ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN SEGREGATING GENERATIONS OF GREENGRAM [*Vigna radiata* (L.) Wilczek]

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UNIVERSITY OF AGRICULTURAL AND HORTICULTURAL SCIENCES

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Thesis submitted to the

KELADI SHIVAPPA NAYAKA
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In partial fulfilment of the requirements
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Shivamogga **December, 2021**

DEPARTMENT OF GENETICS AND PLANT BREEDING
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CERTIFICATE

This is to certify that the thesis entitled **'ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN SEGREGATING GENERATIONS OF GREENGRAM [*Vigna radiata* (L.) Wilczek]'** submitted in partial fulfillment of the requirements for the award of the degree of **MASTER OF SCIENCE (AGRICULTURE)** in **GENETICS AND PLANT BREEDING** to the College of Agriculture, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga is a bonafide record of research work carried out by **ASMA BISTI., ID. No. MA1TAI0342** (asmabisti528@gmail.com) during the period of study in this university under my guidance and supervision and no part of this thesis has previously formed the basis for the award of any other degree, diploma, associateship, fellowship or any other similar titles.

Shivamogga
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ASSESSMENT OF GENETIC VARIABILITY AND DIVERSITY IN SEGREGATING GENERATIONS OF GREENGRAM [*Vigna radiata* (L.) Wilczek]

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ABSTRACT

Genetic analysis of segregating lines of two crosses KKM-3×IPM 205-7 and KKM-3 ×YADADRI in greengram was carried out to assess the genetic variability, diversity and association for yield and its contributing traits to make effective selection for increased yield. Significant mean differences among F_3 families of both the crosses were reported for all the traits through analysis of variance, indicating the adequate amount of genetic variability. The traits like number of pods per plant, seed yield per plant, number of clusters per plant, number of seeds per pod and hundred seed weight exhibited the highest values of phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), broad-sense heritability (h^2_{bs}) and genetic advance as *per cent* of mean (GAM), signifying that selecting certain attributes is highly rewarding to achieve enhanced production. The genetic diversity was assessed using Mahalanobis D^2 statistics. Based on the genetic distance, F_3 populations of Cross 1 and Cross 2 *viz.,* $C1F_3$ and $C2F_3$ were classified into nine and eight clusters, respectively where the number of pods per plant contributed maximum towards divergence. The highest inter-cluster D^2 value was found between clusters VIII and IX and clusters VII and VIII in $C1F_3$ and $C2F_3$ respectively, signifying that the families residing in separate clusters are more diverse. Correlation analysis reported that the seed yield per plant exhibited a positive relationship with all the traits except days to 50 *per cent* flowering in both the crosses. Path-coefficient analysis revealed that traits like hundred seed weight, number of pods per plant and pod length exerted a positive direct effect on seed yield per plant. The superior high yielding segregants were selected from both the populations and advanced to the next generation for the crop improvement in greengram.

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ಹೆಸರು ಬೆಳೆಯ ತಳಿ ಪ್ರಬೇಧಗಳನ್ನು ಪ್ರತ್ಯೇಕಿಸುವಲ್ಲಿ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ ಮತ್ತು ವೈವಿಧ್ಯತೆಯ ಮೌಲ್ಯಮಾಪನ

[ವಿಗ್ನಾ ರೇಡಿಯಾಟಾ (ಎಲ್.) ವಿಲ್ಜೆಕ್]

(ಅಸ್ಮ ಬಿಸ್ತಿ)

ಸಾರಾಂಶ

ಹೆಸರು ಬೆಳೆಯಲ್ಲಿ ಕೆಕೆಎಂ–೩ × ಐಪಿಎಂ ೨೦೫–೭ ಮತ್ತು ಕೆಕೆಎಂ–೩ × ಯಾದಾದ್ರಿ ಎಂಬ ಎರಡು ಸಂಕರಣಿಕೃತ ತಳಿ ಪ್ರಬೇಧಗಳ ಅನುವಂಶಿಕ ವಿಶ್ಲೇಷಣೆಯನ್ನು ಇಳುವರಿಗಾಗಿ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸ, ವೈವಿಧ್ಯತೆ ಮತ್ತು ಸಂಬಂಧದ ಅಧ್ಯಯನಗಳನ್ನು ಹಾಗೂ ಇಳುವರಿ ಹೆಚ್ಚಳಕ್ಕೆ ಪರಿಣಾಮಕಾರಿ ಆಯ್ಕೆಗಳನ್ನು ಮಾಡಲು ಅದರ ಕೊಡುಗೆಯ ಗುಣಲಕ್ಷಣಗಳನ್ನು ನಿರ್ಣಯಿಸಲು ನಡೆಸಲಾಯಿತು. ಎರಡೂ ಸಂಕರಣಿಕೃತ ಎಫ್೩ ಪೀಳಿಗೆ ನಡುವಿನ ಗಮನಾರ್ಹ ಸರಾಸರಿ ವ್ಯತ್ಯಾಸಗಳನ್ನು ಅನೋವಾ ಪರೀಕ್ಷೆ ಮೂಲಕ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳಿಗೆ ವರದಿ ಮಾಡಲಾಗಿದ್ದು, ಇದು ಸಾಕಷ್ಟು ಪ್ರಮಾಣದ ಅನುವಂಶಿಕ ವ್ಯತ್ಯಾಸವನ್ನು ಸೂಚಿಸುತ್ತದೆ. ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಕಾಯಿಯ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಗಿಡದ ಬೀಜದ ಇಳುವರಿ, ಪ್ರತಿ ಗಿಡದ ಗೊಂಚಲುಗಳ ಸಂಖ್ಯೆ, ಪ್ರತಿ ಕಾಯಿಯ ಬೀಜಗಳ ಸಂಖ್ಯೆ ಮತ್ತು ನೂರು ಬೀಜಗಳ ತೂಕದಂತಹ ಗುಣಲಕ್ಷಣಗಳು ಹೆಚ್ಚಿನ ವ್ಯತ್ಯಾಸದ ವಿಭಿನ್ನಾರ್ಥ ಗುಣಾಂಕ (ಫಿನೋಟೈಪಿಕ್ ಕೋಎಫಿಷಿಯಂಟ್ ಆಫ್ ವೇರಿಯೇಷನ್), ವ್ಯತ್ಯಾಸದ ವಂಶವಾಹಿ ಬಗೆಯ ಗುಣಾಂಕ (ಜಿನೋಟೈಪಿಕ್ ಕೋಎಫಿಷಿಯಂಟ್ ಆಫ್ ವೇರಿಯೇಷನ್), ಬ್ರಾಡಸೆನ್ಸ್ ಅನುವಂಶೀಕತೆ ಮತ್ತು ಸರಾಸರಿ ಶೇಕಡಾವಾರು ಅನುವಂಶಿಕ ಮುಂಗಡವನ್ನು ಸೂಚಿಸುವ ಮೂಲಕ ಈ ಮೇಲ್ಕಂಡ ಗುಣಲಕ್ಷಣಗಳ ಆಯ್ಕೆಯ ಮೂಲಕ ವರ್ಧಿತ ಉತ್ಪಾದನೆಯನ್ನು ಸಾಧಿಸಬಹುದು ಎಂದು ಹೇಳಲಾಗಿದೆ. ಮಹಾಲನೋಬಿಸ್ ಡಿ ಸ್ಕ್ವೇರ್ ಸಂಖ್ಯಾಶಾಸ್ತ್ರ ಬಳಸಿಕೊಂಡು ಅನುವಂಶಿಕ ವೈವಿಧ್ಯತೆಯನ್ನು ನಿರ್ಣಯಿಸಲಾಗಿದೆ. ಅನುವಂಶಿಕ ಅಂತರವನ್ನು ಆಧರಿಸಿ, ಸಿ೧ಎಫ್೩ ಮತ್ತು ಸಿ೨ಎಫ್೩ ಸಸ್ಯಸಮೂಹಗಳನ್ನು ಕ್ರಮವಾಗಿ ಒಂಬತ್ತು ಮತ್ತು ಎಂಟು ಸಮೂಹಗಳಾಗಿ ವರ್ಗೀಕರಿಸಲಾಗಿದೆ, ಅದರಲ್ಲಿ ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಕಾಯಿಯ ಸಂಖ್ಯೆಯು ಅನುವಂಶಿಕ ಭಿನ್ನತೆಗೆ ಹೆಚ್ಚಿನ ಕೊಡುಗೆ ನೀಡಿದೆ. ಸಿ೧ಎಫ್೩ ಪೀಳಿಗೆಯ ಗುಂಪಿನ ಸಮೂಹ ಎಂಟು ಮತ್ತು ಸಮೂಹ ಒಂಬತ್ತು ಹಾಗೂ ಸಿ೨ಎಫ್೩ ಪೀಳಿಗೆಯ ಗುಂಪಿನ ಸಮೂಹ ಏಳು ಮತ್ತು ಎಂಟರ ನಡುವೆ ಹೆಚ್ಚಿನ ಸಮೂಹದ ನಡುವಿನ ದೂರ ಕಂಡುಬಂದಿದೆ, ಇದು ಪ್ರತ್ಯೇಕ ಸಮೂಹದಲ್ಲಿರುವ ತಳಿ ಪ್ರಬೇಧಗಳು ಹೆಚ್ಚು ವೈವಿಧ್ಯಮಯವಾಗಿದೆ ಎಂದು ಸೂಚಿಸುತ್ತದೆ. ಗುಣಲಕ್ಷಣಗಳ ನಡುವಿನ ಸಂಬಂಧದ ಅಧ್ಯಯನ (ಕೋರಿಲೇಷನ್ ಕೋಎಫಿಷಿಯಂಟ್ ಅನಾಲೈಸಿಸ್) ಮುಖಾಂತರ ತಿಳಿಯುವುದೇನೆಂದರೆ, ಎರಡೂ ಸಂಕರಣಿಕೃತ ಸಂತತಿಗಳಲ್ಲಿ ಪ್ರತಿ ಗಿಡದ ಬೀಜದ ಇಳುವರಿಯು ಶೇಕಡ ೫೦ ಹೂಬಿಡುವ ದಿನಗಳನ್ನು ಹೊರತುಪಡಿಸಿ ಎಲ್ಲಾ ಗುಣಲಕ್ಷಣಗಳೊಂದಿಗೆ ಸಕಾರಾತ್ಮಕ ಸಂಬಂಧವನ್ನು ಪ್ರದರ್ಶಿಸಿದೆ. ನೂರು ಬೀಜಗಳ ತೂಕ, ಪ್ರತಿ ಗಿಡದಲ್ಲಿನ ಕಾಯಿಯ ಸಂಖ್ಯೆ ಮತ್ತು ಕಾಯಿಯ ಉದ್ದದಂತಹ ಗುಣಲಕ್ಷಣಗಳು ಪ್ರತಿ ಸಸ್ಯದ ಬೀಜದ ಇಳುವರಿ ಮೇಲೆ ಧನಾತ್ಮಕ ನೇರಪರಿಣಾಮ ಬೀರುವುದನ್ನು ಮಾರ್ಗ–ಗುಣಾಂಕದ ವಿಶ್ಲೇಷಣೆಯ ಅಧ್ಯಯನದಿಂದ (ಪಾಥ್ ಕೋಎಫಿಷಿಯಂಟ್ ಅನಾಲೈಸಿಸ್) ತಿಳಿದುಬಂದಿದೆ. ಅತ್ಯುನ್ನತ ಇಳುವರಿ ನೀಡುವ ತಳಿ ಪ್ರಬೇಧಗಳನ್ನು ಎರಡೂ ಪೀಳಿಗೆಯ ಗುಂಪುಗಳಿಂದ ಆಯ್ಕೆ ಮಾಡಲಾಗಿದೆ ಮತ್ತು ಹೆಸರು ಬೆಳೆಯಲ್ಲಿ ಬೆಳೆ ಸುಧಾರಣೆಗಾಗಿ ಮುಂದಿನ ಪೀಳಿಗೆಗೆ ರವಾನೆ ಮಾಡಲಾಗಿದೆ.

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INTRODUCTION

I INTRODUCTION

Green gram [*Vigna radiata* (L.) Wilczek], popularly known as mungbean or moong, is a leguminous plant species belonging to the Fabaceae family. It is a self-pollinated diploid ($2n = 2x = 22$) crop with typical papilionaceous flower bearing 5 sepals, 5 petals, 10 diadelphous (9 +1) stamens and monocarpellary ovary with hairy style. In India, mungbean is grown over an area of 4.5 million hectares with the total production of 2.64 million tonnes and productivity of 548 kg ha^{-1} (Anon., 2020-21).

Pulse crops are an essential group of food legumes that are grown all over the world. The majority of pulses can be farmed with little inputs on marginal areas. Since Asian diets are predominantly cereal based, the pulse protein and cereal protein must complement each other, resulting in much better protein utilization than the individual proteins. Pulses may surmount the rising issue of protein malnutrition, a significant nutrition problem in Asia that rigorously affects children. In India, 29.81 million hectares area has been occupied by pulses with an annual production of 25.58 million tonnes and an average productivity level of 853 kg per hectare as compared to global productivity of 871 kg per hectare (Anon., 2019). For domestic consumption, India still depends on imports from foreign countries.

Green gram is the third most crucial pulse crop of Asia after chickpea and pigeonpea. It is a legume crop with a wide range of adaptations, high versatility and drought tolerance that can improve soil fertility. This crop's high protein, easy digestion and low flatus made it more appealing to people all around the world (Prasanna *et al*., 2013). It is an inseparable ingredient in the diets of the vast majority of people in the Indian subcontinent due to its nutritious profile.

Green gram is a hardy pulse crop that thrives in hot, dry climates and its cultivation enhances soil fertility by contributing 30 to 40 kg N ha^{-1} to the soil after harvest. Therefore, the succeeding crop (usually a cereal) requires approximately 25 % less nitrogen application (Mbeyagala *et al.,* 2017). Despite being the world's biggest producer of greengram, India's productivity is very poor. Thus, there is a great scope for increasing its productivity by developing disease and pest resistance, high yielding varieties with good nutritional value.

The highly self-pollinated nature of this crop reduces the natural variability, which ultimately narrows down the effects of the selection process. The lack of genetic variability for high yield potential is the prime roadblock to a major mungbean breakthrough (Ramanujam, 1977). Investigation and a better understanding of the variability existing in a population constitute a base for efficient and effective breeding work (Bello *et al*., 2012).

The lack of variability in different traits is a bottleneck in its progress, because improving one trait on its own would affect the performance of other traits due to genotypic correlations across traits (Das and Baisakh, 2019). Estimating the extent of variability available in a crop is of immense value to the breeder to efficiently design the breeding procedure for crop improvement. The fruitfulness of selection depends on the nature and magnitude of the genetic variability present in the crop. As a result, knowledge on heritability coupled with genetic advance is critical in choosing a breeding programme.

The majority of agronomic characters in crop plants are quantitative in nature. Yield is one such character that results due to the actions and interactions of various component characters (Grafius, 1960). So, genetic architecture of yield can be resolved better by studying its component characters. This enables the plant breeder to breed for high yielding genotypes with desired combinations of traits (Khan and Dar, 2010). Therefore, studies on correlation and path analysis between different yield components are prerequisite for yield improvement.

The correlation coefficient indicates the degree and direction of association between yield and its component traits at both genotypic and phenotypic levels. But, the correlation coefficient does not always give precise information on the contribution of each trait towards the dependent variable. To understand the characters which contribute towards grain yield, the path analysis is obvious. The path coefficient analysis is simply a standardized partial regression coefficient, which splits the correlation coefficient into the measures of direct and indirect effects.

Genetic diversity analysis is a powerful tool in quantifying the degree of divergence between biological populations and the relative contribution of different components to total divergence. Grouping of mungbean genotypes based on genetic variation for different characters will enable breeders for better selections.

By considering all these assessments, the present study was conducted to estimate genetic variability, diversity and association studies for yield and yield components in early segregating lines (F_3) of greengram. With this premise, the present investigation was formulated with the following objectives.

1. To study genetic variability and diversity in F_3 segregating lines of greengram
2. To study correlation and path analysis in F_3 lines of greengram
3. To identify the superior segregants for yield and its attributing traits in greengram

REVIEW OF LITERATURE

II REVIEW OF LITERATURE

The success of the selection program in plant breeding relies on the magnitude of genetic variability in the population. Genetic variability and their quantification for qualitative and quantitative characters of economic importance are prerequisites for any crop improvement program. Hence, there is a need for knowledge on variability, heritability and genetic advance for efficient breeding, which is significant for the breeder to select the best genotypes for yield enhancement (Degafa *et al*., 2014).

2.1 To study genetic variability and diversity in F_3 segregating lines of greengram

2.2 To study correlation and path analysis in F_3 lines of greengram

2.3 To identify the superior segregants for yield and its attributing traits in greengram

2.1 To study genetic variability and diversity in F_3 segregating lines of greengram

Rao *et al.* (2006) studied genetic variability in sixty mungbean genotypes. High estimates of PCV, GCV, heritability and genetic advance were recorded for seed yield per plant, biological yield per plant, number of clusters per plant and number of pods per plant. These traits can be used for effective selections because of their high genetic variability.

Kumar *et al*. (2010) studied variability parameters in twenty three greengram genotypes. Higher estimates of GCV and PCV were recorded for harvest index and number of pods per plant. On the basis of genetic variability study, only 100 seed weight exhibited high heritability estimates (narrow sense) coupled with high genetic advance, indicating the preponderance of additive gene action.

Tabasum *et al.* (2010) evaluated ten mungbean genotypes to assess variability and the degree to which various plant traits associated with seed yield. Primary and secondary branches, pods per cluster and pod length showed less variability, while clusters per plant, 100 seed weight and harvest index exhibited a moderate range of variability. Sufficient genetic variability was observed for plant height, pods per plant, total plant weight and seed yield.

Abbas *et al*. (2010) studied genetic diversity in forty mungbean genotypes through Metroglyph analysis by distributing into 8 groups. Traits like plant height, clusters per plant, pods per plant, hundred seed weight, biological yield, seed yield and harvest index exhibited considerable genetic variability. The range of total mean index score varied from 12.6 to 17.0. Maximum index scores were obtained by groups I, II and III. In all three groups, biological yield and seed yield contributed more to index scores. NM 6368 (46-40-4 attained highest index score of 18) and VC 3945A, followed by Mung-88 and VC-3476 with an index score of 17. Lowest index score of 10 was attained by 3 genotypes viz., KPS-2, VC2984B and NM-94.

Reddy *et al*. (2011) studied yield and yield attributing characters in thirty five genotypes of greengram. Genotypes differed significantly for all the characters studied. High genetic advance coupled with high heritability was observed for characters like plant height, number of pods per plant and seed yield per plant.

Zaid *et al*. (2012) evaluated twenty mungbean genotypes for genetic variability for different yield contributing traits. Maximum plant height was observed for genotype NFM5-63-19; a maximum number of pods per plant was recorded for genotype NFM5-63-19, while genotypes NFM-12-8 and NFM-6-5 had the maximum pod length. Similarly, the maximum number of seeds per pod, biological yield and grain yield were observed with genotypes NFM-6-5, NFM-12-6 and NM-98, respectively. The high heritability was recorded for pod length (99 %) and plant height (70 %), while pods per plant (29 %) and seed per pod (17 %) had low heritability.

Variability parameters were studied in fifty diverse genotypes of mungbean and revealed that the traits plant height, number of primary branches per plant, number of clusters per plant, number of pods per plant, test weight and seed yield per plant possessing high heritability and genetic advance as *per cent* mean offer much scope for further improvement through simple selection techniques (Prasanna *et al.,* 2013).

Kumar *et al*. (2013) investigated variability in eighty two greengram genotypes. High estimates of PCV were observed for the characters harvest index, seed yield per plant, pod yield per plant and pods per plant, indicating the presence of a high amount of variation in the expression of these characters. However, harvest index and seed yield per plant recorded moderate values of GCV. High heritability in a broad sense was observed for primary branches per plant, followed by pod length. Characters like harvest index, primary branches per plant, seed yield per plant and pods per cluster showed moderate values of genetic advance as *per cent* mean.

Nand and Anuradha (2013) carried out variability studies with fifty genotypes. The genotypic coefficient of variation for all the characters studied was lesser than the phenotypic coefficients of variation, indicating the modifying effects of the environment in association with the characters at the genotypic level. High estimates of PCV and GCV were recorded for number of pods per plant, seed yield per plant.

Gadakh *et al.* (2013) studied genetic divergence and clustering pattern of fifty genotypes of greengram for selecting suitable parents that can be utilized in hybridization programs and to study the genetic parameters attributing to yield. The crosses of genotypes from cluster I, *i.e.*, Kopergaon, Vaibhav, BM-4 and BM-2005-1 with those of genotypes BM-2003-2, PM-203- 18, AKM-9907 and AKM-08-01 belonging to cluster III and RVSM-11, PM-201-19, ML-1354, AKM-0603 belonging to cluster II has the highest intercluster distance and might produce high level of segregating population in regards to yield as well as earliness. High heritability estimates coupled with high genetic advance were observed for harvest index and biological yield per plant, resembling the action of additive genes.

Garje (2013) evaluated forty genotypes of greengram to assess genetic divergence using Mahalanobis' D^2 Statistics. The genotypes were grouped into 13 clusters. Cluster III was largest with ten genotypes, followed by cluster II with eight genotypes. The maximum inter-cluster distance was observed between cluster VIII and IV, suggesting that the genotypes' genetic architecture in one cluster differs entirely from those included in other clusters. Three characters *viz*., seed yield per plant, number of pods per plant and pod length contributed maximum towards genetic diversity. Seed yield per plant had maximum PCV and GCV, followed by the number of pods per plant. High heritability coupled with high genetic advance was observed for plant height and number of pods per plant.

Narasimhulu *et al.* (2013) carried out the genetic variability study in forty mungbean genotypes for different quantitative characters during *Rabi*-2012. The highest GCV and PCV were observed for number of branches per plant, pods per plant, biological yield per plant and harvest index. High heritability coupled with high genetic advance as *per cent* mean was observed for plant height, pods per plant, pods per cluster, biological yield per plant, harvest index seed yield per plant and 100 seed weight, suggesting that these traits were controlled by additive gene action. Hence, direct selection may be exercised for the improvement of these traits.

Ahmad *et al.* (2014) studied genetic variability in fourteen greengram genotypes for yield attributing traits. Genotypic and phenotypic variances were high for number of pods per plant (18.60 and 19.50) and days to maturity (16.39) and 17.69). Heritability was high for 100 seed weight (0.99) and lowest for seed yield per plant (0.42). High heritability with high genetic advance as *per cent* mean for number of pods per plant showed the additive gene effect for these characters. Analysis of variance for parameters showed the significant variations for all variables under consideration.

Titumeer *et al.* (2014) evaluated fifty greengram genotypes to study genetic variability. Higher estimates of GCV was found for number of primary branches per plant and seed yield per plant coupled with close correspondence between them. In all the cases, phenotypic variances were higher than the genotypic variance. High heritability with a low genetic advance in *per cent* mean was observed for days to 50% flowering. High heritability with a high genetic advance in *per cent* mean was observed for number of primary branches per plant and a thousand seed weight.

Genetic analysis of two crosses of greengram studied LM192 × MDU3465 and BL865 × Chinamung along with their F_2 to F_3 generations was conducted to understand the extent of genetic variability. Higher magnitudes of variability were recorded for plant height, primary branches per plant, number of clusters per plant, number of pods per plant, number of pods per cluster, pod yield per plant and seed yield per plant in F_2 and F_3 generations. All the traits recorded high heritability and genetic advance as *per cent* mean except for days to first flowering in both F_2 and F_3 generations that indicate the role of additive gene action. Hence, phenotypic selection would be effective in yield improvement. The PCV values were higher than their corresponding GCV values for most of the traits signifying environmental implications in the expression of those characters (Muralidhara *et al*., 2016).

Anand *et al*. (2016) experimented on F_6 families of greengram to study the genetic variability among the yield and yield contributing characters. High genotypic coefficient of variation was exhibited by plant height, followed by a 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.

Sreethy *et al*. (2017) conducted an experiment to study the extent of variability in greengram for twelve quantitative characters. The magnitude of GCV and PCV was high for primary branches per plant and clusters per plant, indicating the presence of sufficient variation in these traits. Clusters per plant, pods per plant, seeds per pod, seed yield per plant, pod length, primary branches per plant, seed index, plant height, biological yield per plant and harvest index showed high heritability accompanied by high genetic advance.

Rasal and Parhe (2017) studied genetic variability and diversity in fifty genotypes grouped into 10 clusters. High GCV and PCV were recorded for the number of clusters per plant, seed yield per plant and number of pods per plant, indicating a good amount of diversity for these characters. High heritability coupled with high genetic advance was observed for plant height, number of clusters and pods per plant and seed yield per plant.

Chandra *et al.* (2017) used forty genotypes of greengram to study the nature and magnitude of genetic divergence using Mahalanobis D^2 Statistics. Pods per plant had maximum PCV and GCV, followed by clusters per plant. High heritability coupled with high genetic advance was observed for plant height and biological yield. Forty genotypes were grouped into seven clusters. Cluster I and cluster VII were large, with nine genotypes each. Maximum inter-cluster distance was observed between cluster VI and VII, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters. Three characters *viz.,* seed yield per plant, days to 50 *per cent* flowering, and plant height contributed maximum towards genetic diversity.

Thippani *et al.* (2017) investigated genetic diversity among sixty greengram germplasm accessions using the principal component for various morphological traits. Component 1 had the contribution from the traits *viz.,* pod length, 100 seed weight and number of primary branches, which accounted for 21.64 *per cent* of the total variability. Number of pods per cluster, number of pods per plant, number of seeds per pod and seed yield per plant have contributed 17.65 *per cent* to the total variability in component 2. The remaining variability of 11.48 *per cent* , 11.08 *per cent* , 9.30 *per cent* and 7.63 *per cent* was console dated in component 3, component 4 and component 5 by various traits *viz.*, days to 50 *per cent* flowering, plant height, number of pods cluster, number of pods per plant, number of seeds per pod and seed yield per plant. The cumulative variance of 71.07 *per cent* of the total variation among eleven characters was explained by the first five axes. Thus, wide genetic variability exists in these greengram accessions.

Tyagi *et al.* (2017) investigated the genetic divergence and clustering pattern of forty genotypes to study the genetic parameters attributing to yield. Highest inter cluster distance was found between cluster V and cluster II that might produce a high level of segregating population in regards to yield. High heritability estimates coupled with high genetic advance were observed for plant height and the number of pods per plant.

