94	77	55.7	4
	39	30.6	24.2	92	80	156.6	5
October	40	33.1	25.1	86	61	16.7	1
	41	34.1	24.3	81	68	60.9	4
	42	34.5	20.2	72	35	0.0	0
	43	33.1	20.2	78	39	0.0	0
	44	33.9	16.2	69	32	0.0	0

APPENDIX-II

The mean values of 72 genotypes of green gram for 11 characters

Sr. No.	Genotype	DFF	DM	PH	NPBR	NCPP	NPPC	NPP	NSPP	LP	TW	SYPP
1	GM 4	36.00	67.67	52.63	2.27	3.00	4.07	19.67	8.93	6.90	4.59	8.05
2	K 851	38.67	71.33	56.93	1.93	2.27	2.87	15.33	8.80	7.00	3.57	4.96
3	BPMR 145	39.67	73.33	52.00	2.53	2.93	3.67	15.67	9.80	7.07	3.62	5.57
4	AKM 6802	37.00	70.33	50.97	2.33	2.73	3.47	18.13	9.87	6.93	4.70	8.42
5	Kopergaon	38.33	71.00	62.73	3.13	2.87	3.27	17.93	7.67	7.47	4.90	6.74
6	TARM 18	39.00	72.33	52.43	2.27	2.00	3.13	13.87	9.40	7.33	4.38	5.89
7	PM 2	37.67	72.67	54.23	2.00	3.00	3.47	15.60	12.53	7.73	4.51	8.79
8	VAIBHAV	38.33	71.33	56.77	2.80	2.80	4.20	16.67	9.93	7.53	4.60	7.77
9	J 781	40.00	72.33	58.57	2.70	3.20	2.67	14.73	9.00	8.13	5.25	6.94
10	GM 1918	40.33	72.00	57.20	2.47	2.27	2.87	14.00	9.00	7.47	5.26	6.41
11	GM 1924	39.67	71.67	54.40	2.73	2.13	3.60	15.83	10.87	7.73	4.00	6.85
12	GM 1925	40.33	73.67	61.53	3.20	3.27	3.07	15.87	8.20	6.97	5.03	6.68
13	GM 1926	39.67	72.67	57.87	2.27	2.47	3.00	14.93	9.40	6.87	4.76	6.68
14	GM 02-12	41.00	71.67	58.50	2.13	3.20	4.07	20.00	8.27	7.40	5.54	9.25
15	GM 02-13	37.00	69.33	48.93	2.47	3.20	3.87	19.30	8.47	7.33	4.65	7.52
16	GM 02-15	38.33	69.67	51.60	3.00	3.47	4.07	21.67	11.27	7.67	5.42	10.82
17	GM 02-16	37.33	70.00	52.17	2.20	2.80	3.40	17.40	9.73	6.60	3.89	6.36

		DFF	DM	PH	NPBR	NCPP	NPPC	NPP	NSPP	LP	TW	SYPP
18	GM 2K-3	40.67	70.67	51.97	1.93	3.07	3.40	16.27	8.07	7.10	4.14	5.47
19	GM 2K-5	39.00	73.67	57.10	2.93	2.40	2.80	15.73	11.13	7.33	5.10	8.63
20	RMG 62	35.67	68.67	60.20	2.20	2.87	3.73	18.93	10.67	7.40	3.96	8.04
21	RMG 268	38.00	71.67	53.73	2.73	2.87	3.20	16.80	11.93	7.47	4.32	8.58
22	OUM 11-5	36.67	69.67	58.53	3.27	2.93	3.73	19.10	10.27	8.07	4.23	8.29
23	GM 3	37.67	71.67	61.57	2.20	2.07	2.87	13.87	9.53	7.00	4.43	5.84
24	CO 5	38.00	71.00	65.50	2.87	3.13	4.07	18.67	9.00	7.13	3.79	6.36
25	CO 6	38.33	72.00	61.80	2.93	3.27	4.00	20.33	8.73	7.80	4.20	7.29
26	COGG 912	38.67	72.33	67.73	3.27	3.20	4.13	22.60	9.80	7.73	3.74	7.96
27	AKM 8803	37.00	69.67	55.17	2.80	4.00	4.27	25.80	8.67	7.27	3.76	8.39
28	TARM 1	38.00	72.67	53.40	2.93	3.60	3.40	15.80	10.07	8.13	4.17	6.61
29	TARM 2	39.33	73.00	62.10	2.07	2.07	2.67	14.53	8.73	7.93	5.85	7.34
30	ASHA	37.00	73.00	60.83	2.27	3.07	2.87	15.87	9.20	8.40	3.64	5.45
31	PANT M-2	39.00	71.00	58.23	2.47	2.07	3.07	14.27	9.60	7.27	3.61	5.07
32	PANT M-3	39.67	72.33	65.90	2.87	3.07	2.93	18.07	11.40	7.50	4.62	8.80
33	PANT M-4	41.00	71.67	59.63	3.13	2.13	2.73	13.20	9.00	8.40	3.80	4.90
34	PANT M-5	39.00	70.00	50.23	3.27	3.33	4.27	26.27	9.60	7.47	4.70	11.21
35	EC 251557-A	39.00	71.00	61.43	2.93	2.60	3.20	26.27	10.07	7.60	4.63	11.58
36	EC 251810	38.33	69.33	57.20	2.93	4.20	4.67	24.00	10.33	7.87	3.91	9.71
37	EC 314286	40.67	74.00	51.33	3.07	3.20	3.93	20.47	10.40	7.23	3.78	8.03
38	EC 396523	37.33	71.33	73.33	3.27	2.93	3.73	14.33	10.93	7.43	5.96	9.31

