CHARACTER ASSOCIATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREENGRAM (*Vigna radiata* (L.) R. Wilczek.)

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AUGUST – 2023

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[*Vigna radiata* (L.) R. Wilczek.]

A THESIS SUBMITTED TO
JUNAGADH AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILMENT OF THE REQUIREMENTS
FOR THE AWARD OF THE DEGREE OF

MASTER OF SCIENCE
(Agriculture)

IN

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"CHARACTER ASSOCIATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREENGRAM (*Vigna radiata* (L.) R. Wilczek)"

ABSTRACT

Key words: Variability, correlation, path analysis, selection index, genetic diversity, greengram

The present investigation to assess genetic variability, correlation coefficient analysis, path coefficient analysis, selection indices and genetic divergence with respect to seed yield and its components in greengram (*Vigna radiata (*L.) R. Wilczek) genotypes were grown in a Randomized Block Design with three replications at Pulses Research Station, Junagadh Agricultural University, Junagadh during *Kharif* 2022. The characters studied were days to 50 per cent flowering, days to maturity, reproductive phase duration, plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, 100-seed weight and seed yield per plant.

Analysis of variance revealed that the mean square for genotypes was found highly significant for all the characters studied, indicating the presence of a sufficient amount of genetic variability among the genotypes for all the eleven characters. The magnitude of PCV was slightly greater than GCV which revealed that very little influence of environmental variation was observed for all the characters and stated that a sufficient amount of variability was noticed. The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for seed yield per plant, number of pods per plant, number of branches per plant and number of clusters per plant. High heritability coupled with high genetic advance as per cent of mean were recorded for seed yield per plant, number of pods per plant, number of branches per plant, number of clusters per plant and 100-seed weight.

Seed yield per plant had highly significant and positive correlation with number of pods per plant and number of seeds per pod whereas it showed significant and positive correlation with number of clusters per plant, while negative and significant

association with days to 50 per cent flowering at both phenotypic and genotypic levels. Number of pods per plant, number of seeds per pod and 100-seed weight had positive and high to moderate direct effect on seed yield per plant. Number of branches per plant, number of clusters per plant and number of seeds per pod had positive and moderate indirect effect on seed yield per plant through number of pods per plant.

Thirty-one selection indices were constructed using the discriminant function technique revealed that the efficiency of selection increased with the inclusion of more number of characters in the index and it was maximum up to combination of five characters. The selection index based on five characters *viz.,* seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod exhibited maximum relative efficiency and genetic gain would be considered for selection to improve greengram.

The 52 genotypes were grouped into 11 clusters. The inter-cluster distance between cluster IX and XI was highest and it was followed by cluster III and XI. Cluster IX was best for higher number of branches per plant, number of clusters per plant, pod length and 100-seed weight. Cluster XI was desirable for earliest days to 50 per cent flowering, number of pods per plant, number of seeds per pod and seed yield per plant. Inter crossing among the genotypes belonging to different clusters having superior mean performance may help in obtaining superior segregants. The most important traits causing the maximum genetic divergence were seed yield per plant, number of clusters per plant, number of branches per plant, 100-seed weight, number of pods per plant and reproductive phase duration contributing to total diversity. Hence, selection based on these characters would useful for heterosis breeding in greengram.

It can be concluded from the present findings that weightage should be given to number of pods per plant, number of seeds per pod and number of clusters per plant while imposing selection for genetic improvement of seed yield in greengram.

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CERTIFICATE – I

This is to certify that the thesis entitled **"CHARACTER ASSOCIATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREENGRAM (*Vigna radiata* (L.) R. Wilczek)''** submitted by **Mr. N. NARSIMHA RAO (Reg. No. 2010121077)** 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 her 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 prescribe 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 **26th May, 2023** as required under the regulation for post-graduate studies. He has submitted *kachcha* bound thesis on**, July 27th, 2023.**

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Date: 19/08/2023

This is to certify that the thesis entitled **"CHARACTER ASSOCIATION, PATH ANALYSIS AND GENETIC DIVERGENCE IN GREENGRAM (*Vigna radiata* (L.) R. Wilczek)"** submitted by **Mr. N. NARSIMHA RAO (Reg. No. 2010121077)** to Junagadh Agricultural University, Junagadh in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE (AGRICULTURE)** in the subject of **"GENETICS AND PLANT BREEDING"** after recommendation by the external examiner was 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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ACKNOWLEDGEMENT

The long-cherished dream comes true. A journey is easier when you travel together. It is a pleasant aspect that I got a golden opportunity to express my gratitude for all those who helped me during my research work. First and foremost, I thanks to my great caretaker the almighty God for his grace and mercy which made it possible for me to complete this present venture.

First and foremost, I would like to extend my deepest gratitude to my esteemed Major Advisor **Dr. R. M. Javia,** Associate Research Scientist, Pulses Research Station, Junagadh Agricultural University, Junagadh for his keen interest, scientific guidance, constructive criticism and inspiration during the course of research work and preparation of this dissertation.

This memorable occasion provides to me a unique privilege to offer sincere thanks to my minor guide **Dr. G. U. Kulkarni,** Associate Professor, Department of Genetics and Plant Breeding, College of Agriculture, Junagadh Agricultural University, Junagadh. I feel great indulgence in introducing my committee members **Dr. L. K. Sharma,** Assistant Research Scientist, Pulse Research Station, Junagadh Agricultural University, Junagadh and **Dr. D. V. Patel,** Associate Professor, Dept. of Agricultural Statistics, College of Agriculture, Junagadh Agricultural University, Junagadh for their constant encouragement throughout the course of investigation.

I also record my sincere thanks to **Dr. V. P. Chovatia,** Honorable Vice Chancellor J. A. U., Junagadh, **Dr. R. B. Madariya,** Director of Research and Dean P. G., J. A. U., Junagadh, **Dr. S. G. Savalia,** Principal and Dean, College of Agriculture, J. A. U., Junagadh and **Dr. D. R. Mehta,** Professor and Head, Department Genetic and Plant Breeding, J. A. U., Junagadh for providing me necessary facilities during my studies.

I am thankful to **Dr. B. A. Monpara,** Research Scientist (Chickpea), Pulses Research Station, Junagadh Agricultural University, Junagadh for providing field and necessary facilities for the experiment. I am also grateful to **Mr. D. R. Rathod** and all other staff members of Pulses Research Station, Junagadh Agricultural University, Junagadh for their immense help and best co-operation during the study and experimentation.

I am sincerely thankful to **Dr. L. J. Raval, Dr. Rajiv Kumar, Dr. S. B. Chaudhari and Dr. M. H. Sapovadiya** and all the staff members of Department of Genetics and Plant Breeding J.A.U., Junagadh for providing guidance and necessary help to me during period of my study.

The importance of library and role of its staff can never be underestimated, but it is mostly forgotten during acknowledgements. I specially appreciate librarian **Miss P. I. Dave** and staff members for their ever willing help during this study and also 'C' branch of Principal office and examination branch of Registrar office for their cooperation during my study.

Friends bring with them spirit of joy and encouragement and helping hand of friends which play important role in our life. I would like to exprees my indebtness to my dearest friends **Chandu, Vishwa Patil, Kundan, Prateek, Arya, Prerna, Jumbo, Devraj, Navdeep Bhati, Raju, Vishwanath and Uday** and to my juniors **Tangichi, Sai, Jagadeesh, Niranjan, Uday, Prasanna, Nikitha, Yasaswini, Sravya, Tejaswini and leelashankar** for their support and helping hands at the critical junctures during course of project work. I also wish to thank my seniors **Kishor, Durga, Sunitha, Ramya, Mansa, Priyanka, Sravani and Sreevani** for their guidance. Your belief is the reason for my self-confidence. Thanks for being a part of my life.

Words will never be enough to express the support and strength provided by my parents, **Mr. Rama Rao** and **Mrs. Nagaratnmma** for their personal sacrifice my brother **Uday** whose faith, love and affection have always been most vital source of inspiration to me.

To all of you whom I have named please accept my deepest thanks and to whom I have not named please know that even though you are unnamed in this work you are not unknown to me and you are appreciated for more thanks.

There are number of well-wishers to whom I cannot forget and I thank to one and all associated with me directly and indirectly.

Place: Junagadh

Date: 27 / 07 /2023 (**N. Narsimha Rao)**

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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 enriching 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.

Greengram [*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). Greengram (*Vigna radiata* var. radiata) is believed to have originated in the Indian subcontinent (De Candolle, 1884; Vavilov, 1926 and Zukovskij, 1962). Since India has a wide range of genetic diversity of cultivated, as well as of weedy wild types of mungbean, it is considered as the region of its first domestication (Baudoin and Marechal, 1988).

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 million hectares with a production of 69 million tonnes and a productivity of 999 kg per ha. In India, pulses productivity is 892 kg per ha with occupy 28.83 million hectares area and total production of 25.72 million tonnes during 2020-21 (Anon., 2021). Bengalgram, redgram, greengram, blackgram, cowpea, lentil and pea are important pulses crops grown in India. Among, these an ancient and well-known leguminous crop of India is greengram (*Vigna radiata* (L.) R. Wilczek), known for its drought tolerance, early

maturing, nutritional quality and suitability in cropping systems.

According to Vavilov (1926) it 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 greengram (*Vigna radiata* (L.) R. Wilczek). Greengram is cultivated in 1.69 lakh hectares with annual production of 1.37 lakh tonnes leading to an average productivity of 810 kg per ha in Gujarat during 2021-22 (Anon., 2022). It 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 virus resistant varieties provided excellent opportunity for greengram cultivation both in *kharif* as well as in summer season, where adequate irrigation facilities are available.

Greengram (*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. The protein is comparatively rich in lysine, an amino acid that is deficient in cereal grains. So, greengram and cereal grains diet combining form a balanced amino acid diet. 132 mg calcium, 2.251 mg niacin, 4.8 mg ascorbic acid, 0.621 mg thiamine, 0.233 mg riboflavin, 114 IU vitamin A contain in every 100 g greengram seed (Haytowitz and Matthews, 1986). The calorific value of greengram is 334 calories per 100 g and it contains crude fat 1.3 per cent, protein 24.0 per cent and carbohydrate 56.6 per cent.

Greengram is an herbaceous annual plant with erect or sub erect stem, sometime twinning in upper branches, furrowed and moderately or 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.

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 pulses.

For the leading to improved soil fertility and texture should fixes atmospheric nitrogen, there is done by greengram, as a legume crop *via* root rhizobial symbiosis (Graham and Vance, 2003). It is a drought resistant crop and suitable for dry land farming. It is an excellent crop to fit in intercropping system with different major crop or it may be taken as green manure crop to enrich the soil and other biota due to short duration nature. Intercropping greengram in rice-rice and rice-wheat systems increases the yield of the subsequent cereal crop and reduces pest incidence (Yaqub *et al.,* 2010; De Faria *et al.,*1989).

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 non-genetic 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 devised by Wright (1921) provides an effective mean of finding direct and indirect causes of an association under such circumstances.

Yield is governed by polygenic system and is highly influenced by fluctuation in the environment. Hence, selection of plants based directly on yield would not be very reliable in many cases. The effectiveness of component approach to selection breeding is well appreciated. An application of discriminant function developed by Smith (1936) helps to identify important combination of yield component useful for selection by formulating suitable selection indices. The suitable selection index has been found to be superior to direct selection for yield. Thus, selection indices help the breeder to discriminant desirable genotypes on the basis of phenotypic performance.

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 52 diverse greengram genotypes during *kharif* 2022 with the following objectives.

1. To estimate the extent of genetic variability, heritability and genetic advance for different quantitative characters
2. To estimate the phenotypic and genotypic correlations between seed yield and yield contributing characters
3. To determine the direct and indirect effects of different characters on seed yield using path coefficient analysis
4. To construct the selection indices using seed yield and its component traits
5. To find out genetic divergence among the genotypes

CHAPTER II

REVIEW OF LITERATURE

In the present investigation an attempt has been made to study **"Character association, path analysis and genetic divergence in greengram (*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 Selection indices

2.5 Genetic divergence

2.1 GENETIC VARIABILITY PARAMETERS

The presence of genetic variability among different traits is important for breeding and in selecting desirable genotypes. The effectiveness of selection is dependent upon the nature, extent and magnitude of genetic variability present in the material and the extent to which it is heritable. The genetic variability is determined with the help of certain genetic parameters *viz.,* genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance. Heritability of a trait is important in determining its response to selection. Genetic advance provides information on expected genetic gain resulting from selection of superior individuals. Various workers have extensively studied genetic variability parameters in greengram are reviewed as under:

Makeen *et al.* (2007) evaluated 20 diverse greengram genotypes for estimation of genetic variability, heritability and genetic advance for ten quantitative characters. 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 for seed protein, plant height and test weight. They also observed high

heritability coupled with high genetic advance for number of pods per plant, plant height and test weight.

Kumar *et al.* (2010) studied genetic variability in 23 genotypes of mungbean for different quantitative characters. They observed highest GCV and PCV for harvest index and number of pods per plant. High estimates of genetic advance as percent of mean were recorded for 100-seed weight and harvest index.

Narasimhulu *et al.* (2013) studied genetic variability in 40 greengram lines for different quantitative characters. They observed the highest GCV and PCV for the number of branches per plant, number of pods per plant, biological yield per plant and harvest index. High estimates of genetic advance were recorded for 100-seed weight and harvest index. They also observed high heritability coupled with high genetic advances for plant height, number of pods per plant, number of pods per cluster, biological yield per plant, harvest index and seed yield per plant.

Degefa *et al.* (2014) studied genetic variability, heritability in broad sense and genetic advance among 13 mungbean accessions for growth and seed yield characters. They reported high GCV and PCV for number of primary branches per plant, number of pods per plant, number of seeds per plant and harvest index. High genetic advance expected as per cent of mean coupled with high heritability was observed for number of primary branches per plant, number of seeds per plant, number of secondary branches per plant, number of pods per plant and 100-seed weight.

Das and Barua (2015) studied genetic variability in 23 genotypes of greengram. They reported highest genotypic and phenotypic coefficient of variation for seed yield per plant. The highest estimates of heritability in broad sense were recorded for plant height followed by 100-seed weight, pod length, seed yield per plant, days to 50 per cent flowering, number of seeds per pod, days to maturity, pod filling per cent and number of pods per plant. High heritability with high genetic advance were observed for seed yield per plant, number of seeds per pod and plant height.

Hemavathy *et al.* (2015) evaluated 13 diverse greengram genotypes for the estimation of genetic variability, heritability and genetic advance. Higher genotypic and phenotypic coefficient of variation was observed for seed yield per plant, number of pods per plant and number of clusters per plant. High estimates of genetic advance were

recorded for seed yield per plant followed by number of pods per plant and number of pods per cluster. They also observed high heritability coupled with high genetic advance for number of clusters per plant, number of pods per plant and plant height.

Raturi *et al.* (2015) conducted an experiment with 44 promising genotypes of greengram and performed genetic variability analysis. They observed highest GCV for seed yield followed by number of pods per plant. Whereas, highest PCV for seed yield, number of secondary branches per plant, number of pods per plant and number of clusters per plant. The high values of heritability in broad sense were recorded for days to 50 per cent flowering, seed yield, 1000-seed weight and number of pods per plant. High estimates of genetic advance were recorded for seed yield and number of pods per plant.

Anand *et al.* (2016) evaluated 26 greengram genotypes for genetic variability among the yield and yield contributing characters. They found that high genotypic coefficient of variation was exhibited by plant height followed by number of pods per plant and seed yield per plant. The low genotypic coefficient of variation was given by days to 50 per cent flowering. High heritability was shown by seed yield per plant followed by plant height and number of pods per plant. These characters also showed high genetic advance and genotypic coefficient of variation.

Baisakh *et al.* (2016) studied genetic variability and character association in 30 genotypes of greengram for yield attributes and cold tolerance. They observed highest GCV and PCV for plant height, number of clusters per plant, number of seeds per pod, 100-seed weight and seed yield per plant. Plant height and number of pods per plant showed high heritability with high genetic advance indicating additive gene action. Characters like 100-seed weight and number of seeds per pod showed preponderance of non-additive gene effect showing moderate heritability but low genetic advance.

Chandra *et al.* (2017) carried out an experiment to know the genetic variability parameters of 40 greengram genotypes for seed yield characters. They reported high GCV and PCV for number of pods per plant followed by clusters per plant. High heritability in the broad sense was recorded for plant height. High heritability coupled with high genetic advance was observed for plant height and biological yield per plant.

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 per cent flowering. Maximum values of genotypic coefficient of variation were recorded for seed yield per plant, while it was lowest for days to 50 per cent flowering. The PCV for seed yield per plant exhibited maximum and low for days to maturity. Heritability was found high for days to maturity followed by plant height, number of primary branches per plant, pod length and number of pods per plant. 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.

Garg *et al.* (2017a) studied 30 greengram genotypes for estimating genetic variability, heritability and genetic advance. Seed yield per plant followed by harvest index, biological yield per plant and number of pods per plant observed the highest GCV and PCV. High genetic advance coupled with high heritability were observed for plant height, number of branches per plant, pod length, number of seed per pod, 100-seed weight, number of pods per plant, biological yield per plant, seed yield per plant and harvest index.

Perera *et al.* (2017) evaluated 40 greengram genotypes for genetic variability among yield and yield contributing characters. Seed yield per plant followed by pod length observed the highest PCV and GCV. High broad sense heritability along with high genetic advance were recorded for total yield per plant, pod length, number of seeds per pod and plant height.

Yadav *et al.* (2017) conducted experiment on 20 greengram genotypes to estimate genetic variability. 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 number of seeds per pod. High heritability shown by the biological yield per plant followed by harvest index, seed yield per plant, plant height and 100-seed weight.

Abbas *et al.* (2018) conducted an experiment on 58 exotic and indigenous diverse mungbean genotypes for seed yield and yield related traits. They found that high GCV and PCV were exhibited by biological yield per plant, harvest index and seed

yield per plant. They also observed high heritability coupled with high genetic advances for biological yield, harvest index and seed yield per plant.

Azam *et al.* (2018) evaluated 28 greengram genotypes for genetic variability and reported that all the traits showed highly significant differences among genotypes except number of seeds per pod. Number of pods per plant, plant height and 100-seed weight showed high GCV and PCV. They also reported high heritability coupled with moderate genetic advance as per cent of mean for 100-seed weight, days to 50 per cent flowering and number of pods per plant.

Barad *et al.* (2018) evaluated 50 genotypes of chickpea to estimate genetic variability parameters under timely and late sown condition. They observed high PCV and GCV for number of primary branches per plant, seed yield per plant and 100-seed weight under timely and late sowing condition. Number of primary branches per plant, number of secondary branches per plant, plant height, reproductive phase duration, days to 50 per cent flowering, number of pods per plant, seed yield per plant and 100-seed weight noted for high heritability along with high genetic advance as per cent of mean.

Ghimire *et al.* (2018) evaluated seven greengram genotypes for genetic variability and revealed that high genotypic coefficient of variation was exhibited by number of secondary branches per plant and seed yield per plant. Pod length, number of seeds per pod and days to 50 per cent flowering gives the low genotypic coefficient of variation. Test weight, number of secondary branches per plant and seed yield per plant show the high heritability.

Ramakrishnan *et al.* (2018) carried out an experiment to know the genetic variability parameters of 374 greengram germplasm for yield and yield related characters. High GCV and PCV values in the number of clusters per plant, number of pods per plant and number of seeds per pod. Heritability estimates in the broad sense and genetic advance were high for all the characters except for test weight.

Sandhiya and Saravanan (2018) conducted an experiment on 36 greengram germplasm to assess genetic variability, correlation among yield and yield attributing characters. They found that all the quantitative characters *viz.*, days to 50 per cent flowering, plant height, number of primary branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of

seeds per pod and 100-seed weight had a phenotypic coefficient of variation (PCV) higher than the genotypic coefficient of variation (GCV). High heritability coupled with higher genetic advance were recorded for all the ten characters.

Anuradha *et al.* (2019) conducted an experiment on greengram crop with 12 genotypes. Days to 50 per cent flowering, number of branches per plant, number of pods per plant, pod length, number of seeds per pod, plant height, seed yield per plant and Yellow Mosaic Virus per cent had a phenotypic coefficient of variation (PCV) slightly higher than the genotypic coefficient of variation (GCV). Plant height, number of clusters per plant and number of pods per plant exhibited high heritability coupled with moderate to high genetic advance.

Chetariya *et al.* (2019) evaluated 71 genotypes of chickpea to estimate genetic variability parameters under normal and late sown condition. They observed high to moderate values of GCV and PCV for 100-seed weight followed by seed yield per plant, numbers of pods per plant, numbers of primary branches per plant, plant height and reproductive phase duration. High heritability coupled with high to moderate genetic advance expressed as per cent of mean were exhibited by 100-seed weight, seed yield per plant, number of pods per plant, plant height, reproductive phase duration, number of primary branches per plant and days to 50 per cent flowering.