Shiv *et al.* (2017) conducted an experiment to assess the genetic variability for 11 quantitative traits. The material comprises four F_3 generations derived from crosses *viz*., Meha × Pusa Vishal, Meha × GJM-1006, Meha × GM-4 and Meha × GJM-1008 comprising 23, 20, 22 and 15 progenies, respectively. Low to moderate GCV and PCV values were observed for days to 50 *per cent* flowering, days to maturity, plant height, primary branches per plant, seeds per pod and 100 seed weight indicated limited scope for improvement of these traits. While GCV and PCV estimates were moderate to high for pods per plant, seed yield per plant, clusters per plant and harvest index. High heritability estimates coupled with high genetic advance were observed for pods per plant, clusters per plant, seed yield per plant and harvest index coupled with high genetic advance as *per cent* mean suggested the role of additive genes.

Susmitha and Jayamani (2018) studied genetic variability parameters in fifty one greengram genotypes. The estimates of PCV was higher than GCV for all the characters. Plant height, number of primary branches per plant, clusters per plant, pods per plant, and single plant yield recorded high GCV estimates. High heritability coupled with high genetic advance as *per cent* mean was observed for plant height and 100 seed weight. The high degree of variability observed among genotypes for different yield contributing traits could be utilized in the breeding program to improve greengram productivity.

Azam *et al*. (2018) conducted an experiment to estimate the genetic variability parameters in twenty eight greengram genotypes. Analysis of variance revealed that all the traits showed highly significant differences among genotypes except seeds per pod. High GCV and PCV was recorded for the number of pods per plant, plant height and 100 seed weight. High broad sense heritability coupled with moderate genetic advance as *per cent* mean was observed for 100 seed weight, days to flower and pods per plant.

Ramakrishnan *et al*. (2018) studied variability for twelve yield related parameters in 374 diverse genotypes of greengram. The genotypes differed significantly for all characters except for plant height, number of branches per plant and test weight. Number of clusters per plant, number of pods per plant and number of seeds per pod showed high GCV and PCV values. Heritability estimates in a broad sense and genetic advance were high for all the characters except for test weight, indicating that estimates reveal the heritable portion of variability.

Mahalingam (2018) evaluated four hundred and forty five genotypes of greengram for eight quantitative traits. The data were subjected to cluster analysis, and the genotypes were grouped under three discrete clusters. Effective hybridization program including the genotypes between the clusters I, II, and III would produce wider segregation that might be used for the development of improved greengram varieties.

Mohan *et al.* (2019) evaluated forty four greengram genotypes for principal component analysis and cluster analysis based on ten morphological traits. Basic descriptive statistics showed considerable variance for all the traits. PCA revealed 79.12 *per cent* of the variability by the first five components. PC1 was associated mainly with seed yield per plant, number of pod clusters per plant, number of pods per plant and number of branches per plant. The accessions were grouped into six major clusters by the method of hierarchical cluster analysis. The clustering of greengram genotypes based on different morphological traits would be helpful to identify the promising genotypes for effective utilization in future breeding programs.

Karthikeyan *et al.* (2019) conducted a study to estimate the magnitude of genetic divergence for eight morphological characters. Twenty eight genotypes fell into ten clusters by the application of the D^2 clustering technique. Thirteen genotypes were included in Cluster I followed by clusters IV and VI, each with three genotypes. Clusters V and VIII possessed two genotypes each and the clusters II, III, VII, IX, and X had only one genotype each. Cluster I showed minimum intra cluster distance (8.38) and maximum intra cluster distance (9.59) was exhibited by cluster VI. Maximum inter cluster distance existed between the clusters IV and X (53.71) and the least inter cluster distance was recorded between clusters II and III (5.28). Characters such as 100 seed weight, days to first flower, number of pods per cluster and number of seeds per pod contributed much to divergence.

Mariyammal *et al.* (2019) carried out variability studies for eight quantitative traits. Significant variability did exist among F_2 of two crosses for all the traits under investigation. The variation was highest for plant height, followed by the number of pods per plant. Highest GCV and PCV estimates were observed for number of pods per plant in all three crosses. Most of the traits except plant height and single plant yield recorded high heritability and a low genetic advance in all these crosses.

Soni and Mishra (2020) evaluated thirty five genotypes of mungbean to estimate genetic variability for yield and its component traits. The estimates of heritability in broad sense were found higher in seeds per pod, seed yield per plot and branches per plant. The genotypes showed wide and highly significant variation for all the traits. The estimates of GCV and PCV for pods per plant, number of clusters per plant, plant height and seed yield per plot showed very little differences. High heritability and high genetic advance as *per cent* mean were observed for seed yield per plot, days to maturity, plant stand, and plant height preponderance of additive gene action.

Majhi *et al.* (2020) investigated F_3 breeding lines of three crosses *viz.*, DGGV-7 × V-02-709, DGGV-7 × V-02-802, DGGV-2 × SML-1815 along with their parents used as checks. Analysis of variance showed lines from cross DGGV-7 × V-02-709 recorded very high significant variation for the characters like the number of branches per plant, pod length and seed yield per plant. The 100 seed weight was observed in the cross derivative of DGGV-2 × SML-1815 with high heritability moderate genetic advance under mean. The breeding lines of DGGV-7 × V-02-709 have recorded PCV (17.35 %), GCV (14.23 %) was moderate with high heritability (72.12 %) coupled with moderate genetic advance over a mean (17.45 %).

Wesley *et al.* (2020) evaluated hundred greengram genotypes to estimate genetic variability and divergence among genotypes. Number of primary branches per plant showed high GCV and PCV. High heritability was recorded for protein content. High heritability coupled with high genetic advance as percent of mean was observed for days to 50 *per cent* flowering and number of clusters per plant. According to Mahalanobis' D^2statistic, grouped them into 10 clusters. Cluster II was largest with 18 genotypes. The maximum inter cluster distance was observed between cluster III and IV (1128.22), while minimum inter cluster distance was observed between cluster III and X (39). Cluster IV showed the highest mean value for seed yield per plant.

Mathankumar *et al.* (2020) studied genetic divergence in hundred mungbean genotypes using Mahalanobis' D^2 analysis. Among the traits studied, the number of branches contributed the maximum towards the total genetic divergence. The genotypes were grouped into fifteen clusters, with cluster I having the maximum number of genotypes. Maximum intra-cluster distance was recorded in cluster I indicating higher diversity among genotypes of this cluster. Cluster V and XV recorded maximum inter-cluster distance showing wider divergence between genotypes of these clusters. Likewise, clusters III and XII also recorded wider divergence. Hybridization between genotypes of cluster V (VGG 16-035, VGG 17-004) and cluster XV (VGG 17-009) followed by cluster III (VGG 18-012) and cluster XII (ADT3) could yield better segregants.

Mahalingam *et al.* (2020) evaluated seventy four greengram germplasm collections for yield characters through principal component analysis for determining the pattern of genetic diversity. The largest variation was observed for plant height with a CV of 58.98 %, followed by the number of pods per plant. The number of pods per cluster has shown the least variation with a CV of 0.50 *per cent*. The results of PCA revealed that the cumulative variance of 79.90 *per cent* by the first four axes with an Eigenvalue of 1.0 indicates traits within the axes exhibited greater influence of the phenotype. Among the first four PCs, pod length accounted for a high proportion of total variance (32.60 %) and the remaining three principal components *viz.,* number of seeds per pod, number of pods per cluster and single plant yield revealed 20.70, 14.30 and 12.30 *per cent* of the total variance, respectively.

Abhisheka and Mogali (2020) evaluated a hundred and ten advanced breeding lines derived from fourteen families of green gram in F_6 generation in augmented design to estimate genetic variability, heritability, genetic advance for yield and yield attributing traits. High GCV and PCV were recorded 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, hundred seed weight and seed yield per plant.

Prithviraj and Murthy (2020) evaluated the F_2 populations derived from interspecific crosses (KKM-3 × KBR-1 and KKM-3 × RBL-6) for yield and yield attributing traits. Significant variability existed for all the traits studied. In both the populations studied, days to 50 *per cent* flowering, days to maturity and 100 seed weight showed moderate to low PCV and GCV. In contrast, days to 50 *per cent* flowering and days to maturity exhibited high heritability coupled with moderate to low genetic advance. Plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod, seed yield per plant and 100 seed weight recorded high PCV, high GCV and high broad sense heritability coupled with high genetic advance.

Talukdar *et al.* (2020) evaluated thirty eight greengram genotypes to determine the variability and diversity in the phenological traits related to synchronous maturity. Different genotypes were found superior for different characters. The GCV and PCV estimates were high for number of pods per plant. High heritability coupled with high genetic advanced as a *per cent* mean was observed for 13 traits, including yield per plant. Based on D^2 values, the genotypes were grouped into 8 clusters. Maximum inter cluster distance was observed between clusters III and VI, followed by clusters V and VIII. In contrast, the lowest distance was noticed between cluster I and cluster VII. Days to 90 *per cent* pod maturity followed by days to first flowering and days to first pod maturity had the highest contribution towards genetic divergence.

Dutt *et al.* (2020) conducted a study to estimate the genetic variability, heritability and the expected genetic advance upon selection for thirteen characters of F_1s hybrid populations of mungbean. Pod length, cluster per plant and pods per cluster recorded moderate PCV and GCV, heritability along with genetic advance. The remaining characters had low to moderate GCV and PCV values or low to moderate heritability to emerge as poor indices of selection.

Goyal *et al*. (2021) studied genetic divergence in twenty five accessions through cluster analysis by making four clusters. Cluster II and cluster IV showed highest inter cluster distance, signifying that hybridization between genotypes from these two clusters will exploit heterosis at a greater level. Protein content, 100 seed weight and seed yield per plant have high contributions towards total genetic divergence showing scope for selection criteria.

According to the principal component analysis, two principal components (PCs) had eigenvalues more than unity and accounted for 67.37 *per cent* of the variance among six traits. PC1 and PC2 accounted for 39.88 and 27.49 *per cent* proportion of total variance, respectively. All traits were highly loading on PC1 except pod length and 100 seed weight which were loading on PC2. Based on the cluster analysis, it could be recommended that crosses could be made between the genotypes of Cluster VIII and IX, Cluster VIII and X and Cluster X and XI, which are distantly related. Cluster IV had a significantly higher 100 seed weight. Intra class correlation (R2) was the highest for pod length, followed by plant height and seeds per pod, indicating that these traits played an important role in divergence (Patel *et al.*, 2021).

2.2 To study correlation and path analysis in F_3 lines of greengram

Rao *et al.* (2006) studied genetic variability in sixty mungbean genotypes. The estimates of genotypic correlation revealed that seed yield had a highly significant positive association with pods per plant, biological yield per plant and harvest index. Path analysis indicated that pods per plant, biological yield per plant and harvest index had maximum direct contribution on seed yield.

Kumar *et al.* (2010) studied correlation and path analysis in twenty three genotypes of greengram. Number of pods per plant, cluster per branch, number of seeds per pod, plant height, and pod length showed high positive direct effects on yield plant, indicating their significant contribution to yield.

Tabasum *et al.* (2010) conducted an association study in ten mungbean genotypes. Plant height showed positive non-significant and significant genotypic and phenotypic correlation. Pods per cluster exhibited a significantly negative correlation with seed yield. Clusters per plant, pods per plant, total plant weight and harvest index showed positive significant genotypic and phenotypic correlations with seed yield. Positive direct effects were exerted through secondary branches, pods per plant, pod length, 100 seed weight. In contrast, primary branches, plant height, clusters per plant and pods per cluster had negative direct effects.

Correlation analysis indicated that seed yield per plant was positive and significantly associated with days to maturity, plant height, number of pods per plant, number of seeds per pod, and 100 seed weight. Path coefficient analysis revealed that days to flowering, days to maturity, number of pods per plant and 100 seed weight had positive direct effects on seed yield per plant (Reddy *et al.,* 2011).

Sreelakshmi and Reddysekar (2011) carried out association studies among 11 quantitative traits and their contribution towards seed yield in 30 full sib progenies of 2 crosses *viz.,* LGG 410 × LGG 450 and RMG 406 × MGG 330 and their corresponding F_3 bulk populations of greengram. The number of pods per plant, number of clusters per plant and number of seeds per pod had positive and significant association with seed yield in the FSII (RMG 406 × MGG 330) progenies. While, plant height with seed yield, seeds per pod and pods per plant with pod length in FSI (LGG 410 × LGG 450) progenies compared to non- significant positive correlation were observed in their respective F_3 bulk population. Path analysis revealed that positive direct effect of clusters per plant and seeds per pod in FSI and days to 50 *per cent* flowering, plant height, pods per plant and 100 seed weight in FSII were strengthened over their F_3 bulk population.

Twenty mungbean genotypes were tested for correlation and path coefficient among different yield contributing traits. Based on genotypic correlation analysis, characters like plant height, pods per plant, pod length and on the phenotypic basis, grain yield and seed per pod could be the best criteria in any breeding program for increasing yield in mungbean genotypes under agro-climatic conditions of Peshawar (Zaid *et al*., 2012).

Estimates of correlation in fifty greengram genotypes revealed the preponderance of genotypic values over the phenotypic ones. Number of primary branches per plant, number of clusters per plant, numbers of pods per plant, number of seeds per pod and harvest index had a significant and positive correlation with seed yield per plant. Number of pods per plant, harvest index, number of seeds per pod and days to maturity recorded to have a maximum positive direct effect towards seed yield per plant (Prasanna *et al.,* 2013).

Number of secondary branches per plant, number of branches per plant, number of pods per plant, number of grains per pod, pod length and 100 seed weight had shown positive and significant correlation along with their high positive direct effect with grain yield, suggesting that these parameters, may be considered as prime traits during selection to have the higher potential of yield in case of greengram (Kumar *et al*., 2013).

The correlation studies indicated that days to initial flowering, days to 50 *per cent* flowering, no. of branches per plant, no. of pods per plant, no. of seeds per plant, days to full maturity, 100 seed weight, pod length are positively and non-significantly correlated with seed yield and simultaneous improvement of these characters along with seed yield is possible. The path analysis for seed yield revealed that a number of seeds per pod, pod length and 100 seed weight has high positive direct effects and would directly increase seed yield (Nand and Anuradha, 2013).

Narasimhulu *et al.* (2013) conducted character association studies in forty mungbean genotypes for different quantitative characters. Estimates of correlations revealed that seed yield had a positive and significant correlation with the number of pods per plant, clusters per plant, number of pods per cluster and biological yield per plant. All these traits had a significant and positive association with branches per plant might play a vital role in indirect selection for yield.

Singh *et al.* (2014) evaluated thirty six greengram genotypes during *Kharif* 2012 in three environments for analysis of quantitative traits. Association analysis showed significant positive relationship between seed yield and some of the agro-morphological traits *viz.,* days to 50 *per cent* flowering, primary branches per plant, secondary branches per plant, clusters per plant, pods per cluster, pod length, seeds per pod, pod mass, pod wall mass, seed mass, selling percentage, seed index and harvest index. Hence these traits may be used as selection criteria for yield improvement.

Titumeer *et al.* (2014) evaluated fifty genotypes of greengram for conducting an association study. Seed yield per plant showed the highest significant positive correlation with a thousand seed weight. It also has a significant positive correlation with seed per pod at the genotypic level and a non-significant positive correlation with seed per pod at the phenotypic level.

Days to 50 *per cent* flowering showed a negative effect on seed yield *via* a number of pods per plant in eight genotypes of mungbean. Path coefficient measured on seed yield revealed that the number of pods per plant had the maximum direct effect followed by plant height and 1000-seed weight (Raturi *et al*., 2014).

Patel *et al.* (2014) evaluated forty greengram genotypes to study correlation and path analysis. 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 highly significant and positive correlations with seed yield at both genotypic and phenotypic levels.

Muralidhara *et al.* (2016) carried out a genetic analysis of two crosses of greengram LM192 × MDU3465 and BL865 × Chinamung studied along with their F_2 to F_3 generations to assess correlation and path analysis effects on seed yield. Number of pods per plant (0.783) F_2 and (0.884) F_3, pod yield per plant (0.976) F_2 and (0.985) F_3 and threshing percentage (0.452) F_2 and (0.607) F_3 had shown positive and significant correlation along with their high positive direct effect with seed yield.

Anand *et al.* (2016) evaluated twenty six F_6 families of greengram to estimate correlation and path analysis relationships. The days to 50 *per cent* flowering and plant height had a negative correlation and negative direct and indirect effects for grain yield, indicating that dwarf and early maturing produce a higher yield. Number of clusters per plant and the number of pods per plant are the most important yield contributing components as they recorded high direct and indirect effects along with a significant positive correlation towards seed yield.

Sindhu *et al.* (2017) investigated the interrelationship in F_3 generation of three crosses, MGG-347 × MGG351, MGG-351 × LGG-460 and LGG-460 × LGG-528 of green gram. In all the crosses, plant height, cluster per plant, pods per plant, pods per cluster, seeds per pod, harvest index and pod yield showed a significant positive association with seed yield.

Sreethy *et al.* (2017) conducted an association study on seed yield in greengram. Seed yield per plant exhibited a significant positive correlation with pods per plant (0.982), clusters per plant (0.977), primary branches per plant (0.795), harvest index (0.749), seeds per pod (0.417) and biological yield (0.315) at both the phenotypic and genotypic levels. The characters harvest index (0.748), biological yield (0.649), pods per plant (0.133), seeds per pod (0.095) and primary branches per plant (0.016) exhibited a positive direct effect with seed yield. Harvest index and biological yield per plant showed a high positive direct effect accompanied by a significant positive correlation with seed yield.

Azam *et al.* (2018) evaluated twenty eight greengram genotypes for association studies. Seeds per pod, plant height and pods per plant showed positive significant phenotypic and genotypic correlation with yield. The result of path analysis indicated that pods per plant had a maximum direct effect on yield followed by plant height and 100 seed weight and they contributed 31 *per cent* variation in yield.

Association analysis indicated that seed yield per plant showed a significant positive correlation with pod yield per plant, followed by a number of pods per plant, number of clusters per plant and threshing percentage. Among the characters studied, pod yield per plant had the highest positive direct effect followed by the number of pods per plant, threshing percentage and number of clusters per plant on seed yield per plant (Ramakrishnan *et al.*, 2018).

100 seed weight, grains per pod, pod length and harvest index exhibited a highly positive and significant correlation with grain yield per plot. The study of direct effect with grain yield reveals that 100 seed weight, grains per pod and pod length showed positive and highly significant direct effects on grain yield. In this experiment residual effect was very high, indicates that very few of the yield contributing characters were taken understudy, which attributes towards the grain yield of *vigna* (Sinha *et al.*, 2018).

Thirty six mungbean germplasm were investigated to study genetic variability for 10 quantitative characters. Phenotypic correlation is higher than the genotypic correlation for all the characters under study. From the correlation studies, the number of clusters per plant, number of pods per cluster, and number of pods per plant had a significant positive correlation with single plant yield. So, selection for these traits will indirectly increase the seed yield per plant (Sandhiya and Saravanan 2018).

Manivelan *et al.* (2019) conducted an experiment using twenty one mungbean hybrids which were evaluated for yield and its component traits. The estimated correlation coefficient and path coefficient analysis. Among the characters studied, plant height, clusters per plant, number of branches per plant, number of pods per plant, number of seeds per pod showed high direct positive effect in path analysis and a significant positive association with grain yield.

Ahmad and Vikas (2019) studied the association of various plant, pod and seed characters with seed yield in hundred and twelve genotypes of mungbean. Correlation analysis indicated that seed yield showed a significant positive correlation with the number of pods per plant, pod length, 100 seed weight, number of clusters, plant height, number of branches. Path analysis revealed that a number of pod per plant and 100 seed weight exerted a high magnitude of positive direct effect, pod length showed moderate effect while the number of cluster and seed density exerted positive but low magnitude of direct effect on seed yield.

Association analysis indicated that the number of pods per plant, number of pod clusters per plant, number of seeds per pod and number of branches per plant showed a significant positive association with seed yield per plant. Path analysis specified that the highest positive direct effect on single plant yield was exerted by days to 50 *per cent* flowering, number of pods per plant and number of seeds per pod (Mohan *et al*., 2019).

Soni and Mishra (2020) conducted an association study in thirty-five genotypes of mungbean. The characters, seed yield per plant showed a highly significant and positive correlation with number of clusters per plant and plant height.

Majhi *et al.* (2020) conducted an investigation with F_3 breeding lines derived from three crosses viz., DGGV-7 × V-02-709, DGGV-7 × V-02-802, DGGV-2 × SML-1815. A significant positive correlation was observed between plant height, number of clusters per plant, number of pods per plant, number of seeds per pod and seed yield per plant.

Mahalingam *et al.* (2020) evaluated seventy four greengram genotypes to assess association for yield contributing traits. Estimates of correlation coefficient showed a significant positive association of seed yield with the number of pods per plant.

Character association studies revealed that the number of pods per plant, the number of clusters per plant, the number of seeds per pod, the number of primary branches per plant, plant height, days to maturity, pod length and 100 seed weight showed a positive and significant correlation with seed yield per plant. Path analysis revealed that the number of pods per plant had a high positive and direct effect on seed yield (Mohammed *et al*., 2020).

Abhisheka and Mogali (2020) evaluated hundreds and ten advanced breeding lines derived from fourteen families of greengram in F_6 generation in augmented design for estimation of correlation and path coefficient analysis for yield and yield attributing traits. The characters, number of pods per plant and hundred seed weight had the highest positive direct effect and a high positive correlation on seed yield.

Goyal *et al*. (2021) studied the association between yield and its contributing traits in a set of advanced generations of greengram genotypes. Seed yield per plant showed a significant and positive correlation with plant height followed by pod length, pods per cluster and pods per plant. The 100 seed weight and harvest index showed a positive but non-significant correlation. Path analysis indicated that the pod length has the highest positive direct effect on seed yield per plant, followed by harvest index, primary branches per plant, 100 seed weight, pods per cluster, protein content and pods per plant.

Dhunde *et al.* (2021) undertook an investigation to estimate the correlation and path analysis in twenty four F_2 mungbean genotypes. Grain yield per plant showed highly significant and positively associated with days to initiation of flowering, number of grains per pod, plant height, pod length and days to 50 *per cent* flowering at a genotypic level, indicating the possibility of simultaneous improvement for these traits. Days to maturity had highly significant but negatively correlated with grain yield per plant at the genotypic level. Path analysis revealed that the number of branches per plant, pod length, plant height, number of pods per cluster and number of pods per plant recorded the highest direct effect in a desirable direction.

Patel *et al.* (2021) determined an inter-relationship existing between biometrical traits through Pearson's correlation analysis among hundred greengram genotypes. The highest correlation was observed among the seeds per pod and pod length, pod per plant and the number of branches per plant. 100 seed weight had a negative and significant correlation with plant height, the number of branches per plant and pods per plant.

2.3 To identify superior segregants for yield and its attributing traits in greengram

Abbas *et al*. (2010) evaluated forty mungbean genotypes through Metroglyph analysis by distributing into 8 groups. On the basis of this grouping it may be concluded that an effective hybridization program may include the genotypes of group I, II, VII and VIII to produce better segregants that may be used for the development of high yielding mungbean varieties.

Garje *et al.* (2013) evaluated forty genotypes of greengram. The genotypes KM-09-152, KM-09-156, KM-09-183, BM-2005-1, Vaibhav, KM-09-187, KM-09-173 and KM-09-158 were identified as genetically diverse parents, which can be utilized for future crop improvement programme.

Narasimhulu *et al*. (2014) evaluated five lines for yield and its attributing traits in Green gram. Cross combinations *viz.,* MGG-351 × PM-115, TM-96-2 × PM-112, MGG-295 × PM-110, TM-96-2 × WGG-37, WGG-42 × WGG-37 and WGG-42 × PM-110 were found to be good for seed yield per plant and other related desirable traits.

In F_2 generation of the cross BL865 × Chinamung showed high mean performance for seed yield (3.30g), pod yield (4.95) and threshing percentage (63.01) however, least mean performance was observed for yield (1.62 g) in F_3 generation, indicating that there was a greater environmental effect on seed yield in F_2 generation. Family performance in the cross LM-192 × MDU-3465 for seed yield was comparatively superior over the check KKM-3 and Chinamung (Muralidhara *et al*., 2016).

Garg *et al.* (2017) conducted an experiment for the identification of most diverse and promising genotypes. Selection index (I) aimed at selection on several characters simultaneously indicated that genotypes, LGG-460, MH-805, Pusa-0672, IPM-06-5, TBM-11, EC-581523, KM-2241, GP-69, RMG-991 and MH-934 had performed better and were important for further breeding programme aimed at improvement of yield.

Rasal and Parhe (2017) studied genetic variability and genetic diversity in fifty genotypes which were grouped into ten clusters. According to this study, the genotypes Utkarsha, Vaibhav, PKV Green Gold, BPMR-145, BM 2002-1, AKM 09-2-1, AKM 10-13 were found to be the most diverse parents.

Shiv *et al.* (2017) conducted an experiment to assess the genetic variability, heritability and genetic advance in four F_3 populations for 11 quantitative traits including seed yield per plant. The F_3 populations of crosses *viz.,* Meha × GJM-1006 and Meha × GJM-1008 needs to be handled under different selection schemes for improving productivity as they depicted high heritability along with high genetic advance as *per cent* mean for most of the traits.

Seed yield showed significant positive association with plant height, number of cluster per plant, number of pods per plant, number of pods per cluster, number of seeds per pod, harvest index and pod yield in all the three crosses; pod length in two crosses MGG-347 × MGG-351 and MGG-351 × LGG-460; primary branches per plant in two crosses MGG-351 × LGG-460 and LGG-460 × LGG-528. So improvement in seed yield is possible by taking above characters as criteria in selection scheme in these crosses (Sindhu *et al.,* 2017).

Susmitha and Jayamani (2018) evaluated fifty one greengram genotypes to assess variability parameters. Genotypes exhibiting high mean value for yield and its component traits could be employed as parents for the development of high yielding varieties. MS 9724 genotype recorded maximum yield with significant number of primary branches per plant, number of clusters per plant, number of pods per plant and number of seeds per plant which could be utilized as one of the parent for improvement of yield.

Kalpana (2019) evaluated twenty one crosses for combining ability and heterosis for yield and yield attributing traits along with nutrition. Pusa vishal, IPM-2-14 and PM-5 were identified as best genotypes for most of the traits. Among crosses, LGG-574 × Pusa Vishal, LGG-574 × PM-5, LGG-460 × Pusa vishal, LGG-460 × IPM-2-14 and LGG-407 × PM-18 were found to be best as they recorded for yield and quality traits.

Karthikeyan *et al.* (2019) evaluated twenty eight genotypes of greengram to estimate the magnitude of genetic divergence for eight morphological characters. It was reported that variations in leaf shape, serve as marker in the selection of genotypes while bold seeds observed in the study could contribute to the yield if properly exploited in breeding programs.