		DFF	DM	PH	NPBR	NCPP	NPPC	NPP	NSPP	LP	TW	SYPP
39	EC 450446	39.00	72.00	54.07	2.67	2.47	2.93	14.33	10.80	6.67	4.57	6.99
40	EC 450450	37.67	67.33	55.80	3.20	3.00	3.73	17.53	10.07	7.13	3.68	6.51
41	EC 482907	39.00	72.67	54.60	2.73	2.47	3.00	15.13	9.20	7.20	5.77	8.05
42	EC 482908	37.00	72.00	52.00	2.40	2.73	4.27	19.53	9.00	7.20	5.18	8.99
43	EC 482909	37.67	71.33	72.43	2.20	2.73	4.27	16.07	11.20	8.47	4.80	8.55
44	EC 486839	38.33	73.33	69.17	2.93	2.13	2.80	13.40	10.33	7.53	5.58	7.74
45	EC 496841	38.67	71.33	73.67	2.73	3.27	4.07	19.93	10.00	7.27	4.43	8.52
46	EC 501566	38.67	72.00	57.23	3.27	2.33	4.20	16.90	9.47	6.87	4.44	7.05
47	EC 501569	37.33	72.00	70.23	3.47	3.20	3.40	19.73	10.13	8.07	4.13	7.99
48	IC 615-5	39.33	72.33	68.30	3.47	3.20	3.40	18.07	12.00	8.40	4.99	10.26
49	IC8917	40.00	75.33	68.73	2.80	2.93	3.60	16.83	11.00	8.03	5.36	9.85
50	IC 8961-5	39.33	73.33	59.53	3.20	2.93	2.73	15.27	8.87	6.60	5.33	7.06
51	IC 12434	41.67	72.67	71.60	3.00	2.60	4.07	17.73	8.80	6.93	4.25	6.69
52	IC 24789	36.33	71.33	52.40	2.13	2.27	3.73	18.30	8.73	7.20	3.56	5.67
53	IC 73536	39.00	72.00	67.27	2.47	3.07	3.87	20.33	10.33	8.73	3.88	8.14
54	LOCAL COLLECTION-1	38.00	68.33	57.93	2.13	2.73	4.07	16.60	8.60	7.87	4.29	6.12
55	LOCAL COLLECTION-2	39.67	71.33	66.80	2.33	2.60	2.93	15.53	12.33	7.40	4.14	7.91
56	LOCAL COLLECTION-3	38.00	71.33	51.33	2.20	2.33	3.47	15.27	10.30	8.00	4.39	6.91
57	GM 04-02	37.67	71.33	59.00	2.33	2.73	3.07	16.20	9.47	7.80	3.72	5.74
58	GM 04-04	38.00	68.00	56.10	2.27	3.20	4.00	22.73	10.07	8.00	3.87	8.86
59	GM 05-05	36.67	69.33	61.33	3.73	3.53	4.93	25.93	11.40	8.57	4.16	12.03

		DFF	DM	PH	NPBR	NCPP	NPPC	NPP	NSPP	LP	TW	SYPP
60	GM 05-08	38.00	71.00	53.03	3.27	3.20	4.07	19.33	8.53	8.00	4.43	7.30
61	GM 06-08	37.67	68.67	61.30	2.60	4.07	4.27	21.33	8.60	7.20	4.23	7.72
62	GM 02-16	35.33	67.00	64.00	2.67	3.93	3.87	22.73	9.60	7.63	3.99	8.68
63	GJM 1001	36.00	66.33	57.03	2.53	3.93	4.67	25.40	9.87	6.77	4.01	9.97
64	GJM 1002	35.67	67.67	52.37	3.13	4.33	4.60	28.20	8.93	7.47	3.97	9.99
65	GJM 1003	36.00	69.00	59.37	2.47	3.47	3.93	21.20	9.73	8.00	3.85	7.95
66	GJM 1004	37.67	72.33	57.63	3.67	2.80	2.93	15.00	9.47	7.47	5.76	8.19
67	GJM 1005	36.00	72.67	61.47	3.07	2.33	4.47	16.87	12.60	7.73	5.45	11.44
68	GJM 1006	39.33	74.00	71.90	2.20	2.13	2.80	15.07	10.67	7.23	4.55	7.32
69	GJM 1007	38.33	71.33	59.57	3.13	2.73	3.13	14.60	10.47	6.97	5.09	7.73
70	GJM 1008	39.67	73.67	67.60	2.13	2.07	2.53	13.47	11.60	8.27	4.87	7.61
71	GJM 1009	40.33	72.00	54.53	3.27	3.13	3.47	17.33	9.20	7.47	4.97	8.00
72	GJM 1010	39.33	72.00	59.53	3.00	2.60	3.00	15.80	10.20	8.00	5.56	8.94
	Mean	38.37	71.27	59.24	2.72	2.90	3.56	17.99	9.86	7.52	4.50	7.82
	S. Em.±	0.88	1.24	2.17	0.19	0.17	0.19	0.98	0.49	0.17	0.12	0.48
	C. D. at 5 %	2.48	3.46	6.08	0.54	0.46	0.52	2.74	1.37	0.48	0.32	1.35
	C. V. %	4.00	3.01	6.36	12.38	9.89	9.05	9.44	8.59	3.98	4.48	10.70

DFF= Days to 50% flowering, DM = Days to maturity, PH = Plant height, NPBR =Number of primary branches per plant, NCPP = Number of clusters per plant, NPPC = Number of pods per cluster, NPP = Number of pods per plant, NSPP = Number of seeds per pod, LP = Length of pod, TW= 100-seeds weight, SYPP = Seed yield per plant.