Mariyammal *et al.* (2019) conducted an experiment with the F_2 populations of greengram which were derived from the two crosses *viz.*, VBN-2 × RIL-165 and VBN-2 × RIL-169 along with their parents to estimate GCV, PCV, heritability and genetic advance. They observed the highest GCV and PCV for number of pods per plant. They also observed high heritability coupled with high genetic advance for plant height, number of clusters per plant and single plant yield.

Muthuswamy *et al.* (2019) evaluated 100 germplasm accessions of greengram to assess the magnitude of genetic variability and to understand the heritable component of variation for seed yield and its component traits. They observed the highest GCV and PCV for plant height, number of branches per plant, number of clusters per plant, number of pods per cluster, number of pods per plant and seed yield per plant. High value of heritability coupled with high genetic advance as per cent of mean were

recorded for days to 50 per cent flowering, number of primary branches per plant, number of clusters per plant, number of pods per plant and seed yield per plant.

Abhisheka and Mogali (2020) evaluated 110 F_6 generations of greengram to estimate genetic variability, heritability, genetic advance for yield and yield attributing traits. They reported high GCV and PCV for number of pods per plant and seed yield per plant. High heritability and high genetic advance under mean were recorded for plant height, number of branches per plant, number of pods per cluster, number of pods per plant, 100-seed weight and seed yield per plant.

Madhuri *et al.* (2020) conducted an experiment on chickpea crop with 31 genotypes. They observed high heritability accompanied with high to moderate genetic advance for drought tolerant traits like Specific leaf area (SLA), SPAD Chlorophyll Meter Reading (SCMR) and proline. Seed yield, harvest index, 100-seed weight and days to 50 per cent flowering exhibited moderate to high genetic variability, high heritability coupled with high genetic gain under rainfed and irrigated conditions.

Mohammed *et al.* (2020) conducted an experiment with 50 greengram genotypes to estimate the genetic variability, heritability and genetic advance for twelve quantitative characters *viz.*, plant height, days to 50 per cent flowering, days to maturity, number of primary branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, harvest index, 100-seed weight, soil plant analysis development (SPAD) chlorophyll meter reading and seed yield per plant. They found that the genotypic coefficient of variation (GCV) for all the characters was less than phenotypic coefficient of variation (PCV). Number of primary branches per plant, seed yield per plant, plant height, number of pods per plant, 100-seed weight and days to 50 per cent flowering exhibited high heritability coupled with high genetic advance.

Talukdar *et al.* (2020) evaluated 38 greengram genotypes to determine the genetic variation. The GCV and PCV estimates were high for the number of pods per plant followed by the degree of indetermination of plant height from first pod maturity to 90 per cent pod maturity and the number of branches per plant. High heritability coupled with high genetic advanced as per cent of mean was observed for 13 traits including seed yield per plant.

Dhunde *et al.* (2021a) evaluated 35 genotypes of greengram to study the magnitude of genetic variability, heritability and genetic advance for yield and yield contributing traits. The highest and lowest coefficient of variation was noticed in the traits seed yield per plant and days to maturity. Plant height recorded high heritability coupled with high genetic advance as per cent mean, while the number of branches per plant, number of pods per plant and seed yield per plant exhibited moderate to high heritability coupled with moderate genetic advance per cent of mean.

Sabatina *et al.* (2021) conducted an experiment with 30 genotypes of greengram to determine genetic variation. They observed traits like number of branches per plant, number of clusters per plant, number of pods per plant, test weight and seed yield showed high heritability and genetic advance.

Sineka *et al.* (2021) evaluated 60 greengram genotypes for genetic relatedness with 11 quantitative traits. The phenotypic coefficient of variation and genotypic coefficient of variation was found to be high for the number of clusters per pod and the number of pods per plant. High heritability was noticed for single plant yield, plant height and 100-seed weight. The genetic advance was found to be very high for the number of pods per plant.

Bisti *et al.* (2022) evaluated the genetic variability in five F_3 progeny lines, parental lines and check variety of a greengram. High phenotypic coefficient of variation (PCV) and genotypic coefficient of variation (GCV) were recorded for seed yield per plant, number of primary branches per plant and number of secondary branches per plant. High heritability coupled with high genetic advance as percent of mean was observed for the number of seeds per pod, plant height, number of pods per plant, number of primary branches per plant, number of pods per cluster, seed yield per plant, 100-seed weight, number of secondary branches per plant and pod length.

2.2 CORRELATION COEFFICIENT ANALYSIS

Correlation coefficient provides an information about association between two or more components. If its value is found positive it indicated that both variables move in the same direction whereas, negative value indicated that movement is in the reverse direction. It helps in determining the association between several quantitative traits and also in determining component traits where upon selection can be done for improving

the yield genetically. Three types of correlation exist namely phenotypic, genotypic and environmental out of which, phenotypic correlation is observable which consists both genotypic and environmental effects while, the intrinsic association is measured by genotypic correlation. The literature available on correlation analysis of seed yield with other traits in greengram is given below:

Begum *et al.* (2012) estimated genotypic association among yield and related attributes using ten greengram genotypes. Seed yield per plant revealed highly significant phenotypic correlation with number of pods per plant, number of seeds per plant and 100-seed weight. Seed yield per plant showed significant genotypic correlation with number of pods per plant and days to pod formation.

Gadakh *et al.* (2013a) conducted an experiment on 50 greengram genotypes for correlation. Estimates of correlations revealed that seed yield was positively and significantly correlated with the harvest index and 100-seed weight.

Narasimhulu *et al.* (2013) conducted an experiment on 40 greengram genotypes for correlation. Estimates of correlation revealed that seed yield per plant was positively and significantly correlated with the number of pods per plant, number of clusters per plant, number of pods per cluster and biological yield per plant. All these traits showed a significant and positive association with branches per plant.

Prasanna *et al.* (2013) studied fifty greengram genotypes for correlation and revealed that seed yield per plant showed a significant positive correlation with number of primary branches per plant, number of clusters per plant, numbers of pods per plant, number of seeds per pod and harvest index.

Bisht *et al.* (2014) studied 20 mungbean genotypes for correlation and revealed that the seed yield per plant showed a positive significant correlation with the traits *viz.*, number of pods per plant, 100-seed weight and pod length.

Katiyar *et al.* (2015) conducted an experiment on 45 advance lines including four varieties of greengram for correlation among yield contributing traits. Correlation analysis indicated that seed yield per plant showed a positive and significant correlation with 100-seed weight, number of seeds per pod, number of pods per plant and plant height.

Muralidhara *et al.* (2015) conducted an experiment with F_2 and F_3 populations of greengram which was derived from the cross BL-865 × Chinamung to estimate correlation. They revealed that seed yield per plant had a positive significant correlation with the number of pods per plant, pod yield per plant and threshing per cent.

Baisakh *et al.* (2016) analyzed 30 genotypes of greengram for yield and component traits to estimate correlation coefficient. They 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 seed yield per plant.

Garg *et al.* (2017a) evaluated 30 genotypes of greengram to study the magnitude of correlation coefficient for yield and yield contributing traits. They revealed that seed yield per plant had a positive significant 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.

Yadav *et al.* (2017) evaluated 20 greengram genotypes to estimate genotypic and phenotypic correlation coefficient and revealed that the 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-seed weight had a positive significant correlation with seed yield at both genotypic and phenotypic level.

Parihar *et al.* (2018) studied correlation in eight greengram genotypes along with two check varieties. They revealed that days to 50 per cent flowering showed a positive significant correlation with days to maturity, plant height and number of pods per plant. Number of pods per plant had a positive significant correlation with plant height, number of secondary branches per plant and days to maturity. Plant height had a positive significant correlation with days to maturity and number of secondary branches per plant.

Ramakrishnan *et al.* (2018) studied 374 greengram genotypes for correlation and revealed that seed yield per plant showed a significant positive correlation with pod yield per plant followed by the number of pods per plant, number of clusters per plant and threshing per cent. Pod yield per plant had a very high positive direct effect followed by the number of pods per plant, threshing per cent and number of clusters per plant on seed yield per plant.

Sandhiya and Saravanan (2018) studied 36 mungbean germplasm and revealed that the seed yield per plant showed a positive significant correlation with the traits *viz.*, number of pods per plant, number of clusters per plant and number of pods per cluster.

Kanavi *et al.* (2019) conducted an experiment on 200 germplasms of greengram. Number of pods per cluster had highest positive correlation with seed yield per plant followed by number of pods per cluster, number of clusters per plant, plant height, proline content, SPAD chlorophyll meter reading, leaf water potential, harvest index and number of seeds per pod.

Muthuswamy *et al.* (2019) evaluated 100 genotypes of greengram to estimate correlation coefficient. Results revealed that seed yield per plant had significant and positive correlation with the plant height, number of branches per plant, number of clusters per plant, number of pods per cluster and number of pods per plant.

Abhisheka and Mogali (2020) evaluated 110 F_6 generations of greengram to estimate correlation coefficient for yield and yield attributing traits. They revealed that the seed yield per plant had a positive significant correlation with the number of pods per plant and 100-seed weight.

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

Mohammed *et al.* (2020) conducted an experiment on 50 greengram genotypes for correlation. Estimates of correlation revealed that seed yield per plant was positively and significantly correlated with the 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.

Dhunde *et al.* (2021b) carried out correlation coefficient analysis among twelve quantitative traits in 35 greengram genotypes. The results of association study revealed that, grain yield per plant showed highly significant and positive correlation at both

genotypic and phenotypic levels with number of branches per plant, number of pods per plant and 100-seed weight.

Sineka *et al.* (2021) evaluated 60 genotypes of greengram for genetic relatedness and revealed that the single plant yield was significantly correlated with the number of pods per plant followed by the number of pods per cluster, number of clusters per plant and number of seeds per pod.

Gajanan and Lal (2022) investigated 21 genotypes of greengram including one check. A positive and significant correlation was observed for days to maturity, number of clusters per plant, number of pods per plant, number of primary branches per plant, number of seeds per pod, harvest index and biological yield per plant at both phenotypic and genotypic level.

Reshmi *et al.* (2022) conducted an experiment on 50 greengram genotypes for correlation. Correlation analysis indicated that the seed yield per plant showed a positive significant correlation with 100-seed weight, number of clusters per plant, pod length, plant height, number of pods per plant and number of seeds per pod at both genotypic and phenotypic level.

Tejaswini *et al.* (2022) evaluated 189 greengram genotypes along with checks and parents to estimate correlation coefficient. Results revealed that the seed yield per plant had significant and positive correlation with number of pods per plant, number of clusters per plant and plant height.

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 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 coefficient analysis is a standardized partial regression coefficient which splits genotypic correlation coefficient 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 brier review of work related to path coefficient analysis in greengram is presented as under:

Haritha and Sekhar (2002) studied path coefficient analysis in 50 genotypes of mungbean. The path coefficient analysis revealed that maximum direct positive effects were exerted through number of clusters per plant followed by number of pods per cluster and biological yield per plant towards seed yield per plant.

Rao *et al.* (2006) studied path coefficient analysis in 60 genotypes of mungbean and reported that maximum direct positive effects were exerted by number of pods per plant, biological yield per plant and harvest index towards seed yield per plant.

Tabasum *et al.* (2010) performed path analysis for different characters in 10 mungbean genotypes and revealed that highest positive direct effects were exerted through number of pods per plant followed by total plant weight, harvest index, 100-seed weight, pod length and number of secondary branches per plant while the number of primary branches per plant, plant height, number of clusters per plant and number of pods per cluster expressed negative direct effects on seed yield per plant.

Ahmad *et al.* (2013) evaluated 35 greengram genotypes and the 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.

Prasanna *et al.* (2013) evaluated 50 greengram genotypes for path coefficient analysis and reported that maximum direct positive effects were exerted by number of pods per plant, harvest index, number of seeds per pod and days to maturity towards seed yield per plant.

Thippani *et al.* (2013) evaluated 60 genotypes of greengram and reported that maximum direct positive effects were exerted by number of pods per cluster, number of seeds per pod, pod length, plant height and 100-seed weight towards seed yield per plant.

Hemavathy *et al.* (2015) studied path coefficient analysis in 30 diverse greengram genotypes. The path coefficient analysis revealed that the maximum direct effects were exerted by the number of pods per plant, number of pods per cluster, number of clusters per plant and 100 seed-weight towards seed yield per plant.

Katiyar *et al.* (2015) studied 45 advance lines including four varieties of greengram for path coefficient analysis. Results revealed that number of pods per plant had highest direct effect on seed 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 per cent flowering, plant height, number of primary branches per plant and pod length was found to be negative on seed yield per plant.

Raturi *et al.* (2015) used 44 promising genotypes of greengram in their experiment to perform path analysis and results revealed that maximum positive direct contribution to seed yield per plant came from number of pods per plant followed by plant height and1000-seed weight.

Anand *et al.* (2016) evaluated 26 F_6 families of greengram for path coefficient analysis. Results revealed that the number of clusters per plant had high positive direct effect on seed yield per plant followed by number of pods per plant. Days to 50 per cent flowering and plant height had negative direct and indirect effects on seed yield per plant.

Thirty greengram genotypes were used by Garg *et al.* (2017a) to perform path coefficient analysis. Results revealed that harvest index had the highest direct 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 50 per cent flowering.

Kate *et al.* (2017) studied 30 greengram genotypes to estimate genetic variability, heritability, correlation and path analysis. Results revealed that positive direct effect was exhibited by number of pods per plant, 100-seed weight and plant height on seed yield per plant. Number of seeds per pod, 100-seed weight, days to 50 per cent flowering, plant height and days to maturity exhibited indirect effect on seed yield.

Fifty-eight exotic and indigenous diverse greengram genotypes were evaluated by Abbas *et al.* (2018) for seed yield and other related traits. Path coefficient analysis revealed that maximum direct positive effects were exerted by the number of clusters per plant, number of pods per plant, 100-seed weight, biological yield per plant and harvest index. Days to maturity and plant height had negative direct effect on seed yield per plant.

Ghimire *et al.* (2018) studied seven greengram genotypes to estimate path coefficient analysis for yield attributing traits and found the maximum positive direct effect on yield were exhibited by days to 50 per cent flowering, pod length, number of seeds per pod and biological yield per plant.

Parihar *et al.* (2018) carried out an experiment on eight mungbean genotypes including two check varieties and found days to 50 per cent flowering, number of primary branches per plant, number of secondary branches per plant, 100-seed weight and number of seeds per pod had positive direct effect on seed yield per plant while plant height, days to maturity and number of pods per plant had negative direct effects on seed yield per plant.

Ramakrishnan *et al.* (2018) evaluated 374 diverse genotypes of greengram for path coefficient analysis. Results revealed that pod yield per plant had very high positive direct effect on seed yield per plant followed by number of pods per plant, threshing per cent and number of clusters per plant.

Asari *et al.* (2019) studied path coefficient analysis in 44 genotypes of mungbean. The path coefficient analysis revealed that days to 50 per cent flowering had high positive direct effect on seed yield per plant while test weight, number of clusters per plant, number of pods per plant and number of primary branches per plant had low positive direct effect on seed yield per plant.

Mohan *et al.* (2019) studied path coefficient analysis in 44 genotypes of greengram. The path coefficient analysis revealed that the maximum positive direct effect on seed yield was exhibited by days to 50 per cent flowering, number of pods per plant and number of seeds per pod.

Abhisheka and Mogali (2020) evaluated 110 F_6 generations of greengram to estimate path coefficient analysis for yield and yield attributing traits. They revealed that the number of pods per plant and 100-seed weight had highest positive direct effect on seed yield per plant.

Ahmad and Belwal (2020) conducted an experiment on 112 diverse genotypes of greengram, along with five high yielding checks. Path analysis revealed that the number of pods per plant and 100-seed weight exerted a higher magnitude of positive direct effect, pod length showed moderate effect while the number of clusters per plant and seed density exerted a positive but low magnitude of the direct effect on seed yield per plant.

Sineka *et al.* (2021) studied 60 greengram genotypes for genetic relatedness and revealed that days to maturity, number of pods per cluster, pod length and plant height had a higher positive direct effect on single plant yield.

Gajanan and Lal (2022) carried out an experiment on 21 genotypes of greengram including one check and found days to 50 per cent flowering, days to maturity, number of clusters per plant, seed index, number of seeds per pod, biological yield per plant and harvest index had a direct positive effect on seed yield at the genotypic level. Plant height, number of clusters per plant, number of pods per plant, pod length, number of primary branches per plant, biological yield per plant and harvest index had a direct positive effect on seed yield per plant at the phenotypic level.

2.4 SELECTION INDICES

Discriminant function refers to a statistical approach which is used in construction of selection index. The use of discriminant function technique for plant selection was first proposed by Smith (1936). In this technique an index called selection index is constructed with the help of characters associated with dependent trait say yield. Selection index refers to linear combination of characters associated with dependent trait such as economic yield in crop plants. In this technique, since desirable genotypes are discriminated from undesirable ones, based on character combinations, it is called discriminant function technique. Available reports pertaining to the selection indices in pulses and legumes have been reviewed here as under:

Sadiq and Abbas (2007) conducted an experiment on 20 elite lines of mungbean and revealed that the harvest index showed a positive and significant association with seed yield per plant. Days to 50 per cent flowering and plant height showed a positive and significant relationship with biological yield per plant. The magnitude of a direct effect of harvest index was maximum and 100-seed weight had the highest indirect effect *via* harvest index.

Khanpara *et al.* (2012) studied 58 diverse genotypes of a greengram to construct selection indices under rainfed conditions. Thirty-one selection indices involving seed yield per plant and four yield components were constructed using the discriminant function technique. Among the single character indices, the number of pods per plant exhibited higher genetic advance and relative efficiency over straight selection for seed yield per plant. The index based on four characters *viz.,* seed yield per plant, number of pods per plant, number of clusters per plant and number of pods per cluster recorded the highest genetic advance and relative efficiency.

Sodavadiya *et al.* (2012) evaluated 40 genotypes of pigeonpea to construct sixty-three selection indices involving seed yield and five yield components using the discriminant function technique. They observed that efficiency of selection increased with the inclusion of a greater number of the characters in the index. The index based on all six characters *viz.,* seed yield per plant, number of pods per plant, days to maturity, number of branches per plant, 100-seed weight and pod length recorded the highest genetic advance and relative efficiency followed by an index based on five characters *viz.,* seed yield per plant, number of pods per plant, days to maturity, number of branches per plant and 100-seed weight.

Sarker *et al.* (2013) conducted an experiment on 8 lines of chickpea for selection indices involving eleven agronomical characters by using the discriminant function technique. Results revealed that among all the selection indices, the highest expected genetic gain was obtained when two characters were included in a combination *viz.,* number of primary branches at maximum flower + root weight after fully dry followed by the number of primary branches at maximum flower + number of secondary branches at maximum flower and number of primary branches at maximum flower + seed weight per plant. They concluded that number of primary branches at maximum

flower is most important for selection because it gave high expected genetic gain in yield and it also showed moderate heritability.

Adsul and Monpara (2014) constructed 63 selection indices involving six characters in 100 germplasm lines of soybean. Results revealed that selection efficiency was higher over straight selection when the selection was based on individual components. The highest genetic gain and selection efficiency were observed with combination of six characters *i.e.*, seed yield per plant, number of pods per cluster, number of clusters per plant, number of pods per plant, biological yield per plant and harvest index. They suggested that from practical view point, the selection index based on four characters *viz.*, number of clusters per plant, number of pods per plant, biological yield per plant, harvest index showing higher genetic gain and selection efficiency, was recommended for yield improvement in soybean.

Khanpara *et al.* (2015) evaluated 60 diverse genotypes of vegetable cowpea for selection indices on four characters. Results revealed that selection indices containing single trait were not efficient to bring genetic improvement in vegetable cowpea for green pod yield per plant. Selection index involving green pod yield per plant, number of pods per plant, pod length and 10-pod weight followed by green pod yield per plant, number of pods per plant and 10-pod weight or green pod yield per plant, pod length and 10-pod weight could be advantageously exploited in the vegetable cowpea breeding programmes. They suggested that there was an increase in the genetic gain as well as relative efficiency with inclusion of an additional trait in the character combination.

Kumar *et al.* (2016) studied 40 greengram genotypes to find out suitable selection indices. Seed yield showed a positive and significant association with days to maturity (DM), growing degree days (GDD), relative temperature depression (RTD) and heat use efficiency (HUE). Stepwise regression analysis showed that maximum contribution was made by HUE followed by photo thermal index (PTI) and DM. The comparison of different functions revealed that among the single character selection index heat use efficiency (HUE) was the key component to construct the selection index for terminal heat tolerance in greengram.