Manivelan *et al.* (2019) evaluated twenty one mungbean hybrids for yield and its component traits. Selection based on number of plant height, number of clusters per plant, number of branches per plant, number of pods per plant, number of seed per pod will be effective to improve yield potential as they showed high direct positive effect in path analysis and positive significant association with grain yield.

Mohan *et al.* (2019) evaluated forty four greengram genotypes for cluster analysis based on ten morphological traits. Reported that genotypes grouped under cluster II, having more number of branches, number of pods per clusters, number of seeds per pod and single plant yield can be utilized as potential donors in crossing program for improving yield.

Abhisheka and Mogali (2020) concluded that number of pods per plant and hundred seed weight should be given topmost priority during selection while working with hundred and ten breeding lines in F_6 generation for improvement of yield in greengram.

Aruna *et al.* (2020) conducted an investigation to assess variability for yield and its attributing traits in a set of eighty one mungbean genotypes. Among which thirteen genotypes were identified as high yielding based on seed yield per plant.

Dutt *et al*. (2020) conducted a study to estimate the genetic variability, heritability and the expected genetic advance upon selection for thirteen characters of F_1s hybrid populations of mungbean. Pod length, number of clusters per plant and number of pods per cluster recorded moderate PCV and GCV, heritability along with genetic advance. Thus, selection for these traits among these genotypes would be effective.

It is concluded that plant height, the number of primary branches, the number of clusters per plant, the number of pods per cluster and the number of pods per plant are the major yield contributing characters and hence during selection, priority should be given to these characters for the development of high yielding cultivars of greengram (Mahalingam *et al.,* 2020).

Mathankumar *et al.* (2020) evaluated hundred mungbean genotypes using Mahalanobis D^2 analysis. High mean performances for the number of clusters per plant, the number of pods per cluster, the total number of pods per plant and seed yield per plant was observed in cluster XIII (VGG 15-030). This genotype can be utilized for further crop improvement programme in mungbean.

Prithviraj and Murthy (2020) evaluated the F_2 populations derived from interspecific crosses (KKM-3 × KBR-1 and KKM-3 × RBL-6) for yield and yield attributing traits. Revealed that limited genetic variability for characters such as day to 50 *per cent* flowering and days to maturity whereas higher variability for plant height, number of branches per plant, number of clusters per plant, number of pods per plant, pod length, number of seeds per pod and seed yield per plant which may give an idea of the direction and intensity of selection to be practiced to achieve desired recombination of traits of interest followed by the stabilization of the evaluated material.

Soni and Mishra (2020) were evaluated thirty five genotypes of mungbean. Number of cluster per plant and plant height were significant and positively correlated with seed yield per plant. Hence, these traits should be given consideration while selecting for increasing yield.

Singh *et al*. (2020) reported that desirable transgressive segregants were observed in F_2 progenies for plant height, number of primary branches, number of cluster per plant and number of pods per plant. From this study it maybe concluded that interspecific hybridization may be used to produce elite population for effective selection for the improvement of these important pulse crops.

Talukdar *et al*. (2020) evaluated thirty eight greengram genotypes to determine the variability and diversity in the phenological traits related to synchronous maturity. It is concluded from the present study, the best genotypes for yield and yield attributing characters identified were KM 2355, AKM 12-24, AKM 12-28, MH 2-15, IPM 312-20 and HUM 1. PantM-4, AKM 12-24, AKM 12-28, MH 2-15, KM 2355, IPM 312-20 and COGG 13-39 could be useful for exploitation of hybrid vigor and for getting good recombinant.

Dhunde *et al.* (2021) evaluated twenty four F_2 mungbean genotypes and concluded that, number of branches per plant, number of pods per cluster, number of clusters per plant, number of pods per plant and hundred seed weight were the major yield contributing characters. Therefore, due emphasis should be given on these characters in the selection which would help in isolating high yielding genotypes from highly segregating population to improve yield potential of mungbean.

Selection for traits like pod length, number of pods per cluster, protein content, 100 seed weight and seed yield per plant will lead to generate an improved population through a breeding programme enhancing the yield of greengram (Goyal *et al*., 2021).

MATERIAL AND METHODS

III MATERIAL AND METHODS

Genetic analysis of two populations, $C1F_3$ and $C2F_3$ of greengram was carried out along with parents and checks to assess genetic variability and diversity. The experiment was conducted during *Kharif*-2020 at the experimental plots of the Department of Genetics and Plant Breeding (GPB), College of Agriculture, Keladi Shivappa Nayaka University of Agricultural and Horticultural Sciences, Shivamogga, Karnataka, India.

3.1 Experimental material

The experimental material consisted of two populations *i.e.,* $C1F_3$ (KKM-3 × IPM 205-7) and $C2F_3$ (KKM-3 × YADADRI) each involving thirty progeny lines evaluated with parental lines and checks (IPM 205-7, YADADRI, KKM-3, China mung). Salient features of greengram varieties used as parents in the crosses and checks are shown in table 1.

3.2 Experimental details and the layout of the experimental field

The experiment was laid out at research plots of the College of Agriculture, Shivamogga. F_3 generation of both the crosses was raised on a plant-to-row progeny basis in an augmented design with twelve blocks. Each block was comprised of 5 F_3 progeny lines, parental lines and check variety. Each progeny was sown in a single row of 3 m length with 30 cm spacing between rows and 10 cm spacing between plants in a row on 6th July *Kharif* -2020. Each progeny row consists of 10 plants. Individual plant data of 600 plants from both the crosses were analyzed for the experiment. All the recommended field management practices were followed to raise a healthy and better crop. The layout of the experimental design is depicted in figure 1. General view of the research plots of both the populations are presented in plate 1 and 2, respectively.

3.3 Data collection

The observations were recorded for both F_3 populations on individual plant basis for following growth and yield contributing traits by counting/measurement using appropriate scale depending on the traits (Table 2).

Table 1. Salient features of greengram varieties used as parents in the crosses and checks

Parents	Characteristics
KKM-3	Late maturing, high net returns, low *MYMV* incidence
IPM 205-7	Early maturing, high yielding, *MYMV* resistance
YADADRI	High yielding, moderately *MYMV* resistance
China mung (Check)	Early maturing with bold seeds, susceptible to *MYMV* and powdery mildew

Table 2. Protocol for counting quantitative traits in F_3 progenies of greengram

SI. No.	Traits	Procedure of counting/ measurement
1	Days to 50 *per cent* flowering	Number of days taken from the date of sowing to 50 *per cent* of the plants to attain flowering
2	Primary branches per plant	Number of primary branches of individual plants counted at the prematurity stage and averaged
3	Secondary branches per plant	Number of secondary branches of individual plants counted at the prematurity stage and averaged
4	Plant height (cm)	Height of the individual plants from the base of the plants to the tip of the main stem was measured and averaged
5	Number of clusters per plant	Number of clusters per plant recorded by counting the total number of pod bearing clusters on individual plants and averaged
6	Number of pods per cluster	Number of well-filled pods from all the effective clusters of each plant was counted and averaged per cluster
7	Number of pods per plant	Number of pods were counted at the harvest stage on individual plants averaged
8	Pod length (cm)	Measured pod length of selected pods in each plant and averaged
9	Number of seeds per pod	Counted seeds per pod by taking seeds from selected pods in each plant and averaged
10	100 seed weight (g)	Weight of 100 randomly chosen well-filled dried seeds of selected pods was recorded
11	Seed yield per plant (g)	Total weight of pods from individual plants was recorded and averaged

N

C1F$_3$ POPULATION (KKM-3 × IPM 205-7)	C2F$_3$ POPULATION (KKM-3 × YADADRI)
BLOCK I PROGENY LINES 1 TO 5	BLOCK VII PROGENY LINES 1 TO 5
BLOCK II PROGENY LINES 6 TO 10	BLOCK VIII PROGENY LINES 6 TO 10
BLOCK III PROGENY LINES 11 TO 15	BLOCK IX PROGENY LINES 11 TO 15
BLOCK IV PROGENY LINES 16 TO 20	BLOCK X PROGENY LINES 16 TO 20
BLOCK V PROGENY LINES 21 TO 25	BLOCK XI PROGENY LINES 21 TO 25
BLOCK VI PROGENY LINES 26 TO 30	BLOCK XII PROGENY LINES 26 TO 30

Fig. 1: Layout of the experimental design in research plots of the College of Agriculture, Shivamogga

Plate 1: General view of experimental plot of $C1F_3$ population of greengram

Plate 2: General view of experimental plot of $C2F_3$ population of greengram

3.4 Statistical analysis

The experimental data were compiled and subjected to statistical analysis using the adjusted trait means of F_3 progenies from both the crosses.

3.4.1 Analysis of Variance (ANOVA)

ANOVA was performed following Augmented design (Federer, 1961) using R 4.0.3 software to examine statistical significance or otherwise of the differences among F_3 families for eleven quantitative traits. Structure of ANOVA (Augmented Design; Federer, 1961) is depicted in table 3.

Adjusted quantitative trait values of each of the individuals in F_3 progenies were estimated by subtracting observed quantitative trait value of the individuals of F_3 progenies from the block effect, 'a_j' of j^{th} block; 'a_j' was estimated as 'a_j' = (x_j – x...), x_j = trait mean of checks in the j^{th} block and x...= the experimental quantitative trait means of parents as checks in the experiment (Federer, 1961).

3.4.2 Estimation of descriptive statistics

3.4.2.1 Mean

The mean value of every trait was computed on the basis of observations recorded on individual plants.

$$\bar{X} = \sum_{i=1}^{n} X_i/n$$

Where,

$\bar{X}$ = Trait mean

$\sum_{i=1}^{n} X_i$= Sum of observations of all the plants of each progeny row

n = Number of plants

3.4.2.2 Range

Range was calculated by the difference between the highest mean value and the lowest mean value of each character on individual plant.

$$\text{Range} = X_{max} - X_{min}$$

Where,

X_{max} = the highest mean value of the character

X_{min} = the lowest mean value of the character

Table 3. Structure of ANOVA (Augmented Design; Federer, 1961) of F$_3$ progenies

Sources of variations	**Degrees of freedom**	**Mean sum of squares (MSS)**	**‘F’ ratio**
Blocks (b) (Eliminating F$_3$ progenies)	b-1	MSS(b)	MSS(b)/EMSS
Entries (e) (F$_3$ progenies + checks) (Eliminating blocks)	e-1	MSS(e)	MSS(e)/EMSS
F$_3$ progenies (p)	p-1	MSS(p)	MSS(p)/EMSS
Checks (c)	c-1	MSS(c)	MSS(c)/EMSS
F$_3$ progenies *vs*. Checks (pc)	1	MSS(pc)	MSS(pc)/EMSS
Error	(b-1) (c-1)	EMSS	

Where,

b = Number of blocks

f = Number of F$_3$ progenies

c = Number of checks

e = Number of entries

3.4.2.3 Standard error of mean

It is the measure of uncontrolled variation present in a sample, which is estimated by dividing the standard deviation (SD) by the square root of the number of observations (n) in the sample and denoted by SEm.

$$\mathrm{SEm} = \frac{\mathrm{SD}}{\sqrt{\mathrm{n}}}$$

3.4.3 Variance and covariance

3.4.3.1 Variance

Variance is defined as the average of the squared deviation from the mean and is expressed as the sum of squares of the deviations of all the observations of a sample from its mean and divided by (n-1), where n is the number of observations. It is estimated by the following formula.

$$\mathrm{Variance} = \frac{\sum(\mathrm{Xi} - \bar{\mathrm{X}})^2}{\mathrm{n} - 1}$$

Where,

X_i = i^{th} observation of a population

n = Number of observations

3.4.3.2 Genotypic and phenotypic variances

The genetic parameters such as genotypic and phenotypic variances were estimated to assess and quantify the genetic variability for the traits among the F_3 progenies using the formula given by Cochran and Cox (1957).

$$\text{Genotypic variance } (\sigma^2_g) = \frac{\text{MSS (genotype)} - \text{MSS (error)}}{\text{Number of blocks}}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + \text{MSS (error)}$$

3.4.3.3 Covariance

The analysis of covariance was carried out by taking two characters at a time. The genotypic and phenotypic covariances were calculated as per the formula described by Singh and Chaudhary (1977).

Environmental covariance = EMSP

$$\text{Genotypic covariance} = \frac{\text{TrMSP} - \text{EMSP}}{\text{r}}$$

Phenotypic covariance = Genotypic covariance + Environmental covariance

Where,

EMSP = Error mean sum of products

TrMSP = Treatment mean sum of products

r = number of replications

3.4.4 Coefficient of variation

The phenotypic coefficient of variation and genotypic coefficient of variation for all the traits were calculated by the formula suggested by Burton and De vane (1953) using the components *viz*., phenotypic, genotypic and environmental variances.

$$\text{PCV} = \frac{\text{Phenotypic standard deviation}}{\text{General mean}} \times 100$$

$$\text{PCV} = \frac{\sigma_p}{\bar{X}} \times 100$$

$$\text{GCV} = \frac{\text{Genotypic standard deviation}}{\text{General mean}} \times 100$$

$$\text{GCV} = \frac{\sigma_g}{\bar{X}} \times 100$$

Categorization of the range of variability as proposed by Sivasubramanian and Madhavamenon (1973) is as follows.

Scales	**Value of GCV (%) and PCV (%)**
Low	Less than 10
Moderate	10 to 20
High	More than 20

3.4.5 Heritability and Genetic advance

3.4.5.1 Heritability

Hanson *et al.* (1956) defined heritability in broad sense as the ratio of genotypic variance to the total variance. Heritability was calculated by the formula given by Allard (1960).

$$\text{H} = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

Where,

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

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* (1955), Heritability (h^2_{bs}) estimates were categorized as follows:

Scales	**Values of heritability in broad sense (%)**
Low	Less than 30
Moderate	30 to 60
High	More than 60

3.4.5.2 Genetic Advance (Expected)

Genetic advance denotes the improvement in the genotypic value of the new population over the base population, and it is estimated by the following formula suggested by Allard (1960).

$$\text{Genetic Advance (Expected)} = H \times \sqrt{\sigma^2_p} \times K$$

Where,

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

$\sqrt{\sigma^2_p}$= Phenotypic standard deviation

K = Selection differential in the standard units, which is 2.06 at 5 *per cent* selection intensity

3.4.5.3 Genetic advance as per cent mean (GAM)

Genetic advance as *per cent* mean was calculated by the following formula.

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Expected genetic advance

$\bar{X}$ = General mean of the character in the population

The range of GAM was classified as suggested by Johnson *et al.* (1955).

Scales	Value of GAM (%)
Low	Less than 10
Moderate	10 to 20
High	More than 20

3.4.6 Genetic divergence studies by Mahalanobis' D^2 Statistics

Genetic divergence is the process in which two or more populations of an ancestral species accumulate independent genetic changes when they become reproductively isolated. Mahalanobis' D^2 statistics was initially developed by Mahalanobis' in 1928 and is one of the most effective tools to measure the genetic distance between genotypes. The genetic distance can be defined as the extent of gene difference between cultivars, as measured by allele frequencies at a sample of loci (Nei, 1987). Diversity analysis was carried out using WINDOSTAT version 9.2 software for both $C1F_3$ and $C2F_3$ populations of greengram.

3.4.6.1 Mahalanobis' D^2 statistics

Genetic divergence was assessed based on Mahalanobis' generalized distance described by Rao (1952) in the present investigation. Original variable means were transformed into uncorrelated variables by the essential condensation method of the inversion matrix. The following formula gives the square of the Mahalanobis' generalized distance between any two populations.

$$D^2 = \sum s_i s_j \lambda_{ij}$$

Where,

D^2 = Square of generalized distances

$s_i = (x_{i1} - x_{i2})$

$s_j = (x_{j1} - x_{j2})$

x = Vector of mean values for all the characters

λ_{ij} = Reciprocal of the common dispersion matrix

Since inverting the matrix is complicated when the number of variables under study is large, the original correlated variables (x_i) were transformed to non-correlated variables (y_i) using Dwyer's square root method Dwyer (1945). Thus, computation of D^2 values reduces to a simple summation of the squares of the difference between the values of transformed variables of two populations.

The newly transformed uncorrelated variables were used to calculate the D^2 values using the formula given below:

$$D^2 = \sum_{i=1}^{p}(Y_i^1 - Y_i^2)^2$$

Where,

y = Vector of transformed mean values.

p = Number of characters

The significance of D^2 values was tested by treating them as chi-square (χ^2) at p degree of freedom.

3.4.6.2 *Contribution of individual character towards divergence*

Each trait was ranked in all the trait combinations based on their contribution towards the divergence between two entries $d_i = Y_i^j - Y_i^k$ values. Rank '1' was given to the highest mean difference and rank 'p' to the lowest mean difference where 'p' is the total number of characters considered.

Where,

d_i = mean deviation

Y_i^j = mean value of the jth genotype for the ith character

Y_i^k = mean value of the kth genotype for the ith character

The number of cases where a particular trait ranked first was counted; the proportion of this to the total number of trait combinations expressed in percentage will quantify that character's contribution to the overall genetic divergence between the genotypes.

$$X = \left(\frac{N}{M}\right) \times 100$$

Where,

X = *Per cent* contribution of character

N = Number of genotype combinations where the character ranked first

M = All possible combinations of the genotypes concerned

3.4.6.3 Clustering of D^2 values

All the F_3 progenies considered in the experiment were clustered using Tocher's method, as Rao (1952) described.

3.4.6.3.1 Intra-cluster distance

The intra-cluster distances were calculated by the following formula given by Singh and Chaudhary (1977).

$$\text{Square of intra} - \text{cluster distance} = \frac{\sum D_i^2}{n}$$

Where,

$\sum D_i^2$ = Sum of distances between all possible combinations of the entries in a cluster

n = Number of all possible combinations

3.4.6.3.2 Inter-cluster distance

The inter-cluster distances were calculated by the following formula given by Singh and Chaudhary (1977).

$$\text{Square of inter} - \text{cluster distance} = \frac{\sum D_i^2}{n_i n_j}$$

Where,

$\sum D_i^2$= Sum of distances between all possible combinations ($n_i n_j$) of the entries included in the clusters(i and j).

n_i= Number of entries in cluster i

n_j = Number of entries in cluster j

3.4.7 Correlation coefficient and path analysis

The correlation coefficients and path analysis for both $C1F_3$ and $C2F_3$ populations of greengram were carried out using WINDOSTAT version 9.2 software.

3.4.7.1 Correlation coefficient analysis

The concept of correlation was first given by Galton (1889), which was further elaborated by Fisher (1919) to initiate an effective selection program aimed at genetic enhancement of the economic yield of the crop plants.

The correlation coefficients were calculated to determine the degree of association among different yield contributing characters. Phenotypic correlation coefficients were estimated in F_3 generations using the variance and covariance components, as suggested by Johnson *et al.* (1955).

$$r_p(xy) = \frac{Cov_p(xy)}{\sqrt{\sigma_p^2(x) \times \sigma_p^2(y)}}$$

Where,

r_p (xy) = Phenotypic correlation coefficients between x & y traits

Cov_p (xy) = Phenotypic covariance between x & y traits

$\sigma_p^2(x)$ = Phenotypic variance of x character

$\sigma_p^2(y)$ = Phenotypic variance of y character

x and y are the two traits for which the correlation coefficient is estimated.

For testing the significance of correlation coefficients, the estimated values were compared with the table value (Fisher and Yates, 1938) at n-2 degrees of freedom (where n denotes the number of genotypes tested) at 5% and 1% levels of significance.

The range of correlation coefficients was classified as suggested by Searle (1965).

Scales	**Value of Correlation Coefficients**
Very strong	More than 0.65
Moderately strong	0.50 to 0.64
Moderately weak	0.30 to 0.49
Very weak	Less than 0.30

3.4.7.2 Path coefficient analysis

Path coefficient analysis is a standardized partial regression coefficient that splits the correlation coefficients into the measures of direct and indirect effects. Wright (1934), suggested Path coefficient analysis, and it was further elaborated by Dewey and Lu (1959). The whole system of variables represented in the form of a diagram called a path diagram.

Path coefficient is the ratio of the standard deviation of the effect due to a given cause to the total standard deviation of the effect, *i.e.* if seed yield per plant (Y) is the function of the causal factor X_1, then path coefficient for the path from causal factor X_1 to the effect Y is given by the formula, σ_{X_1}/σ_Y

In this experiment, seed yield per plant (Y) was taken as an effect of the other traits (X) like the number of days to 50 *per cent* flowering, plant height, number of primary branches per plant, number of secondary 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, hundred seed weight and seed yield per plant as the causal factors.

3.4.7.3 The path-coefficients were obtained by solving a set of simultaneous equations given below

$$rx_{1Y} = Px_{1Y} + rx_{1X_2}Px_{2Y} + rx_{1X_3}Px_{3Y} + \dots\dots\dots\dots\dots\dots\dots\dots + rx_{1X_{11}}Px_{11Y}$$

$$rx_{2Y} = rx_{2X_1}Px_{1Y} + Px_{2Y} + rx_{2X_3}Px_{3Y} + \dots\dots\dots\dots\dots\dots\dots\dots + rx_{2X_{11}}Px_{11Y}$$

$$\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots$$

$$\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots$$

$$rx_{11Y} = rx_{11X_1}Px_{1Y} + rx_{11X_2}Px_{2Y} + rx_{11X_3}Px_{3Y} + \dots\dots\dots\dots\dots\dots\dots\dots + Px_{11Y}$$

Where,

rx_{1Y} to rx_{11Y} denotes the coefficient of correlation between independent characters X_1 to X_{11} and dependent character Y

rx_{1X_2} to $rx_{10X_{11}}$ denotes the coefficient of correlation between all possible combinations of independent characters.

Px_{1Y} to Px_{11Y} indicates direct effects of characters X_1 to X_{11} on Y

3.4.7.4 The indirect effects of the causal factors were calculated by the formula given below

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

Where,

$i = 1 \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots n$

$j = 1 \dots\dots\dots\dots\dots\dots\dots\dots\dots\dots\dots n$

$P_{ij} = P_{1Y}, P_{2Y}, P_{3Y} \dots\dots\dots\dots\dots P_{nY}$

3.4.7.5 The residual factor(P_{RY})

The variation in yield unaccounted by the causal effects under consideration is called the residual effect and is calculated using the following formula.

$$(P_{RY}) = \sqrt{1 - R^2}$$

$$(R^2) = \sum_{i=1}^{15} P_{X_iY} r_{X_iY}$$

Therefore,

$$(P_{RY}) = \sqrt{1 - P_{1Y}\, r_{1Y} + P_{2Y}\, r_{2Y} + \ldots\ldots\ldots\ldots\ldots\ldots\ldots + P_{11Y}\, r_{11Y}}$$

Where,

P_{RY} = Residual effect

R^2 = Coefficient of determination

P_{iY} = Direct effect of X_i on Y

r_{iY} = Correlation coefficient of X_i and Y

The range of path coefficients was classified as suggested by Lenka and Misra (1973).

Scales	**Value of direct and indirect effects**
Negligible	0.00 to 0.09
Low	0.10 to 0.19
Moderate	0.20 to 0.29
High	0.30 to 0.99
Very high	More than 1.00

EXPERIMENTAL RESULTS

IV EXPERIMENTAL RESULTS

The findings of the current research conducted during *Kharif*-2020 are specified under the following subheads:

4.1 Analysis of variance

4.2 Genetic variability parameters

4.3 Genetic divergence

4.4 Correlation coefficient analysis

4.5 Path coefficient analysis

4.6 High yielding superior segregants identified with respect to seed yield

4.1 Analysis of variance

Analysis of variance between F_3 families of the cross KKM-3 × IPM 205-7 revealed highly significant differences among the F_3 progenies for all characters under study, indicating the existence of sufficient genetic variability within families and between families and scope for improvement (Table 4).

Analysis of variance in F_3 progenies of the cross KKM-3 × YADADRI exhibited significant mean squares for all the traits studied, suggesting the presence of an adequate amount of genetic variability among F_3 progenies (Table 5).

4.2 Genetic variability parameters

The genetic variability parameters for yield and yield contributing traits were estimated in F_3 generations derived from the crosses, KKM-3 × IPM 205-7 (C1) and KKM-3 × YADADRI (C2). Results of variability parameters *viz*., mean, range, genotypic coefficient variation (GCV), phenotypic coefficient variation (PCV), broad-sense heritability (h^2_{bs}) and genetic advance expressed as *per cent* mean (GAM) concerning all the traits of two populations *viz*., $C1F_3$ and $C2F_3$ of greengram are presented in tables 6 and 7, respectively.

4.2.1 Mean and range

4.2.1.1 Days to 50 per cent flowering

This trait recorded the mean value of 30.04 days and 32.17 days in $C1F_3$ and $C2F_3$, respectively. The lowest and highest value ranged from 25.14 to 39.15 and 28.57 to 39.15 for $C1F_3$ and $C2F_3$, respectively.