Choudhary *et al.* (2017) conducted an experiment on 18 greengram genotypes along with two parents were studied to assess the selection indices among the yield

components. The highest genetic advance and relative efficiency was observed for the selection index containing days to 50 per cent flowering, days to maturity, plant height, pod length, number of seeds per pod and biological yield per plant.

Indu and Saxena (2017) evaluated 50 diverse genotypes of mungbean. They constructed thirty-one selection indices in five characters. Results revealed that among the single character indices, biological yield per plant exhibited higher genetic advance and relative efficiency over straight selection for seed yield per plant. The index based on five characters *viz.*, seed yield per plant, biological yield per plant, number of primary branches per plant, number of seeds per pod and plant height recorded the highest genetic advance as well as relative efficiency and selection efficiency.

Sana *et al.* (2017) constructed thirty-one selection indices in F_2 progenies derived from of 26 crosses of mungbean by using discriminant function. Results revealed that the best selection index was made by discriminant function with four-character index *viz.*, seed yield per plant, number of pods per plant, number of seeds per pod and plant height followed by an index of three characters *viz.*, seed yield per plant, number of pods per plant and plant height.

Fifty diverse genotypes of Indian bean were evaluated by Hadavani *et al.* (2018) for construction of selection indices. Results exhibited that five component characters *viz.*, green pod yield per plant, number of pods per plant, 10-green pod weight, plant height and reproductive phase duration exhibited maximum relative efficiency. They suggested that selection based on these characters increased pod yield in Indian bean. The expected genetic advance and relative efficiency assessed for different indices increased considerably when selection was based on two or more characters.

Das and Baisakh (2019) studied 90 mutants of greengram for estimation of selection indices. The highest genetic advance in seed yield per plant was obtained on a linear combination of traits such as days to 50 per cent flowering, pod length, number of pods per plant, 100-seed weight, number of seeds per pod and seed yield per plant suggesting that the above characteristics could be advantageously exploited in the greengram breeding programs.

Girase *et al.* (2020) evaluated 60 genotypes of mungbean in an RBD with two replications. The seed yield per plant showed a highly significant and positive

association with pod length followed by 100-seed weight, number of seeds per pod, number of pods per plant, number of clusters per plant, plant height and number of primary branches per plant at a genotypic level, indicated that these are the important yield contributing traits and due weightage should be given to these traits during the selection for improvement of yield and its components for the development of genotype sustainable for climate change.

Rukhsar *et al.* (2021) constructed sixty-three selection indices using 42 genotypes of cowpea through discriminant function techniques. The maximum efficiency in selection for seed yield per plant was exhibited by a discriminant function involving the number of pods per plant and number of seeds per pod which had a genetic advance and relative efficiency followed by an index of three characters *viz.*, seed yield per plant, number of clusters per plant and number of pods per plant.

2.5 GENETIC DIVERGENCE

Genetic diversity plays a crucial role because it is the base for survival of plants in nature and for crop improvement. In plant breeding genetic diversity plays an important role because hybrids between lines of diverse origin, generally, display a greater heterosis than those between closely related parents. It helps to find out the genetically divergent parents by using Mahalanobis D^2 statistics. D^2 measures the extent of variability at genotypic level and also determines the comparative ratio of each component trait to the total divergence. It is measured at inter-cluster and intra-cluster levels. This statistic can assess several germplasms at a time and provides reliable approximations of diversity. It is depicted by cluster diagram. The reviews of genetic divergence are listed below:

Manivannan (2002) studied genetic diversity in 33 greengram genotypes. The cluster II and VI, cluster V and VII, cluster VI and VII were highly divergent. Among the characters studied, 100-seed weight followed by powdery mildew reaction contributed the most towards the total divergence.

Patel and Patel (2012) carried out diversity analysis using 40 genotypes of greengram. Based on D^2 values, 40 genotypes were grouped into 11 clusters. The maximum inter-cluster distance was observed between cluster III and IX, II and IX, III

and VII, III and VI. Iron content contributed maximum towards the genetic divergence followed by phosphorous content, harvest index and seed yield per plant.

Gadakh *et al.* (2013b) studied the genetic divergence and clustering pattern among 50 genotypes of greengram. Based on D^2 values, 50 genotypes grouped into 7 clusters. 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. Protein content contributed maximum towards divergence followed by biological yield per plant, number of primary branches per plant, plant height, pod length and seed yield per plant.

Mehandi *et al.* (2015) carried out an experiment to perform the multivariate analysis in greengram using 21 greengram genotypes. The highest intra-cluster distance was found in cluster VI. The maximum inter-cluster distance was found between cluster IV and V followed by the cluster combinations VI and IX, VI and VIII, IV and VI, VI and X. The maximum contribution towards total divergence was recorded from number of pods per plant, plant height and number of clusters per plant.

Sarkar and Kundagrami (2016) evaluated 11 agro-morphological traits in 23 genotypes of mungbean. Cluster analysis using UPGMA method grouped the genotypes into five clusters. Cluster V showed the maximum mean value for plant height, number of branches per plant, number of pods per plant, number of seeds per pod, seed yield per plant and lowest values for days to 50 per cent maturity, 1st picking and days to maturity. Principal component analysis revealed that the first five main PCAs amounted 71.11 per cent of the total variation among genotypes.

Garg *et al.* (2017b) studied the genetic diversity in 30 greengram genotypes. Based on D^2 values, 30 genotypes were grouped into six clusters. The highest intra-cluster distance was observed for cluster III and the lowest was observed for cluster II. While, the highest inter-cluster distance was observed between cluster I and VI. Cluster III showed the maximum mean value for harvest index, plant height and seed yield per plant. The maximum contribution towards total divergence was recorded from harvest index, plant height, days to maturity and biological yield per plant.

Jeeva and Saravanan (2017) estimated the genetic divergence in greengram 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 and minimum in cluster VI and VII. The maximum inter-cluster distance was found between clusters III and cluster VII followed by cluster II and cluster IV. Plant height contributed the highest for genetic divergence followed by days to 50 per cent flowering, number of pods per plant and number of seeds per pod.

Rasal and Parhe (2017) studied genetic diversity in 50 genotypes of greengram. Based on D^2 values, 50 genotypes were grouped into 10 clusters. The highest intra-cluster distance was observed for cluster V followed by cluster IV, cluster VI, cluster III and cluster I. The maximum inter-cluster distance was observed between cluster VII and VI followed by cluster X and VI, cluster VII and II and cluster VII and IV. Seed yield per plant contributed the highest for genetic divergence followed by plant height.

Sen and De (2017) estimated genetic divergence in greengram using D^2 statistics. The 30 genotypes were grouped into 6 clusters. The maximum intra-cluster distance was obtained for cluster VI while the highest inter-cluster distance was found between cluster III and VI. Shelling per cent contributed the highest for genetic divergence followed by seed yield per plant and number of clusters per plant.

Sofia *et al.* (2017) studied 35 greengram genotypes to genetic diversity for yield and physiological traits. Based on D^2 values, 35 genotypes were grouped into 7 clusters. The maximum intra-cluster distance was recorded by cluster IV, while the maximum inter-cluster value was observed between cluster III and IV followed by cluster II and IV and cluster IV and VII. Leaf area duration, chlorophyll content, seed yield per plant, 100-seed weight and net assimilation rate showed maximum percent contribution towards total genetic divergence.

Jakhar and Kumar (2018) carried out an experiment to determine the relationship and genetic diversity among 30 greengram germplasm. The maximum intra-cluster distance was obtained for cluster II followed by cluster I while the highest inter-cluster value was found between cluster III and VI followed by cluster I and III.

Biological yield per plant, seed index and plant height showed maximum percent contribution towards total genetic divergence.

Sixty-four greengram genotypes were evaluated by Sharma *et al.* (2018) to explore the extent of genetic diversity. On the basis of Tocher's method, 64 genotypes were grouped into eight clusters. The maximum inter-cluster distance was observed between cluster VI and VI while the lowest was found between cluster VIII and VII. 100-seed weight contributed highest for genetic diversity followed by number of clusters per plant, days to 50 per cent flowering and days to maturity.

Kumar *et al.* (2019) studied genetic divergence in 79 greengram genotypes. On the basis of D^2 statistics genotypes were grouped into 15 clusters. The maximum intra-cluster distance was recorded for cluster IV followed by cluster II, cluster III, cluster XI and cluster I. The highest inter-cluster distance was found between cluster II and cluster IX. Days to 50 per cent flowering exhibited a maximum contribution to genetic divergence followed by 100-seed weight, biological yield per plant, number of branches per plant and number of pods per plant.

Tomar and Upadhyay (2019) conducted an experiment involving 45 genotypes of mungbean during *kharif* 2018. All the forty-five genotypes were grouped into seven different clusters using D^2 statistics. The greatest inter-cluster distance was between cluster II and cluster V. 100-seed weight was maximum contribution toward divergence followed by seed yield per plant, plant height, days to 50 per cent flowering, number of pods per plant, pod length, number of clusters per plant, number of primary branches per plant, number of seeds per pod and days to maturity.

Mathankumar *et al.* (2020) studied genetic diversity in 100 genotypes of mungbean. Based on D^2 values, 100 genotypes were grouped into 15 clusters. The maximum intra-cluster distance was observed in cluster I while highest inter-cluster distance was found between cluster V and cluster XV. The number of branches per plant contributed maximum towards divergence followed by days to 50 per cent flowering and 100-seed weight.

Nagda *et al.* (2020) evaluated 12 greengram genotypes to determine genetic divergence using D^2 statistics. The genotypes were grouped into four clusters. The maximum intra-cluster distance was observed in cluster II followed by cluster I while

the highest inter-cluster was found between cluster IV and III followed by cluster I and IV and cluster II and III.

Sneha *et al.* (2020) studied 110 mungbean genotypes to determine genetic diversity for yield related traits. 110 genotypes grouped into 15 clusters, cluster XV showed maximum intra-cluster distance while the highest inter-cluster distance was observed between cluster VI and XIII. Seed yield per plant exhibited a maximum contribution to genetic divergence followed by days to 50 per cent flowering and plant height.

Talukdar *et al.* (2020) evaluated 38 greengram genotypes to determine genetic divergence using D^2 statistics. The genotypes were grouped into eight clusters. The highest intra-cluster distance was found in cluster IV. The maximum inter-cluster distance was observed between clusters III and cluster VI followed by cluster V and cluster VIII. Days to 90 per cent pod maturity contributed highest for genetic divergence followed by days to first flowering and days to first pod maturity.

Goyal *et al.* (2021) carried out an experiment with a set of 20 greengram genotypes of advance generation along with five check varieties. The intra-cluster distance for cluster IV was highest followed by cluster III, cluster I and cluster II while the highest inter-cluster distance was observed between cluster I and II. The maximum contribution towards total divergence was recorded from the protein content.

Ram and Saxena (2022) conducted an experiment on 60 genotypes of mungbean to ascertain the information about the magnitude and extent of genetic diversity of agro-morphological characters. The highest intra-cluster distance was observed for cluster IX and the lowest was observed for cluster V, VIII, X and the maximum inter-cluster distance was observed between cluster IX and X. Seed yield per plant contributed the highest for genetic divergence followed by number of pods per plant, 100-seed weight and days to 50 per cent flowering.

CHAPTER III

MATERIALS AND METHODS

The present investigation was carried out to assess the character association, path analysis and genetic divergence in greengram (*Vigna radiata* (L.) R. Wilczek). The study was conducted during *kharif* 2022 at Pulses Research Station, Junagadh Agricultural University, Junagadh. Geographically Junagadh is situated at 21.5^0 N latitude and 70.5^0 E longitude with an altitude of 60 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 semi-arid type. The details of weather parameters recorded for the year 2022 during which the experiment was conducted is presented in the Appendix I. The details of material used and different methods adopted in the investigation are described under the following headings:

3.1 EXPERIMENTAL MATERIAL

The experimental material consisted of fifty-two genotypes of greengram from different origins which were obtained from the Pulses Research Station, Junagadh Agricultural University, Junagadh. Name of the genotypes are summarized in Table 3.1.

3.2 EXPERIMENTAL DETAILS

Fifty-two genotypes of greengram were sown in a Randomized Block Design (RBD) with three replications during *kharif* 2022 at Pulses Research Station, Junagadh Agricultural University, Junagadh. 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.

Table 3.1 Details of greengram genotypes used in present study

Sr. No	Name of genotype	Sr. No	Name of genotype
1	Virat	27	GJM 2009
2	VMS 6	28	GJM 2011
3	Meha	29	GJM 2012
4	Sona mung	30	GJM 2013
5	IPM 409-4	31	GJM 2015
6	RMG 268	32	GJM 2017
7	COGG 13-39	33	GJM 2018
8	GM 04-04	34	GJM 2019
9	GJM 1024	35	GJM 2020
10	GJM 1701	36	GJM 2021
11	GJM 1703	37	GJM 2026
12	GJM 1818	38	GJM 2032
13	GJM 1819	39	ANDG 1800
14	GJM 1822	40	ANDG 1801
15	GJM 1826	41	SKNM 1901
16	GJM 1835	42	SKNM 1910
17	GJM 1902	43	SKNM 1911
18	GJM 1907	44	SML 1827
19	GJM 1909	45	SML 1901
20	GJM 1911	46	SKM 1911
21	GJM 1912	47	Pusa 1501
22	GJM 1916	48	Pusa 1842
23	GJM 2003	49	VGG 16-036
24	GJM 2004	50	VGG 16-027
25	GJM 2005	51	LC 1
26	GJM 2008	52	LC 2

3.3 CHARACTERS STUDIED

The observations were recorded on five randomly selected plants from each genotype per replication for the following characters. Observations on days to 50 per cent flowering and days to maturity were taken on plot basis:

3.3.1 Days to 50 per cent flowering

Number of days from date of sowing to the date of appearance of flower in 50 per cent of the plants in a plot were recorded.

3.3.2 Days to maturity

The total numbers of days were calculated from sowing to maturity when 80 per cent of the plants per plot turned yellow and started drying at physiological maturity.

3.3.3 Reproductive phase duration

Reproductive phase duration was calculated by taking difference between days to maturity and days to 50 per cent flowering.

3.3.4 Plant height (cm)

Height of plant was measured in centimeters from base of plant to the tip of main shoot at the time of harvesting.

3.3.5 Number of branches per plant

Number of fruiting branches arising from the main shoot were counted at the time of harvest.

3.3.6 Number of clusters per plant

The number of clusters arising from branches were counted from each of the selected plant at the time of harvesting.

3.3.7 Number of pods per plant

Total number of seed-bearing matured pods were counted from each selected plant at the time of harvesting.

3.3.8 Pod Length (cm)

Pod length was measured from base to the tip of pod from randomly selected five pods from individual plant at the time of maturity.

3.3.9 Number of seeds per pod

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

3.3.10 100-seed weight (g)

After threshing and cleaning the seeds, random 100-seeds were taken and weighed in grams.

3.3.11 Seed yield per plant (g)

At the time of harvesting, all the pods of selected plants were threshed, cleaned and their seeds weighed in grams and averaged.

3.4 STATISTICAL ANALYSIS:

The replication wise mean value of each genotype was worked out. These values were used for the statistical analysis for eleven 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 Agricultural University, Junagadh for various parameters *viz.*, genetic variability, heritability, genetic advance, genotypic and phenotypic correlations, path coefficient analysis, selection indices and genetic divergence.

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

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

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

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

Where,

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

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

(b) Phenotypic coefficient of variation (PCV)

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

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

Where,

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

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

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973).

GCV and PCV values	Classification
0 – 10	Low
10 – 20	Medium
20 and above	High

(c) Phenotypic range and range coefficient

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

Range = Maximum value – Minimum value

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

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

(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 indicated by Hanson *et al.* (1956) 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 (value of 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:

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

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

The phenotypic and genotypic 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 of analysis of covariance between two characters

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

Where,

r = Number of replications

g = Number of genotypes

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

Cov_{gxy}= Genotypic 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 significance of the genotypic and phenotypic correlation coefficients was tested against standardized tabulated values of 'r' with (n-2) error degree of freedom (Fisher and Yates, 1963).

r value	Classification
+ 0.70 or higher	Very strong positive relationship
+ 0.40 to + 0.69	Strong positive relationship
+ 0.30 to + 0.39	Moderate positive relationship
+ 0.20 to + 0.29	Weak positive relationship
+ 0.01 to + 0.19	No or negligible relationship
0	No relationship
- 0.01 to - 0.19	No or negligible relationship
- 0.20 to - 0.29	Weak negative relationship
- 0.30 to - 0.39	Moderate negative relationship
- 0.40 to - 0.69	Strong negative relationship
- 0.70 or lower	Very strong negative relationship

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 phenotypic as well as genotypic path coefficient analysis was done as per the method suggested by Dewey and Lu (1959).

Phenotypic as well as genotypic correlation coefficients of ten variables with seed yield were used to estimate the phenotypic path coefficient and genotypic path coefficient, respectively 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 of the form given below:

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

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

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$R_{9y} = P_{1y}\, r_{1.10} + P_{2y}\, r_{2.10} + ..., +P_{10y}$

Where,

r_{1y}, r_{2y}, r_{3y},…,..., r_{10y} are the genotypic correlations of days to 50 per cent flowering, days to maturity, reproductive phase duration, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod and 100-seed weight (g) on seed yield per plant, respectively.

P_{1y}, P_{2y}, P_{3y},…,…,…,..,P_{10y} are the direct effects of characters *viz*., days to 50 per cent flowering, days to maturity, reproductive phase duration, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) on seed yield per plant, respectively.

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

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

The residual variable was computed from the following formula:

Residual variable (X) = $1- R^2$

Where,

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

Path coefficients were rated as suggested by Lenka and Mishra (1973).

Scales	Classification
> 1.0	Very high
0.30 - 0.99	High
0.20 - 0.29	Moderate
0.10 - 0.19	Low
0.00 - 0.09	Negligible

3.4.5 Selection indices

Application of discriminant function as a basis for making the selection on several characters simultaneously is aimed at discriminating the desirable genotypes from undesirable ones based on their phenotypic performance. The concept of the selection index was first proposed by Smith (1936) on the basis of the discriminant function of Fisher (1936). The model suggested by Robinson *et al.* (1951) was used for the construction of selection indices and the development of a required discriminant function. Smith (1936) defined the genetic worth (H) of an individual as,

$$H = a_1G_1 + a_2G_2 + \ldots + a_nG_n$$

Where,

G_1, G_2,..., G_n is the genotypic values of individual characters and a_1,a_2, ...,a_n signify their relative economic importance.

Another function (I), based on phenotypic performance of various characters was defined as:

$$I = b_1p_1 + b_2p_2 + \ldots + b_np_n$$

Where,

b_1, b_2,...,b_n are to be estimated such that the correlation between H and I *i.e.*, r(H, I) becomes maximum. One such function is obtained, discrimination of good genotypes/characters from the undesirable ones will be possible based on phenotypic performance *i.e.*, p_1, p_2,..., p_n directly.

The maximization of r (H, I) leads to a set of simultaneous equations which upon solving give the desired estimate of "bi" values. Considering three characters as an example, the simultaneous equations look like as follows:

$$b_1X_{11} + b_2X_{12} + b_1X_{13} = a_1G_{11} + a_1G_{12} + a_1G_{13}$$

$$b_1X_{21} + b_2X_{22} + b_3X_{23} = a_1G_{21} + a_2G_{22} + a_3G_{23}$$

$$b_1X_{31} + b_2X_{32} + b_3X_{33} = a_1G_{31} + a_2G_{32} + a_3G_{33}$$

The matrix form of the above simultaneous equations is as under:

$$\begin{pmatrix} X_{11} & X_{12} & X_{13} \\ X_{21} & X_{22} & X_{23} \\ X_{31} & X_{32} & X_{33} \end{pmatrix} \times \begin{pmatrix} b_1 \\ b_2 \\ b_3 \end{pmatrix} = \begin{pmatrix} G_{11} & G_{12} & G_{13} \\ G_{21} & G_{22} & G_{23} \\ G_{31} & G_{32} & G_{33} \end{pmatrix} \times \begin{pmatrix} a_1 \\ a_2 \\ a_3 \end{pmatrix}$$

X b G a

Where,

X = Phenotypic variance-covariance matrix

b = Discriminant function coefficient column matrix

G = Genotypic variance-covariance matrix

a = Economic weightage column matrix

The solution of these equations gives the estimate of 'b_i' values in the following manner:

$$b_i = X^{-1}.G.a$$

Where,

X^{-1} = Inverse matrix of X

G = Genotypic variance-covariance matrix

a = Economic weightage column matrix

The mathematical description of the function (I) is known as selection index:

$$I = b_1p_1 + b_2p_2 + ..., + b_np_n$$

Using this function, it is possible to discriminate among the superior and inferior characters or combination of characters. The selection index or score is calculated for all the characters or combinations of characters and those with the highest values are considered.

a) Expected genetic advance

The expected genetic advance through selection was calculated as per the formula suggested by Robinson *et al.* (1951).

$$G = \frac{Z}{P} \frac{\Sigma\Sigma a_i b_j G_{ij}}{(\Sigma\Sigma b_i b_j P_{ij})^{1/2}}$$

Where,

Z/P = Standardized selection differential (s) indicating the intensity of selection (i) at 5% (k= 2.06)

a_i = Economic weightage

b_i = Regression coefficient

G_{ij} = Genotypic variance-covariance matrix

P_{ij} = Phenotypic variance-covariance matrix

b) Relative efficiency

The relative efficiency of different discriminant functions was calculated according to Robinson *et al.* (1951), assuming the efficiency of selection for seed yield per plant as 100 per cent.

$$RI(\%) = \frac{GA(D)}{GA(S)} \times 100$$

Where,

RI = Relative efficiency

GA (D) = Genetic advance through discriminant function

GA (S) = Genetic advance through straight selection

3.4.5 Genetic divergence

D^2 statistic is a measure for group distance which is based on multiple characters and its concept was initially developed by P.C. Mahalanobis (1936). With x_1, x_2, x_3 ...x_p as the multiple measurements available on each individual and d_1, d_2, d_3….d_p as x_1^{-1} - x_1^{-2}, x_2^{-1} - x_2^{-2}, …..x_p^{-1} - x_p^{-2}, respectively, being the difference in the means of two populations, Mahalanobis D^2 statistics is defined as follows :

$$pD^2 = b_1d_1 + b_2d_2 + \ldots\ldots b_pd_p$$

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

$$pD^2 = W_{ij} (x_i^{-1} - x_i^{-2}) (x_j^{-1} - x_j^{-2})$$

Where,

W_{ij} = inverse of estimated variance and covariance matrix.

3.4.5.1 Steps involved in estimation of D^2 values

3.4.5.1.1 Collection of data

Data have been measured on each individual considering "v" populations and "p" characters.

3.4.5.1.2 Test of significance

According to wilk's criteria a simultaneous test of differences between mean values of a no. of correlated variables is done.

With an implementation of pivotal condensation method, determinants of error and error + variety matrix will be calculated.

$$\wedge = \left|\frac{D}{S}\right| \left|\frac{\text{Determinant of matrix}}{\text{Determinant of error+variety of matrix}}\right|$$

$$V\,(Stat) = -m \log e \wedge = -\,[n - (p + g + 1)/2] \log e \wedge$$

Where,

$m = n - (p+q+1)/2$,

p = number of variance or characters,

q = number of varieties – 1 (or d. f. for populations)

n = degree of freedom for error + varieties

e = 2.7183 (constant) or

$\log_e \wedge = 2.3026 \log_{10} \wedge$

V $(Stat)$ is distributed as X^2 with Pq degrees of freedom.

The tabulated value of χ^2 for Pq degree of freedom at 5% level is compared with the χ^2 value for testing the significance.

3.4.5.2 Computation of D^2 values

"The D^2 value obtained for a pair of population was taken as the calculated value of χ^2 and tested against the tabulated value of χ^2 at "P" degree of freedom, where "P" was considered as the no. of traits".

3.4.5.3 Contribution of individual characters towards divergence

In each combination, individual trait was ranked on the basis of $di = Y_{ij} - Y_{ik}$ values and the trait having highest mean difference was ranked 1st where, "P" was considered as the no. of traits.

3.4.5.4 Grouping of genotypes into various clusters by Tocher's method

The first step of grouping the genotypes into different clusters is grouping of genotypes in order to their relative genetic distance from each other. Two genotypes having smallest distance from each other are considered first, then the third genotype having least D^2 value from the first two genotypes is added, then comes to the fourth genotype and so on. When it is felt that there is sudden increase in the average D^2 at certain point by including a specific genotype, then this genotype is not added into that cluster.

In the same way, second cluster is formed. This process is continued till entire genotypes are added into one or another cluster.

3.4.5.5 Average intra-cluster distance

Formula used for measuring the intra cluster distance is $\Sigma D_i^2/n$.

Where,

ΣD_i^2 = Sum of distance between all possible combination of the genotypes included in the cluster

n = Number of populations in the cluster

3.4.5.6 Average inter-cluster distance

Formula used for measuring the inter cluster distance is $\Sigma D_{ij}^2/n_i \times n_j$

Where,

ΣD_{ij}^2 = Sum of distance between all possible combination of the two cluster

n_i = Number of populations in the cluster i

n_j = Number of populations in the cluster j

At first, distance between cluster I and II, I and III, I and IV, I and V, I and VI, I and VII, I and VIII between II and III, II and IV and so on are measured. In other words, clusters are taken one by one and their distance from other clusters are computed.

CHAPTER IV

EXPERIMENTAL RESULTS

The current analysis was done using fifty-two greengram genotypes. The results presented in this chapter comprised of different aspects undertaken during the present study on **"Character association, path analysis and genetic divergence in greengram (*Vigna radiata* (L.) R. Wilczek)"**. The results of the experiment are given and discussed under the following aspects:

4.1 Analysis of variance

4.2 Genetic variability parameters

4.3 Correlation coefficient analysis

4.4 Path coefficient analysis

4.5 Selection indices

4.6 Genetic divergence

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 significant for all the eleven characters 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 PARAMETERS

Presence of genetic variability is unambiguously the most important prerequisite for crop improvement programme. 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 showing mean squares for various characters in 52 genotypes of greengram

		Mean squares										
Source	**d. f.**	**DF**	**DM**	**RPD**	**PH (cm)**	**NBP**	**NCP**	**NPP**	**PL (cm)**	**NSP**	**100-SW (g)**	**SYP (g)**
Replications	2	6.33	0.54	0.95	2.45	0.14	0.17	0.77	0.56	1.27	0.00	0.04
Genotypes	51	7.62**	16.25**	18.98**	118.22**	1.01**	4.35**	180.79**	1.01**	1.95*	0.67**	15.90**
Error	102	2.22	2.36	1.68	19.21	0.06	0.22	8.75	0.33	1.22	0.04	0.44

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

Here; DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod, 100-SW= 100-seed weight and SYP= Seed yield per plant.

4.2.1 Mean performance and range

The mean value of 52 genotypes of greengram for eleven characters along with the standard error of mean (S.Em), critical difference (CD) and coefficient of variance (CV per cent) are given in Appendix II, the summary of which is also presented in Table 4.2.

4.2.1.1 Days to 50 per cent flowering

Earliness in flowering is a desirable trait in greengram. This character ranged from 37 days to 46 days. The genotype SKNM 1901 found the earliest (37 days) followed GM 04-04 (38 days), GJM 1701 (38 days) and GJM 2005 (38 days). Whereas, the genotype VGG 16-036 took the maximum days to 50 per cent flowering (46 days). Out of fifty-two genotypes, thirty-nine genotypes were equal to or early and thirteen genotypes were late than the mean days to 50 per cent flowering (41 days). The range coefficient for days to 50 per cent flowering was 10.40 per cent.

4.2.1.2 Days to maturity

With respect to days to maturity, mean values ranged from 68 days to 78 days. The genotypes GJM 1703 (68 days), GJM 1818 (68 days), GJM 1819 (68 days), GJM 1909 (68 days), GJM 1912 (68 days), SKNM 1901 (68 days) and SKNM 1911 (68 days) were earliest to mature while, the genotype Meha took maximum days for maturity (78 days). Out of fifty-two genotypes, twenty-five genotypes were equal to or early and twenty-seven genotypes were late than mean values (72 days). The range coefficient for days to maturity was 6.93 per cent.

4.2.1.3 Reproductive phase duration

The range of reproductive phase duration was noticed from 27 days to 38 days and the mean value was 32 days. The genotypes GJM 1909 and GJM 1912 exhibited the shortest (27 days) reproductive phase duration. VMS 6 took maximum days for reproductive phase duration (38.00 days). Out of fifty-two genotypes, twenty-nine genotypes take lower than or equal to the mean value (32 days) and remaining twenty-three genotypes were more than mean value of reproductive phase duration. The coefficient of range was found 16.92 per cent for this trait.

4.2.1.3 Plant height (cm)

The range for plant height in material was 48.47 cm to 77.13 cm. The genotype RMG 268 (77.13 cm) found the tallest followed by GJM 1024 (74.13 cm), GJM 1822 (72.60 cm) whereas, Sona mung (48.47 cm) had the shortest plant height. Twenty-five, out of 52 genotypes remained above the mean value (60.84 cm) and remaining 27 genotypes below the mean value. The range coefficient for plant height was 22.82 per cent.

4.2.1.5 Number of branches per plant

The range for number of branches per plant was 1.00 to 3.07. The number of branches per plant was highest in GJM 2026 (3.07) followed by GJM 1902 (3.00), Meha (2.93) and RMG 268 (2.93). Whereas, minimum number of branches per plant were observed in GJM 1912 (1.00) and GJM 2009 (1.00). Twenty-five genotypes were recorded more than the mean value of number of branches per plant (1.96). The range coefficient for number of branches per plant was 50.86 per cent.

4.2.1.6 Number of clusters per plant

An average value for number of clusters per plant was 4.65. Among 52 genotypes, GJM 1703 possessed the maximum number of clusters per plant (7.20) and minimum in IPM 409-4 (2.47). The number of clusters per plant ranged from 2.47 to 7.20. Twenty-four genotypes exhibited more than mean value for number of clusters per plant. The range of coefficient for number of clusters per plant was 48.91 per cent.

4.2.1.7 Number of pods per plant

Number of pods per plant ranged from 11.27 to 54.07. The genotype GJM 1911 exhibited the maximum number of pods per plant (54.07) followed by GJM 1902 (44.07), GJM 1024 (39.53) and Meha (36.47). The genotype VGG 16-027 (11.27) had minimum number of pods per plant. Twenty-seven genotypes exhibited more than the mean value of number of pods per plant. The range of coefficient for number of pods per plant was 65.50 per cent.

Table 4.2 Genetic parameters of variability for yield and its components in greengram genotypes

Characters	Phenotypic range	Mean	Range coefficient (%)	Genotypic coefficient of variation (%)	Phenotypic coefficient of variation (%)	Heritability in broad sense (%)	Genetic advance (GA)	GA expressed as per cent of mean
Days to 50 per cent flowering	37.33-46.00	40.68	10.40	3.30	3.92	70.80	2.33	5.72
Days to maturity	67.67-77.67	72.17	6.93	2.98	3.23	85.50	4.10	5.68
Reproductive phase duration	27.00-38.00	31.87	16.92	7.54	7.89	91.10	4.72	14.82
Plant height (cm)	48.47-77.13	60.84	22.82	9.44	10.32	83.80	10.83	17.80
Number of branches per plant	1.00-3.07	1.96	50.86	28.81	29.64	94.50	1.13	57.71
Number of clusters per plant	2.47-7.20	4.65	48.91	25.23	25.88	95.00	2.36	50.65
Number of pods per plant	11.27-54.07	26.04	65.50	29.08	29.81	95.20	15.22	58.44
Pod length (cm)	6.37-8.77	7.46	15.85	6.39	7.79	67.40	0.81	10.80
Number of seeds per pod	8.87-12.33	10.37	16.32	4.76	7.78	37.30	0.62	5.98
100- seed weight (g)	2.03-4.13	3.27	34.09	13.98	14.42	94.00	0.91	27.91
Seed yield per plant (g)	3.57-14.70	7.59	60.92	29.89	30.32	97.20	4.61	60.71

4.2.1.8 Pod length (cm)

Pod length (cm) ranged from 6.37 cm to 8.77 cm. The genotype VGG 16-036 (8.77 cm) expressed maximum pod length followed by SKNM 1911 (8.67 cm), SKNM 1910 (8.60 cm), GJM 2003 (8.63 cm) and GJM 2005 (8.53 cm). The genotype Sona mung (6.37 cm) expressed minimum pod length. Twenty-two genotypes exhibited more than the mean value for pod length (7.46). The range of coefficient for length of pod was 15.85 per cent.

4.2.1.9 Number of seeds per pod

The mean value for number of seeds per pod ranged from 8.87 to 12.33. The genotype GJM 2004 (12.33) registered the maximum number of seeds per pod followed by GJM 2015 (12.13), GJM 2008 (11.87), GJM 2009 (11.57) and LC 1 (11.23). The genotype Sona mung (8.87) had minimum number of seeds per pod. Twenty-seven genotypes were more than the mean value of number of seeds per pod. The range coefficient for number of seeds per pod was 16.32 per cent.

4.2.1.10 100-seed weight (g)

The range of this character was 2.03 to 4.13 g. Mean value was registered to be 3.27 g. The genotype GJM 2008 had the maximum 100-seed weight (4.13 g) followed by VMS 6 (4.07 g) and SKNM 1910 (4.10 g). On the contrary, minimum weight of 100-seed was found in genotype Sona mung (2.033 g). Out of fifty-two genotypes of greengram, twenty-four genotypes were exceeded for 100-seed weight over its mean value (3.27 g). The range coefficient for 100-seed weight was 34.09 per cent.

4.2.1.11 Seed yield per plant (g)

The range for seed yield per plant exhibited from 3.57 to 14.70 g. The genotype GJM 1911 gave the maximum seed yield per plant (14.70 g) followed by GJM 1024 (11.43 g) and GJM 2026 (11.10 g) whereas, the minimum seed yield per plant was noted by the genotype VGG 16-027 (3.57 g). Out of fifty-two genotypes, twenty-nine genotypes were more than the mean value of seed yield per plant (7.59 g). The range coefficient for seed yield per plant was 60.92 per cent.

4.2.2 Genotypic coefficient of variation

Genotypic coefficients of variation for all eleven characters of greengram are furnished in Table 4.2. The highest genotypic coefficient of variation was observed for seed yield per plant (29.89 per cent) followed by number of pods per plant (29.08 per cent), number of branches per plant (28.81 per cent), number of clusters per plant (25.23 per cent) while 100-seed weight (13.98 per cent) exhibited moderate values for genotypic coefficient of variation. Days to maturity (2.98 per cent), days to 50 per cent flowering (3.30 per cent), number of seeds per pod (4.76 per cent), pod length (6.39 per cent), reproductive phase duration (7.54 per cent) and plant height (9.44 per cent) had low genotypic coefficient of variation.

4.2.3 Phenotypic coefficient of variation

Phenotypic coefficients of variation for all eleven characters of greengram are furnished in Table 4.2. The highest phenotypic coefficient of variation was observed for seed yield per plant (30.32 per cent) followed by number of pods per plant (29.81 per cent), number of branches per plant (29.64 per cent), number of clusters per plant (25.88 per cent) while plant height (10.32 per cent) and 100-seed weight (14.42 per cent) exhibited moderate values for phenotypic coefficient of variation. Days to maturity (3.23 per cent), days to 50 per cent flowering (3.92 per cent), number of seeds per pod (7.78 per cent), pod length (7.79 per cent) and reproductive phase duration (7.89 per cent) had low phenotypic coefficient of variation. Phenotypic coefficient of variation was slightly higher than that of genotypic coefficient of variation 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 greengram are given Table 4.2. High heritability estimates were observed for seed yield per plant (97.20 per cent) followed by number of pods per plant (95.20 per cent), number of clusters per plant (95.00 per cent), number of branches per plant (94.50 per cent), 100-seed weight (94.00 per cent), reproductive phase duration (91.10

per cent), days to maturity (85.50 per cent), plant height (83.80 per cent), days to 50 per cent flowering (70.80 per cent) and pod length (67.40 per cent). Whereas number of seeds per pod (37.30 per cent) expressed moderate heritability.

4.2.5 Genetic advance

The values of genetic advance estimated for different characters in greengram are summarized in Table 4.2. Genetic advance at 5 per cent selection intensity (k=2.06) was estimated for different characters. Moderate value of genetic advance was observed for number of pods per plant (15.22) and plant height (10.83). Low values of genetic advance were observed for reproductive phase duration (4.72), seed yield per plant (4.61), days to maturity (4.10), number of clusters per plant (2.36), days to 50 per cent flowering (2.33), number of branches per plant (1.13), 100-seed weight (0.91), pod length (0.81) and number of seeds per pod (0.62).

4.2.6 Genetic advance expressed as per cent of mean

Genetic advance expressed as per cent of mean (Table 4.2) was found high for seed yield per plant (60.71 per cent) followed by number of pods per plant (58.44 per cent), number of branches per plant (57.71 per cent), number of clusters per plant (50.65 per cent) and 100-seed weight (27.91 per cent). It was moderate for plant height (17.80 per cent), reproductive phase duration (14.82 per cent) and pod length (10.80 per cent). The values were low for number of seeds per pod (5.98 per cent), days to 50 per cent flowering (5.72 per cent) and days to maturity (5.68 per cent).

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. 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 Seed yield per plant

The seed yield per plant exhibited highly significant and positive correlation at phenotypic and genotypic levels with number of pods per plant (r_p=0.816, r_g=0.844)

and number of seeds per pod (r_p=0.525, r_g=0.883). Seed yield per plant had positively and significantly correlated with number of clusters per plant (r_p=0.342, r_g=0.352) at both phenotypic and genotypic levels. Number of branches per plant (r_p=0.240, r_g=0.251), plant height (r_p=0.231, r_g=0.258), 100-seed weight (r_p=0.179, r_g=0.187), reproductive phase duration (r_p=0.166, r_g=0.182) and days to maturity (r_p=0.011, r_g=0.013) were positively and non-significantly correlated with seed yield per plant at both phenotypic and genotypic levels. Seed yield per plant was negatively and significantly correlated with days to 50 per cent flowering (r_p=-0.273, r_g=-0.334) at both phenotypic and genotypic levels, while negative and non-significant association correlation with pod length (r_p=-0.030, r_g=-0.037) at both phenotypic and genotypic levels.

4.3.2 Days to 50 per cent flowering

Days to 50 per cent flowering had positive and significant correlation at both phenotypic and genotypic levels with days to maturity (r_p=0.297, r_g=0.319). Days to 50 per cent flowering had positive and non-significant correlation with plant height (r_p=0.078, r_g=0.122) and pod length (r_p=0.023, r_g=0.037) at both phenotypic and genotypic levels, while number of branches per plant (r_p=0.001) at phenotypic level. It showed negative and significant correlation with seed yield per plant (r_p=-0.273, r_g=-0.334) at both phenotypic and genotypic levels. Days to 50 per cent flowering showed negative and non-significant correlation with reproductive phase duration (r_p=-0.268, r_g=-0.240), number of pods per plant (r_p=-0.255, r_g=-0.309), 100-seed weight (r_p=-0.181, r_g=-0.236), number of clusters per plant (r_p=-0.141, r_g=-0.164) and number of seeds per pod (r_p=-0.108, r_g=-0.163) at both phenotypic and genotypic levels, while number of branches per plant (r_g=-0.008) at genotypic level.

4.3.3 Days to maturity

Days to maturity at both phenotypic and genotypic levels was positive and highly significant correlation with reproductive phase duration (r_p=0.778, r_g=0.865) while, plant height (r_g=0.390) at genotypic level. Days to 50 per cent flowering (r_p=0.297, r_g=0.319) and number of branches per plant (r_p=0.291, r_g=0.328) showed significant and positive association at both phenotypic and genotypic levels, while plant height (r_p=0.309) at phenotypic level only. Days to maturity showed positive and non-

Table 4.3 Phenotypic (r_p) and genotypic (r_g) correlation coefficients among eleven characters of greengram

Characters		DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	SYP
DF	r_p	1.000	0.297*	-0.268	0.078	0.001	-0.141	-0.255	0.023	-0.108	-0.181	-0.273*
	r_g	1.000	0.319*	-0.240	0.122	-0.008	-0.164	-0.309	0.037	-0.163	-0.236	-0.334*
DM	r_p		1.000	0.778**	0.309*	0.291*	0.027	-0.027	0.080	-0.115	-0.074	0.011
	r_g		1.000	0.865**	0.390**	0.328*	0.027	-0.024	0.083	-0.243	-0.096	0.013
RPD	r_p			1.000	0.316*	0.262	0.061	0.074	0.075	-0.044	0.104	0.166
	r_g			1.000	0.358**	0.290*	0.071	0.079	0.121	-0.104	0.118	0.182
PH	r_p				1.000	-0.009	0.089	0.140	0.277*	0.018	0.058	0.231
	r_g				1.000	-0.021	0.098	0.137	0.427**	0.084	0.076	0.258
NBP	r_p					1.000	0.529**	0.347*	-0.224	0.183	-0.173	0.240
	r_g					1.000	0.556**	0.352*	-0.267	0.299*	-0.180	0.251
NCP	r_p						1.000	0.336*	-0.126	0.237	0.008	0.342*
	r_g						1.000	0.345*	-0.149	0.403**	0.013	0.352*
NPP	r_p							1.000	-0.337*	0.276*	-0.204	0.816**
	r_g							1.000	-0.406**	0.411**	-0.214	0.844**
PL	r_p								1.000	0.072	0.549**	-0.030
	r_g								1.000	0.008	0.690**	-0.037
NSP	r_p									1.000	0.183	0.525**
	r_g									1.000	0.264	0.883**
100-SW	r_p										1.000	0.179
	r_g										1.000	0.187

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

Here; DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod,100-SW= 100-seed weight and SYP= Seed yield per plant.

significant correlation with pod length (r_p=0.080, r_g=0.083), number of clusters per plant (r_p=0.027, r_g=0.027) and seed yield per plant (r_p=0.011, r_g=0.013) at both phenotypic and genotypic levels, while negative and non-significant correlation with number of seeds per pod (r_p=-0.115, r_g=-0.243), 100-seed weight (r_p=-0.074, r_g=-0.096) and number of pods per plant (r_p=-0.027, r_g=-0.024).