Table 4. ANOVA for seed yield and its component traits for C1F$_3$ population (KKM-3 × IPM 205-7) in greengram

Source of Variation	Degrees of freedom	Mean Sum of Square										
		DFF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
Blocks	5	1.62	6.06	0.06	0.1	0.67	0.09	0.15	0.03	0.03	0.07	0.12
Entries (F$_3$ progenies + Checks)	33	20.02 **	226.02 **	0.23 **	1.73**	3.21 **	0.85 **	63.36 **	1.85 **	2.2 **	0.39 **	1.31 **
F$_3$ progenies	29	4.87 **	35.56 **	0.21 **	1.82 **	1.5 *	0.61 **	17.13 **	0.94 **	1.74 **	0.26 **	1.03 **
Checks	3	135.13 **	1531.71 **	0.22 *	0.65 *	17.28 **	1.94 **	51.33 **	9.86 **	1.92 **	0.41 **	1.92 **
Checks *vs.* F$_3$ progenies	1	131.74 **	1819.22 **	1.32 **	2.29 **	9.07 **	5.38 **	1453.34 **	5.31 **	25.4 **	3.87 **	8.63 **
Error	15	0.77	3.29	0.04	0.12	0.67	0.05	0.63	0.03	0.14	0.06	0.12

*Significant @ P= 0.05 level; **Significant @ P= 0.01 level

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant
NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)
NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

Table 5. ANOVA for seed yield and its component traits for C2F3 population (KKM-3 × YADADRI) in greengram

Source of Variation	Degrees of freedom	Mean Sum of Square										
		DFF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
Blocks	5	0.28	5.64	0.04	0.15	0.47	0.05	2.69	0.03	0.29	0.01	0.11
Entries (F_3 progenies + Checks)	33	13.88 **	240.63 **	0.23 **	1.04 **	7.04**	0.38 *	90.21 **	2.1 **	6.39 **	0.36 **	1.25 **
F_3 progenies	29	3.6 *	12.15 *	0.25 **	1.07 **	6.85 **	0.27 *	26.64 **	1.67 **	5.76 **	0.24 **	1.32 **
Checks	3	117.48 **	2083.86 **	0.13	1.32 **	20.36 **	1.04 **	71.02 **	6.67 **	12.51 **	0.26 *	1.18 **
Checks *vs*. F_3 progenies	1	18.25 **	1374.54 **	0.89 **	0.71 *	0.7	2.95 **	2133.18 **	3.75 **	19.96 **	4.54 **	0.27*
Error	15	1.26	8.07	0.05	0.12	0.37	0.13	3.33	0.07	0.53	0.05	0.2

*Significant @ P= 0.05 level; **Significant @ P= 0.01 level

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant
NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)
NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

Table 6. Estimates of genetic variability parameters for seed yield and its component traits in C1F$_3$ population (KKM-3 × IPM 205-7) of greengram

Sl. No.	Traits	Mean ± SEm	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)	CV (%)
			Lowest	Highest					
1	Days to 50 *per cent* flowering	30.04 ± 1.06	25.14	39.15	6.74	7.35	84.17	12.76	2.83
2	Plant height (cm)	40.43 ± 2.19	28.19	66.32	14.05	14.75	90 .75	27.61	4.1
3	Primary branches per plant	2.16 ± 0.25	1.14	2.99	18.76	21.09	79.14	34.43	9.2
4	Secondary branches per plant	4.91 ± 0.43	3.15	8.65	26.55	27.5	93.18	52.87	7.39
5	Number of clusters per plant	8.44 ± 0.99	5.22	10.54	10.84	14.54	55.62	16.68	10.01
6	Number of pods per cluster	4.49 ± 0.27	2.93	6.45	16.68	17.4	91.88	32.99	4.74
7	Number of pods per plant	30.26 ± 0.96	18.28	39.78	13.42	13.68	96.31	27.18	2.96
8	Pod length (cm)	7.68 ± 0.22	6.19	9.68	12.39	12.62	96.3	25.07	2.36
9	Number of seeds per pod	8.48 ± 0.45	6.17	10.58	14.91	15.54	92.03	29.51	4.17
10	100 seed weight (g)	3.62 ± 0.3	2.6	4.66	12.41	14.19	76.52	22.39	6.55
11	Seed yield per plant (g)	3.64 ± 0.42	1.94	5.78	26.18	27.9	88.1	50.7	8.98

Where,

SEm = Standard error of mean
GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2_{bs} = Broad sense heritability
GAM = Genetic advance in *per cent* mean

Table 7. Descriptive statistics for seed yield and its component traits in C2F$_3$ population (KKM-3 × YADADRI) of greengram

Sl. No.	Traits	Mean ± SEm	Range		GCV (%)	PCV (%)	h^2_{bs} (%)	GAM (%)	CV (%)
			Lowest	Highest					
1	Days to 50 *per cent* flowering	32.17 ± 1.36	28.57	39.15	4.75	5.9	64.99	7.91	3.45
2	Plant height (cm)	41.82 ± 3.43	25.92	71.04	4.83	8.33	30.55	5.77	6.29
3	Primary branches per plant	2.15 ± 0.27	1.00	3.08	20.76	23.15	80.43	38.42	9.85
4	Secondary branches per plant	4.85 ± 0.41	3.25	7.25	20.17	21.36	89.18	39.3	7.14
5	Number of clusters per plant	7.64 ± 0.73	2.52	12.27	33.34	34.27	94.67	66.92	7.99
6	Number of pods per cluster	4.64 ± 0.43	3.89	5.63	8.11	11.14	53.04	12.19	7.39
7	Number of pods per plant	31.92 ± 2.2	16.86	46.71	15.12	16.17	87.49	29.19	6.57
8	Pod length (cm)	7.8 ± 0.32	6.11	10.63	16.24	16.59	95.78	32.79	3.33
9	Number of seeds per pod	9.4 ± 0.88	6.13	14.33	24.33	25.54	90.73	47.8	7.46
10	100 seed weight (g)	3.56 ± 0.27	2.79	4.6	12.17	13.65	79.49	22.38	5.87
11	Seed yield per plant (g)	4.6 ± 0.54	2.82	6.56	23.01	24.95	85.04	43.78	9.65

Where,

SEm = Standard error of mean
GCV = Genotypic coefficient of variation
PCV = Phenotypic coefficient of variation
h^2_{bs} = Broad sense heritability
GAM = Genetic advance in *per cent* mean

4.2.1.2 Plant height (cm)

The mean value of 40.43 cm and 41.82 cm in C1F$_3$ and C2F$_3$, respectively were documented for this trait. The lowest and highest value ranged from 28.19 to 66.32 and 25.92 to 71.04 for C1F$_3$ and C2F$_3$, respectively.

4.2.1.3 Number of primary branches per plant

This trait recorded an average value of 2.16 in C1F$_3$ and 2.15 in C2F$_3$, respectively. Range of 1.14 to 2.99 and 1.00 to 3.08 were documented in C1F$_3$ and C2F$_3$, respectively.

4.2.1.4 Number of secondary branches per plant

This trait was found to have an average value of 4.91 in C1F$_3$ and 4.85 in C2F$_3$, with a range of 3.15 to 8.65 and 3.25 to 7.25 in C1F$_3$ and C2F$_3$, respectively.

4.2.1.5 Number of clusters per plant

The mean value of 8.44 in C1F$_3$ and 7.64 in C2F$_3$ with a range of 5.22 to 10.54 and 2.52 to 12.27 were documented for this trait in C1F$_3$ and C2F$_3$, respectively.

4.2.1.6 Number of pods per cluster

The average value of the trait was 4.49 and 4.64 in C1F$_3$ and C2F$_3$, respectively. The range of 2.93 to 6.45 and 3.89 to 5.63 respectively in C1F$_3$ and C2F$_3$ were reported.

4.2.1.7 Number of pods per plant

The average value of the trait was 30.26 and 31.92 in C1F$_3$ and C2F$_3$, respectively. The range was 18.28 to 39.78 and 16.86 to 46.71 in C1F$_3$ and C2F$_3$, respectively.

4.2.1.8 Pod length (cm)

This trait was found to have a mean value of 7.68 cm and 7.80 cm in C1F$_3$ and C2F$_3$, respectively. Range of 6.19 to 9.68 cm and 6.11 to 10.63 cm were documented for this trait in C1F$_3$ and C2F$_3$, respectively.

4.2.1.9 Number of seeds per pod

The average value for this trait was 8.48 and 9.40 in C1F$_3$ and C2F$_3$, respectively. Range of 6.17 to 10.58 and 6.13 to 14.33 was found in C1F$_3$ and C2F$_3$, respectively.

4.2.1.10 Hundred seed weight (g)

The mean value of 3.62 g and 3.56 g was recorded for this trait in C1F$_3$ and C2F$_3$, respectively. Range of 2.60 to 4.66 g and 2.79 to 4.60 g was documented in C1F$_3$ and C2F$_3$, respectively.

4.2.1.11 Seed yield per plant (g)

The average of 3.64 g and 4.6 g was recorded in C1F$_3$ and C2F$_3$, respectively. Range of 1.94 to 5.78 g and 2.82 to 6.56 g was reported in C1F$_3$ and C2F$_3$, respectively for this trait.

4.2.2 Phenotypic and genotypic coefficient of variation

4.2.2.1 Phenotypic coefficient of variation

PCV values for the C1F$_3$ population were estimated to vary from 7.35 % to 27.90 %. High PCV values were recorded for the seed yield per plant (27.90), followed by the number of secondary branches per plant (27.50), number of primary branches per plant (21.09), whereas the moderate PCV values were recorded for the number of pods per cluster (17.40), number of seeds per pod (15.54), plant height (14.75), number of clusters per plant (14.54), hundred seed weight (14.19), number of pods per plant (13.68) followed by pod length (12.62) and low PCV value for days to 50 *per cent* flowering (7.35).

For C2F$_3$ population, PCV values ranged from 5.90 % to 34.27 %. The highest PCV values were documented for the number of clusters per plant (34.27), followed by the number of seeds per pod (25.54), seed yield per plant (24.95), number of primary branches per plant (23.15), number of secondary branches per plant (21.36). In contrast, moderate PCV values were noted for pod length (16.59), number of pods per plant (16.17), hundred seed weight (13.65), number of pods per cluster (11.14) and low PCV values for the plant height (8.33) followed by days to 50 *per cent* flowering (5.90).

4.2.2.2 Genotypic coefficient of variation

For C1F$_3$ population, GCV values ranged from 6.74 % to 26.55 %. High GCV values were recorded for the number of secondary branches per plant (26.55) and seed yield per plant (26.18). Moderate GCV values were followed by the number of primary branches per plant (18.76), number of pods per cluster (16.68), number of seeds per pod (14.91), plant height (14.05), number of pods per plant (13.42), hundred seed weight (12.41), pod length (12.39), number of clusters per plant (10.84) and low GCV values were followed for days to 50 *per cent* flowering (6.74).

The estimated GCV values for the $C2F_3$ population ranged from 4.75 % to 33.34 %. High GCV values were recorded for the number of clusters per plant (33.34) followed by the number of seeds per pod (24.33), seed yield per plant (23.01), number of primary branches per plant (20.76), number of secondary branches per plant (20.17), moderate GCV values were recorded for the pod length (16.24), number of pods per plant (15.12), hundred seed weight (12.17) and low GCV values for the number of pods per cluster (8.11), plant height (4.83) and days to 50 *per cent* flowering (4.75).

4.2.3 Heritability

In $C1F_3$ population, the high heritability values were documented for the number of pods per plant (96.31 %) followed by pod length (96.30 %), number of secondary branches per plant (93.18 %), number of seeds per pod (92.03 %), number of pods per cluster (91.88 %), plant height (90.75 %), seed yield per plant (88.10 %), days to 50 *per cent* flowering (84.17 %), number of primary branches per plant (79.14 %) and hundred seed weight (76.52 %), whereas the moderate heritability values were documented for the number of clusters per plant (55.62 %).

In $C2F_3$ population, the high heritability values were recorded for the pod length (95.78 %) followed by the number of clusters per plant (94.67 %), number of seeds per pod (90.73 %), number of secondary branches per plant (89.18 %), number of pods per plant (87.49 %), seed yield per plant (85.04 %), number of primary branches per plant (80.43 %), hundred seed weight (79.49 %) and days to 50 *per cent* flowering (64.99 %). In contrast, the moderate heritability estimates were documented for the number of pods per cluster (53.04 %) and plant height (33.55 %).

4.2.4 Genetic advance as per cent mean

In $C1F_3$ population, high values of genetic advance as *per cent* mean was documented for the number of secondary branches per plant (52.87 %), seed yield per plant (50.70 %), number of primary branches per plant (34.43 %), number of pods per cluster (32.99 %), number of seeds per pod (29.51 %), plant height (27.61 %), number of pods per plant (27.18 %) followed by pod length (25.07 %), hundred seed weight (22.39 %), whereas moderate GAM values were reported for number of clusters per plant (16.68 %) and days to 50 *per cent* flowering (12.76 %).

In $C2F_3$ population, high values of genetic advance as *per cent* mean was observed for the number of clusters per plant (66.92 %), number of seeds per pod (47.80 %), seed yield per plant (43.78 %), number of secondary branches per plant (39.30 %), number of primary branches per plant (38.42%) followed by pod length (32.79 %), number of pods per plant (29.19 %), hundred seed weight (22.38 %), whereas the moderate values were recorded for the number of pods per cluster (12.19 %) and low GAM values were observed for days of 50 *per cent* flowering (7.91 %) followed by the plant height (5.77 %).

4.3 Genetic divergence

4.3.1 Contribution of individual character towards total divergence

The genetic diversity was examined for both $C1F_3$ and $C2F_3$ populations using Mahalanobis' D^2 statistics which yielded nine and eight clusters, respectively by Tocher's method.

In $C1F_3$ population, the trait number of pods per plant contributed maximum towards the total genetic divergence with 50.09 *per cent*, followed by plant height (33.51 %), days to 50 *per cent* flowering (7.66 %), number of seeds per pod (5.35 %), number of clusters per plant (2.32 %), number of secondary branches per plant (0.71 %), seed yield per plant (0.18 %) and primary branches per plant (0.18 %). Details are presented in figure 2.

In $C2F_3$ population, the trait number of pods per plant contributed maximum towards the total genetic divergence with 58.65 *per cent*, followed by plant height (29.41 %), number of clusters per plant (5.17 %), days to 50 *per cent* flowering (3.03 %), seed yield per plant (2.14 %), number of seeds per pod (1.07 %), number of secondary branches per plant (0.53 %). Details are depicted in figure 3.

4.3.2 Grouping of genotypes into various clusters

In $C1F_3$ population, cluster II emerged as the largest cluster with 18 progenies, followed by 6 progenies in cluster I, cluster VI with 3 progenies, cluster VII with 2 progenies, clusters III, IV, V, VIII and IX each with solitary progeny. The details are presented in figure 4.

In $C2F_3$ population, cluster II emerged as the largest cluster with 17 progenies, followed by cluster I with 7 progenies, cluster V with 5 progenies, clusters III, IV, VI, VII and VIII, each with unitary progeny. The details are presented in figure 6.

4.3.3 Inter and intra-cluster distances

4.3.3.1 Inter-cluster distances

For $C1F_3$ population, inter-cluster D^2 values were ranged from 24.69 to 2138.29. The highest inter-cluster D^2value (2138.29) was noticed between clusters VIII and IX, followed by 1450.15 between cluster I and cluster VIII. In contrast, the least inter-cluster distance (24.69) was recorded between clusters III and IV. The details are presented in figure 5.

For $C2F_3$ population, inter-cluster D^2 values were ranged from 66.23 to 1814.69. The highest inter-cluster D^2value (1814.69) was documented between clusters VII and VIII, followed by 1515.13 between cluster I and cluster VIII. In contrast, the least inter-cluster distance (66.23) was recorded between clusters IV and VI. The details are depicted in figure 7.

4.3.3.2 Intra-cluster distances

For C1F$_3$ population, the intra-cluster distance ranged from 0 to 50.35, whereas the highest intra-cluster distance (50.35) was noted in cluster VII, followed by 37.61 in cluster VI, 34.47 in cluster II, 25.87 in cluster I. In contrast, no intra-cluster D^2 value was found in clusters III, IV, V, VIII and IX. The details are presented in figure 5.

For C2F$_3$ population, the intra-cluster distance ranged from 0 to 74.57, where the highest intra-cluster distance (74.57) was noted in cluster V, followed by 68.86 in cluster II, 56.50 in cluster I, whereas no intra-cluster D^2 value was found in the clusters III, IV, VI, VII, VIII. The details are presented in figure 7.

4.3.4 Cluster means for various characters

The detailed cluster mean values for different yield attributing traits in C1F$_3$ and C2F$_3$ populations are presented in tables 8 and 9, respectively.

4.3.4.1 Days to 50 per cent flowering

For C1F$_3$ population, the cluster mean values for this trait ranged from 26 to 39 days, where the progenies of cluster III were early flowering and progenies belonging to cluster VIII were late to flower.

Cluster mean values for this trait in C2F$_3$ population ranged from 28.30 to 39 days, where the progenies of cluster VII were early blooming and progenies of cluster VIII were flowering late.

4.3.4.2 Plant height (cm)

For C1F$_3$ population, the cluster means for the trait ranged from 22.10 cm to 66.50 cm. Progenies belonging to cluster IX were shorter in contrast to the progenies included in cluster VIII, which were taller.

The cluster means for the trait in the C2F$_3$ population ranged from 25.80 cm to 66.50 cm. Cluster VII progenies were shorter than cluster VIII progenies, which were taller.

4.3.4.3 Number of primary branches per plant

For C1F$_3$ population, cluster means for the trait ranged from 1.87 to 2.70, where the progenies from cluster VI had a low number of primary branches compared to the progenies belonging to clusters I and VII, which had fewer primary branches more primary branches per plant.

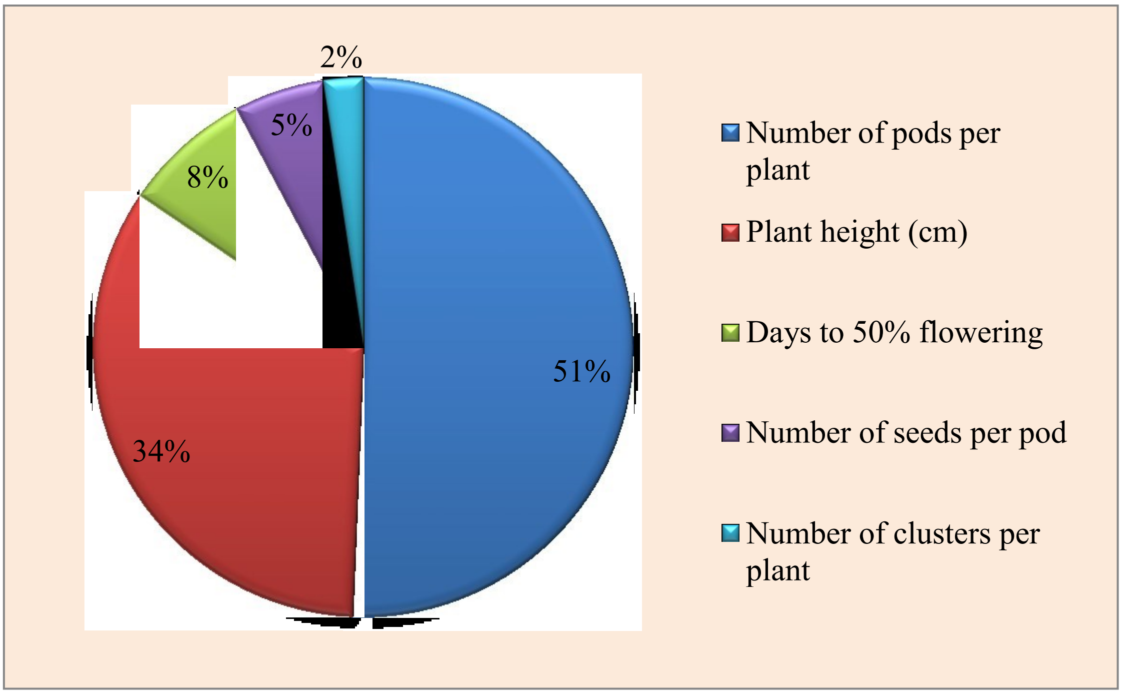

Fig. 2: ***Per cent*** **contribution of different traits towards genetic diversity in C1F$_3$ population of greengram**

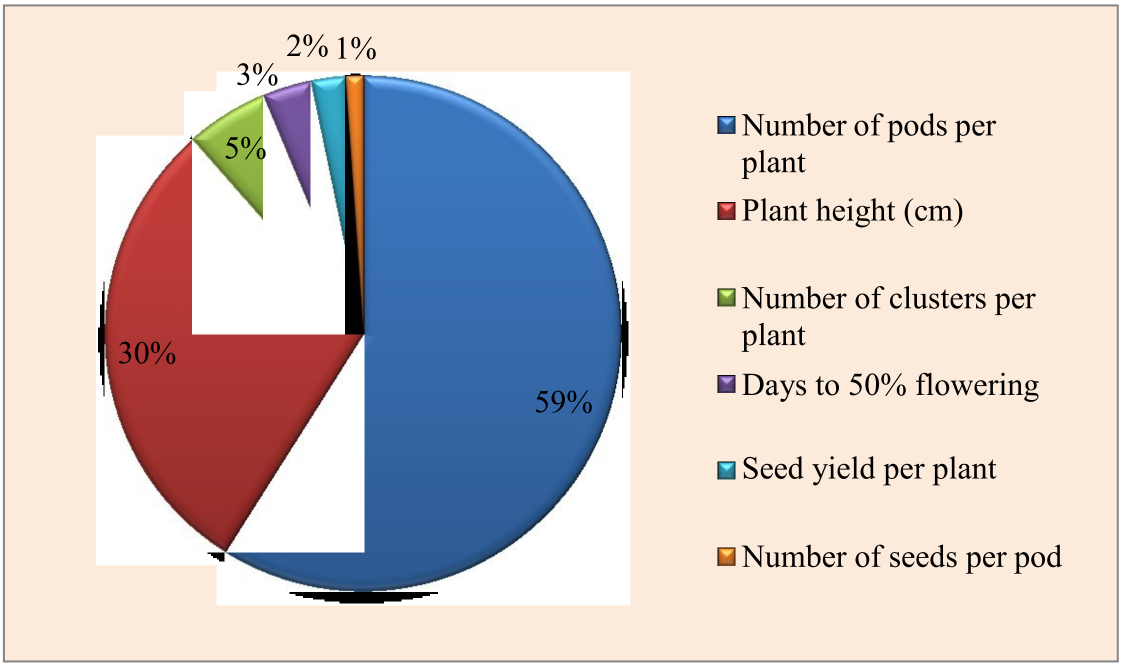

Fig. 3: ***Per cent*** **contribution of different traits towards genetic diversity in C2F$_3$ population of greengram**

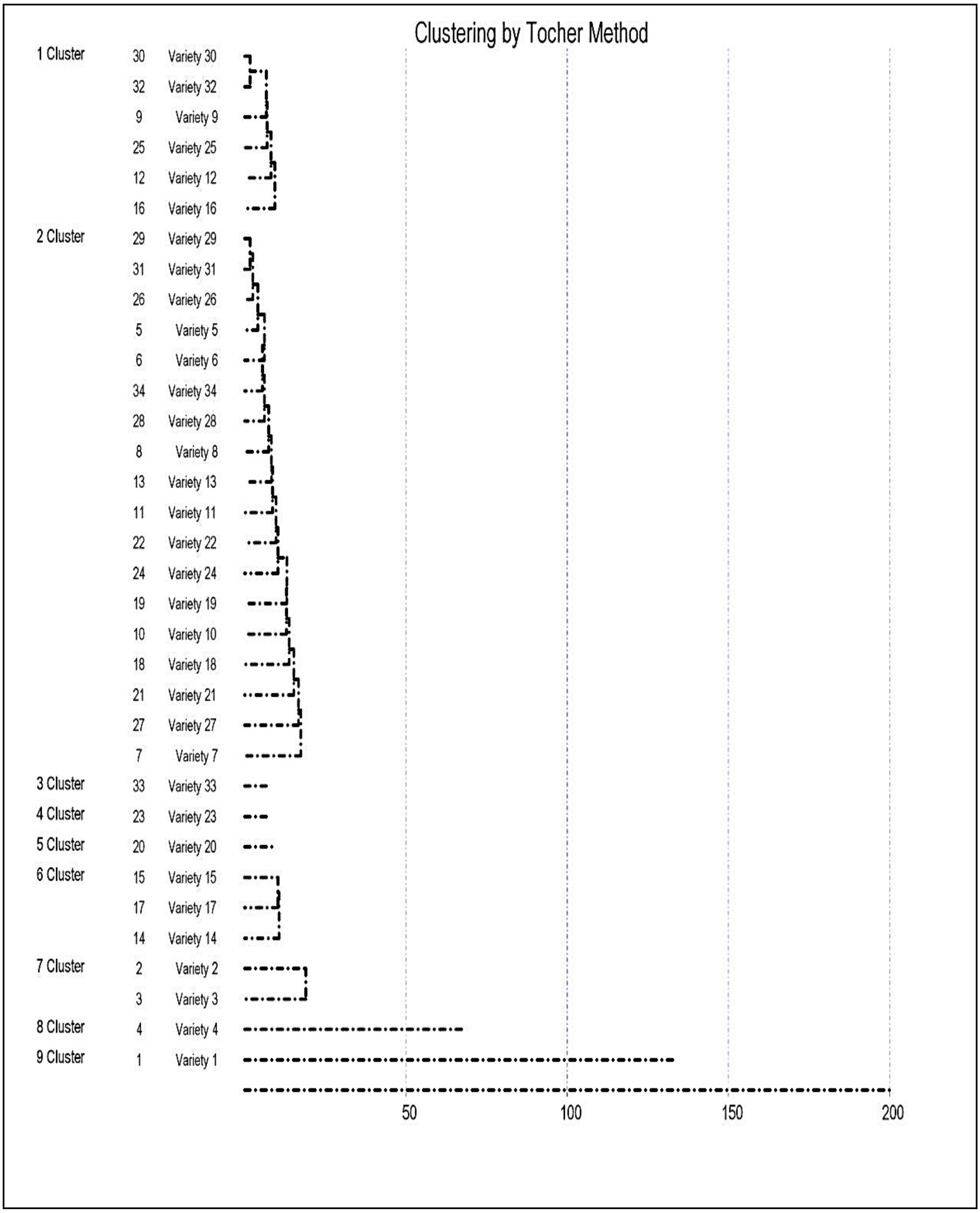

Fig. 4: Clustering pattern of C1F$_3$ population (KKM-3 × IPM 205-7) based on D^2 values in greengram