4.3.4 Reproductive phase duration

Reproductive phase duration had highly significant and positive association with days to maturity (r_p=0.778, r_g=0.865) at both phenotypic and genotypic levels, while plant height (r_g=0.358) at genotypic level only. This trait showed positive and significant correlation with plant height (r_p=0.316) at phenotypic level and number of branches per plant (r_g=0.290) at genotypic level. Reproductive phase duration exhibited non-significant and positive correlation with number of branches per plant (r_p=0.262) at phenotypic level, while at both phenotypic and genotypic levels, seed yield per plant (r_p=0.166, r_g=0.182), 100-seed weight (r_p=0.104, r_g=0.118), pod length (r_p=0.075, r_g=0.121), number of pods per plant (r_p=0.074, r_g=0.079) and number of clusters per plant (r_p=0.061, r_g=0.071) was positively and non-significantly correlated. Days to 50 per cent flowering (r_p=-0.268, r_g=-0.240) and number of seeds per pod (r_p=-0.044, r_g=-0.104) expressed negative and non-significant correlation at both phenotypic and genotypic levels.

4.3.5 Plant height

Plant height expressed highly significant and positive correlation with pod length (r_g=0.427), days to maturity (r_g=0.390) and reproductive phase duration (r_g=0.358) at genotypic level. This trait showed positive and significant correlation with reproductive phase duration (r_p=0.316), days to maturity (r_p=0.309) and pod length (r_p=0.277) at phenotypic level. Seed yield per plant (r_p=0.231, r_g=0.258), number of pods per plant (r_p=0.140, r_g=0.137), number of clusters per plant (r_p=0.089, r_g=0.098), days to 50 per cent flowering (r_p=0.078, r_g=0.122), 100-seed weight (r_p=0.058, r_g=0.076) and number of seeds per pod (r_p=0.018, r_g=0.084) showed positive and non-significant correlation at both phenotypic and genotypic levels. Plant height showed negative and non-significant correlation with number of branches per plant (r_p=-0.009, r_g=-0.021) at both phenotypic and genotypic levels.

4.3.6 Number of branches per plant

Number of branches per plant exhibited positive and highly significant correlation with number of clusters per plant (r_p=0.529, r_g=0.556) at both phenotypic and genotypic levels. It showed positive and significant correlation with number of pods per plant (r_p=0.347, r_g=0.352) and days to maturity (r_p=0.291, r_g=0.328) at both phenotypic and genotypic levels, while number of seeds per pod (r_g=0.299) and reproductive phase duration (r_g=0.290) at genotypic level only. Number of branches per plant exhibited positive and non-significant correlation with seed yield per plant (r_p=0.240, r_g=0.251) at both phenotypic and genotypic levels, while reproductive phase duration (r_p=0.262), number of seeds per pod (r_p=0.183) and days to 50 per cent flowering (r_p=0.001) at phenotypic level only. Number of branches per plant exhibited negative and non-significant correlation with pod length (r_p=-0.224, r_g=-0.267), 100-seed weight (r_p=-0.173, r_g=-0.180) and plant height (r_p=-0.009, r_g=-0.021) at both genotypic and phenotypic levels, while days to 50 per cent flowering (r_g=-0.008) at genotypic level only.

4.3.7 Number of clusters per plant

Number of clusters per plant had positive highly significant and positive correlation with number of branches per plant (r_p=0.529, r_g=0.556) at both phenotypic and genotypic levels, while number of seeds per pod (r_g=0.403) at genotypic level only. Number of clusters per plant exhibited positive and significant correlation with seed yield per plant (r_p=0.342, r_g=0.352) and number of pods per plant (r_p=0.336, r_g=0.345) at both phenotypic and genotypic levels. It had positive and non-significant correlation with number of seeds per pod (r_p=0.237) at phenotypic level while, plant height (r_p=0.089, r_g=0.098), reproductive phase duration (r_p=0.061, r_g=0.071), days to maturity (r_p=0.027, r_g=0.027) and 100-seed weight (r_p=0.008, r_p=0.013) at both phenotypic and genotypic levels. It had negative and non-significant association with days to 50 per cent flowering (r_p=-0.141, r_g=-0.164) and pod length (r_p=-0.126, r_g=-0.149) at both phenotypic and genotypic levels.

4.3.8 Number of pods per plant

Number of pods per plant showed positive and highly significant association with seed yield per plant (r_p=0.816, r_g=0.844) at both phenotypic and genotypic levels,

while number of seeds per pod (r_g=0.411) at genotypic level only. It showed positive and significant correlation with number of branches per plant (r_p=0.347, r_g=0.352) and number of clusters per plant (r_g=0.336, r_p=0.345) at both phenotypic and genotypic levels, while number of seeds per pod (r_p=0.276) at phenotypic level only. Number of pods per plant was positively and non-significantly correlated with plant height (r_p=0.140, r_g=0.137) and reproductive phase duration (r_p=0.074, r_g=0.079) at both phenotypic and genotypic levels. It showed negative and highly significant association with pod length (r_g=-0.406) at genotypic level, while at phenotypic level pod length (r_p=-0.337) was negatively and significantly correlated. Number of pods per plant showed negative and non-significant association with days to 50 per cent flowering (r_p=-0.255, r_g=-0.309), 100-seed weight (r_p=-0.204, r_g=-0.214) and days to maturity (r_p=-0.027, r_g=-0.024) at both phenotypic and genotypic levels.

4.3.9 Pod length (cm)

Pod length showed highly significant and positive correlation with 100-seed weight (r_p=0.549, r_g=0.690) at both phenotypic and genotypic levels, while plant height (r_g=0.427) at genotypic level. Pod length showed positive and significant correlation with plant height (r_p=0.277) at phenotypic level, while positive and non-significant correlation with days to maturity (r_p=0.080, r_g=0.083), reproductive phase duration (r_p=0.075, r_g=0.121), number of seeds per pod (r_p=0.072, r_g=0.008) and days to 50 per cent flowering (r_p=0.023, r_g=0.037) at both phenotypic and genotypic levels. Pod length was negative and high significant correlation with number of pods per plant at genotypic level (r_g=-0.406), while at phenotypic level, number of pods per plant (r_p=-0.337) was significantly and negatively correlated. Number of branches per plant (r_p=-0.224, r_g=-0.267), number of clusters per plant (r_p=-0.126, r_g=-0.149) and seed yield per plant (r_p=-0.030, r_g=-0.037) showed negative and non-significant correlation with pod length at both phenotypic and genotypic levels.

4.3.10 Number of seeds per pod

Number of seeds per pod expressed highly significant and positive correlation with seed yield per plant (r_p=0.525, r_g=0.883) at both phenotypic and genotypic levels, while number of clusters per plant (r_g=0.403) and number of pods per plant (r_g=0.411) at genotypic level only. Number of seeds per pod showed positive and significant

correlation with number of branches per plant (r_g=0.299) at genotypic level and number of pods per plant (r_p=0.276) at phenotypic level while, positive and non-significant correlation with number of clusters per plant (r_p=0.237) at phenotypic level. Pod length (r_p=0.072, r_g=0.008) and plant height (r_p=0.018, r_g=0.084) showed positive and non-significant correlation at both phenotypic and genotypic levels, while number of branches per plant (r_p=0.183) at phenotypic level only. Days to maturity (r_p=-0.115, r_g=-0.243), days to 50 per cent flowering (r_p=-0.108, r_g=-0.163) and reproductive phase duration (r_p=-0.044, r_g=-0.104) showed negative and non-significant correlation at both phenotypic and genotypic levels.

4.3.11 100-seed weight

100-seed weight had positive and high significant correlation with pod length (r_p=0.549, r_g=0.690) at both phenotypic and genotypic levels. 100-seed weight exhibited positive and non-significant correlation with number of seeds per pod (r_p=0.183, r_g=0.264), seed yield per plant (r_p=0.179, r_g=0.187), reproductive phase duration (r_p=0.104, r_g=0.118), plant height (r_p=0.058, r_g=0.076) and number of clusters per plant (r_p=0.008, r_g=0.013) at both phenotypic and genotypic levels, while negative and non-significant correlation with number of pods per plant (r_p=-0.204, r_g=-0.214), days to 50 per cent flowering (r_p=-0.181, r_g=-0.236), number of branches per plant (r_p=-0.173, r_g=-0.180) and days to maturity (r_p=-0.074, r_g=-0.096) at both phenotypic and genotypic levels.

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 per cent flowering, days to maturity, reproductive phase duration, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod and 100-seed weight (g) 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 and Table 4.5, respectively. The path coefficient analysis revealed the cause-and-effect

Table 4.4 Genotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 52 genotypes of greengram

Characters	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	Genotypic correlation with SYP
DF	**0.220**	-0.076	-0.138	-0.021	0.002	-0.002	-0.240	0.011	-0.118	0.028	-0.334*
DM	0.070	**-0.240**	0.498	-0.067	-0.091	0.001	-0.018	0.025	-0.176	0.012	0.013
RPD	-0.053	-0.208	**0.576**	-0.062	-0.081	0.001	0.061	0.036	-0.075	-0.014	0.182
PH	0.027	-0.093	0.206	**-0.173**	0.006	0.001	0.106	0.127	0.061	-0.009	0.258
NBP	-0.002	-0.079	0.167	0.004	**-0.278**	0.007	0.274	-0.079	0.217	0.022	0.251
NCP	-0.036	-0.007	0.041	-0.017	-0.154	**0.012**	0.268	-0.044	0.291	-0.002	0.352*
NPP	-0.068	0.006	0.045	-0.024	-0.098	0.004	**0.777**	-0.121	0.297	0.026	0.844**
PL	0.008	-0.020	0.070	-0.074	0.074	-0.002	-0.315	**0.298**	0.006	-0.082	-0.037
NSP	-0.036	0.058	-0.060	-0.015	-0.083	0.005	0.319	0.003	**0.723**	-0.032	0.883**
100-SW	-0.052	0.023	0.068	-0.013	0.050	0.001	-0.166	0.205	0.191	**-0.119**	0.187

***, ** Significant at 5 % and 1 % levels, respectively** **Residual effect = 0.422**

Here; DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod and 100-SW= 100-seed weight.

relationship which is shown at genotypic level in Fig 4.1 and for phenotypic level in Fig. 4.2.

4.4.1 Genotypic path coefficient analysis

The genotypic path coefficient analysis (Table 4.4) revealed that number of pods per plant (0.777), number of seeds per pod (0.723) and reproductive phase duration (0.576) expressed positive and high direct effect on seed yield. Pod length (0.298) and days to 50 per cent flowering (0.220) showed moderate positive direct effect on seed yield per plant while, number of clusters per plant (0.012) had negligible and positive direct effect on seed yield per plant. However, negative direct effect on seed yield per plant were contributed through number of branches per plant (-0.278), days to maturity (-0.240), plant height (-0.173) and 100-seed weight (-0.119) at genotypic level. The characters which had shown significant genotypic correlation with seed yield per plant were considered for results and discussion.

4.4.1.1 Days to 50 per cent flowering *vs* seed yield per plant

Days to 50 per cent flowering had negative and significant association with seed yield per plant (r_g=-0.334). This trait exhibited positive and moderate (0.220) direct effect on seed yield in genotypic path coefficient analysis. Days to 50 per cent flowering had positive and negligible indirect effect *via* 100-seed weight (0.028), pod length (0.011) and number of branches per plant (0.002) while, negative indirect effect *via* number of pods per plant (-0.240), reproductive phase duration (-0.138), number of seeds per pod (-0.118), days to maturity (-0.076), plant height (-0.021) and number of clusters per plant (-0.002).

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

This character showed positive and significant association with seed yield per plant (r_g=0.352). This trait exhibited positive and negligible direct effect (0.012) on seed yield per plant. Number of clusters per plant expressed positive indirect effect on seed yield per plant *via* number of seeds per pod (0.291), number of pods per plant (0.268) and reproductive phase duration (0.041). Number of clusters per plant had negative indirect effect *via* number of branches per plant (-0.154), pod length (-0.044),

days to 50 per cent flowering (-0.036), plant height (-0.017), days to maturity (-0.007) and 100-seed weight (-0.002).

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

Number of pods per plant (r_g=0.844) had positive and highly significant correlation with seed yield per plant. It showed positive and high direct effect (0.777) on seed yield per plant in genotypic path coefficient analysis. Number of pods per plant exhibited positive and moderate indirect effect on seed yield *via* number of seeds per pod (0.297) while positive and negligible indirect effect *via* reproductive phase duration (0.045), 100-seed weight (0.026), days to maturity (0.006) and number of clusters per plant (0.004). This trait shows negative indirect effect *via* pod length (-0.121), number of branches per plant (-0.098), days to 50 per cent flowering (-0.068) and plant height (-0.024).

4.4.1.4 Number of seeds per pod vs seed yield per plant

Number of seeds per pod (r_g=0.883) was positive and highly significant association with seed yield per plant. It also showed positive and high direct effect (0.723) on seed yield per plant in genotypic path coefficient analysis. It exhibited positive indirect effect *via* number of pods per plant (0.319), days to maturity (0.058), number of clusters per plant (0.005) and pod length (0.003) while, negative indirect effect *via* number of branches per plant (-0.083), reproductive phase duration (-0.060), days to 50 per cent flowering (-0.036), 100-seed weight (-0.032) and plant height (-0.015).

4.4.2 Phenotypic path coefficient analysis

The phenotypic path coefficient analysis (Table 4.5) revealed that number of pods per plant (0.830), number of seeds per pod (0.259) and 100-seed weight (0.239) expressed positive and high to moderate direct effect on seed yield. While, reproductive phase duration (0.152) followed by days to 50 per cent flowering (0.068), pod length (0.067), number of clusters per plant (0.056) and plant height (0.034) had low to negligible positive direct effect on seed yield per plant. However, negative direct effect on seed yield per plant were contributed through number of branches per plant (-0.094)

Table 4.5 Phenotypic path coefficient analysis showing direct (diagonal and bold) and indirect effects of different characters on seed yield per plant in 52 genotypes of greengram

Characters	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	Phenotypic correlation with SYP
DF	**0.068**	-0.014	-0.041	0.003	0.001	-0.008	-0.212	0.002	-0.028	-0.043	-0.273*
DM	0.020	**-0.048**	0.118	0.010	-0.027	0.002	-0.022	0.005	-0.030	-0.018	0.011
RPD	-0.018	-0.037	**0.152**	0.011	-0.025	0.003	0.062	0.005	-0.011	0.025	0.166
PH	0.005	-0.015	0.048	**0.034**	0.001	0.005	0.116	0.019	0.005	0.014	0.231
NBP	0.001	-0.014	0.040	0.001	**-0.094**	0.030	0.288	-0.015	0.047	-0.041	0.240
NCP	-0.010	-0.001	0.009	0.003	-0.050	**0.056**	0.279	-0.008	0.061	0.002	0.342*
NPP	-0.018	0.001	0.011	0.005	-0.033	0.019	**0.830**	-0.023	0.072	-0.049	0.816**
PL	0.002	-0.004	0.011	0.009	0.021	-0.007	-0.279	**0.067**	0.019	0.131	-0.030
NSP	-0.007	0.006	-0.007	0.001	-0.017	0.013	0.229	0.005	**0.259**	0.044	0.525**
100-SW	-0.012	0.004	0.016	0.002	0.016	0.001	-0.169	0.037	0.047	**0.239**	0.179

***, ** Significant at 5 % and 1 % levels, respectively** **Residual effect = 0.369**

Here; DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod and 100-SW= 100-seed weight

and days to maturity (-0.048). The characters which had shown significant phenotypic correlation with seed yield per plant were considered for results.

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

Days to 50 per cent flowering had negative and significant association with seed yield per plant (r_p=-0.273). This trait exhibited positive and negligible (0.068) direct effect on seed yield per plant in phenotypic path coefficient analysis, while negative indirect effects *via* number of pods per plant (-0.212), 100-seed weight (-0.043), reproductive phase duration (-0.041), number of seeds per pod (-0.028), days to maturity (-0.014) and number of clusters per plant (-0.008). Days to 50 per cent flowering showed positive and negligible indirect effect *via* plant height (0.003), pod length (0.002) and number of branches per plant (0.001).

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

Number of clusters per plant had positive and significant association with seed yield per plant (r_p=0.342). It also had positive and negligible direct effect (0.056) on seed yield. Number of clusters per plant showed positive indirect effect on seed yield *via* number of pods per plant (0.279), number of seeds per pod (0.061), reproductive phase duration (0.009), plant height (0.003) and 100-seed weight (0.002). Whereas, negative indirect effect exhibited *via* number of branches per plant (-0.050), days to 50 per cent flowering (-0.010), pod length (-0.008) and days to maturity (-0.001).

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

The phenotypic correlation between number of pods per plant and seed yield per plant was highly significant and positive (r_p=0.816) and also exerted positive and high direct effect (0.830) on seed yield per plant. Number of pods per plant exhibited positive and negligible effect through number of seeds per pod (0.072), number of clusters per plant (0.019), reproductive phase duration (0.011), plant height (0.005) and days to maturity (0.001). However, negative indirect effect was observed *via* 100-seed weight (-0.049), number of branches per plant (-0.033), pod length (-0.023) and days to 50 per cent flowering (-0.018).

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

The phenotypic correlation between number of seeds per pod and seed yield per plant was highly significant and positive (r_p=0.525) and also exerted positive and moderate direct effect (0.259) on seed yield per plant. Number of seeds per pod exhibited positive and moderate indirect effect on seed yield per plant through number of pods per plant (0.229), while positive and negligible indirect effect on seed yield per plant through 100-seed weight (0.044), number of clusters per plant (0.013), days to maturity (0.006), pod length (0.005) and plant height (0.001). Number of seeds per pod exhibited negative and negligible indirect effect on seed yield per plant through number of branches per plant (-0.017), days to 50 per cent flowering (-0.007) and reproductive phase duration (-0.007).

4.5 SELECTION INDICES

For estimation of selection indices, the characters which had a significant correlation with seed yield per plant and positive direct effects on seed yield were considered. Seed yield per plant (X_1) along with its four components *viz*., days to 50 per cent flowering (X_2), number of clusters per plant (X_3), number of pods per plant (X_4) and number of seeds per pod (X_5) were identified and considered.

Thirty-one selection indices were assembled in all the possible combinations of seed yield and four yield contributing characters. The genetic advances were calculated and the relative efficiency of different discriminant functions concerning the straight selection for seed yield was compared. The data on selection index that depicts discriminant functions, genetic gain, relative efficiency and relative efficiency per character are given in Table 4.6, emphasizing the efficiency of selection for seed yield as 100 per cent.

As a consequence, this illustrated that consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. The surged efficiency was noticed when four or five characters were considered together.

When the relative efficiency of the single trait index was calculated, it was observed that maximum efficiency of 330.15 per cent was noticed for number of pods

per plant which was followed by seed yield per plant (100.00 per cent), number of clusters per plant (51.19 per cent), days to 50 per cent flowering (50.54 per cent) and number of seeds per pod (13.45 per cent).

Among the combinations involving two component characters, seed yield per plant and number of pods per plant (X_1X_4) exhibited maximum relative efficiency of 349.92 per cent followed by number of clusters and number of pods per plant (X_3X_4), number of pods per plant and number of seeds per pod (X_4X_5), days to 50 per cent flowering and number of pods per plant (X_2X_4) and seed yield per plant and number of seeds per pod (X_1X_5) had relative efficiency of 336.15 per cent, 333.17 per cent, 331.91 per cent and 121.04 per cent, respectively. Seed yield per plant and number of clusters per plant (X_1X_3), seed yield per plant and days to 50 per cent flowering (X_1X_2), number of clusters per plant and number of seeds per pod (X_3X_5), plant height and 100-seeds weight (X_2X_3) and days to 50 per cent flowering and number of seeds per pod (X_2X_5) had relative efficiency of 118.56 per cent, 105.19 per cent, 69.12 per cent, 66.80 per cent and 46.62 per cent, respectively.

The selection index based on three-character combinations indicated that a discriminant function based on days to 50 per cent flowering, number of clusters per plant and number of seeds per pod ($X_2X_3X_5$) possessed maximum relative efficiency of 522.07 per cent followed by seed yield per plant, days to 50 per cent flowering and number of pods per plant ($X_1X_2X_4$, 452.82 per cent), number of clusters per plant, number of pods per plant and number of seeds per pod ($X_3X_4X_5$, 443.79 per cent), seed yield per plant, number of clusters per plant and number of seeds per pod ($X_1X_3X_5$, 421.30 per cent), days to 50 per cent flowering, number of pods per plant and number of seeds per pod ($X_2X_4X_5$, 411.23 per cent). Seed yield per plant, days to 50 per cent flowering and number of seeds per pod ($X_1X_2X_5$), seed yield per plant, number of clusters per plant and number of pods per plant ($X_1X_3X_4$), days to 50 per cent flowering, number of clusters per plant and number of pods per plant ($X_2X_3X_4$), seed yield per plant, number of pods per plant and number of seeds per pod ($X_1X_4X_5$) and seed yield per plant, days to 50 per cent flowering and number of clusters per plant ($X_1X_2X_3$) had relative efficiency of 349.61 per cent, 321.62 per cent, 291.47 per cent, 212.40 per cent and 196.94 per cent, respectively.

Table 4.6 Selection index, discriminant function and expected genetic advance in yield and relative efficiency from the use of different selection indices in greengram.

Sr. no.	Selection index	Discriminant function	Expected genetic advance (GA)	Relative efficiency (%)	Relative efficiency per character (%)
1	X_1	0.9721 X_1 (Seed yield per plant)	4.61	100.00	100.00
2	X_2	0.7084 X_2 (Days to 50 per cent flowering)	2.33	50.54	50.54
3	X_3	0.9502 X_3 (Number of clusters per plant)	2.36	51.19	51.19
4	X_4	0.9516 X_4 (Number of pods per plant)	15.22	330.15	330.15
5	X_5	0.3733 X_5 (Number of seeds per pod)	0.62	13.45	13.45
6	X_1+ X_2	0.9440 X_1 + 0.6783 X_2	4.85	105.19	52.60
7	X_1+ X_3	0.9765 X_1 + 0.9627 X_3	5.47	118.56	59.28
8	X_1+ X_4	0.9847 X_1 + 0.9523 X_4	16.13	349.92	174.96
9	X_1+ X_5	1.0514 X_1 + 0.8817 X_5	5.58	121.04	60.52
10	X_2+ X_3	0.6942 X_2 + 0.9048 X_3	3.08	66.80	33.40
11	X_2+ X_4	0.6822 X_2 + 0.9494 X_4	15.30	331.91	165.95
12	X_2+ X_5	0.6539 X_2 + 0.2311 X_5	2.15	46.62	23.31
13	X_3+ X_4	0.9676 X_3 + 0.9520 X_4	15.50	336.15	168.08
14	X_3+ X_5	1.1331 X_3 + 0.5798 X_5	3.19	69.12	34.56
15	X_4+ X_5	0.9557 X_4 + 0.5983 X_5	15.36	333.17	166.59
16	X_1+ X_2+ X_3	1.0302 X_1 + 0.9279 X_2 + 0.9159 X_3	9.08	196.94	65.65
17	X_1+ X_2+ X_4	1.2014 X_1 + 1.0951 X_2 + 0.8805 X_4	20.88	452.82	150.94
18	X_1+ X_2+ X_5	1.3894 X_1 + 0.5864 X_2 + 0.7415 X_5	16.12	349.61	116.54
19	X_1+ X_3+ X_4	1.2191 X_1 + 1.0119 X_3 + 0.8893 X_4	14.83	321.62	107.21
20	X_1+ X_3+ X_5	1.2788 X_1 + 0.6292 X_3 + 0.7431 X_5	19.42	421.30	140.43
21	X_1+ X_4+ X_5	1.5605 X_1 + 0.8307 X_4 + 0.7627 X_5	9.79	212.40	70.80
22	X_2+ X_3+ X_4	1.1504 X_2 + 1.0205 X_3 + 0.9558 X_4	13.44	291.47	97.16
23	X_2+ X_3+ X_5	1.1576 X_2 + 0.8647 X_3 + 0.8457 X_5	24.07	522.07	174.02
24	X_2+ X_4+ X_5	0.7932 X_2 + 1.0716 X_4 + 0.8968 X_5	18.96	411.23	137.08
25	X_3+ X_4+ X_5	0.7729 X_3 + 1.0533 X_4 + 0.8850 X_5	20.46	443.79	147.93
26	X_1+ X_2+ X_3+ X_4	1.1965 X_1 + 1.1010 X_2 + 1.0321 X_3 + 0.8796 X_4	21.75	471.75	117.94
27	X_1+ X_2+ X_3+ X_5	1.5972 X_1 + 0.3779 X_2 + 0.4650 X_3 + 0.6786 X_5	15.33	332.55	83.14
28	X_1+ X_2+ X_4+ X_5	1.5349 X_1 + 0.7751 X_2 + 0.8799 X_4 + 0.7697 X_5	26.29	570.27	142.57
29	X_1+ X_3+ X_4+ X_5	1.5986 X_1 + 0.7464 X_3 + 0.8370 X_4 + 0.7425 X_5	24.79	537.71	134.43
30	X_2+ X_3+ X_4+ X_5	0.6533 X_2 + 0.6759 X_3 + 1.1216 X_4 + 0.8853 X_5	21.15	458.84	114.71
31	X_1+ X_2+ X_3+ X_4+ X_5	1.5874 X_1 + 0.6209 X_2 + 0.6412 X_3 + 0.9157 X_4 + 0.7457 X_5	26.99	585.53	117.11

In four-character selection index, a function involving seed yield per plant, days to 50 per cent flowering, number of pods per plant and number of seeds per pod ($X_1X_2X_4X_5$) exerted maximum relative efficiency and genetic advance of 570.27 per cent and 26.29 g, respectively. This was followed by seed yield per plant, number of clusters per plant, number of pods per plant and number of seeds per pod ($X_1X_3X_4X_5$), seed yield per plant, days to 50 per cent flowering, number of clusters per plant and number of pods per plant ($X_1X_2X_3X_4$), days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod ($X_2X_3X_4X_5$) and seed yield per plant, days to 50 per cent flowering, number of clusters per plant and number of seeds per pod ($X_1X_2X_3X_5$) had relative efficiency of 537.71 per cent, 471.75 per cent, 458.84 per cent and 332.55 per cent, respectively.

The selection index based on five characters combination *viz.*, seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod ($X_1X_2X_3X_4X_5$) had relative efficiency of 585.53 per cent and genetic advance of 26.99 g.

Among all the 31 selection indices, the highest relative efficiency (585.53 per cent) and genetic advance (26.99 g) was noticed by a selection index involving five-component characters *viz.*, seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod ($X_1X_2X_3X_4X_5$) as compared to straight selection for seed yield per plant only.

While calculating relative efficiency per character, it was observed that direct selection of number of pods per plant exerted maximum relative efficiency per character of 330.15 per cent. The selection index based on two component characters *viz.*, seed yield per plant and number of pods per plant (X_1X_4) exhibited second highest relative efficiency per character of 174.96 per cent. The selection index involving three component characters *viz.*, days to 50 per cent flowering, number of clusters per plant and number of seeds per pod ($X_2X_3X_5$) exerted relative efficiency per character of 174.02 per cent. The selection index based on four characters *viz.*, seed yield per plant, days to 50 per cent flowering, number of pods per plant and number of seeds per pod ($X_1X_2X_4X_5$) possessed relative efficiency per character of 142.57 per cent. The selection based on all five characters *viz.*, seed yield per plant, days to 50 per cent

flowering, number of clusters per plant, number of pods per plant and number of seeds per pod ($X_1X_2X_3X_4X_5$) exerted relative efficiency per character of 117.11 per cent.

4.6 GENETIC DIVERGENCE

Breeding programme depends on the genetic diversity present among genotypes for its accomplishment. Clustering and divergence analysis are pre-requisite to know the expansion of diversity among genotypes. It is measured in the form of phenotypic and genotypic diversity out of which genetic divergence is of enormous importance for choosing the parents for further use in hybridization programme for obtaining desirable genetic combination. Genetic divergence gives an idea about more genetically divergence genotypes and help in their identification and selection. Genetically diverse parents can be further used in any crop improvement programme for obtaining desirable segregants.

To estimate D^2 values, correlated means of characters were transformed to standard uncorrelated means using Tocher's method. The statistical distance (Mahalanobis D^2) between pair of genotypes were obtained as the sum of squares of the difference between the pairs of corresponding uncorrelated value of any two genotypes considered at a time.

4.6.1 Grouping of genotypes into various clusters

Fifty-two genotypes of greengram were grouped into 11 clusters based on divergence analysis. Distributions of genotypes into different clusters were presented in Table 4.7. Cluster I was the largest among all the clusters comprising 35 genotypes each, followed by cluster III consist of 5 genotypes and cluster II consist of 4 genotypes, whereas cluster IV, V, VI, VII, VIII, IX, X and XI comprising 1 genotype in each.

Table 4.7 Distribution of greengram genotypes into various cluster

Cluster no.	No. of genotypes	Name of genotypes
I	35	Virat, GJM 2013, GJM 2012, GJM 2021, GJM 2032, COGG 13-39, GM 04-04, GJM 2019, GJM 2004, GJM 1916, GJM 2015, ANDG 1800, ANDG 1801, GJM 1835, GJM 2020, GJM 2011, SML 1901, GJM 2018, GJM 2005, GJM 2003, GJM 1826, GJM 1819, GJM 2009, GJM 1818, SKNM 1901, GJM 1701, LC 1, Pusa 1842, SKM 1911, GJM 1909, Pusa 1501, IPM 409-4, SKNM 1911, LC 2 and SML 1827
II	4	RMG 268, GJM 1822, Meha and VMS 6
III	5	VGG 16-036, VGG 16-027, GJM 1912, Sona mung and GJM 1907
IV	1	GJM 2026
V	1	GJM 1024
VI	1	GJM 2017
VII	1	GJM 1703
VIII	1	GJM 2008
IX	1	SKNM 1910
X	1	GJM 1902
XI	1	GJM 1911

4.6.2 Average intra and inter-cluster distances among 11 clusters in greengram

The intra and inter-cluster D^2 mean values are presented in Table 4.8. The maximum inter-cluster distance was found between cluster IX and XI (22.79) followed by cluster III and XI (20.18), cluster II and XI (18.25), cluster VI and XI (17.03), cluster I and XI (16.79) and cluster VII and XI (16.74). The minimum inter-cluster distance was observed between cluster IV and VIII (6.30) followed by cluster IV and VI (6.77), cluster VI and VII (8.31), cluster V and VIII (8.86), cluster VI and VIII (8.91) and cluster V and XI (9.00). The intra-cluster distance (D) ranged from 0.00 to 9.57. Cluster III showed highest intra-cluster value (9.57), followed by cluster I (7.64) and cluster II

(7.52). The clusters IV, V, VI, VII, VIII, IX, X and XI contained only single genotype and therefore, their intra-cluster distance was zero.

4.6.3 Cluster Mean

The cluster mean for different characters are presented in Table 4.9. Wide range of variation was noted for all the characters under study.

In case of days to 50 per cent flowering, cluster III and cluster IV showed maximum value 42.87 days and 42.33 days, respectively and cluster XI showed minimum value of 39.33 days. Days to maturity was found maximum in cluster II, 75.83 day and minimum value was noticed for cluster VII, 67.67 days. Reproductive phase duration was found maximum in cluster II and IX, 36.08 days and 34.33 days, respectively while, cluster VII and cluster X showed minimum value of 27.67 days. Plant height had maximum in cluster V, 74.13 cm and minimum in cluster VI, 52.60 cm. Number of branches per plant showed maximum in cluster IV and cluster X, 3.07 and 3.00 respectively. Number of branches per plant showed minimum in cluster XI, 1.20. Number of clusters per plant showed maximum in cluster VII, 7.20 whereas cluster III and cluster XI showed minimum value of 3.47. Number of pods per plant was recorded maximum in cluster XI, 54.07 and minimum in cluster IX, 15.93. Pod length showed maximum in cluster IX, 8.60 cm and minimum in cluster X, 6.67 cm. Number of seeds per pod was maximum in cluster IV, 11.97 and minimum in cluster VII, 9.17. The mean value for 100-seed weight was recorded maximum in cluster VIII and cluster IX, 4.13 and 4.10 g respectively and minimum in cluster X, 2.30 g. The mean value for seed yield per plant was recorded maximum in cluster XI, 14.70 g followed by cluster VIII and V, 12.67 g and 11.43 g, respectively and minimum was found in cluster III, 4.83 g.

4.6.4 Contribution of individual character towards genetic divergence

The percentage contributions towards genetic divergence by 11 characters under study are presented in Table 4.10. The percent contribution of individual characters toward the total divergence was found high for seed yield per plant (27.15 per cent) followed by number of clusters per plant (18.25 per cent), number of branches per plant (18.02 per cent), 100-seed weight (15.23 per cent), number of pods per plant (8.82 per cent) and reproductive phase duration (5.73 per cent). These six characters accounted

Table 4.8: Inter and intra-cluster D^2 values for different clusters

Clusters	I	II	III	IV	V	VI	VII	VIII	IX	X	XI
I	**7.64**	10.25	10.11	10.15	10.48	9.27	9.83	10.76	10.19	11.46	16.79
II		**7.52**	13.46	10.21	10.99	10.15	12.73	11.75	10.25	12.01	18.25
III			**9.57**	14.93	13.97	13.64	12.17	16.26	13.24	13.15	20.18
IV				**0.00**	10.84	6.77	12.17	6.30	11.31	10.97	15.98
V					**0.00**	12.05	11.64	8.86	15.88	11.22	9.00
VI						**0.00**	8.31	8.91	9.48	10.13	17.03
VII							**0.00**	12.19	13.36	9.85	16.74
VIII								**0.00**	12.95	13.99	13.28
IX									**0.00**	15.97	22.79
X										**0.00**	14.96
XI											**0.00**

Table 4.9: Cluster mean for yield and its component traits of greengram genotypes: Tocher's Method

Clusters	DF	DM	RPD	PH (cm)	NBP	NCP	NPP	PL (cm)	NSP	100-SW (g)	SYP (g)
I	40.41	71.89	31.90	60.05	1.86	4.48	24.50	7.52	10.44	3.34	7.37
II	40.25	75.83	36.08	70.33	2.83	5.88	30.18	7.30	10.40	2.96	8.03
III	42.87	72.33	29.87	58.28	1.71	3.47	18.95	7.23	9.67	2.75	4.83
IV	42.33	71.67	29.33	58.07	3.07	5.53	31.53	7.40	11.97	3.93	11.10
V	41.33	74.00	33.00	74.13	1.67	4.07	39.53	7.47	10.47	2.93	11.43
VI	42.00	72.00	30.00	52.60	2.37	7.13	33.70	7.03	10.73	3.90	8.63
VII	40.00	67.67	27.67	65.47	1.30	7.20	31.63	6.73	9.17	2.97	8.00
VIII	40.33	71.67	32.33	62.27	1.87	5.33	30.53	7.87	11.87	4.13	12.67
IX	39.67	74.00	34.33	59.40	2.47	5.87	15.93	8.60	9.27	4.10	5.23
X	40.67	69.00	27.67	56.87	3.00	5.87	44.07	6.67	10.37	2.30	8.80
XI	39.33	72.00	32.67	60.47	1.20	3.47	54.07	7.53	10.10	3.03	14.70

Here; DF= Days to 50 per cent flowering, DM= Days to maturity, RPD= Reproductive phase duration, PH= Plant height, NBP= Number of branches per plant, NCP= Number of clusters per plant, NPP= Number of pods per plant, PL= Pod length, NSP= Number of seeds per pod,100-SW= 100-seed weight and SYP= Seed yield per plant.

for more than 90 per cent of total divergence in the material studied. Days to 50 per cent flowering, days to maturity, plant height, pod length and number of seeds per pod contributed low or negligible genetic divergence towards total divergence.

Table 4.10: Contribution of different characters towards clustering in greengram genotypes

Sr. No.	Character	Times Ranked 1st	Contribution towards divergence per cent
1	Days to 50 per cent flowering	12	0.90%
2	Days to maturity	15	1.13%
3	Reproductive phase duration	76	5.73%
4	Plant height (cm)	45	3.39%
5	Number of branches per plant	239	18.02%
6	Number of clusters per plant	242	18.25%
7	Number of pods per plant	117	8.82%
8	Pod length (cm)	17	1.28%
9	Number of seeds per pod	1	0.08%
10	100-seed weight (g)	202	15.23%
11	Seed yield per plant (g)	360	27.15%

CHAPTER-V

DISCUSSION

Plant breeding is an art and science used in crop plants for improving the genetic architecture about their economic use; it has become a technology or an industry in the course of its development. Most of the plant breeding programmes are geared towards the precept goal of enhancing genotypes or populace of genotypes to expand crop cultivars that are advanced in single or greater tendencies to the prevailing high-quality varieties in a crop. The yield of produce continually being the top hobby for the plant breeders as a completely complicated polygenic character and is stricken by a huge wide variety of genetic and non-genetic factors. As such the inheritance of this character is pretty complicated and hard to control in breeding programmes.

Global population explosion is triggering the serious problem of malnutrition. Pulses are one of the reliable options to overcome malnutrition. Greengram (*Vigna radiata* (L.) R. Wilczek) is the third important pulse crop of India grown in nearly 8 per cent of the total pulse area of the country. The seed contains 24.7 per cent protein due to its supply of cheaper protein source, it is designated as “poor man’s meat” (Potter and Hotchkiss, 1997). Every 100 g of mungbean seeds contains 132 mg calcium, 6.74 mg iron, 189 mg magnesium, 367 mg phosphorus, 124 mg potassium and vitamins (Haytowitz and Matthews, 1986). It has high digestibility and palatability; its pods are used as green vegetable. Its whole grains and split grains are used as dal and curry. Being highly digestible, its curry is generally recommended for patients. Its flour is used in various preparations like halwa, savoury dishes, snacks, pakoras and fried dal, to get very delicious and nutritious products. Its green plants, chopped and mixed with other fodders are palatable feed for animals. It is also used as green manuring crop, which adds nitrogen in addition to humus to the soil. It is a soil protecting crop in rainy season.

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.

The information on the phenotypic and genotypic relationships of seed yield in the greengram with its component characters and also among the characters themselves would be very useful to the breeders in developing an appropriate breeding strategy, since seed yield is a complex character and is influenced by number of traits as well as the environmental factors. Hence, selection of genotype with desirable characters would be greatly enhanced, if significant correlations between seed yield and its component characters are established. In order to improve seed yield by accumulating optimum combination of yield contributing characters in a single genotype, it is essential to know the implication of the inter relationship of various characters. The information on correlation and path coefficient provides an opportunity to know the magnitude and direction of association of yield with its direct and indirect components. Yield is a complex character influenced by the number of factors. Direct selection on the basis of yield may not be beneficial because many morphological traits affect it. Therefore, to make effective selection for higher yield, it is necessary to determine the relative efficiency of selection through discriminant function over straight selection.

Further, it is well known that the success of any breeding programme depends upon the availability of adequate genetic diversity. The major factor responsible for limited success in increasing the seed yield of greengram has been the narrow genetic base of the material available. It has been observed that genetically diverse parents show the maximum heterosis and offer the maximum chances of isolating transgressive segregates. Mahalanobis (1936) D^2 statistic is being used as an efficient tool in quantitative estimation of genetic diversity and for choice of parents in hybridization programme. In the present study, analysis of variance revealed that mean square due to genotypes was highly significant for all the traits indicating the presence of sufficient amount of genetic variability among the genotypes for all the 11 characters studied.

5.1 ANALYSIS OF VARIANCE

In the present experiment, fifty-two greengram 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 square due to all the traits exhibited significant difference among genotypes indicating the presence of sufficient amount of variability in the experimental material used. These findings are in accordance with findings of Makeen *et al.* (2007), Kumar *et al.* (2010), Hemavathy *et al.* (2015), Baisakh *et al.* (2016), Chandra *et al.* (2017), Garg *et al.* (2017a) and Bisti *et al.* (2022) 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 PARAMETERS

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 genotypic 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 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 observed was 2.98 per cent to 29.89 per cent whereas, it was 3.23 per cent to 30.32 per cent for phenotypic coefficient of variation indicating extent of GCV and PCV in the material studied. This finding is in agreement with earlier reports of Tabasum *et al.* (2010), Raturi *et al*. (2015), Sandhiya and Saravanan (2018), Anuradha *et al.* (2019), Mohammed *et al.* (2020) and Dhunde *et al.* (2021a).