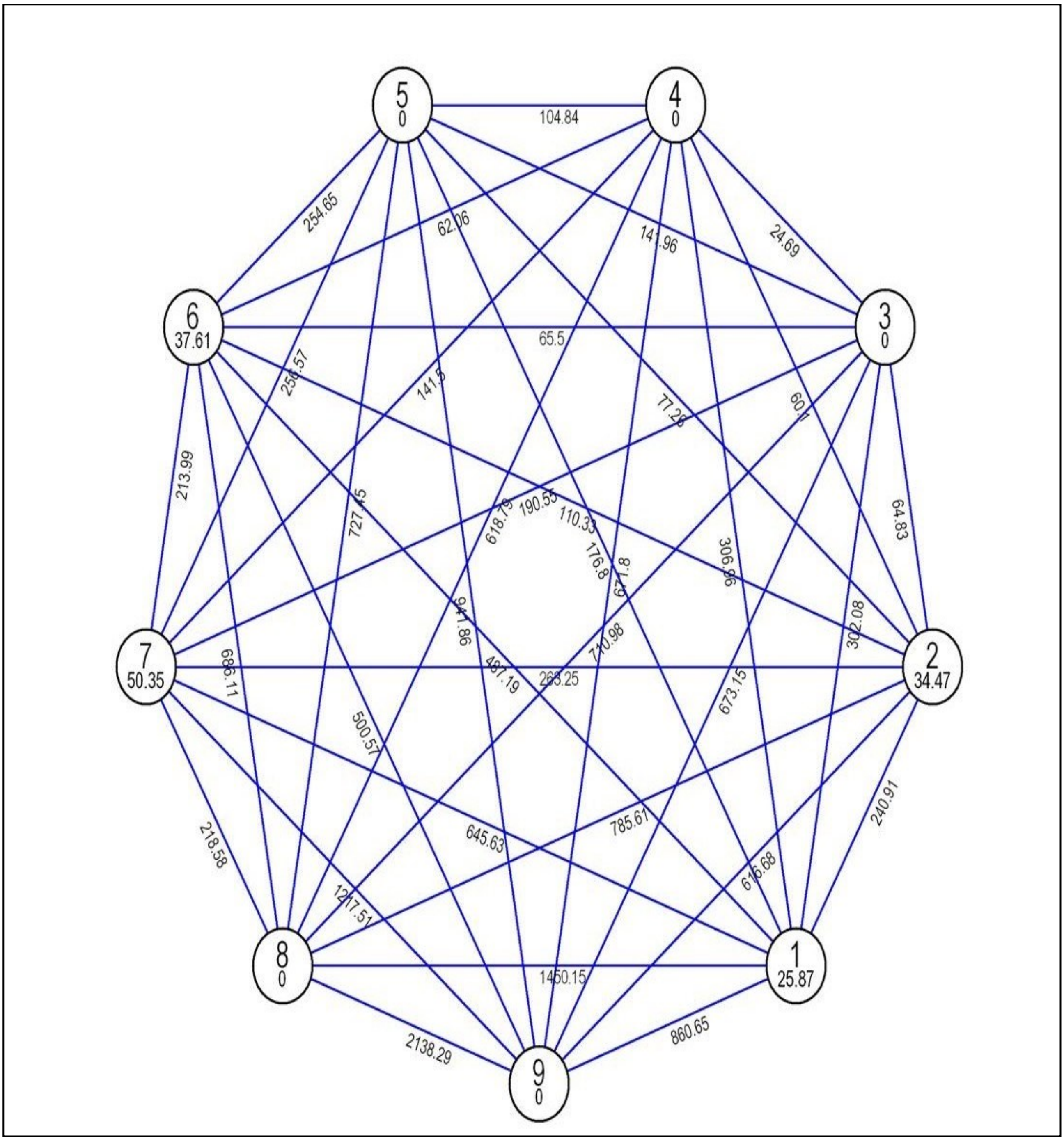

Fig. 5: Average intra and inter cluster distances for yield and its components in C1F$_3$ population (KKM-3 × IPM 205-7) of greengram

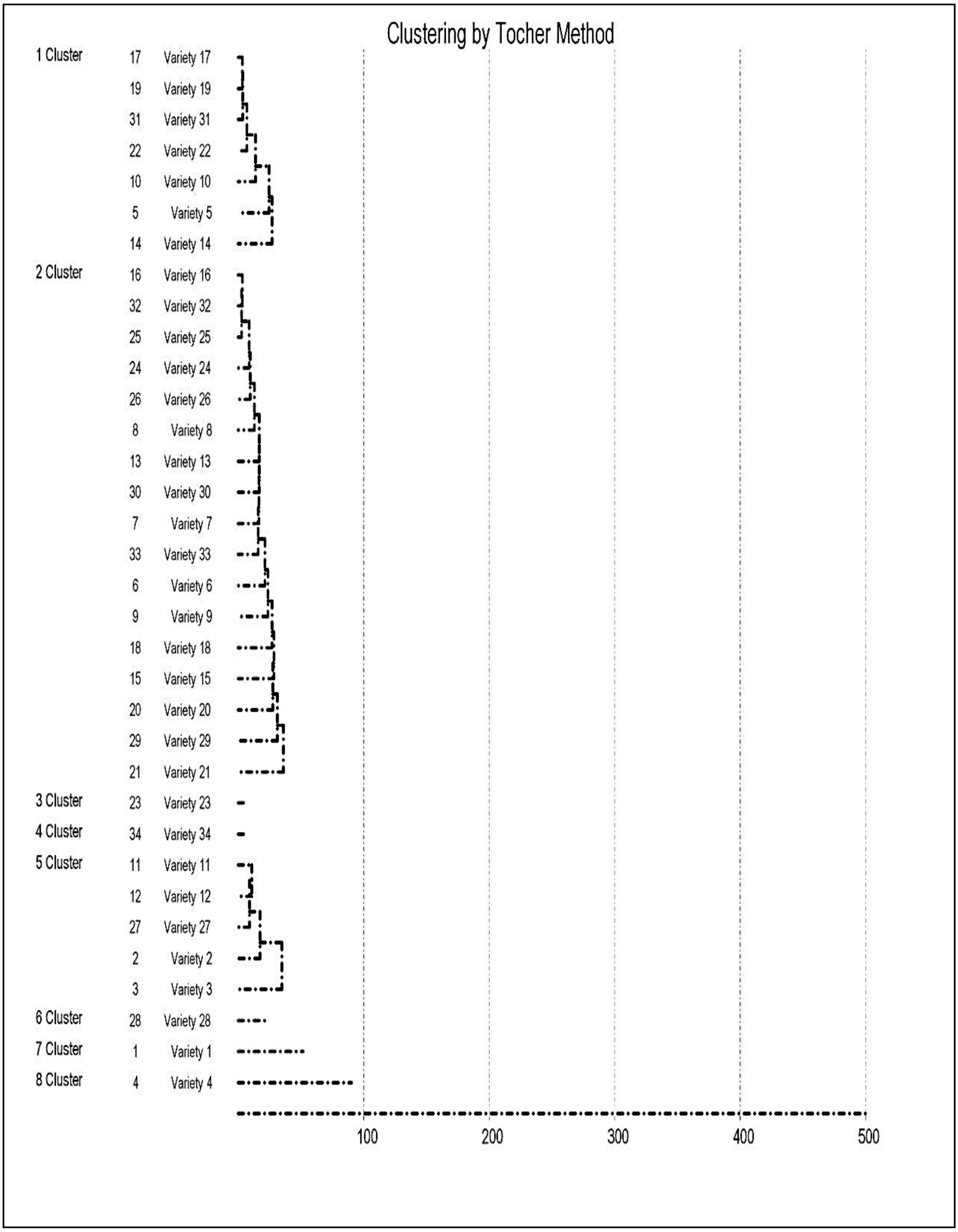

Fig. 6: Clustering pattern of C2F$_3$ population (KKM-3 × YADADRI) based on D^2 values in greengram

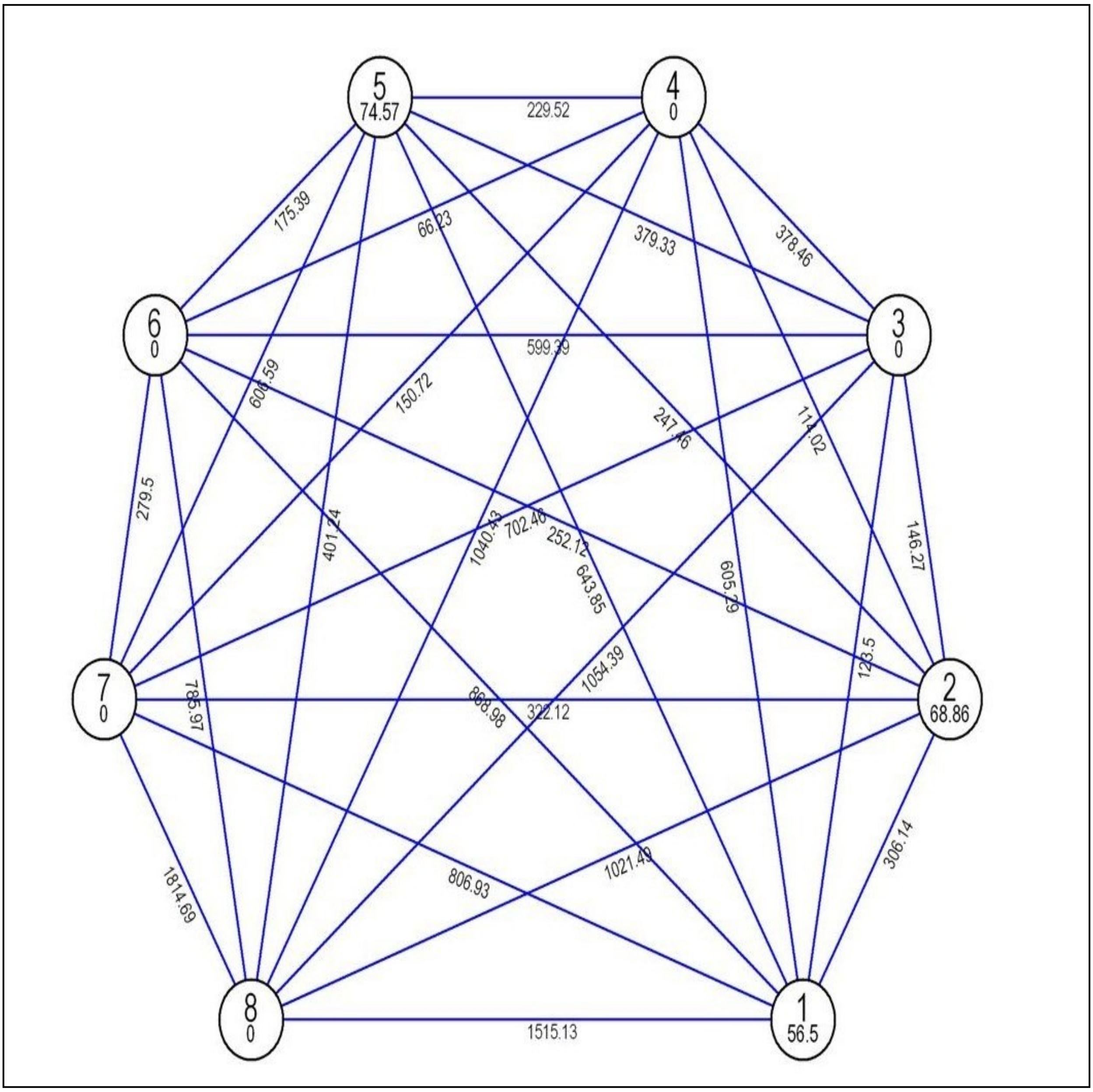

Fig. 7: Average intra and inter cluster distances for yield and its component in $C2F_3$ population (KKM-3 × YADADRI) of greengram

Table 8: Cluster means for yield and yield attributing traits in $C1F_3$ population (KKM-3 × IPM 205-7) of greengram

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII	Cluster IX
Days to 50 *per cent* flowering	27.32	30.82	26.00	28.00	32.50	28.37	31.50	39.00	28.00
Plant height (cm)	42.08	44.41	46.90	47.30	48.80	43.93	56.45	66.50	22.10
Primary branches per plant	2.50	2.02	2.00	2.40	2.40	1.87	2.70	2.20	2.40
Secondary branches per plant	6.60	4.46	6.80	5.20	4.60	4.13	4.70	4.20	4.60
Number of clusters per plant	10.02	8.51	10.20	8.90	6.95	9.04	7.50	4.80	8.50
Number of pods per cluster	5.64	3.97	4.60	3.80	4.60	4.73	5.30	4.68	5.20
Number of pods per plant	40.54	29.65	26.50	25.70	34.50	21.05	21.35	15.60	20.42
Pod length (cm)	9.29	7.16	7.40	6.86	6.86	7.43	9.10	8.30	6.14
Number of seeds per pod	13.30	8.32	7.80	11.60	11.80	7.92	11.00	9.20	9.82
100 seed weight (g)	4.41	3.37	3.60	3.30	3.10	3.13	4.24	4.12	3.47
Seed yield per plant (g)	8.88	2.77	3.10	3.25	3.12	2.78	5.04	3.14	4.89

Table 9: Cluster means for yield and yield attributing traits in $C2F_3$ population (KKM-3 × YADADRI) of greengram

Trait	Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI	Cluster VII	Cluster VIII
Days to 50 *per cent* flowering	31.24	32.38	35.00	30.50	32.44	30.00	28.30	39.00
Plant height (cm)	41.56	39.29	44.20	36.30	49.40	40.20	25.80	66.50
Primary branches per plant	2.35	2.05	2.40	2.20	2.36	1.20	2.40	2.20
Secondary branches per plant	5.46	4.78	5.20	3.20	4.78	4.40	4.80	4.20
Number of clusters per plant	10.43	6.92	9.25	4.80	7.56	2.50	8.50	4.80
Number of pods per cluster	5.26	4.39	4.20	4.00	4.88	4.40	5.20	4.68
Number of pods per plant	42.01	29.62	38.20	22.09	20.61	15.80	20.42	15.60
Pod length (cm)	9.63	7.27	6.10	6.40	7.73	7.80	6.80	8.30
Number of seeds per pod	13.00	8.29	9.10	6.50	8.99	7.04	9.82	9.20
100 seed weight (g)	4.14	3.32	3.70	2.84	3.62	3.05	3.47	4.12
Seed yield per plant (g)	10.97	4.08	5.20	3.01	4.63	4.02	4.89	3.14

For $C2F_3$ population, cluster means for the trait ranged from 1.20 to 2.40. The progenies from cluster VI had a low number of primary branches compared to the progenies belonging to the cluster I, III and VII, which were having more number of primary branches per plant.

4.3.4.4 Number of secondary branches per plant

For $C1F_3$ population, cluster means for the trait ranged from 4.13 to 6.80, where the progenies from cluster VI were having a low number of secondary branches, whereas the progenies from cluster III had more number of secondary branches per plant.

For $C2F_3$ population, cluster means for the trait ranged from 3.20 to 5.46, where the progenies from cluster IV were having a low number of secondary branches, whereas the progenies from cluster I had more number of secondary branches per plant.

4.3.4.5 Number of clusters per plant

Cluster means for this trait in $C1F_3$ population ranged from 4.80 to 10.20. The progenies included in cluster VIII had the lowest number of clusters per plant whereas, the progenies belonging to cluster III had more number of clusters per plant.

For $C2F_3$ population, cluster means for this trait ranged from 2.50 to 10.43. The progenies from cluster VI had the lowest number of clusters per plant whereas, the progenies belonging to cluster I had more number of clusters per plant.

4.3.4.6 Number of pods per cluster

For $C1F_3$ population, the cluster means for the trait ranged from 3.80 to 5.64, where the progenies belonging to cluster IV had fewer pods per cluster compared to the progenies from the cluster I had more pods per cluster.

Cluster means for the trait in $C2F_3$ population ranged from 4.00 to 5.26, with progenies from cluster IV having less pods per cluster than progenies from cluster I and VII, which had more pods per cluster.

4.3.4.7 Number of pods per plant

For $C1F_3$ population, cluster means for the trait ranged from 15.60 to 40.54, where the progenies from cluster VIII had fewer number of pods per plant, compared to the progenies belonging to cluster I had more number of pods per plant.

For C2F$_3$ population, cluster means for the trait ranged from 15.60 to 42.01, with progenies from cluster VIII having less pods per plant than progenies from cluster I, which had more pods per plant.

4.3.4.8 Pod length (cm)

For the C1F$_3$ population, the cluster means for the trait ranged from 6.14 cm to 9.29 cm, where the progenies belonging to cluster IX had shorter pod lengths than the progenies belonging to cluster I, which had longer pod lengths.

Cluster means for the trait in C2F$_3$ population ranged from 6.10 cm to 9.63 cm, where the progenies included in cluster III had shorter pod lengths than the progenies from cluster I, which had longer pod lengths.

4.3.4.9 Number of seeds per pod

For C1F$_3$ population, the cluster means for the trait ranged from 7.80 to 13.30, where the progenies grouped into cluster III had fewer seeds per pod compared to the progenies belonging to cluster I, which had more number of seeds per pod.

In C2F$_3$ population, the cluster means for the trait ranged from 6.50 to 13.00. The progenies grouped into cluster IV had fewer seeds per pod as compared to the progenies belonging to the cluster I, which had more number of seeds per pod.

4.3.4.10 Hundred seed weight (g)

For C1F$_3$ population, the cluster means for the trait ranged from 3.10 g to 4.41 g. The progenies belonging to cluster V had less test weight when compared to the progenies from cluster I had high test weight.

For C2F$_3$ population, the cluster means for the trait ranged from 2.84 g to 4.14 g. The progenies belonging to cluster IV had less test weight. In contrast, the progenies from clusters I and VIII had high test weight.

4.3.4.11 Seed yield per plant (g)

Cluster means for C1F$_3$ population ranged from 2.77 g to 8.88 g. The progenies included in cluster II were exhibiting low seed yield per plant, when compared to the progenies of cluster I, which had high seed yield per plant.

For C2F$_3$ population, the cluster means ranged from 3.01 g to 10.97 g. The progenies contained in cluster IV had low seed yield per plant as compared to the progenies of cluster I, which had high seed yield per plant.

4.4 Correlation coefficient analysis

The action and interplay of numerous agro-morphological attributes governs the economic yield of crop plants, which is a complex trait. Association of economic yield with other agro-morphological component characters should be investigated because, due to low heritability, selecting directly for high seed yield per plant may be ineffective. Correlation studies will provide reliable information, particularly when the breeder wants to combine superior yield potential with desirable agronomic attributes. The Phenotypic relations between yield and yield attributing component traits for $C1F_3$ and $C2F_3$ populations are studied and presented in tables 10 and 11, respectively.

4.4.1 Days to 50 per cent flowering

In $C1F_3$ population, this trait exhibited a significant positive association with plant height (0.510). In contrast, a significant negative association was observed with the number of secondary branches per plant (-0.34), number of seeds per pod (-0.340), number of pods per plant(-0.437), seed yield per plant (-0.442), number of clusters per plant(-0.534) and a non-significant negative correlation with the number of primary branches per plant (-0.0493), hundred seed weight (-0.153), pod length (-0.218), number of pods per cluster (-0.268).

In $C2F_3$ population, this trait has shown a significant positive association with plant height (0.523) and a non-significant positive association with hundred seed weight (0.144), number of primary branches per plant (0.117), number of secondary branches per plant (0.054). In contrast, a non-significant negative correlation was exhibited with the number of pods per cluster (-0.019), pod length (-0.066), number of seeds per pod (-0.134), number of pods per plant (-0.175), number of clusters per plant (-0.214) and seed yield per plant (-0.227).

4.4.2 Plant height (cm)

In $C1F_3$ population, this trait exhibited a significant positive correlation with days to 50 *per cent* flowering (0.510) and a non-significant positive correlation with pod length (0.27) followed by hundred seed weight (0.195), number of primary branches per plant (0.099). In contrast, a significant negative correlation was noticed with the number of clusters per plant (-0.452) and a non-significant negative correlation was found for the number of pods per cluster (-0.032), number of seeds per pod (-0.048), seed yield per plant (-0.161), number of secondary branches per plant (-0.185), number of pods per plant (-0.300).

Table 10. Phenotypic correlation coefficient for C1F$_3$ population (KKM-3 × IPM 205-7) of greengram

	DFF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
DFF	**1.0000**	0.5100**	-0.0493	-0.3480*	-0.5344**	-0.2683	-0.4376**	-0.2186	-0.3409*	-0.1533	-0.4426**
PH		**1.0000**	0.0993	-0.1859	-0.4521**	-0.0329	-0.3000	0.2716	-0.0485	0.1955	-0.1614
PBP			**1.0000**	0.3336	0.0446	0.3733*	0.1939	0.4831**	0.4272*	0.4288*	0.4631**
SBP				**1.0000**	0.2239	0.3994*	0.4950**	0.4838**	0.4591**	0.5513**	0.5808**
NCP					**1.0000**	0.3178	0.3867*	0.1982	0.2268	0.1183	0.4093**
NPC						**1.0000**	0.2438	0.6674**	0.6462**	0.6732**	0.7610**
NPP							**1.0000**	0.4532**	0.5612**	0.4286*	0.6513**
PL								**1.0000**	0.6898**	0.7764**	0.8031**
NSP									**1.0000**	0.6390**	0.8097**
100SW										**1.0000**	0.8039**
SYP											**1.0000**

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant
NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)
NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

Table 11. Phenotypic correlation coefficient for C2F_3 population (KKM-3 × YADADRI) of greengram

	DFF	**PH**	**PBP**	**SBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**100SW**	**SYP**
DFF	**1.0000**	0.5234**	0.1175	0.0549	-0.2148	-0.0194	-0.1758	-0.0661	-0.1345	0.1446	-0.2272
PH		**1.0000**	0.1400	0.0119	-0.0114	0.2126	-0.1947	0.2420	0.1118	0.3606*	0.0114
PBP			**1.0000**	0.4756**	0.3605*	0.3887*	0.2274	0.2973	0.2559	0.2352	0.2538
SBP				**1.0000**	0.3238	0.3408*	0.4367**	0.2937	0.2602	0.1375	0.3757*
NCP					**1.0000**	0.5337**	0.5622**	0.5219**	0.6042**	0.3294	0.6044**
NPC						**1.0000**	0.2680	0.6352**	0.6573**	0.5377**	0.5965**
NPP							**1.0000**	0.5049**	0.6235**	0.3930*	0.7494**
PL								**1.0000**	0.7846**	0.6045**	0.7423**
NSP									**1.0000**	0.7193**	0.7992**
100SW										**1.0000**	0.6280**
SYP											**1.0000**

**Significance at 0.01 probability level *Significance at 0.05 probability level

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant

NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)

NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

In C2F$_3$ population, this trait exhibited a significant positive correlation with days to 50 *per cent* flowering (0.523), hundred seed weight (0.360), and a non-significant positive correlation with pod length (0.242), number of pods per cluster (0.212), the number of primary branches per plant (0.140), number of seeds per pod (0.111) and seed yield per plant (0.011) and secondary branches per plant (0.011). In contrast, a significant negative correlation was observed with the number of clusters per plant (-0.011) and number of pods per plant (-0.194).

4.4.3 Number of primary branches per plant

In C1F$_3$ population, this trait had a significant positive correlation with pod length (0.483), seed yield per plant (0.463), hundred seed weight (0.428), number of seeds per pod (0.427), number of pods per cluster (0.373) and a non-significant positive correlation with secondary branches per plant (0.333), number of pods per plant (0.193), plant height (0.099), number of clusters per plant (0.044), whereas, a non-significant negative correlation was found with days to 50 *per cent* flowering (-0.049).

In C2F$_3$ population, this trait has shown a significant positive correlation with the number of secondary branches per plant (0.475), number of pods per cluster (0.388), number of clusters per plant (0.360), and a non-significant positive association with pod length (0.297), number of seeds per pod (0.255), seed yield per plant (0.253), hundred seed weight (0.235), number of pods per plant (0.227) plant height (0.140) and days to 50 *per cent* flowering (0.117).

4.4.4 Number of secondary branches per plant

In C1F$_3$ population, this trait exhibited a significant positive correlation with seed yield per plant (0.580), hundred seed weight (0.551), number of pods per plant (0.495), pod length (0.483), number of seeds per pod (0.459), number of pods per cluster (0.399) and a non-significant positive association with primary branches per plant (0.333), number of clusters per plant (0.223). In contrast, a significant negative correlation was observed with days to 50 *per cent* flowering (-0.348) and a non-significant negative correlation with plant height (-0.185).

In C2F$_3$ population, this trait had a significant positive relation with the number of primary branches per plant (0.475), number of pods per plant (0.436), seed yield per plant (0.375), number of pods per cluster (0.340) and a non-significant positive association with the pod length (0.293), number of seeds per pod (0.260), hundred seed weight (0.137), number of days to 50 *per cent* flowering (0.054), number of clusters per plant (0.032), plant height (0.011).

4.4.5 Number of clusters per plant

In C1F$_3$ population, this trait has shown a significant positive correlation with seed yield per plant (0.409), number of pods per plant (0.386) and a non-significant positive relation with the number of pods per cluster (0.317) and the number of seeds per pod (0.226), secondary branches per plant (0.223), pod length (0.198), hundred seed weight (0.118), number of primary branches per plant (0.044). In contrast, a significant negative relation was observed with plant height (-0.452) and days to 50 *per cent* flowering (-0.534).

In C2F$_3$ population, this trait exhibited a significant positive relation with the number of seeds per pod (0.604) and seed yield per plant (0.604), number of pods per plant (0.562), number of pods per cluster (0.533), pod length (0.521), primary branches per plant (0.360), and a non-significant positive relation with hundred seed weight (0.329), secondary branches per plant (0.323). In contrast, a non-significant negative correlation was observed with plant height (-0.011) and days 50 *per cent* flowering (-0.214).

4.4.6 Number of pods per cluster

In C1F$_3$ population, this trait has shown a significant positive association with seed yield per plant (0.761), hundred seed weight (0.673), pod length (0.667), number of seeds per pod (0.646), secondary branches per plant (0.399), primary branches per plant (0.373) and a non-significant positive relation with the number of clusters per plant (0.317), number of pods per plant (0.243). In contrast, a non-significant negative association was reported with plant height (-0.032) followed by days to 50 *per cent* flowering (-0.263).

In C2F$_3$ population, this trait had a significant positive correlation with the number of seeds per pod (0.657), pod length (0.635), seed yield per plant (0.596), hundred seed weight (0.537), number of clusters per plant (0.533), primary branches per plant (0.388), secondary branches per plant (0.340), and positive relation with plant height (0.212), number of pods per plant (0.268). In contrast, a non-significant negative association was noticed with days to 50 *per cent* flowering (-0.019).

4.4.7 Number of pods per plant

In C1F$_3$ population, this trait had a significant positive relation with seed yield per plant (0.651), number of seeds per pod (0.561), number of secondary branches per plant (0.495), pod length (0.453), hundred seed weight (0.428), number of clusters per plant (0.386), and a non-significant positive association with the number of pods per cluster (0.243) and the number of primary branches per plant (0.193). In contrast, a significant negative relation was observed with days to 50 *per cent* flowering (-0.437) and a non-significant negative association with plant height (-0.300).

In $C2F_3$ population, this trait had a positive correlation significantly with seed yield per plant (0.749), number of seeds per pod (0.623), number of clusters per plant (0.562), pod length (0.504), number of secondary branches per plant (0.436), hundred seed weight (0.393) and a non-significant positive relation with the number of pods per cluster (0.268), number of primary branches per plant (0.227). In contrast, a non-significant negative association was observed with number of days to 50 *per cent* flowering (-0.175), plant height (-0.194).

4.4.8 Pod length (cm)

In $C1F_3$ population, this trait exhibited a significant positive association with the seed yield per plant (0.803), hundred seed weight (0.776), number of seeds per pod (0.689), number of pods per cluster (0.667), number of primary branches per plant (0.483), number of secondary branches per plant (0.483), number of pods per plant (0.453), whereas a non-significant positive correlation was found with plant height (0.271) and number of clusters per plant (0.198). In contrast, a non-significant negative association with the number of days to 50 *per cent* flowering (-0.218).