The high genotypic coefficient of variation and phenotypic coefficient of variation was observed for seed yield per plant, number of pods per plant, number of branches per plant and number of clusters per plant. The high genotypic coefficient of variation indicated the presence of wide variation for the characters under study to allow

selection for individual traits. Similar findings were also reported earlier by Yadav *et al.* (2017) and Muthuswamy *et al.* (2019). Similar results were observed by Chandra *et al.* (2017) for number of clusters per plant and number of pods per plant. Similar results with Raturi *et al.* (2015) and Abhishek and Mogali (2020) for seed yield per plant and number of pods per plant. Similar results with Hemavathy *et al.* (2015) for seed yield per plant, number of pods per plant and number of clusters per plant.

In the present study moderate value for phenotypic coefficient of variation (PCV) was observed for 100-seed weight and plant height. Similar findings were also reported earlier by Garg *et al.* (2017a) and Abhisheka and Mogali (2020). Similar results with Ramakrishnan *et al.* (2018) and Dhunde *et al.* (2021a) for plant height. Moderated GCV for 100-seed weight were in agreement of Garg *et al.* (2017a) and Abhisheka and Mogali (2020).

Low value for phenotypic and genotypic coefficient of variation was observed for days to maturity, days to 50 per cent flowering, number of seeds per pod, pod length and reproductive phase duration. Similar results were observed by Yadav *et al.* (2017) and Dhunde *et al.* (2021a) for days to 50 per cent flowering, pod length and days to maturity. Similar results with Kumar *et al.* (2010) and Garg *et al.* (2017a) for days to 50 per cent flowering and days to maturity. Similar results with Muthuswamy *et al.* (2019) for number of seeds per pod. Similar results with Madhuri *et al.* (2020) for reproductive phase duration. Low genotypic coefficient of variation was observed for plant height also, this was in accordance with the finding of Sabatina *et al.* (2021).

5.2.2 Heritability

The genotypic coefficient of variation (GCV per cent) 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 in broad sense estimates (Table 4.2) were observed for seed yield per plant followed by number of pods per plant, number of clusters per plant, number of branches per plant, 100-seed weight, reproductive phase

duration, days to maturity, plant height, days to 50 per cent flowering and pod length. Similar conclusion was derived by Muthuswamy *et al.* (2019). Abbas *et al.* (2018) for plant height, number of clusters per plant, number of pods per plant, 100-seed weight and seed yield per plant; Barad *et al.* (2018) for reproductive phase duration; Mohammed *et al.* (2020) for number of branches per plant, days to 50 per cent flowering, 100-seed weight, plant height, pod length, seed yield per plant and number of pods per plant.

Moderate heritability in broad sense estimates was observed for number of seeds per pod. This finding is in agreement with earlier report of Hemavathy *et al.* (2015) and Azam *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 (Table 4.2) was high for seed yield per plant (60.71 per cent) followed by number of pods per plant (58.44 per cent), number of branches per plant (57.71 per cent), number of clusters per plant (50.65 per cent) and 100-seed weight (27.91 per cent). Similar findings were reported by Muthuswamy *et al.* (2019). Hemavathy *et al.* (2015) for number of clusters per plant and number of pods per plant. The similar results corroborated by Raturi *et al.* (2015) for seed yield per plant and number of pods per plant. Garg *et al.* (2017a) for number of branches per plant, 100-seed weight and seed yield per plant

The moderate estimate of genetic advance as per cent of mean was observed for plant height (17.80 per cent), reproductive phase duration (14.82 per cent) and pod length (10.80 per cent). Results are in conformity of Katiyar *et al.* (2015) and Dangi *et al.* (2017) for plant height and pod length; Chetariya *et al.* (2019) for reproductive phase duration.

The lower genetic advance as per cent of mean was observed for days to maturity (4.10), days to 50 per cent flowering (2.33) and number of seeds per pod (0.62). The similar finding was also obtained by Baisakh *et al.* (2016) and Azam *et al.* (2018) for number of seeds per pod. Baisakh *et al.* (2016) for days to 50 per cent flowering. Abbas *et al.* (2018) for days to maturity.

Heritability estimates reported here was based on broad sense only and hence the total genetic variance may include dominance and epistatic components which are not available for selection. Heritability being a single numerical expression on the ratio of two variances, may not lead to success if selection is based on heritability estimates alone. Shift in gene frequency under selection pressure towards desirable side is also termed as genetic advance. Therefore, high heritability coupled with high genetic advance expressed as per cent of mean is more valuable in predicting the effect of selection.

In the present investigation, the estimates of high heritability coupled with high genetic advance expressed as per cent of mean was observed for seed yield per plant, number of pods per plant, number of branches per plant, number of clusters per plant and 100-seed weight. 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 has been reported by Muthuswamy *et al.* (2019), Abhisheka and Mogali (2020). Similar results with Degefa *et al.* (2014), Garg *et al.* (2017a), Mohammed *et al.* (2020), Bisti *et al.* (2022) for seed yield per plant, number of branches per plant, number of pods per plant and 100-seed weight. Narasimhulu *et al.* (2013) also observed similar results for number of pods per plant and seed yield per plant. Hemavathy *et al.* (2015) observed for number of clusters per plant and number of pods per plant. This may be contributed to the preponderance of additive gene action and selection pressure could profitably be applied on this character for improving the seed yield.

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 between the traits, 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 plant characters.

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 greengram has 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 pods per plant and number of seeds per pod at both genotypic and phenotypic levels. Such result also reported by Prasanna *et al.* (2013), Sandhiya and Saravanan (2018) and Kanavi *et al.* (2019) for number of pods per plant. Similar results with Garg *et al.* (2017a), Abhisheka and Mogali (2020), Mohammed *et al.* (2020) and Dhunde *et al.* (2021b) for number of seeds per pod and number of pods per plant. While significant and positive correlation at both phenotypic and genotypic levels with number of clusters per plant. Similar findings were reported by Prasanna *et al.* (2013), Mohammed *et al.* (2020) and Reshmi *et al.* (2022) for number of clusters

per plant. Seed yield per plant had significant and negative correlation with days to 50 per cent flowering at phenotypic and genotypic levels, this findings are in accordance with Kanavi *et al.* (2019). This indicated that the character seed yield was more influenced by these attributes in greengram and therefore, were important for bringing improvement in seed yield. Johnson *et al.* (1955) emphasized that these correlated yield attributes can serve as indicator characters for improving seed yield. They have further emphasized that such improvement depends not only on genotypic correlations but phenotypic correlations also play an important role.

Days to 50 per cent flowering had a positive and significant association at both phenotypic and genotypic levels with days to maturity. Similar results were reported by Gadakh *et al.* (2013a), Prasanna *et al.* (2013), Kanavi *et al.* (2019), Mohammed *et al.* (2020) and Reshmi *et al.* (2022) for days to maturity. Days to maturity had a positive and highly significant association at genotypic level with plant height. Such results also reported by Gajanan and Lal (2022). Days to maturity had a positive and significant association at both genotypic and phenotypic levels with number of branches per plant. Similar results were reported by Gadakh *et al.* (2013a).

Plant height exhibited highly significant and positive correlation with pod length at genotypic level. Similar findings were reported by Gadakh *et al.* (2013a), Garg *et al.* (2017a), Kanavi *et al.* (2019), Gajanan and Lal (2022) and Tejaswini *et al.* (2022) for pod length. Number of branches per plant showed positive and highly significant correlation with number of clusters per plant at both genotypic and phenotypic levels. Similar findings were reported by Narasimhulu *et al.* (2013) and Mohammed *et al.* (2020). Number of branches per plant showed positive and significant correlation with number of pods per plant at both genotypic and phenotypic levels. Similar finding confounded by Prasanna *et al.* (2013) and Mohammed *et al.* (2020).

Number of clusters per plant showed positive and significant correlation with number of pods per plant at both genotypic and phenotypic levels. Similar results were obtained by Gadakh *et al.* (2013a), Muralidhara *et al.* (2015), Kanavi *et al.* (2019), Gajanan and Lal (2022) and Reshmi *et al.* (2022). Number of clusters per plant showed positive and highly significant correlation with number of seeds per pod at genotypic level. Similar findings were confounded by Muralidhara *et al.* (2015) and Reshmi *et al.* (2022). Number of pods per plant showed positive and significant correlation with number of seeds per pod at phenotypic level. Similar results were obtained by

Muralidhara *et al.* (2015), Kanavi *et al.* (2019) and Reshmi *et al.* (2022). Number of pods per plant showed negative and highly significant correlation with pod length at genotypic level. Similar results were reported by Muthuswamy *et al.* (2019). Number of pods per plant showed positive and significant correlation with number of seeds per pod at phenotypic level. Similar results were reported by Kanavi *et al.* (2019) and Reshmi *et al.* (2022). Pod length showed positive and highly significant correlation with 100-seed weight at both genotypic and phenotypic levels. Similar results were obtained by Muthuswamy *et al.* (2019).

The present results on correlation coefficients revealed that number of pods per plant and number of seeds per pod 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 as well as phenotypic correlation coefficient of different characters with seed yield was parted into their direct and indirect effects (Table 4.4 and Table 4.5). 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, number of seeds per pod and reproductive phase duration had positive and higher direct effect on seed yield per plant. These results were in conformity with earlier report of Rao *et al.* (2006), Prasanna *et al.* (2013), Azam *et al.* (2018), Goyal *et al.* (2021) for number of pods per plant. Thippani *et al.* (2013) for number of seeds per pod.

While, 100-seed weight, plant height, days to maturity and number of branches per plant had negative and direct effect on seed yield at genotypic level. Similar conclusion also derived by Tabasum *et al.* (2010) and Katiyar *et al.* (2015) for number of branches per plant; Abbas *et al.* (2018), Parihar *et al.* (2018) and Asari *et al.* (2019) for days to maturity and plant height; Mohan *et al.* (2019) for 100-seed weight.

Days to 50 per cent flowering exerted negative and moderate indirect effect through number of pods per plant on seed yield per plant. Days to maturity exhibited positive and high indirect effect on seed yield per plant through reproductive phase duration. Reproductive phase duration exerted negative and moderate indirect effect on seed yield per plant through days to maturity. Plant height exerted positive and moderate indirect effect on seed yield per plant through reproductive phase duration. Number of branches per plant exhibited positive and moderate indirect on seed yield per plant through number of pods per plant. Number of clusters per plant and number of pods per plant exhibited positive and moderate indirect effect on seed yield per plant through number of seeds per pod. Pod length exhibited negative and high indirect effect on seed yield per plant through number of pods per plant. Number of seeds per pod exhibited positive and high indirect effect on seed yield per plant through number of pods per plant. 100-seed weight exhibited positive and moderate indirect effect on seed yield per plant through pod length.

5.4.2 Phenotypic path coefficient analysis

The phenotypic path coefficient analysis (Table 4.5) revealed that positive direct effect on seed yield were exerted through number of pods per plant followed by number of seeds per pod and 100-seed weight. So, emphasis should be given to these traits in selection program for improvement of seed yield in greengram. Which coincides with

earlier reports of Tabasum *et al.* (2010) for number of pods per plant and 100-seed weight; Ahmad *et al.* (2013) and Prasanna *et al.* (2013) for number of seeds per pod, 100-seed weight and number of pods per plant; Parihar *et al.* (2018) for 100-seed weight and number of seeds per pod.

However, negative direct effect on seed yield per plant were contributed through days to maturity and number of branches per plant. Similar results were reported by Thippani *et al.* (2013) and Mohan *et al.* (2019). Similar conclusion also derived by Muthuswamy *et al.* (2019) for number of branches per plant and Mohammed *et al.* (2020) for days to maturity.

Pod length and days to 50 per cent flowering exerted negative and moderate indirect effect on seed yield per plant through number of pods per plant. Number of branches per plant, number of clusters per plant and number of seeds per pod exhibited positive and moderate indirect effect on seed yield per plant through number of pods per plant.

The residual effect was found to be 0.422 for genotypic path coefficient analysis, while it was 0.369 at phenotypic path coefficient analysis. This indicated that other attributing character were also important and may play a critical role in greengram improvement. These results are in accordance with the reports of Ghimire *et al.* (2018), Mohan *et al.* (2019), Abhisheka and Mogali (2020) and Mohammed *et al.* (2020).

5.5 SELECTION INDICES

Seed yield in greengram is a complex entity associated with many contributing traits which are interrelated among them. The interdependence of contributory traits affects the selection criteria. The objective of this study to construct suitable selection indices for obtaining high genetic gain for seed yield. The plant breeder has certain desired plant characteristics in his mind while selecting for particular genotypes and he applies various weights to different traits for arriving at decisions. This suggests the use of a selection index that gives proper weight to each of the two or more characters to be considered. Hazel and Lush (1943) showed that the selection based on such an index is more efficient than selecting individuals for the various characters. The basis for the development of the selection indices has been provided by Smith (1936), Hazel (1943) and Robinson *et al.* (1951).

Hazel and Lush (1943) stated that the superiority of selection based on index increases with an increase in the number of characters under selection. In the present study the maximum genetic advance (GA) and relative efficiency in single character (number of pods per plant) discriminant function was 15.22 g and 330.15 per cent, respectively. In two-character combinations, seed yield per plant and number of pods per plant had maximum genetic advance (GA) and relative efficiency of 16.13 g and 349.92 per cent, respectively. In three characters combination days to 50 per cent flowering, number of clusters per plant and number of seeds per pod had the highest genetic advance (GA) and relative efficiency of 24.07 g and 522.07 per cent, respectively. In four-character combinations *viz.*, seed yield per plant, days to 50 per cent flowering, number of pods per plant and number of seeds per pod weight had the highest genetic advance and relative efficiency of 26.29 g and 570.27 per cent, respectively.

The maximum efficiency in selection for seed yield was exhibited by a discriminant function involving five characters combination *viz.*, seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod had the highest genetic advance (26.99 g) and relative efficiency (585.53 per cent).

In the present study showed consistent increase in the relative efficiency of the succeeding index with simultaneous inclusion of each character. This was in agreement with the findings of Choudhary *et al.* (2017), Indu and Saxena (2017), Sana *et al.* (2017), Hadavani *et al.* (2018) and Das and Baisakh (2019).

Further, it was observed that the straight selection for yield was not that much rewarded (GA=4.61 g, RE=100.00 per cent) as it was through its components like days to 50 per cent flowering (GA=2.33 g, RE=50.54 per cent), number of clusters per plant (GA=2.36 g, RE=51.19 per cent), number of pods per plant (GA=15.22 g, RE=330.15 per cent) and number of seeds per pod (GA=0.62 g, RE= 13.45 per cent).

Relative efficiency per character was also worked out for each selection index in greengram. It was observed that number of pods per plant (X_4, 330.15 per cent) exerted maximum relative efficiency per character. Therefore, due weightage should be given to number of pods per plant while formulating selection index in greengram.

The present study also revealed that the discriminant function method of making selections in plants appears to be the most useful than the straight selection for seed yield per plant. Hence, the weightage should be given to the important selection indices while making the selection for yield advancement in greengram.

5.6 GENETIC DIVERGENCE ANALYSIS

Success of any breeding programme depends upon the amount of genetic variability present in the population. The use of Mahalanobis 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).

5.6.1 Clustering pattern

With the help of Tocher's method, 11 clusters were formed from fifty-two genotypes of greengram. The composition of clusters is given in Table 4.7. The result revealed that cluster I having largest number of genotypes (35) followed by cluster III (5) and cluster II (4). On the other hand, cluster IV, cluster V, cluster VI, cluster VII, cluster VIII, cluster IX, cluster X and cluster XI are solitary clusters.

In the present study, D^2 statistic estimated on 52 genotypes of greengram for 11 characters showed that the generalised distance between two entries varied from 7.52 to 9.57, which was an indicator of considerable diversity available in the material evaluated. The maximum intra-cluster distance was observed for cluster III (9.57) followed by cluster I (7.64) and cluster II (7.52). The clusters IV, V, VI, VII, VIII, IX, X and XI 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 IX and XI (22.79) followed by cluster III and XI (20.18), cluster II and XI (18.25), cluster VI and XI (17.03), cluster I and XI (16.79) and cluster VII and XI (16.74). The minimum inter-cluster distance was observed between cluster IV and VIII (6.30). 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 greengram.

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.

5.6.2 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. Cluster XI had high mean value for number of pods per plant, seed yield per plant and desirable for days to 50 per cent flowering. Cluster VII was desirable for days to maturity, reproductive phase duration and number of clusters per plant. Whereas, cluster IV had high mean value for number of branches per plant and number of seeds per pod. Cluster IX had high mean value for pod length. Cluster V had high mean value for plant height. Cluster VIII had high mean value for 100-seed weight. Therefore, intercrossing of genotypes involved in these clusters could be practiced for inducing variability in their respective characters and their rational improvement for increasing seed yield. On the basis of these characters, superior genotypes should be selected from two clusters having wide inter-cluster distance to create maximum variability in segregating generation. Heterosis is generally attributed to genetic divergence among the parental lines involved in the crosses.

5.6.3 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 (27.15 per cent) and was responsible for differentiating the genotypes studied. Number of clusters per plant (18.25 per cent), number of branches per plant (18.02 per cent), 100-seed weight (15.23 per cent), number of pods per plant (8.82 per cent) and reproductive phase duration (5.73 per cent) were the next important traits contributed to total genetic divergence. A considerable diversity of 93.20 per cent was observed due to these six characters. Hence selection for divergent parents based on these six characters would be useful for heterosis breeding in greengram. 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 per cent flowering, days to maturity, plant height, pod length and number of seeds per pod contributed low or 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 per cent flowering, days to maturity and number of seeds per pod. Nagda *et al.* (2020) for days to 50 per cent flowering and number of seeds per pod. Similar results for pod length were observed by Garg *et al.* (2017b), Jakhar and Kumar (2018) and Kumar *et al.* (2019). Similar results for plant height were observed by Sharma *et al.* (2018), Mathankumar *et al.* (2020), Goyal *et al.* (2021) and Ram and Saxena (2022).

CHAPTER VI
SUMMARY AND CONCLUSION

The present investigation entitled “Character association, path analysis and genetic divergence in greengram (*Vigna radiata* (L.) R. Wilczek)” was conducted at, Pulses Research Station, Junagadh Agricultural University, Junagadh during *kharif* 2022. The material consisted of fifty-two greengram 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 on five randomly selected plants in each entry and from each replication except days to 50 per cent flowering and days to maturity which was calculated on plot basis and their mean values were used for statistical analysis. The characters studied were days to 50 per cent flowering, days to maturity, reproductive phase duration, plant height (cm), number of branches per plant, number of clusters per plant, number of pods per plant, pod length (cm), number of seeds per pod, 100-seed weight (g) and seed yield per plant (g).

The salient features of the findings are as under:

1. The analysis of variance revealed the significant differences among the mean square due to genotypes for all the characters studied, suggesting the presence of sufficient amount of variability in the material used.

2. The values of phenotypic coefficient of variation were slightly higher than that of genotypic coefficient of variation for all the traits studied, indicating little effect of environment on the expression of characters studied. This suggests that phenotypic variation can be used to judge genetic variation.

3. High values of GCV and PCV were observed for seed yield per plant, number of pods per plant, number of branches per plant and number of clusters per plant. This indicated presence of genetic variation for these characters.

4. High heritability (broad sense) estimates were observed for seed yield per plant followed by number of pods per plant, number of clusters per plant, number of branches per plant, 100-seed weight, reproductive phase duration, days to maturity,

plant height, days to 50 per cent flowering and pod length. Whereas number of seeds per pod expressed moderate heritability. High heritability values suggested presence of sufficient amount of heritable variation in these characters.

5. High estimates of genetic advance as per cent of mean were found for seed yield per plant followed by number of pods per plant, number of branches per plant, number of clusters per plant and 100-seed weight. Moderate values of genetic advance as per cent of mean were observed for plant height, reproductive phase duration and pod length. On the other hand, low values of genetic advance as per cent of mean was observed for number of seeds per pod, days to 50 per cent flowering and days to maturity.

6. High heritability coupled with high genetic advance expressed as per cent of mean were observed for seed yield per plant, number of pods per plant, number of branches per plant, number of clusters per plant and 100-seed weight suggesting the role of additive gene action in inheritance of these character and selection based on these traits may be effective and sufficient improvement in seed yield may be achieved through selection of these traits.

7. 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, phenotypic expression of characters was altered due to influence of environmental factors.

8. Seed yield per plant was found highly significant and positively correlated with number of pods per plant and number of seeds per pod whereas it showed significant and positive correlation with number of clusters per plant at both genotypic and phenotypic levels. Hence, genetic improvement of seed yield can be done by giving prime importance to these traits throughout the selection procedure.