In $C2F_3$ population, this trait had a significant positive association with the number of seeds per pod (0.784), seed yield per plant (0.743), number of pods per cluster (0.635), hundred seed weight (0.604), number of clusters per plant (0.521), number of pods per plant (0.504) and a non-significant positive association with a number of primary branches per plant (0.297) and number of secondary branches per plant (0.293), plant height (0.242), whereas a non-significant negative relation was observed with days to 50 *per cent* flowering (-0.066).

4.4.9 Number of seeds per pod

In $C1F_3$ population, this trait exhibited a significant positive association with seed yield per plant (0.809), pod length (0.689), number of pods per cluster (0.646), hundred seed weight (0.639), number of pods per plant (0.561), secondary branches per plant (0.459), number of primary branches per plant (0.427), whereas a non-significant positive association with the number of clusters per plant (0.226). In contrast, a significant negative association was observed with the number of days to 50 *per cent* flowering (-0.340) and a non-significant negative association with plant height (-0.048).

In $C2F_3$ population, this trait had a significant positive correlation with seed yield per plant (0.799), pod length (0.784), hundred seed weight (0.719), number of pods per cluster (0.657), number of pods per plant (0.623), number of clusters per plant (0.604) and a non-significant positive relation with the number of secondary branches per plant (0.260), number of primary branches per plant (0.255) and the plant height (0.118). In contrast, a non-significant negative correlation was observed with the number of days to 50 *per cent* flowering (-0.134).

4.4.10 Hundred seed weight (g)

In C1F$_3$ population, this trait had a significant positive association with the primary branches per plant (0.428), number of secondary branches per plant (0.551), number of pods per cluster (0.673), number of pods per plant (0.428), pod length (0.776), number of seeds per pod (0.639), seed yield per plant (0.803) and a non-significant positive relation with plant height (0.195), number of clusters per plant (0.118). In contrast, a non-significant negative correlation was recorded with days to 50 *per cent* flowering (-0.153).

In C2F$_3$ population, this trait shown a significant positive association with the number of seeds per pod (0.713), seed yield per plant (0.628), pod length (0.604), number of pods per cluster (0.537), number of pods per plant (0.393), plant height (0.360) and a non-significant positive relation with the number of clusters per plant (0.329), number of primary branches per plant (0.235), days to 50 *per cent* flowering (0.144), number of secondary branches per plant (0.137).

4.4.11 Seed yield per plant (g)

In C1F$_3$ population, this trait has shown a significant positive association with the number of seeds per pod (0.809), pod length (0.803), hundred seed weight (0.803), number of pods per cluster (0.761), number of pods per plant (0.651), secondary branches per plant (0.580), primary branches per plant (0.463), number of clusters per plant (0.409). In contrast, a significant negative relation was observed with days to 50 *per cent* flowering (-0.442) and a non-significant negative relation with plant height (-0.1614).

In C2F$_3$ population, this trait exhibited a significant positive association with the number of seeds per pod (0.799), number of pods per plant (0.749), pod length (0.742), hundred seed weight (0.628), number of clusters per plant (0.604), number of pods per cluster (0.596), secondary branches per plant (0.375) and a non-significant positive relation with the number of primary branches per plant (0.253) followed by plant height (0.011), whereas a negative non-significant association reported with days to 50 *per cent* flowering (-0.227).

4.5 Path coefficient analysis

Seed yield is generally under polygenic control; selecting for economic yield for the sake of increasing yield will not be fruitful as it affects the other related traits and vice versa. To understand the influence of different agro-morphological traits on seed yield, the association of these traits with seed yield was divided into direct and indirect effects; this gives more clarity while selecting for essential traits, which may contribute towards increased seed yield per plant. The results of path analysis between yield and yield-related traits in C1F$_3$ and C2F$_3$ populations are estimated and depicted in tables 12 and 13, respectively.

Table 12. Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects of different traits on seed yield per plant in C1F$_3$ population (KKM-3 × IPM 205-7) of greengram

Effect of trait	***Via* Character**									
	DFF	**PH**	**PBP**	**SBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**100SW**
DFF	**-0.0315**	-0.0160	0.0015	0.0109	0.0168	0.0084	0.0138	0.0069	0.0107	0.0048
PH	-0.1078	**-0.2113**	-0.0210	0.0393	0.0955	0.0070	0.0634	-0.0574	0.0102	-0.0413
PBP	-0.0025	0.0050	**0.0501**	0.0167	0.0022	0.0187	0.0097	0.0242	0.0214	0.0215
SBP	0.0130	0.0070	-0.0125	**-0.0375**	-0.0084	-0.0150	-0.0186	-0.0181	-0.0172	-0.0207
NCP	-0.0297	-0.0252	0.0025	0.0125	**0.0557**	0.0177	0.0215	0.0110	0.0126	0.0066
NPC	-0.0449	-0.0055	0.0624	0.0668	0.0531	**0.1672**	0.0408	0.1116	0.1080	0.1125
NPP	-0.0682	-0.0468	0.0302	0.0772	0.0603	0.0380	**0.1559**	0.0707	0.0875	0.0668
PL	-0.0621	0.0772	0.1373	0.1375	0.0563	0.1897	0.1288	**0.2842**	0.1961	0.2206
NSP	-0.0597	-0.0085	0.0748	0.0804	0.0397	0.1132	0.0983	0.1208	**0.1752**	0.1120
100SW	-0.0492	0.0628	0.1376	0.1770	0.0380	0.2161	0.1376	0.2492	0.2051	**0.3210**
r values	**-0.4426****	**-0.1614**	**0.4631****	**0.5808****	**0.4093****	**0.7610****	**0.6513****	**0.8031****	**0.8097****	**0.8039****

* Significant at 0.05 level of probability; ** Significant at 0.01 level of probability; r: Correlation coefficient with seed yield per plant

Residual effect: 0.2661

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant

NCP = Number of cluster per plant
NPC = Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)

NSP = Number of seeds per pod
100 SW = 100 seed weight (g)

Table 13. Phenotypic path coefficient analysis showing direct (diagonal) and indirect effects of different traits on seed yield per plant in C2F$_3$ population (KKM-3 × YADADRI) of greengram

Effect of trait	*Via* Character									
	DFF	**PH**	**PBP**	**SBP**	**NCP**	**NPC**	**NPP**	**PL**	**NSP**	**100SW**
DFF	**-0.1513**	-0.0792	-0.0178	-0.0083	0.0325	0.0029	0.0266	0.0100	0.0203	-0.0219
PH	0.0050	**0.0096**	0.0013	0.0001	-0.0001	0.0020	-0.0019	0.0023	0.0011	0.0035
PBP	-0.0066	-0.0079	**-0.0562**	-0.0267	-0.0203	-0.0218	-0.0128	-0.0167	-0.0144	-0.0132
SBP	0.0026	0.0006	0.0224	**0.0470**	0.0152	0.0160	0.0205	0.0138	0.0122	0.0065
NCP	-0.0043	-0.0002	0.0072	0.0065	**0.0199**	0.0106	0.0112	0.0104	0.0121	0.0066
NPC	-0.0035	0.0387	0.0708	0.0621	0.0972	**0.1821**	0.0488	0.1157	0.1197	0.0979
NPP	-0.0749	-0.0830	0.0969	0.1861	0.2397	0.1142	**0.4262**	0.2152	0.2657	0.1675
PL	-0.0144	0.0526	0.0646	0.0638	0.1134	0.1380	0.1097	**0.2172**	0.1704	0.1313
NSP	-0.0090	0.0075	0.0171	0.0174	0.0404	0.0439	0.0416	0.0524	**0.0668**	0.0480
100SW	0.0292	0.0728	0.0475	0.0278	0.0665	0.1085	0.0793	0.1220	0.1452	**0.2019**
r values	**-0.2272**	**0.0114**	**0.2538**	**0.3757****	**0.6044****	**0.5965****	**0.7494****	**0.7423****	**0.7992****	**0.6280****

* Significant at 0.05 level of probability; ** Significant at 0.01 level of probability; r: Correlation coefficient with seed yield per plant

Residual effect: 0.4250

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant

NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)

NSP = Number of seeds per pod
100 SW = 100 seed weight (g)

4.5.1 Days to 50 per cent flowering

In C1F$_3$ population, the number of days to 50 *per cent* flowering showed a negative direct effect on seed yield per plant (-0.0315) *via* positive indirect effects of the number of clusters per plant (0.0168), number of pods per plant (0.0138), number of secondary branches per plant (0.0109), number of seeds per pod (0.0107), number of pods per cluster (0.0084), pod length (0.0069), hundred seed weight (0.0048), primary branches per plant (0.0015) and negative indirect effects of plant height (-0.0160).

In C2F$_3$ population, the number of days to 50 *per cent* flowering showed a negative direct effect on seed yield per plant (-0.1513) through positive indirect effects of the number of clusters per plant (0.0325), number of pods per plant (0.0266), number of seeds per pod (0.0203), pod length (0.0100), number of pods per cluster (0.0029) and negative indirect effects of the number of secondary branches per plant (-0.0083), plant height (-0.0792), hundred seed weight (-0.0219), primary branches per plant (-0.0178).

4.5.2 Plant height (cm)

In C1F$_3$ population, plant height exerted a negative direct effect on seed yield per plant (-0.2113) through a positive indirect effect of the number of clusters per plant (0.0955), number of pods per plant (0.0634), number of secondary branches per plant (0.0393), number of seeds per pod (0.0102), number of pods per cluster (0.0070) and a negative indirect effect of the number of primary branches per plant (-0.0210), pod length (-0.0574), hundred seed weight (-0.0413), days to 50 *per cent* flowering (-0.1078).

In C2F$_3$ population, plant height exerted a positive direct effect on seed yield per plant (0.0096) through a positive indirect effect of days to 50 *per cent* flowering (0.0050), hundred seed weight (0.0035), pod length (0.0023), number of pods per cluster (0.0020), number of primary branches per plant (0.0013), number of seeds per pod (0.0011), secondary branches per plant (0.0001) and a negative indirect effect of number of clusters per plant (-0.0001), number of pods per plant (-0.0019).

4.5.3 Number of primary branches per plant

In C1F$_3$ population, the number of primary branches per plant exhibited a positive direct effect on seed yield per plant (0.0501) through positive indirect effects of pod length (0.0242), hundred seed weight (0.215), number of seeds per pod (0.214), number of pods per cluster (0.0187), secondary branches per plant (0.0167), number of pods per plant (0.0097), plant height (0.0050), number of clusters per plant (0.0022) and a negative indirect effects of days to 50 *per cent* flowering (-0.0025).

In C2F$_3$ population, the number of primary branches per plant exhibited a negative direct effect on seed yield per plant (-0.0562) through negative indirect effects of days to 50 *per cent* flowering (-0.0066), plant height (-0.0079), number of pods per plant (-0.0128), hundred seed weight (-0.0132), number of seeds per pod (-0.0144), pod length (-0.0167), number of clusters per plant (-0.0203), number of pods per cluster (-0.0218) and number of secondary branches per plant (-0.0267).

4.5.4 Number of secondary branches per plant

In C1F$_3$ population, the number of secondary branches per plant exerted a negative direct effect on seed yield per plant (-0.0375) through positive indirect effects of days to 50 *per cent* flowering (0.0130), plant height (0.0070) and negative indirect effects of the number of clusters per plant (-0.0084), primary branches per plant (-0.0125), number of pods per cluster (-0.0150), number of seeds per pod (-0.0172), pod length (-0.0181), number of pods per plant (-0.0186), hundred seed weight (-0.0207).

In C2F$_3$ population, the number of secondary branches per plant exerted a positive direct effect on seed yield per plant (0.0470) through positive indirect effects of primary branches per plant (0.0224), number of pods per plant (0.0205), number of pods per cluster (0.0160), number of clusters per plant (0.0152), pod length (0.0138), number of seeds per pod (0.0122), hundred seed weight (0.0065), days to 50 *per cent* flowering (0.0026) and plant height (0.0006).

4.5.5 Number of clusters per plant

In C1F$_3$ population, the number of clusters per plant had a positive direct effect on seed yield per plant (0.0557) through positive indirect effects of number of pods per plant (0.0215), number of pods per cluster (0.0177), number of seeds per pod (0.0126), secondary branches per plant (0.0125), pod length (0.0110), hundred seed weight (0.0066), number of primary branches per plant (0.0025) and negative indirect effects of plant height (-0.0252), days to 50 *per cent* flowering (-0.0297).

In C2F$_3$ population, the number of clusters per plant had a positive direct effect on seed yield per plant (0.0199) through positive indirect effects of the number of seeds per pod (0.0121), number of pods per plant (0.0112), number of pods per cluster (0.0106), pod length (0.0104), number of primary branches per plant (0.0072), hundred seed weight (0.0066), secondary branches per plant (0.0065), number and negative indirect effects of plant height (-0.0002), days to 50 *per cent* flowering (-0.0043).

4.5.6 Number of pods per cluster

In $C1F_3$ population, the number of pods per cluster exerted a positive direct effect on seed yield per plant (0.1672) through positive indirect effects of hundred seed weight (0.1125), pod length (0.1116), number of seeds per pod (0.1080), secondary branches per plant (0.0668), primary branches per plant (0.0624), number of clusters per plant (0.0531), number of pods per plant (0.0408) and negative indirect effects of days to 50 *per cent* flowering (-0.0449), plant height (-0.0055).

In $C2F_3$ population, the number of pods per cluster exerted a positive direct effect on seed yield per plant (0.1821) through positive indirect effects of the number of seeds per pod (0.1197), pod length (0.1157), hundred seed weight (0.0979), number of clusters per plant (0.0972), primary branches per plant (0.0708), secondary branches per plant (0.0621), number of pods per plant (0.0488), plant height (0.0387) and negative indirect effect of days to 50 *per cent* flowering (-0.0035).

4.5.7 Number of pods per plant

In $C1F_3$ population, the number of pods per plant exerted a positive direct effect on seed yield per plant (0.1559) through positive indirect effects of the number of seeds per pod (0.0875), number of secondary branches per plant (0.0772), pod length (0.0707), hundred seed weight (0.0668), number of clusters per plant (0.0603), number of pods per cluster (0.0380), and primary branches per plant (0.0302) and negative indirect effects of plant height (-0.0468), days to 50 *per cent* flowering (-0.0682).

In $C2F_3$ population, the number of pods per plant exerted a positive direct effect on seed yield per plant (0.4262) through positive indirect effects of the number of seeds per pod (0.2657), number of clusters per plant (0.2397), pod length (0.2152), number of secondary branches per plant (0.1861), hundred seed weight (0.1675), number of pods per cluster (0.1142), primary branches per plant (0.0969) and negative indirect effects of days to 50 *per cent* flowering (-0.0749), plant height (-0.0830).

4.5.8 Pod length (cm)

In $C1F_3$ population, pod length exerted a positive direct effect on seed yield per plant (0.2842) through positive indirect effects of hundred seed weight (0.2206), number of seeds per pod (0.1961), number of pods per cluster (0.1897), secondary branches per plant (0.1375), primary branches per plant (0.1373), number of pods per plant (0.1288), plant height (0.0772), number of clusters per plant (0.0563) and negative indirect effects of days to 50 *per cent* flowering (-0.0621).

In C2F$_3$ population, pod length exerted a positive direct effect on seed yield per plant (0.2172) through positive indirect effects of the number of seeds per pod (0.1704) followed by the number of pods per cluster (0.1380), hundred seed weight (0.1313), number of clusters per plant (0.1134), number of pods per plant (0.1097), primary branches per plant (0.0646), number of secondary branches per plant (0.0638), plant height (0.0526) and negative indirect effects of days to 50 *per cent* flowering (-0.0144).

4.5.9 Number of seeds per pod

In C1F$_3$ population, the number of seeds per pod exerted a positive direct effect on seed yield per plant (0.1752) through positive indirect effects of pod length (0.1208), number of pods per cluster (0.1132), hundred seed weight (0.1120), number of pods per plant (0.0983), secondary branches per plant (0.0804), number of primary branches per plant (0.0748), number of clusters per plant (0.0397) and negative indirect effects of plant height (-0.0085) followed by days to 50 *per cent* flowering (-0.0597).

In C2F$_3$ population, the number of seeds per pod exerted a positive direct effect on seed yield per plant (0.0668) through positive indirect effects of pod length (0.0524), number of pods per cluster (0.0439), hundred seed weight (0.0480), number of pods per plant (0.0416), number of clusters per plant (0.0404), secondary branches per plant (0.0174), number of primary branches per plant (0.0171), plant height (0.0075) and negative indirect effects of days to 50 *per cent* flowering (-0.0090).

4.5.10 Hundred seed weight (g)

In C1F$_3$ population, hundred seed weight exerted a positive direct effect on seed yield per plant (0.3210) through indirect positive effects of the number of pods per cluster (0.2161), number of pods per plant (0.1376), number of clusters per plant (0.0380) and negative indirect effects of the number of secondary branches per plant (0.1770), primary branches per plant (0.1376), number of seeds per pod (0.2051), pod length (0.2492) and plant height (0.0628) and negative indirect effects of days to 50 *per cent* flowering (-0.0492).

In C2F$_3$ population, hundred seed weight exerted a positive direct effect on seed yield per plant (0.2019) through indirect positive effects of number of seeds per pod (0.1452), pod length (0.1220) followed by the number of pods per cluster (0.1085), the number of pods per plant (0.0793), primary branches per plant (0.0728), plant height (0.0728), number of clusters per plant (0.0665), days to 50 *per cent* flowering (0.0292) and number of secondary branches per plant (0.0278).

4.6 High yielding superior segregants identified concerning seed yield

The progeny lines 32, 9, 25, 12 were contributing more number of pods per plant (39.59, 39.14, 36.15, 39.78) and high seed yield per plant (5.42 g, 5.32 g, 5.19 g, 5.78 g) when compared with better parent KKM-3 (4.10g) in C1F_3 population. Progeny lines 9 and 12 were identified as early flowering (27.82 days, 28.84 days) as compared to KKM-3. However, other yield attributing traits like pod length, number of seeds per pod and hundred seed weight were on par with the parental lines. Hence, these progeny lines were identified as superior segregants for yield and its contributing traits. The details are furnished in table 14.

Among the different C2F_3 families, progeny lines *viz.,* 19, 31, 22, 14 were found to be outperforming over better parent YADADRI (18.50) with respect to number of pods per plant (36.03, 39.04, 38.75, 37.68) and high seed yield per plant (6.42 g, 6.26 g, 6.56 g, 6.31g) as that of YADADRI (4.90 g). All selected progenies were exhibiting longer pod lengths (9.89 cm, 10.55 cm, 10.63 cm, 10.27 cm) and more number of seeds per pod (13.50, 14.33, 12.70, 13.55). The trait hundred seed weight was on par with the parental lines. Hence, these progeny lines were selected as high yielding superior segregants for yield and its contributing traits. The detailed view is presented in table 15.

Table 14: Superior segregants identified for yield and its component traits in C1F$_3$ population (KKM-3 × IPM 205-7) of greengram

Progeny lines	DFF	NPP	PL	NSP	100SW	SYP
32	25.64	39.59	9.49	9.80	4.58	5.42
9	27.82	39.14	9.47	9.95	4.47	5.32
25	29.04	36.15	9.60	10.16	4.44	5.19
12	28.84	39.78	9.68	9.99	4.23	5.78
KKM-3	31.08	25.23	9.51	11.20	4.09	4.10
IPM 205-7	27.88	20.23	6.45	9.35	3.77	3.90
CD@5%	2.26	2.05	0.48	0.96	0.64	0.90

DFF = Days to 50 *per cent* flowering
NPP = Number of pods per plant
PL = Pod length (cm)
NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

Table 15: Selected superior segregants for yield and its component traits in C2F$_3$ population (KKM-3 × YADADRI) of greengram

Progeny lines	DFF	NPP	PL	NSP	100SW	SYP
19	30.80	36.03	9.89	13.50	4.44	6.42
31	29.60	39.04	10.55	14.33	4.29	6.26
22	33.07	38.75	10.63	12.70	3.82	6.56
14	34.20	37.68	10.27	13.55	4.25	6.31
KKM-3	31.08	25.23	9.51	11.20	4.09	4.10
YADADRI	32.50	18.50	8.60	10.20	4.20	4.90
CD@5%	2.89	4.70	0.68	1.88	0.57	1.14

DFF = Days to 50 *per cent* flowering
NPP = Number of pods per plant
PL = Pod length (cm)
NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)

DISCUSSION

V DISCUSSION

The current study, titled "Assessment of Genetic Variability and Diversity in Segregating Generations of Greengram [*Vigna radiata* (L.) Wilczek]" used two populations, C1F$_3$ (KKM-3 × IPM 205-7) and C2F$_3$ (KKM-3 × YADADRI) to evaluate the direct selection parameters (variability, heritability and genetic advance), as well as indirect selection parameters (correlation and path coefficient) and estimation of genetic diversity using Mahalanobis' D^2 statistics for identifying superior segregants from the base population. The findings from the field data for eleven quantitative traits have been explored in light of previous researchers' explanations in the following sections:

5.1 Analysis of variance

It is marked from the analysis of variance that the F$_3$ families of both crosses varied significantly for all the traits. This indicated that the F$_3$ progenies had sufficient genetic variability, providing ample scope for selection for the identification of superior high yielding segregants to be used in a crop improvement program to enhance the seed yield of greengram. The present findings were in accordance with Narasimhulu *et al.* (2013) and Muralidhara *et al.* (2016).

5.2 Heritability and Genetic advance

The effectiveness of selection is determined by the magnitude of genetic variation associated with high heritability and greater genetic advance, so the success of any crop breeding programme is dependent on the extent of variability, which is heritable. Therefore, criteria like PCV, GCV, heritability and genetic advance will help in estimating the heritable genetic variation and frame better breeding programs by having the proper knowledge about the kind of gene action.

From the results of genetic variability estimates, both C1F$_3$ and C2F$_3$ populations exhibited higher PCV values than their corresponding GCV values for all the component traits. The difference between them was smaller, indicating that the environment had less influence on the expression of those characters, implying that phenotypic selection may be given due consideration. In case of number of primary branches per plant, number of clusters per plant, hundred seed weight of C1F$_3$, and the number of pods per cluster and plant height of C2F$_3$, the difference was relatively higher, indicating a significant effect of the environment on these traits where other variability parameters like heritability may also be considered for selection. Similar results were reported by Narasimhulu *et al*. (2013) and Muralidhara *et al.* (2016).

From the above results, $C1F_3$ population showed high PCV and GCV values for seed yield per plant, number of secondary branches per plant. Moderate values observed for number of clusters per plant, number of pods per cluster, number of pods per plant, plant height, number of seeds per pod, pod length and hundred seed weight, suggesting that the practicing selection for these traits will be effective. In contrast, lesser extent of genetic variation noticed for days to 50 *per cent* flowering, indicating the presence of non- additive gene action making the selection relatively less effective for this character.

In the $C2F_3$ population, high PCV and GCV values were recorded for the number of clusters per plant, number of seeds per pod, seed yield per plant, number of primary branches per plant and number of secondary branches per plant. The number of pods per plant, pod length and hundred seed weight had moderate values, but the days to 50 *per cent* flowering and plant height had low values. These findings were in close agreement with the reports of Rao *et al.* (2006), Narasimhulu *et al.* (2013) and Muralidhara *et al.* (2016).

GCV gives a measure of variability present in a particular character. However, it does not determine the proportion of heritable variation present in the total variation. Hence, heritability in combination with genetic advance is considered for finding out heritable variation existing in character with a greater degree of accuracy (Dudley and Moll, 1969).

In $C1F_3$ population, high heritability coupled with high genetic advance as *per cent* 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, hundred seed weight, number of secondary branches per plant and pod length confirming the additive gene action hence effective selection can be made for these traits. Whereas high heritability along with moderate GAM was observed for days to 50 *per cent* flowering, indicating the role of non-fixable genetic variance.

In $C2F_3$ population, high heritability associated with more genetic advance as *per cent* mean was reported for the number of secondary branches per plant, pod length, number of seeds per pod, number of pods per plant, number of primary branches per plant, seed yield per plant, hundred seed weight, number of clusters per plant were under the control of additive genes, simple selection may be effective. Whereas high heritability along with low GAM was observed for days to 50 *per cent* flowering, indicating the role of non-additive gene action. These results were in harmony with the findings of Prasanna *et al.* (2013), Titumeer *et al.* (2014), Muralidhara *et al*. (2016), Sreethy *et al*. (2017), Rasal and Parhe (2017), Abhisheka and Mogali (2020), Prithviraj and Murthy (2020).

The results of the current field experiment clearly show that the number of pods per plant, number of seeds per pod, seed yield per plant, number of clusters per plant and hundred seed weight exhibited the greater values of PCV, GCV, heritability and genetic advance. It is strongly recommended that these traits can be chosen in order to increase yield.

5.3 Diversity analysis

Information about the genetic divergence of a population is essential in any breeding program since it aids in the differentiation of accessions, identification of contrasting genotypes and the making of future crosses, thus providing a database for the identification of possible groups with a higher degree of heterosis (Silva *et al.*, 2014).

Based on their level of divergence, the $C1F_3$ population was classified into nine different clusters. The greater intra-cluster D^2 values were noticed in cluster VII. The intra-cluster distances for clusters III, IV, V, VIII and IX were found to be zero. The genotypes with close relatedness fall into the same cluster, owing to be less divergent than those positioned in a different cluster. The greater inter-cluster D^2 values were noticed between clusters VIII and IX, followed by between clusters I and VIII, suggesting that the genetic architecture of the genotypes in one cluster differ entirely from those included in other clusters.

The $C2F_3$ population was divided into eight different clusters. The highest intra-cluster D^2 distance was noted in cluster V, whereas clusters III, IV, VI, VII and VIII found no intra-cluster D2 values. The highest inter-cluster D^2value was noticed between clusters VII and VIII, followed by between cluster I and cluster VIII, signifying that the hybridization between the genotypes fall in diverse clusters would yield desirable segregants with the accumulation of favorable genes in the segregating generations.

Cluster means revealed the presence of considerable differences in the mean values of different characters. The traits contributing to the overall divergence were identified by the distribution of the highest and lowest mean values for various characters in a distinct cluster.

The trait number of pods per plant contributed maximum towards the overall genetic divergence, followed by plant height in both $C1F_3$ and $C2F_3$ populations. These findings were in line with the findings of Garje (2013), Chandra *et al.* (2017) and Saidaiah *et al.* (2021).

The F_3 progenies of C1 and C2 belonging to clusters III and VII respectively, were found to be early flowering. The F_3 plants falling into the cluster I had a higher number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight and seed yield per plant. Hence, cluster I can be selected for superior segregants with high yielding and early maturing types. China mung and IPM 205-7 were found to be more divergent through diversity analysis. Variations among F_3 progenies for the traits like pod length and seed size were observed and depicted in plate 3 and 4, respectively.

5.4 Correlation coefficient analysis

Correlation coefficient analysis provides the idea about the mutual relationship between the various component traits and seed yield. Traits exhibit association due to linkage or pleiotropy. If the linkage is between two desirable traits, it will be helpful as selecting such traits leads to the simultaneous improvement of both the attributes. Selection for seed yield directly is not always fruitful since seed yield is a complex trait controlled by minor genes and dependent on many factors for its expression. As a result, it is more desirable to select the yield attributing traits that show significant positive relation with seed yield for the yield improvement.

From the results of correlation studies, seed yield per plant possessed a significant positive association with the number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, primary branches per plant, secondary branches per plant, whereas days to 50 *per cent* flowering and plant height were negatively correlated in C1F_3 population.

In C2F_3 population, seed yield per plant possessed a positive correlation with the number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, plant height, number of primary branches per plant, secondary branches per plant. In contrast, days to 50 *per cent* flowering showed a negative association with seed yield per plant. These findings were in accordance with the reports of Rao *et al.* (2006), Narasimhulu *et al.* (2013), Muralidhara *et al.* (2016), Anand *et al.* (2016), Aruna (2020) and Dhunde *et al.* (2021).

The results indicate that selecting the genotypes with a more number of pods per plant for the breeding program is beneficial for crop improvement. Selection for pods per plant has frequently been regarded as important for seed yield improvement of mungbean by various authors (Gul *et al.*, 2008; Hakim, 2008; Tabasum *et al.,* 2010).

5.5 Path coefficient analysis

Plate 3: Variations observed in pod length among F_3 populations of greengram

Plate 4: Variations observed in seed size among F_3 populations of greengram

Path coefficient analysis is a method for partitioning the correlation coefficient into direct and indirect effects and thus providing a clear picture of whether the association of a component trait with seed yield is due to a direct effect or an indirect effect through another component character. It is useful for indirect selection and helps breeders to determine the yield components.

In $C1F_3$ population, the 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 hundred seed weight exerted a positive direct effect on seed yield per plant. The traits such as days to 50 *per cent* flowering, plant height and number of secondary branches per plant exerted negative direct effects. Selection would be rewarding if these traits were considered accordingly.

In $C2F_3$ population, the number of secondary 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 hundred seed weight exerted a positive direct effect on seed yield per plant. The traits such as days to 50 *per cent* flowering and number of primary branches per plant exerted negative direct effects.

From the results of path analysis, hundred seed weight and pod length exerted the highest positive direct effects on seed yield per plant and hundred seed weight exerted the highest positive indirect effect on seed yield per plant *via* pod length in $C1F_3$ population. The number of pods per plant and pod length exhibited the highest positive direct effect on seed yield per plant and number of pods per cluster and pod length through the number of seeds per pod exerted the highest positive indirect effect on seed yield per plant in $C2F_3$ population. As a result, taking these traits into account during the selection process for the breeding program would be beneficial. These results were in compliance with the findings of Kumar *et al*. (2010), Tabasum *et al.* (2010), Kumar *et al*. (2013), Nand and Anuradha (2013), Raturi *et al*. (2014), Sinha *et al.* (2018), Ahmad and Vikas (2019), Abhisheka and Mogali (2020), Aruna (2020) and Goyal *et al*. (2021).

5.6 Superior segregants identified for yield and yield attributing traits

According to the findings, $C1F_3$ progeny lines *viz.,* 32, 9, 25, 12 contributed significantly more number of pods per plant and significantly higher seed yield per plant compared to better parent KKM-3. However, other yield attributing traits like pod length, number of seeds per pod and hundred seed weight were on par with the parental lines. Hence, these progeny lines have been identified as superior segregants for yield and its contributing traits.

Among the different $C2F_3$ families, progeny lines *viz.,* 19, 31, 22, 14 were found to be significantly outperforming with respect to number of pods per plant and seed yield per plant over better parent YADADRI. All selected segregants were exhibiting significantly longer pod lengths and more number of seeds per pod compared to better parent. The trait hundred seed weight was on par with the parental lines. Hence, these progeny lines were selected as high yielding superior segregants for yield and its attributing traits.

Conclusion

1. ANOVA results revealed that both $C1F_3$ and $C2F_3$ populations showed significant mean differences among F_3 progenies for all the yield traits studied.
2. Traits like number of pods per plant, seed yield per plant, number of clusters per plant, number of seeds per pod and hundred seed weight exhibited the highest values of PCV, GCV, broad-sense heritability and genetic advance as *per cent* mean.
3. The F_3 progenies of C1 and C2 belonging to clusters III and VII respectively, were found to be early flowering. The F_3 plants of the cluster I exhibited higher number of pods per cluster, number of pods per plant, number of seeds per pod, seed yield per plant, test weight and greater pod length.
4. Correlation analysis reported that seed yield per plant exhibited a positive relationship with the traits *viz.,* number of seeds per pod, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, number of primary branches per plant and number of secondary branches per plant in both the populations.
5. Path coefficient analysis revealed that traits like hundred seed weight, number of pods per plant and pod length exerted a positive direct effect on seed yield per plant in both the populations.
6. High yielding progeny lines were selected as superior segregants for yield and yield contributing traits.

Future line of work

- ✓ The present segregating material showed significant genetic variability for all the characters studied, which helps in finding out superior segregants intended for yield improvement.
- ✓ Progeny lines identified as high yielding could be subjected to *MYMV* disease screening.
- ✓ The characters which unveiled high heritability and high genetic advance as *per cent* mean could be further enhanced through simple selection practises.
- ✓ The study reported strong positive correlation of seed yield per plant with different yield attributes. Hence, it will be helpful in working out the selection indices by taking consideration of more than one character during selection to attain desired selection response.

- ✓ Diversity analysis revealed that the progenies belonging to cluster I of both the crosses were elite with respect to major yield attributing traits and early flowering types. These progeny lines could be advanced to F_5 or F_6 to stabilize the genotypes.

SUMMARY

VI SUMMARY

The present research experiment entitled “Assessment of Genetic Variability and Diversity in Segregating Generations of Greengram [*Vigna radiata* (L.) Wilczek]” was carried out to evaluate 600 F_3 plants from both the crosses for the selection parameters such as variability, heritability, genetic advance and association studies for yield and yield attributing traits as well as to estimate genetic divergence among the families using Mahalanobis’ D^2 statistics.

According to the results of analysis of variance, the F_3 families of both crosses varied significantly for all the yield attributing traits, showing that there was enough genetic variability to allow for selection of superior high yielding segregants for use in a crop development programme to boost greengram seed yield.

The differences between PCV and GCV values were small for several traits studied, implying that there was less environmental effect on those traits' expression, suggesting that the genotypes may be selected based on the differences in their phenotypes.

In both the crosses, greater values of PCV and GCV were documented for the traits *viz.,* number of clusters per plant, number of pods per cluster, number of pods per plant, hundred seed weight, number of seeds per pod, seed yield per plant, number of primary branches per plant and secondary branches per plant, insisting that the selection would be desirable for these characters. In contrast, days to 50 *per cent* flowering recorded less PCV and GCV, suggesting that the selection would generally be less effective for this trait.

Further, greater heritability values along with more genetic advance as *per cent* mean was recorded for the number of pods per plant, seed yield per plant, number of secondary branches per plant, number of primary branches per plant, hundred seed weight, pod length, number of pods per cluster and number of seeds per pod in both the populations, indicating the efficacy of selection for the crop improvement.

By taking into consideration of the above-mentioned selection parameters, it is evident that the traits like the number of pods per plant, seed yield per plant, number of clusters per plant, number of seeds per pod and hundred seed weight exhibited the highest values of PCV, GCV, broad-sense heritability and genetic advance. Selecting certain attributes is highly suggested to achieve enhanced production.

The genetic diversity was assessed using Mahalanobis D^2 statistics. Based on the genetic distance, $C1F_3$ and $C2F_3$ were classified into nine clusters and eight clusters, respectively. For $C1F_3$ population, Cluster II emerged as the largest cluster with 18 progenies, followed by cluster I with 6 progenies, cluster VI with 3 progenies, cluster VII with 2 progenies, clusters III, IV, V, VIII, and IX, each with unitary progenies. In $C2F_3$ population, cluster II emerged as the largest cluster with 17 progenies, followed by cluster I with 7 progenies, cluster V with 5 progenies and clusters III, IV, VI, VII and VIII, each with solitary progenies. The genotypes that show close relationships were grouped together, whereas those with much more distinctiveness were divided into separate clusters.

In $C1F_3$ population, the highest inter-cluster D^2value was documented between clusters VIII and IX, followed by between cluster I and cluster VIII. In $C2F_3$ population, the highest inter-cluster D^2 value was reported between the clusters VII and VIII, followed by between cluster I and cluster VIII, which signifies that the genotypes residing in separate clusters are more diverse and maybe hybridized to get high competency segregants with aggregation of favorable alleles.

In both the crosses, the trait number of pods per plant contributed maximum towards divergence, followed by the plant height. Depending on the findings of the D^2 investigation report, genotypes belonging to more diverse groups with more average values and relevant attributes may be included in a selective breeding programme to combine favourable alleles and desirable characteristics into a single genotypic background, allowing improved cultivars to evolve more effectively.

Correlation analysis reported that the seed yield per plant exhibited a positive relationship with the number of seeds per pod, number of clusters per plant, number of pods per cluster, number of pods per plant, pod length, number of seeds per pod, hundred seed weight, number of primary branches per plant and number of secondary branches per plant in both the populations.

In both the crosses, the path coefficient analysis revealed that traits like hundred seed weight, the number of pods per plant and pod length exerted a positive direct effect on seed yield per plant. In contrast, the traits, number of primary and secondary branches per plant, number of days to 50 *per cent* flowering exerted direct negative effects. Selection would be rewarding if these traits were considered accordingly.

The superior high yielding segregants were selected based on yield and yield attributing traits from both $C1F_3$ and $C2F_3$ populations and advanced to the next generations for the crop improvement in greengram.

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APPENDICES

VIII APPENDIX

Appendix I: Performance of C1F$_3$ population (KKM-3 × IPM 205-7) for quantitative traits

Plant No.	DFF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
1	28.50	35	2	4	11	6	33	6.5	10	3.5	2.50
2	33.00	43	3	5	9	5	18	7	10	2.8	3.14
3	30.00	38	1	3	10	5	30	6.5	9	2.9	3.03
4	39.00	42	1	4	11	5	32	8	10	3.2	2.12
5	28.50	44	2	4	9	6	36	7	11	3	5.50
6	31.80	45	3	6	10	3	40	7.5	11	3.8	2.92
7	30.20	45	3	3	8	2	40	7	9	3.5	3.82
8	26.00	43	2	3	12	3	48	7	10	3.2	5.68
9	31.00	38	2	6	12	3	54	7.5	10	2.6	3.18
10	26.50	42	1	4	9	4	20	8.5	9	3.2	2.40
11	26.00	50	3	3	10	4	44	8.5	9	3.9	3.52
12	32.00	48	3	4	11	5	50	8	9	3.5	4.95
13	36.00	46	2	5	10	5	36	8	9	4.2	2.43
14	26.00	45	1	3	9	4	50	6.5	10	3.2	3.56
15	31.00	50	2	5	10	4	48	7	10	3.2	2.82
16	30.50	48	3	3	12	6	45	6.5	12	3.8	3.12
17	33.00	34	2	4	9	2	36	8	10	3.5	2.62
18	30.00	38	2	5	9	4	56	6.5	10	3.2	4.06
19	39.00	48	2	5	14	5	40	7.5	9	3.5	3.25
20	28.50	46	3	3	10	4	78	6.2	10	3.8	2.60
21	27.50	42	1	5	13	5	70	9	14	4.5	5.37
22	40.00	45	2	4	14	5	65	9.5	14	4.5	3.23

23	26.00	42	1	6	13	4	84	10	15	4.2	3.40
24	32.00	40	2	4	12	4	60	9.5	14	4	3.52
25	28.00	38	3	5	13	4	36	9.5	14	4.2	4.95
26	32.00	45	2	5	9	4	65	8.5	14	3.8	2.43
27	36.00	46	3	6	13	5	52	6.5	12	4	4.10
28	42.00	45	2	5	13	6	84	7.5	12	4.2	2.62
29	45.00	48	1	5	11	6	60	7	11	3.8	4.80
30	31.80	35	1	4	14	5	36	7.5	10	2.5	4.28
31	26.00	47	2	5	11	5	65	6.8	13	2.8	5.25
32	32.00	40	3	6	10	4	52	6.5	12	4.2	3.10
33	36.00	30	3	4	12	5	55	7.5	10	3.8	3.06
34	28.50	48	2	5	12	4	70	7	10	2.5	4.06
35	30.50	38	1	3	11	5	44	7.4	12	2.6	3.25
36	28.50	46	2	6	10	5	40	6.6	12	4.2	2.60
37	33.00	49	3	5	12	4	60	7.3	12	3.6	5.37
38	30.00	45	2	4	11	5	60	7.5	14	4.5	3.23
39	39.00	43	3	5	12	4	66	7.5	14	2.8	3.40
40	28.50	46	1	6	11	4	52	6.8	12	3.5	3.52
41	30.50	44	2	4	14	4	44	9.5	12	3.8	4.95
42	31.80	42	2	5	13	4	60	10	11	4.2	2.50
43	26.00	38	2	6	14	6	65	9.5	10	3.5	3.14
44	32.00	35	3	4	12	6	35	10	12	3.8	3.03
45	36.00	42	3	5	14	4	56	9.5	12	2.6	2.12
46	28.50	42	1	5	10	5	78	7.5	15	4.5	5.50
47	33.00	48	3	5	12	5	56	7.5	13	4.5	2.92
48	30.00	43	2	6	10	6	60	6.5	13	4.2	3.82

49	39.00	46	3	4	12	4	80	7.5	14	4	5.68
50	28.50	46	3	5	11	5	60	7	13	4.6	2.50
51	28.60	42	2	5	9	5	64	7	12	3.8	3.14
52	40.00	38	3	6	9	4	60	6.2	10	4	3.03
53	26.00	35	2	5	10	6	62	7.5	11	4.2	2.12
54	32.00	41	1	4	12	4	55	7	12	3.8	3.10
55	28.00	44	2	3	8	5	56	8	10	2.5	3.06
56	32.00	48	3	6	9	5	42	9	13	2.8	4.06
57	36.00	50	2	4	12	4	50	8	11	4.2	3.25
58	42.00	42	2	5	12	5	33	8.5	13	3.8	3.25
59	45.00	45	1	4	13	6	30	8.5	11	4.2	2.60
60	31.80	40	2	3	12	5	35	9.2	12	2.6	5.37
61	30.20	48	2	4	10	4	60	7.5	11	3.4	3.23
62	28.50	35	3	5	10	5	52	8.5	12	3.6	3.10
63	30.00	43	2	6	12	5	6	7.5	10	4.2	3.06
64	28.50	48	3	4	12	5	60	8.5	10	3.4	4.06
65	30.50	50	2	3	9	4	48	7.5	12	4.2	3.25
66	28.50	35	2	4	14	3	42	9.2	11	4.5	3.56
67	28.60	38	3	5	13	4	60	9	11	4.2	5.37
68	26.60	45	2	6	12	4	55	8.5	12	4.6	3.23
69	28.00	42	2	4	13	5	40	9	12	4.2	3.40
70	30.20	38	1	5	14	3	36	9.5	10	4.5	3.52
71	32.00	42	2	4	9	4	60	8.5	10	2.5	4.95
72	32.50	46	3	5	10	4	48	8.2	13	4	4.06
73	35.20	48	3	4	12	5	50	7.5	13	2.8	3.25
74	30.00	50	2	3	10	6	40	7	12	3.4	2.60

75	28.00	45	3	6	12	5	65	6.5	11	3.8	5.37
76	31.20	32	2	4	10	4	38	7.6	11	4.3	3.23
77	28.80	50	2	5	10	4	40	9	11	4.8	3.40
78	30.50	46	2	3	14	3	28	7.5	10	4.5	3.52
79	31.50	45	2	5	11	6	44	7	10	4.6	4.95
80	32.50	49	3	6	10	5	40	6.5	12	4.2	3.80
81	30.20	35	2	4	10	3	60	8.5	12	3.8	2.62
82	26.00	48	3	4	12	5	40	8.5	14	4.2	4.20
83	31.00	45	3	5	12	4	65	7	12	3.2	4.06
84	26.50	52	3	6	13	3	30	6.5	12	3.8	3.25
85	26.00	36	2	4	10	5	36	5.5	11	3.5	2.60
86	32.00	44	2	5	9	6	52	5.5	12	3.8	5.37
87	35.00	38	2	4	10	4	45	6.8	14	4.2	3.23
88	40.00	48	2	5	1	5	68	6.5	10	3.2	3.40
89	26.00	35	3	6	12	3	52	8.5	12	3.8	3.52
90	32.00	46	3	5	9	4	38	8.5	10	4.2	4.95
91	28.00	48	3	6	10	5	54	7.6	12	2.8	4.20
92	32.00	45	3	4	12	6	65	6.5	10	3.8	3.20
93	36.00	48	1	5	12	4	70	7.5	10	3.5	3.06
94	42.00	50	3	4	10	4	68	6.2	10	4.2	4.06
95	45.00	46	1	3	12	5	70	7.5	10	3.2	3.25
96	31.80	42	3	4	10	5	75	7.5	14	3.5	2.60
97	35.00	44	2	6	9	3	65	6.5	13	3.2	5.37
98	38.00	42	2	5	10	6	72	7.8	12	2.8	3.23
99	40.00	44	1	4	11	6	65	6.5	14	3.8	3.40
100	42.50	46	3	5	10	5	68	7.2	14	3.5	3.52

101	28.80	41	2	6	10	6	36	6.5	12	3.4	2.50
102	26.50	38	2	5	12	5	35	6.5	15	2.5	3.14
103	48.00	35	3	4	12	6	38	7	15	3.2	3.03
104	50.00	51	1	5	13	5	42	8.5	14	3	2.12
105	46.00	48	3	4	14	4	36	8.5	14	3.8	5.50
106	30.50	44	2	6	9	3	48	6.8	11	4.2	2.92
107	32.50	47	3	4	12	6	52	7.5	10	3.8	3.82
108	36.00	50	2	3	12	6	48	8	9	3.5	5.68
109	42.50	44	3	3	14	5	70	6.5	11	3.2	3.25
110	28.50	50	3	5	12	5	36	5.5	11	3.5	2.60
111	31.50	38	2	4	9	4	40	5.6	13	3.9	5.37
112	29.50	46	2	5	12	5	30	7	9	3.8	3.23
113	35.50	43	3	6	10	5	65	8.5	10	2.6	3.40
114	42.00	35	3	5	10	5	29	6.8	12	3.2	3.52
115	32.00	45	1	4	9	6	39	6.5	10	3.8	4.95
116	32.50	43	2	6	9	4	36	9	10	3.4	2.50
117	36.40	46	2	4	10	4	45	10	9	2.8	3.20
118	26.20	38	3	5	9	6	49	8	13	3.2	4.20
119	28.50	48	2	4	10	5	52	9.5	9	3.5	2.50
120	31.80	45	3	3	12	5	45	10.2	11	3.5	3.14
121	28.00	38	1	5	8	5	38	9.5	9	3.8	3.03
122	30.50	42	2	6	12	4	50	10	12	2.8	2.12
123	27.50	45	3	4	10	5	34	9	10	3.5	5.50
124	28.50	43	2	5	9	4	42	10	9	3.2	2.92
125	30.00	35	3	4	12	6	28	9.2	10	2.8	3.82
126	28.50	40	3	6	9	5	28	8.5	12	4.5	5.68

127	30.50	35	2	4	10	4	35	7.5	10	4.5	5.37
128	28.50	42	2	5	8	4	30	6.5	13	4.1	3.23
129	28.60	45	2	6	11	3	32	7.5	12	4.2	2.50
130	26.60	38	3	4	10	4	38	6.5	13	4.6	3.14
131	28.00	50	3	5	8	5	40	8.8	9	4.6	3.03
132	30.20	47	2	6	10	4	46	7	10	4.3	2.12
133	32.00	45	2	4	9	5	48	8	9	4	5.50
134	32.50	51	1	5	9	6	44	7	10	4.2	2.92
135	35.20	46	2	5	10	4	46	6.5	11	2.8	3.82
136	30.00	39	3	6	11	5	55	7.5	10	2.5	5.68
137	28.00	48	3	5	10	6	50	5.5	9	3.5	3.06
138	31.80	36	3	4	9	5	48	6.5	12	3.8	4.06
139	28.80	49	2	3	10	4	50	7.5	10	3.2	3.25
140	30.50	43	2	5	12	5	52	8.5	10	2.5	2.60
141	31.50	46	2	6	11	6	48	6.5	11	3.2	5.37
142	32.50	42	3	4	9	4	46	6.5	10	3.5	3.23
143	30.20	38	3	5	10	3	50	7.5	10	3.8	3.40
144	26.00	48	2	4	11	3	42	7	11	3.6	3.52
145	31.00	36	2	3	10	4	38	7.5	9	3.4	2.50
146	26.50	38	3	5	10	5	40	7.5	10	3	3.14
147	26.00	48	2	4	12	5	42	5.5	10	3.5	3.03
148	32.00	45	3	3	12	6	38	6.5	11	3.8	2.12
149	36.00	48	2	4	10	5	44	5.5	9	3.6	5.50
150	28.00	35	3	5	12	5	46	5.5	12	3.4	2.92
151	30.00	43	2	6	12	5	6	7.5	10	4.2	3.06
152	28.50	48	3	4	12	5	60	8.5	10	3.4	4.06

153	30.50	50	2	3	9	4	48	7.5	12	4.2	3.25
154	28.50	35	2	4	8	3	42	9.2	11	4.5	3.56
155	28.60	38	3	5	10	4	60	9	11	4.2	5.37
156	26.60	45	2	6	12	4	55	8.5	12	4.6	3.23
157	28.00	42	2	4	13	5	40	9	12	4.2	3.40
158	30.20	38	1	5	14	3	36	9.5	10	4.5	3.52
159	32.00	42	2	4	9	4	60	8.5	10	2.5	4.95
160	32.50	46	3	5	10	4	48	8.2	13	4	4.06
161	35.20	40	3	4	12	5	50	7.5	13	2.8	3.25
162	30.00	36	2	3	10	6	40	7	12	3.4	2.60
163	28.00	45	3	6	12	5	65	6.5	11	3.8	5.37
164	31.80	32	2	4	10	4	38	7.6	11	4.3	3.23
165	28.80	50	2	5	10	4	40	9	11	4.8	3.40
166	30.50	42	2	3	14	3	28	7.5	10	4.5	3.52
167	31.50	45	2	5	11	6	44	7	10	4.6	4.95
168	32.50	35	3	6	10	5	40	6.5	12	4.2	3.80
169	30.20	32	2	4	10	3	60	8.5	12	3.8	2.62
170	26.00	48	3	4	12	5	40	8.5	14	4.2	4.20
171	31.00	45	3	5	12	4	65	7	12	3.2	4.06
172	26.50	52	3	6	13	3	30	6.5	12	3.8	3.25
173	26.00	46	2	4	10	5	36	5.5	11	3.5	2.60
174	32.00	44	2	5	9	6	52	5.5	12	3.8	5.37
175	35.00	38	2	4	10	4	45	6.8	14	4.2	3.23
176	32.00	46	3	6	10	4	52	6.5	12	4.2	3.10
177	36.00	45	3	4	12	5	55	7.5	10	3.8	3.06
178	28.50	48	2	5	12	4	70	7	10	2.5	4.06

179	30.50	48	1	3	11	5	44	7.4	12	2.6	3.25
180	26.50	52	3	6	13	3	30	6.5	12	3.8	3.25
181	30.00	43	2	6	12	5	6	7.5	10	4.2	3.06
182	28.50	48	3	4	12	5	60	8.5	10	3.4	4.06
183	30.50	50	2	3	9	4	48	7.5	12	4.2	3.25
184	28.50	35	2	4	14	3	42	9.2	11	4.5	3.56
185	28.60	31	3	5	13	4	60	9	11	4.2	5.37
186	26.60	45	2	6	12	4	55	8.5	12	4.6	3.23
187	28.00	42	2	4	13	5	40	9	12	4.2	3.40
188	30.20	38	1	5	14	3	36	9.5	10	4.5	3.52
189	32.00	42	2	4	9	4	60	8.5	10	2.5	4.95
190	32.50	46	3	5	10	4	48	8.2	13	4	4.06
191	35.20	48	3	4	12	5	50	7.5	13	2.8	3.25
192	30.00	45	2	3	10	6	40	7	12	3.4	2.60
193	28.00	42	3	6	12	5	65	6.5	11	3.8	5.37
194	31.80	45	2	4	10	4	38	7.6	11	4.3	3.23
195	28.80	50	2	5	10	4	40	9	11	4.8	3.40
196	42.00	45	2	5	13	6	84	7.5	12	4.2	2.62
197	45.20	48	1	5	11	6	60	7	11	3.8	4.80
198	31.80	32	1	4	14	5	36	7.5	10	2.5	4.28
199	26.00	47	2	5	11	5	65	6.8	13	2.8	5.25
200	32.00	36	3	6	10	4	52	6.5	12	4.2	3.10
201	36.00	28	3	4	12	5	55	7.5	10	3.8	3.06
202	28.50	42	2	5	12	4	70	7	10	2.5	4.06
203	30.50	44	1	3	11	5	44	7.4	12	2.6	3.25
204	28.50	46	2	6	10	5	40	6.6	12	4.2	2.60

205	33.00	42	3	5	12	4	60	7.3	12	3.6	5.37
206	30.00	45	2	4	11	5	60	7.5	14	4.5	3.23
207	39.00	43	3	5	12	4	66	7.5	14	2.8	3.40
208	28.50	46	1	6	11	4	52	6.8	12	3.5	3.52
209	30.50	38	2	4	14	4	44	9.5	12	3.8	4.95
210	31.80	42	2	5	13	4	60	10	11	4.2	2.50
211	26.00	38	2	6	14	6	65	9.5	10	3.5	3.14
212	32.00	35	3	4	12	6	35	10	12	3.8	3.03
213	36.00	42	3	5	14	4	56	9.5	12	2.6	2.12
214	28.50	45	1	5	10	5	78	7.5	15	4.5	5.50
215	33.00	48	3	5	12	5	56	7.5	13	4.5	2.92
216	30.00	43	2	6	10	6	60	6.5	13	4.2	3.82
217	39.00	46	3	4	12	4	80	7.5	14	4	5.68
218	28.50	46	3	5	11	5	60	7	13	4.6	2.50
219	31.80	42	3	3	12	5	45	10.2	11	3.5	3.14
220	28.00	38	1	5	12	5	38	9.5	9	3.8	3.03
221	30.50	42	2	6	12	4	50	10	12	2.8	2.12
222	27.50	45	3	4	14	5	34	9	10	3.5	5.50
223	28.50	43	2	5	10	4	42	10	9	3.2	2.92
224	30.00	35	3	4	12	6	28	9.2	10	2.8	3.82
225	28.50	40	3	6	9	5	28	8.5	12	4.5	5.68
226	30.50	35	2	4	10	4	35	7.5	10	4.5	5.37
227	28.50	42	2	5	10	4	30	6.5	13	4.1	3.23
228	28.60	45	2	6	11	3	32	7.5	12	4.2	2.50
229	26.60	38	3	4	10	4	38	6.5	13	4.6	3.14
230	28.00	50	3	5	12	5	40	8.8	9	4.6	3.03