9. The genotypic path analysis revealed that number of pods per plant, number of seeds per pod and reproductive phase duration had positive and higher direct effect on seed yield per plant.

10. The phenotypic path analysis revealed that number of pods per plant, number of seeds per pod and 100-seed weight had positive and high to moderate direct effect

on seed yield per plant and that was found to be the most important yield components.

11. The residual effect indicated that other attributing character were also important and may play a critical role in greengram improvement.

12. The index comprising 31 selection indices involving seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod were constructed. The efficiency of selection increase with the inclusion of more number of characters in the index. The selection index based on five characters *viz.,* seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod recorded highest genetic advance and relative efficiency. So, this combination should be considered for seed yield improvement in greengram.

13. The genetic diversity analysis grouped genotypes in 11 clusters suggested the presence of considerable genetic diversity among the fifty-two genotypes studied.

14. The clustering pattern showed no parallelism between geographic distribution and genetic diversity.

15. The analysis of per cent contribution of various characters towards the expression of total genetic divergence indicated that seed yield per plant contributed most towards genetic divergence followed by number of clusters per plant, number of branches per plant, 100-seed weight, number of pods per plant and reproductive phase duration.

16. Based on the maximum genetic distance, it is advisable to attempt crossing of the genotypes from cluster IX with the genotypes of cluster XI and genotypes of cluster III with genotypes of cluster XI, which may lead to the generation of high genetic variability for yield improvement also can be utilized for hybridization and superior recombinants can be obtained from these clusters, which can be exploited in further breeding programmes.

CONCLUSION

It could be concluded from the present findings that additive gene action was operating for seed yield per plant, number of pods per plant, number of branches per plant, number of clusters per plant and 100-seed weight indicating high heritability coupled with high genetic advance. Study of correlation coefficient showed that number of pods per plant, number of seeds per pod and number of clusters per plant were the characters that displayed positive and significant association with seed yield per plant, while days to 50 per cent flowering showed negative and significant association with seed yield per plant. Number of pods per plant, number of seeds per pod and 100-seed weight displayed a high and positive direct effect on seed yield per plant. Hence, these traits deserve strategic importance while formulating effective breeding strategies with the aim of yield enhancement. Combination of five traits *viz.*, seed yield per plant, days to 50 per cent flowering, number of clusters per plant, number of pods per plant and number of seeds per pod were found as the most useful combination than straight selection for the seed yield alone. Seed yield per plant followed by number of clusters per plant, number of branches per plant, 100-seed weight, number of pods per plant and reproductive phase duration had maximum contribution towards the total genetic divergence, a considerable diversity was observed due to these characters. Hence, selection for divergent parents based on these characters would be useful for development of hybrids and selection in F_2 and subsequent generations for isolation of transgressive segregants for traits of interest in future breeding programme for improvement of greengram.

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Appendix I: Meteorological data for the duration of crop season in *Rabi* 2021-22 (Weekly data)

Month	Standard week	Temperature (c)		Mean relative humidity (%)		Wind speed (KMPH)
		Max.	Min.	Max.	Min.	
	45	33.7	17.4	63	28	2.7
November	46	32.8	15.9	68	35	4.2
	47	32.7	20.8	73	49	3.7
	48	32.1	16.2	77	49	2.8
December	49	28.6	16.8	70	45	4.5
	50	29.9	15.4	59	35	4.3
	51	28.6	10.9	60	32	3.8
	52	27.9	14.8	77	48	4.1
January	1	29.2	15.9	87	55	3.1
	2	24.7	9.4	75	35	5.5
	3	29.2	12.8	83	42	3.8
	4	26.7	10.1	76	31	4.7
	5	30.2	12.6	83	33	3.5
February	6	29.0	14.3	74	42	5.0
	7	31.3	12.7	73	33	4.1
	8	33.4	15.5	68	26	4.9
	9	34.5	17.1	61	21	5.4
March	10	36.0	18.8	49	20	6.2
	11	40.0	22.2	50	18	4.7
	12	38.7	22.4	58	22	6.2
	13	40.3	21.5	76	17	4.4

Appendix II: The mean values of greengram genotypes for 11 characters along with the standard error of mean (S.Em), critical difference (CD) and coefficient of variation (CV per cent)

Sr. No.	Name of genotype	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	SYP
1	Virat	41.33	70.67	29.33	55.07	2.07	5.70	26.87	6.73	9.30	2.90	7.00
2	VMS 6	38.67	76.33	38.00	64.13	2.47	5.93	28.60	7.50	9.57	4.07	8.97
3	Meha	41.33	77.67	36.67	67.47	2.93	5.53	36.47	6.97	10.13	2.27	7.93
4	Sona mung	42.67	75.33	33.00	48.47	2.47	4.00	18.37	6.37	8.87	2.03	4.03
5	IPM 409-4	38.67	74.00	35.00	56.30	2.20	2.47	27.00	7.20	9.47	3.10	5.07
6	RMG 268	40.33	73.33	34.33	77.13	2.93	6.67	27.80	7.27	10.97	2.67	7.60
7	COGG 13-39	42.33	74.00	31.67	64.20	2.37	4.87	29.00	7.63	9.80	3.13	8.03
8	GM 04-04	38.00	72.00	34.00	65.13	2.07	5.27	28.73	7.17	10.13	3.07	8.37
9	GJM 1024	41.33	74.00	33.00	74.13	1.67	4.07	39.53	7.47	10.47	2.93	11.43
10	GJM 1701	38.33	71.67	33.33	53.07	1.53	2.73	26.60	7.30	9.50	3.60	8.37
11	GJM 1703	40.00	67.67	27.67	65.47	1.30	7.20	31.63	6.73	9.17	2.97	8.00
12	GJM 1818	40.00	68.33	28.00	66.00	1.60	4.47	23.23	7.70	10.00	3.03	7.20
13	GJM 1819	39.33	68.33	32.67	69.13	1.80	3.53	32.10	7.27	10.67	3.47	9.63
14	GJM 1822	40.67	76.00	35.33	72.60	3.00	5.40	27.83	7.47	10.93	2.83	7.63

Cont…

Appendix II: Continue…

Sr. No.	Name of genotype	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	SYP
15	GJM 1826	40.33	70.67	30.33	69.00	1.87	3.93	31.70	7.60	10.50	3.97	7.83
16	GJM 1835	39.00	71.67	32.67	62.60	2.93	5.27	29.27	7.27	9.97	3.60	9.70
17	GJM 1902	40.67	69.00	27.67	56.87	3.00	5.87	44.07	6.67	10.37	2.30	8.80
18	GJM 1907	40.67	69.00	28.33	50.00	2.27	3.87	31.00	6.60	10.93	2.57	7.27
19	GJM 1909	40.33	67.67	27.33	60.13	1.53	4.40	21.20	8.13	10.40	3.60	5.47
20	GJM 1911	39.33	72.00	32.67	60.47	1.20	3.47	54.07	7.53	10.10	3.03	14.70
21	GJM 1912	40.33	68.33	27.00	58.00	1.00	3.07	18.60	7.00	9.97	3.13	5.13
22	GJM 1916	39.33	71.33	33.67	59.53	1.80	5.67	27.20	7.23	11.13	3.50	9.37
23	GJM 2003	40.00	73.33	33.33	64.07	1.40	4.33	19.40	8.63	10.47	3.67	9.20
24	GJM 2004	39.00	72.67	33.67	54.27	2.33	5.33	28.87	7.53	12.33	3.17	9.57
25	GJM 2005	38.00	73.33	35.33	65.07	2.27	6.40	27.10	8.53	11.17	3.43	9.13
26	GJM 2008	40.33	71.67	32.33	62.27	1.87	5.33	30.53	7.87	11.87	4.13	12.67
27	GJM 2009	41.67	72.67	31.33	61.00	1.00	3.67	22.87	7.97	11.57	3.37	7.93
28	GJM 2011	41.33	72.67	31.33	65.07	1.80	4.93	20.67	8.50	9.93	3.67	6.60
29	GJM 2012	40.67	69.67	29.00	49.87	2.20	4.67	21.87	6.83	10.77	2.93	5.97
30	GJM 2013	41.33	70.67	29.33	54.80	2.23	6.53	26.27	7.03	10.57	3.00	7.07
31	GJM 2015	42.00	72.67	30.67	60.93	2.00	5.93	33.13	7.13	12.13	3.20	10.20

Cont…

Appendix II: Continue…

Sr. No.	Name of genotype	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	SYP
32	GJM 2017	42.00	72.00	30.00	52.60	2.37	7.13	33.70	7.03	10.73	3.90	8.63
33	GJM 2018	41.33	72.67	33.33	60.47	1.53	3.53	20.13	7.40	10.53	3.33	6.37
34	GJM 2019	41.00	73.00	34.00	55.80	2.13	4.47	25.47	7.33	10.53	3.53	7.83
35	GJM 2020	41.67	73.67	32.00	68.53	1.60	4.80	27.33	7.13	10.73	3.43	10.03
36	GJM 2021	42.00	72.00	30.00	54.20	2.33	4.47	26.67	7.20	10.67	3.10	8.13
37	GJM 2026	42.33	71.67	29.33	58.07	3.07	5.53	31.53	7.40	11.97	3.93	11.10
38	GJM 2032	41.67	73.00	32.33	58.40	2.67	5.60	28.60	7.07	10.20	3.00	8.03
39	ANDG 1800	42.00	72.67	32.00	59.07	2.87	4.27	22.53	7.83	11.17	3.47	7.93
40	ANDG 1801	40.33	75.00	34.67	63.00	2.20	4.60	34.20	7.57	10.00	3.20	9.47
41	SKNM 1901	37.33	68.00	30.67	55.87	1.53	3.80	21.73	7.33	10.47	3.23	6.00
42	SKNM 1910	39.67	74.00	34.33	59.40	2.47	5.87	15.93	8.60	9.27	4.10	5.23
43	SKNM 1911	40.00	68.00	28.00	53.33	1.30	3.73	16.60	8.67	10.20	3.80	5.33
44	SML 1827	40.00	72.00	32.00	56.67	1.27	4.33	18.20	7.50	9.30	2.70	3.80
45	SML 1901	39.00	72.67	33.67	59.00	1.53	6.53	23.27	7.40	10.90	3.57	7.03
46	SKM 1911	40.67	72.67	32.00	57.40	1.53	3.47	15.13	7.77	9.67	3.77	4.57
47	Pusa 1501	40.67	72.33	31.67	55.20	1.27	3.27	19.87	6.73	10.83	2.87	5.00
48	Pusa 1842	41.33	74.67	33.33	64.40	1.27	3.40	22.20	6.60	9.87	3.20	5.73
49	VGG 16-036	46.00	74.33	29.00	66.07	1.47	3.60	15.53	8.77	9.50	2.90	4.17

Appendix II: Continue…

Sr. No.	Name of genotype	DF	DM	RPD	PH	NBP	NCP	NPP	PL	NSP	100-SW	SYP
50	VGG 16-027	44.67	74.67	32.00	68.87	1.33	2.80	11.27	7.40	9.07	3.13	3.57
51	LC 1	41.33	72.33	31.00	65.33	1.33	2.80	19.00	8.40	11.23	3.60	6.83
52	LC 2	43.00	73.33	34.00	61.27	1.60	3.53	14.27	7.70	9.27	3.77	4.17
	Mean	**40.68**	**72.17**	**31.87**	**60.84**	**1.96**	**4.65**	**26.04**	**7.46**	**10.37**	**3.27**	**7.59**
	S.Em. ±	0.86	0.89	0.75	2.53	0.14	0.27	1.71	0.33	0.64	0.12	0.38
	CV%	3.66	2.13	4.07	7.20	12.02	10.01	11.36	7.70	10.67	6.14	8.77
	C.D. 5%	2.41	2.49	2.10	7.10	0.38	0.75	4.79	0.93	1.79	0.32	1.08
	C.D. 1%	3.19	3.29	2.78	9.39	0.50	1.00	6.34	1.23	2.37	0.43	1.43

Fig. 3.1: Field view of greengram experiment at Pulses Research Station, JAU, Junagadh during *Kharif* 2022

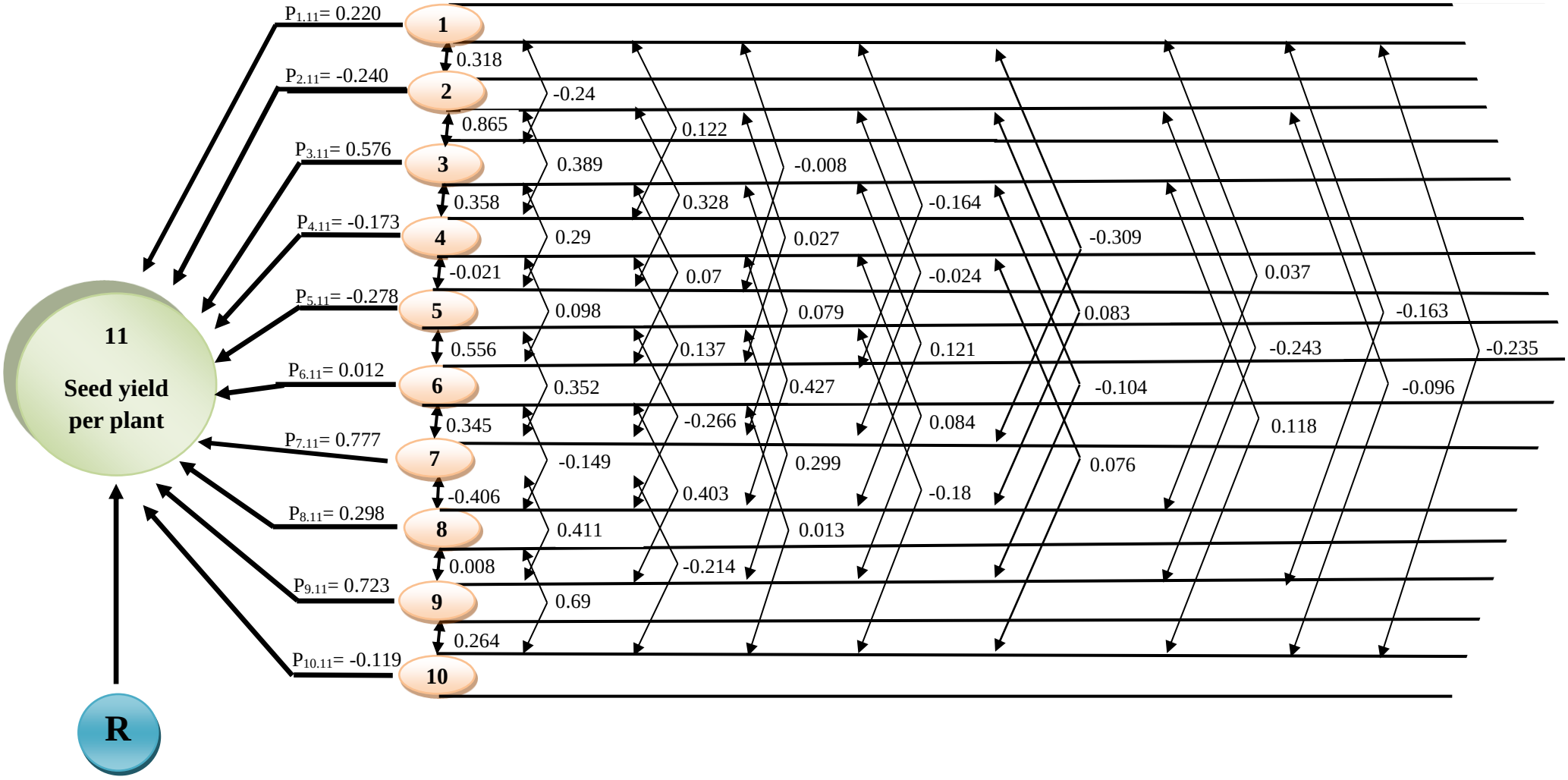

Fig 4.1: Diagrammatic representation of genotypic path analysis using 11 characters of greengram

Where, double arrowed lines indicate genotypic correlation coefficient and single arrowed lines indicate direct effect

1. **Days to 50 per cent flowering**
2. **Days to maturity**
3. **Reprodutive phase duration**
4. **Plant height (cm)**
5. **Number of branches per plant**
6. **Number of clusters per plant**
7. **Number of pods per plant**
8. **Pod length (cm)**
9. **Number of seeds per pod**
10. **100-seed weight (g)**
11. **Seed yield per plant (g)**

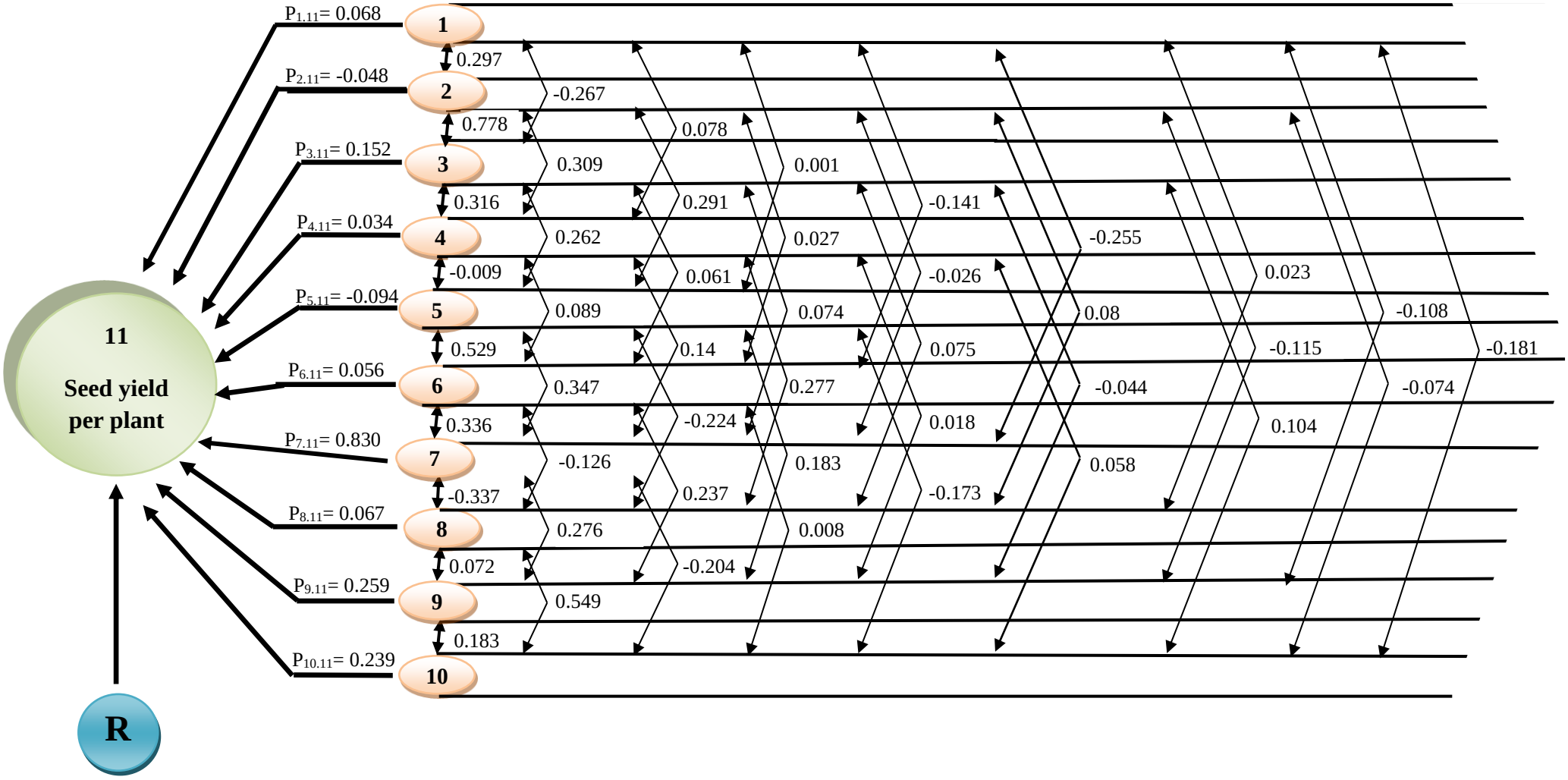

Fig 4.2: Diagrammatic representation of phenotypic path analysis using 11 characters in greengram

Where, double arrowed lines indicate phenotypic correlation coefficient and single arrowed lines indicate direct effect

1. **Days to 50 per cent flowering**
2. **Days to maturity**
3. **Reprodutive phase duration**
4. **Plant height (cm)**
5. **Number of branches per plant**
6. **Number of clusters per plant**
7. **Number of pods per plant**
8. **Pod length (cm)**
9. **Number of seeds per pod**
10. **100-seed weight (g)**
11. **Seed yield per plant (g)**