231	30.20	42	2	6	10	4	46	7	10	4.3	2.12
232	32.00	45	2	4	9	5	48	8	9	4	5.50
233	32.50	52	1	5	9	6	44	7	10	4.2	2.92
234	35.20	46	2	5	10	4	46	6.5	11	2.8	3.82
235	30.00	38	3	6	11	5	55	7.5	10	2.5	5.68
236	28.00	48	3	5	10	6	50	5.5	9	3.5	3.06
237	31.80	36	3	4	12	5	48	6.5	12	3.8	4.06
238	28.80	42	2	3	10	4	50	7.5	10	3.2	3.25
239	30.50	45	2	5	12	5	52	8.5	10	2.5	2.60
240	31.50	44	2	6	9	6	48	6.5	11	3.2	5.37
241	32.50	42	3	4	9	4	46	6.5	10	3.5	3.23
242	30.20	38	3	5	10	3	50	7.5	10	3.8	3.40
243	26.00	48	2	4	11	3	42	7	11	3.6	3.52
244	31.00	36	2	3	10	4	38	7.5	9	3.4	2.50
245	26.50	38	3	5	10	5	40	7.5	10	3	3.14
246	26.00	45	2	4	12	5	35	5.5	10	3.5	3.03
247	32.00	42	3	6	10	4	56	6.5	12	4.2	3.10
248	36.00	45	3	4	12	5	78	7.5	10	3.8	3.06
249	28.50	48	2	5	12	4	56	7	10	2.5	4.06
250	30.50	42	1	3	11	5	60	7.4	12	2.6	3.25
251	42.00	45	2	5	13	6	80	7.5	12	4.2	2.62
252	45.30	48	1	5	11	6	60	7	11	3.8	4.80
253	31.80	46	1	4	14	5	45	7.5	10	2.5	4.28
254	26.00	42	2	5	11	5	38	6.8	13	2.8	5.25
255	32.00	46	3	6	10	4	50	6.5	12	4.2	3.10
256	36.00	40	3	4	12	5	34	7.5	10	3.8	3.06

257	28.50	48	2	5	12	4	42	7	10	2.5	4.06
258	30.50	42	1	3	11	5	28	7.4	12	2.6	3.25
259	28.50	40	2	6	10	5	28	6.6	12	4.2	2.60
260	33.00	38	3	5	12	4	35	7.3	12	3.6	5.37
261	30.00	45	2	4	11	5	30	7.5	14	4.5	3.23
262	39.00	43	3	5	12	4	35	7.5	14	2.8	3.40
263	28.50	46	1	6	11	4	52	6.8	12	3.5	3.52
264	30.50	44	2	4	14	4	44	9.5	12	3.8	4.95
265	31.80	42	2	5	13	4	60	10	11	4.2	2.50
266	26.00	38	2	6	14	6	65	9.5	10	3.5	3.14
267	32.00	35	3	4	12	6	35	10	12	3.8	3.03
268	36.00	42	3	5	14	4	56	9.5	12	2.6	2.12
269	28.50	40	1	5	10	5	78	7.5	15	4.5	5.50
270	33.00	28	3	5	12	5	56	7.5	13	4.5	2.92
271	30.00	42	2	6	10	6	60	6.5	13	4.2	3.82
272	39.00	30	3	4	12	4	80	7.5	14	4	5.68
273	28.50	46	3	5	11	5	60	7	13	4.6	2.50
274	33.00	28	3	5	12	4	35	7.3	12	3.6	5.37
275	30.00	45	2	4	11	5	56	7.5	14	4.5	3.23
276	39.00	35	3	5	12	4	78	7.5	14	2.8	3.40
277	28.50	46	1	6	11	4	56	6.8	12	3.5	3.52
278	42.00	40	2	5	13	6	60	7.5	12	4.2	2.62
279	45.20	38	1	5	11	6	80	7	11	3.8	4.80
280	31.80	32	1	4	14	5	60	7.5	10	2.5	4.28
281	26.00	45	2	5	11	5	45	6.8	13	2.8	5.25
282	32.00	40	3	6	10	4	38	6.5	12	4.2	3.10

283	36.00	46	3	4	12	5	50	7.5	10	3.8	3.06
284	28.50	48	2	5	12	4	34	7	10	2.5	4.06
285	30.50	42	1	3	11	5	42	7.4	12	2.6	3.25
286	28.50	46	2	6	10	5	28	6.6	12	4.2	2.60
287	33.00	49	3	5	12	4	40	7.3	12	3.6	5.37
288	30.00	45	2	4	11	5	35	7.5	14	4.5	3.23
289	39.00	43	3	5	12	4	28	7.5	14	2.8	3.40
290	28.50	46	1	6	11	5	52	6.8	12	3.5	3.52
291	30.50	44	2	4	14	4	44	9.5	12	3.8	4.95
292	31.80	42	2	5	13	4	28	10	11	4.2	2.50
293	26.00	38	2	6	14	6	25	9.5	10	3.5	3.14
294	32.00	35	3	4	12	6	35	10	12	3.8	3.03
295	36.00	40	3	5	14	4	50	9.5	12	2.6	2.12
296	28.50	42	1	5	10	5	42	7.5	15	4.5	5.50
297	33.00	48	3	5	12	5	56	7.5	13	4.5	2.92
298	30.00	43	2	6	10	6	32	6.5	13	4.2	3.82
299	39.00	46	3	4	12	4	45	7.5	14	4	5.68
300	28.50	29	3	5	11	5	40	7	13	4.6	2.50
Mean	**32.50**	**38.62**	**1.98**	**4.85**	**12.40**	**4.82**	**44.58**	**7.28**	**10.20**	**3.08**	**5.02**

Appendix II: Performance of $C2F_3$ population (KKM-3 ×YADADRI) for quantitative traits

Plant No.	DFF	PH	PBP	SBP	NCP	NPC	NPP	PL	NSP	100SW	SYP
1	32.50	40.80	2	3	8	4	38	7.20	8	4.50	6.02
2	32.50	34.40	2	4	10	5	39	7.20	9	4.50	6.02
3	30.00	36.90	3	4	11	6	29	8.50	9	2.96	5.05
4	30.50	39.90	3	6	9	3	34	7.20	10	3.38	4.05
5	32.00	35.80	2	3	10	2	26	6.50	10	3.70	4.92
6	30.00	46.20	2	3	8	3	27	7.50	12	3.00	3.20
7	28.50	46.40	1	6	12	3	38	10.00	10	3.19	5.98
8	32.20	47.00	3	4	12	4	32	7.20	10	2.90	3.03
9	30.00	39.80	3	3	9	4	38	6.50	9	3.58	4.93
10	29.30	35.90	2	4	10	5	32	7.50	10	3.62	3.21
11	34.00	39.10	1	5	11	5	38	7.00	14	4.26	6.35
12	33.50	35.50	2	3	10	4	29	6.80	14	3.18	3.18
13	34.50	42.20	3	5	9	4	30	7.20	15	3.24	4.05
14	30.00	44.30	2	3	10	6	37	8.50	14	4.42	5.64
15	32.50	41.30	2	4	12	2	27	7.20	14	3.56	5.20
16	30.50	40.00	2	5	9	4	36	6.50	14	4.44	6.58
17	34.50	44.80	3	5	9	5	48	7.50	12	3.18	3.90
18	34.00	41.20	1	3	14	4	35	10.00	12	3.32	4.28
19	33.20	44.20	2	5	10	5	40	7.20	11	3.86	6.30
20	35.00	40.00	1	4	13	5	28	6.50	10	3.70	5.20
21	32.50	39.10	2	6	14	4	29	7.50	13	3.44	3.08
22	35.00	37.40	3	4	13	4	32	7.00	12	3.54	5.04
24	30.00	41.20	2	4	11	4	28	8.00	10	2.98	4.20
25	34.00	40.20	3	5	13	4	30	6.50	10	3.30	5.12
26	30.00	35.20	2	6	9	5	27	7.00	12	3.05	4.02
27	32.00	39.90	1	5	13	6	32	7.30	12	3.20	3.07
28	31.20	43.30	1	5	13	6	35	7.00	12	3.52	5.01

29	30.00	41.20	2	4	11	5	39	6.20	14	4.34	6.45
30	34.50	40.20	3	5	14	5	32	7.50	14	3.54	4.03
31	32.50	36.30	3	6	11	4	35	8.50	12	3.01	3.86
32	30.50	45.90	2	4	10	5	39	7.20	12	2.84	3.01
33	34.00	40.20	1	5	12	4	39	6.50	11	4.50	6.02
34	30.00	35.20	2	3	12	5	29	7.22	10	2.96	5.05
35	32.00	39.90	3	6	11	5	34	10.00	12	3.38	4.05
36	31.20	43.30	2	5	10	4	26	7.20	12	3.70	4.92
37	30.00	41.20	3	4	12	5	27	7.20	15	3.00	3.20
38	34.50	40.20	1	5	11	4	38	8.00	13	3.19	5.98
39	32.50	39.90	2	6	12	4	32	8.50	13	2.90	3.03
40	30.50	43.30	2	4	11	4	38	9.00	14	3.58	4.93
41	32.00	41.20	2	5	14	4	32	6.20	13	3.62	3.21
42	29.30	40.20	3	6	13	6	38	7.50	12	4.26	6.35
43	32.50	40.20	3	4	9	6	29	9.50	10	3.18	3.18
44	30.00	35.20	1	5	13	4	30	6.10	11	3.24	4.05
45	30.50	39.90	3	5	13	5	37	7.20	12	4.42	5.64
46	32.00	43.30	2	5	11	5	27	7.50	10	3.56	5.20
47	30.00	41.20	3	6	14	6	36	7.60	13	4.44	6.58
48	28.50	40.20	3	4	11	4	48	6.96	9	3.18	3.90
49	32.20	55.20	2	5	10	5	35	7.80	9	3.32	4.28
50	30.00	50.50	2	5	12	5	40	7.40	10	3.86	6.30
51	29.30	40.80	1	6	12	4	28	7.58	10	3.70	5.20
52	34.00	34.40	3	5	11	6	29	10.00	12	3.44	3.08
53	33.50	36.90	3	4	10	4	32	7.10	10	3.54	5.04
54	34.50	39.90	2	3	12	5	28	7.40	10	2.98	4.20
55	30.00	35.80	1	6	11	5	30	6.40	9	3.30	5.12
56	32.50	46.20	2	4	12	4	27	7.20	10	3.05	4.02
57	30.50	46.40	3	4	11	5	32	8.50	14	3.20	3.07

58	34.50	47.00	2	6	9	6	35	7.20	14	3.52	5.01
59	34.00	38.00	2	3	10	5	39	6.50	15	4.34	6.45
60	33.20	35.90	2	3	8	4	32	7.50	14	3.54	4.03
61	35.00	39.10	3	6	12	5	35	10.00	14	3.01	3.86
62	32.50	65.00	1	4	12	5	39	7.20	14	2.84	3.01
63	35.00	42.20	2	3	9	5	39	8.50	12	4.50	6.02
64	32.00	44.30	1	4	10	4	29	7.20	12	2.96	5.05
65	34.00	41.30	2	5	11	3	34	7.30	11	3.38	4.05
66	30.00	40.00	3	3	10	6	26	7.00	10	3.70	4.92
67	32.00	44.80	2	5	9	5	27	6.20	13	3.00	3.20
68	31.20	41.20	3	3	10	6	38	7.20	12	3.19	5.98
69	30.00	44.20	2	4	12	3	32	8.50	10	2.90	3.03
70	34.50	40.00	1	5	9	2	38	7.20	10	3.58	4.93
71	32.50	39.10	1	5	9	3	32	6.50	12	3.62	3.21
72	30.50	37.40	2	3	14	3	38	7.50	12	4.26	6.35
73	32.50	45.90	3	5	10	4	29	10.00	12	3.18	3.18
74	30.00	40.20	3	4	13	4	30	7.20	14	3.24	4.05
75	30.50	55.50	2	6	14	5	37	7.00	14	4.42	5.64
76	32.00	39.90	1	4	13	5	27	9.50	12	3.56	5.20
77	30.00	43.30	2	5	12	4	36	8.50	12	4.44	6.58
78	28.50	41.20	3	5	13	4	48	9.70	11	3.18	3.90
79	32.20	40.20	2	6	9	6	35	6.20	10	3.32	4.28
80	30.00	36.30	3	5	13	2	40	7.50	12	3.86	6.30
81	29.30	47.00	1	5	13	4	28	10.00	12	3.70	5.20
82	34.00	39.80	2	4	11	5	29	6.10	15	3.44	3.08
83	33.50	40.00	2	5	14	4	32	7.20	13	3.54	5.04
84	34.50	44.80	2	6	11	5	28	7.50	13	2.98	4.20
85	30.00	41.20	3	4	10	5	30	7.60	14	3.30	5.12
86	32.50	44.20	3	5	12	4	27	6.96	13	3.05	4.02

87	30.50	40.00	1	3	12	4	32	7.80	12	3.20	3.07
88	34.50	39.10	3	6	11	4	35	7.40	10	3.52	5.01
89	34.00	52.50	2	5	10	4	39	7.50	11	4.34	6.45
90	33.20	45.90	3	4	12	5	32	10.50	8	3.54	4.03
91	35.00	40.20	3	5	11	6	35	7.16	10	3.01	3.86
92	32.50	35.20	2	6	12	6	39	7.40	13	2.84	3.01
93	35.00	39.90	2	4	11	5	39	6.40	9	4.50	6.02
94	32.00	43.30	1	5	14	5	29	8.50	9	2.96	5.05
95	34.00	41.20	3	6	13	4	34	7.20	9	3.38	4.05
96	30.00	40.00	3	4	9	5	26	7.30	10	3.70	4.92
97	32.00	39.10	2	5	10	4	27	7.19	10	3.00	3.20
98	31.20	37.40	1	5	8	5	38	6.20	12	3.19	5.98
99	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
100	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
101	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
102	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
103	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18
104	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05
105	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
106	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
107	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58
108	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
109	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
110	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
111	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
112	34.00	39.90	2	3	10	4	29	10.60	10	3.44	3.08
113	33.50	42.20	1	3	11	5	32	6.10	13	3.54	5.04
114	34.50	44.30	1	6	10	5	28	7.20	12	2.98	4.20
115	30.00	41.30	2	4	9	4	30	7.50	10	3.30	5.12

116	32.50	40.00	3	3	10	6	27	7.60	10	3.05	4.02
117	30.50	44.80	3	4	12	4	32	6.50	12	3.20	3.07
118	34.50	41.20	2	5	9	5	35	7.80	12	3.52	5.01
119	34.00	44.20	1	3	9	5	39	7.40	12	4.34	6.45
120	33.20	40.00	2	5	14	4	32	7.00	14	3.54	4.03
121	35.00	39.10	3	3	10	5	35	10.50	14	3.01	3.86
122	32.50	37.40	2	4	13	6	39	7.10	12	2.84	3.01
123	35.00	45.90	3	5	14	5	42	7.40	12	4.50	6.02
124	32.00	40.20	1	5	13	4	38	6.40	11	2.96	5.05
125	34.00	35.20	2	3	12	5	25	8.50	10	3.38	4.05
126	30.00	39.90	2	5	13	5	40	7.20	12	3.70	4.92
127	32.00	43.30	2	4	9	5	39	7.30	12	3.00	3.20
128	31.20	41.20	3	6	13	4	29	7.00	15	3.19	5.98
129	30.00	40.20	3	4	13	3	34	6.20	13	2.90	3.03
130	34.50	36.30	1	5	11	2	26	7.30	13	3.58	4.93
131	32.50	40.80	3	5	14	3	27	8.94	14	3.62	3.21
132	30.50	34.40	2	6	11	3	38	7.20	13	4.26	6.35
133	34.00	36.90	2	5	10	4	32	6.50	12	3.18	3.18
134	30.00	39.90	2	5	12	4	38	7.20	10	3.24	4.05
135	29.50	52.50	3	4	12	5	32	10.00	11	4.42	5.64
136	34.50	35.80	1	5	11	5	38	7.20	12	3.56	5.20
137	30.50	46.20	2	6	10	4	29	7.50	10	4.44	6.58
138	34.50	46.40	1	4	12	4	30	10.00	12	3.18	3.90
139	34.00	47.00	2	5	11	6	37	8.50	12	3.32	4.28
140	33.20	39.80	3	3	12	2	27	9.70	12	3.86	6.30
141	35.00	47.00	2	6	11	4	36	6.20	12	3.70	5.20
142	32.50	39.80	3	5	14	5	48	7.50	11	3.44	3.08
143	30.50	45.30	2	4	13	4	35	10.20	10	3.54	5.04
144	34.50	40.80	1	5	9	5	40	6.10	12	2.98	4.20

145	34.00	34.40	1	6	10	5	28	7.20	12	3.30	5.12
146	33.20	36.90	2	4	12	4	29	7.50	12	3.05	4.02
147	35.00	39.90	3	5	12	6	32	7.60	12	3.20	3.07
148	32.50	35.80	2	6	14	5	28	6.50	11	3.52	5.01
149	30.00	46.20	2	4	8	3	30	7.80	10	4.34	6.45
150	34.50	54.50	3	5	11	5	27	7.40	12	3.54	4.03
151	30.00	36.90	3	4	11	6	29	8.50	9	2.96	5.05
152	30.50	39.90	3	6	9	3	34	7.20	10	3.38	4.05
153	32.00	35.80	2	3	10	2	26	6.50	10	3.70	4.92
154	30.00	46.20	2	3	8	3	27	7.50	12	3.00	3.20
155	28.50	46.40	1	6	12	3	38	10.00	10	3.19	5.98
156	32.20	47.00	3	4	12	4	32	7.20	10	2.90	3.03
157	30.00	39.80	3	3	9	4	38	6.50	9	3.58	4.93
158	29.30	35.90	2	4	10	5	32	7.50	10	3.62	3.21
159	34.00	39.10	1	5	11	5	38	7.00	14	4.26	6.35
160	33.50	39.90	2	3	10	4	29	6.80	14	3.18	3.18
161	34.50	42.20	3	5	9	4	30	7.20	15	3.24	4.05
162	30.00	44.30	2	3	10	6	37	8.50	14	4.42	5.64
163	32.50	41.30	2	4	12	2	27	7.20	14	3.56	5.20
164	30.50	40.00	2	5	9	4	36	6.50	14	4.44	6.58
165	34.50	44.80	3	5	9	5	48	7.50	12	3.18	3.90
166	34.00	41.20	1	3	14	4	35	10.00	12	3.32	4.28
167	33.20	44.20	2	5	10	5	40	7.20	11	3.86	6.30
168	35.00	40.00	1	4	13	5	28	6.50	10	3.70	5.20
169	32.50	39.10	2	6	14	4	29	7.50	13	3.44	3.08
170	35.00	37.40	3	4	13	4	32	7.00	12	3.54	5.04
171	30.00	41.20	2	4	11	4	28	8.00	10	2.98	4.20
172	34.50	39.10	3	6	11	4	35	7.40	10	3.52	5.01
173	34.00	52.50	2	5	10	4	39	7.50	11	4.34	6.45

174	33.20	45.90	3	4	12	5	32	10.50	8	3.54	4.03
175	35.00	40.20	3	5	11	6	35	7.16	10	3.01	3.86
176	32.50	35.20	2	6	12	6	39	7.40	13	2.84	3.01
177	35.00	39.90	2	4	11	5	39	6.40	9	4.50	6.02
178	32.00	43.30	1	5	14	5	29	8.50	9	2.96	5.05
179	34.00	41.20	3	6	13	4	34	7.20	9	3.38	4.05
180	30.00	40.00	3	4	9	5	26	7.30	10	3.70	4.92
181	32.00	39.10	2	5	10	4	27	7.19	10	3.00	3.20
182	31.20	37.40	1	5	8	5	38	6.20	12	3.19	5.98
183	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
184	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
185	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
186	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
187	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18
188	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05
189	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
190	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
191	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58
192	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
193	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
194	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
195	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
196	34.00	39.90	2	3	10	4	29	10.60	10	3.44	3.08
197	33.50	42.20	1	3	11	5	32	6.10	13	3.54	5.04
198	34.50	44.30	1	6	10	5	28	7.20	12	2.98	4.20
199	30.00	41.30	2	4	9	4	30	7.50	10	3.30	5.12
200	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
201	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
202	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35

203	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18
204	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05
205	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
206	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
207	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58
208	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
209	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
210	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
211	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
212	34.50	39.10	3	6	11	4	35	7.40	10	3.52	5.01
213	34.00	52.50	2	5	10	4	39	7.50	11	4.34	6.45
214	33.20	45.90	3	4	12	5	32	10.50	8	3.54	4.03
215	35.00	40.20	3	5	11	6	35	7.16	10	3.01	3.86
216	32.50	35.20	2	6	12	6	39	7.40	13	2.84	3.01
217	35.00	39.90	2	4	11	5	39	6.40	9	4.50	6.02
218	32.00	43.30	1	5	14	5	29	8.50	9	2.96	5.05
219	34.00	41.20	3	6	13	4	34	7.20	9	3.38	4.05
220	30.00	40.00	3	4	9	5	26	7.30	10	3.70	4.92
221	32.00	39.10	2	5	10	4	27	7.19	10	3.00	3.20
222	31.20	37.40	1	5	8	5	38	6.20	12	3.19	5.98
223	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
224	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
225	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
226	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
227	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18
228	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05
229	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
230	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
231	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58

232	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
233	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
234	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
235	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
236	34.00	39.90	2	3	10	4	29	10.60	10	3.44	3.08
237	33.50	42.20	1	3	11	5	32	6.10	13	3.54	5.04
238	34.50	44.30	1	6	10	5	28	7.20	12	2.98	4.20
239	30.00	41.30	2	4	9	4	30	7.50	10	3.30	5.12
240	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
241	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
242	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
243	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
244	34.50	39.10	3	6	11	4	35	7.40	10	3.52	5.01
245	34.00	52.50	2	5	10	4	39	7.50	11	4.34	6.45
246	33.20	45.90	3	4	12	5	32	10.50	8	3.54	4.03
247	35.00	40.20	3	5	11	6	35	7.16	10	3.01	3.86
248	32.50	35.20	2	6	12	6	39	7.40	13	2.84	3.01
249	35.00	39.90	2	4	11	5	39	6.40	9	4.50	6.02
250	32.00	43.30	1	5	14	5	29	8.50	9	2.96	5.05
251	34.00	41.20	3	6	13	4	34	7.20	9	3.38	4.05
252	30.00	40.00	3	4	9	5	26	7.30	10	3.70	4.92
253	32.00	39.10	2	5	10	4	27	7.19	10	3.00	3.20
254	31.20	37.40	1	5	8	5	38	6.20	12	3.19	5.98
255	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
256	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
257	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
258	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
259	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18
260	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05

261	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
262	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
263	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58
264	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
265	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
266	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
267	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
268	34.00	39.90	2	3	10	4	29	10.60	10	3.44	3.08
269	33.50	42.20	1	3	11	5	32	6.10	13	3.54	5.04
270	34.50	44.30	1	6	10	5	28	7.20	12	2.98	4.20
271	30.00	41.30	2	4	9	4	30	7.50	10	3.30	5.12
272	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
273	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
274	34.50	39.10	3	6	11	4	35	7.40	10	3.52	5.01
275	34.00	52.50	2	5	10	4	39	7.50	11	4.34	6.45
276	33.20	45.90	3	4	12	5	32	10.50	8	3.54	4.03
277	35.00	40.20	3	5	11	6	35	7.16	10	3.01	3.86
278	32.50	35.20	2	6	12	6	39	7.40	13	2.84	3.01
279	35.00	39.90	2	4	11	5	39	6.40	9	4.50	6.02
280	32.00	43.30	1	5	14	5	29	8.50	9	2.96	5.05
281	34.00	41.20	3	6	13	4	34	7.20	9	3.38	4.05
282	30.00	40.00	3	4	9	5	26	7.30	10	3.70	4.92
283	32.00	39.10	2	5	10	4	27	7.19	10	3.00	3.20
284	31.20	37.40	1	5	8	5	38	6.20	12	3.19	5.98
285	30.00	42.50	2	5	12	5	32	7.36	10	2.90	3.03
286	34.50	38.80	3	6	12	4	38	8.94	10	3.58	4.93
287	32.50	40.80	2	4	9	5	32	7.20	9	3.62	3.21
288	30.50	34.40	2	5	10	4	38	6.50	10	4.26	6.35
289	32.50	36.90	2	5	11	4	29	7.20	14	3.18	3.18

290	30.00	50.20	3	6	10	4	30	10.00	14	3.24	4.05
291	30.50	35.80	1	5	9	4	37	7.20	15	4.42	5.64
292	32.00	46.20	2	4	10	6	27	7.16	14	3.56	5.20
293	30.00	46.40	1	3	10	6	36	10.00	14	4.44	6.58
294	28.50	47.00	2	6	8	4	48	8.50	14	3.18	3.90
295	32.20	39.80	3	4	12	5	35	9.70	12	3.32	4.28
296	30.00	35.90	2	4	12	5	40	6.20	12	3.86	6.30
297	29.30	39.10	3	6	9	6	28	7.50	11	3.70	5.20
298	34.00	39.90	2	3	10	4	29	10.60	10	3.44	3.08
299	33.50	42.20	1	3	11	5	32	6.10	13	3.54	5.04
300	34.50	44.30	1	6	10	5	28	7.20	12	2.98	4.20
Mean	**38.50**	**48.20**	**1.96**	**4.32**	**12.42**	**4.05**	**42.58**	**6.26**	**6.92**	**3.28**	**6.20**

DFF = Days to 50 *per cent* flowering
PH = Plant height (cm)
PBP = Primary branches per plant
SBP = Secondary branches per plant

NCP = Number of cluster per plant
NPC =Number of pods per cluster
NPP = Number of pods per plant
PL = Pod length (cm)

NSP = Number of seeds per pod
100 SW = 100 seed weight (g)
SYP = Seed yield per plant (g)