GENETIC ANALYSIS IN GREEN GRAM
(*Vigna radiata* (L.) Wilczek)

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(2018-11-020)

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KERALA, INDIA

2020

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by

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THESIS
Submitted in partial fulfilment of the
requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture
Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS
COLLEGE OF AGRICULTURE
VELLAYANI, THIRUVANANTHAPURAM – 695 522
KERALA, INDIA

2020

DECLARATION

I, hereby declare that this thesis entitled **“GENETIC ANALYSIS IN GREEN GRAM (*Vigna radiata* (L.) Wilczek).”** is a bonafide record of research work done by me during the course of research and the thesis has not previously formed the basis for the award to me of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Reshma

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Date: 21-08-2020 **(2018 -11-020)**

CERTIFICATE

Certified that this thesis entitled **"GENETIC ANALYSIS IN GREEN GRAM (*Vigna radiata* (L.) Wilczek)."** is a record of research work done independently by Miss **RESHMA S. NAIR** under my guidance and supervision and that it has not previously formed the basis for the award of any degree, diploma, fellowship or associateship to her.

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We, the undersigned members of the advisory committee of Miss **RESHMA S. NAIR**, a candidate for the degree of Master of Science in Agriculture, with major in Plant Breeding and Genetics, agree that the thesis entitled **"GENETIC ANALYSIS IN GREEN GRAM (*Vigna radiata* (L.) Wilczek)"** may be submitted by Miss **RESHMA S. NAIR**, in partial fulfilment of the requirement for the degree.

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Acknowledgement

*I bow my head before the Almighty **God** for the blessings and enlightenment throughout my work and enabled me to complete my thesis work successfully on time.*

*With great respect and privilege, I would like to express my sincere gratitude and indebtedness to **Dr. Arya. K**, Professor and Head, Plant Breeding and Genetics, College of Agriculture, Vellayani and Chairperson of my Advisory Committee for her constant encouragement, valuable suggestions, motherly approach, everlasting patience and support that she has given throughout the course of thesis work. It was her sincerity, dedication and perfectionism that I could finish my work on time.*

*I am extremely thankful to **Dr. Dijee Bastian**, Professor, Department of Seed Science, College of Horticulture, Vellanikkara, for her valuable suggestions, fruitful criticism and timely help for the successful completion of the thesis.*

*I am grateful to the worthy members of my advisory committee, **Dr. Roy Stephen, Dr. Manorama Thampatti** and **Dr. Beena Thomas** for their valuable suggestions and support during the course of these investigations.*

*I extend my acknowledgement to **Dr. G. Sreenivas**, Assistant Professor, ARS, Amadalavalasa, Andhra Pradesh, **Dr. S. Gangaprasad**, Professor, Genetics and Plant Breeding, University of Agriculture and Horticulture Sciences, Shivamogga and **NBPGR**, New Delhi for providing germplasm for the research work.*

*I sincerely express my obligation and respect to teachers of Department of Plant Breeding and Genetics, **Dr. Lekha Rani, Dr. Mareen Abraham**, and **Dr. G. Gayathri** for their constant encouragement, support, and valuable advice. I also express my gratitude to **Dr. Jayalekshmi V.G.,** Professor (RC), Department of Seed Science and technology for sincere co- operation throughout my course work.*

*I am grateful to **Anju chechi, Radhamani chechi, Beena chechi** and other office staffs for their sincere cooperation and support. I also express my sincere thanks to*

***Soumya chechi**, Research Assistant, Dept. of Soil science and. Agricultural chemistry for her help and support in completing my work.*

*Words are inadequate to express my thanks to my classmates **Bhoomika, Mythri, Darshana, Smera** and **Roshin** for being there with me from beginning of course study and playing big part in completion of my research work.*

*I also express my sincere thanks to my seniors **Swathy, Anand, Arun, Ankitha, Govind** and **Bhaskar** for their valuable advice, suggestions and support. I wish to express my heartfelt thanks to my seniors **Shahiba, Arya, Thouseem, Anju** and **Amrutha** and dear **juniors** for their help and suggestions during the research period.*

*I express my heartfelt thanks to my friends **Anna, Rose, Sarin, Shinu, Arun, Nayana, Deena, Amritha, Aparna, Aashika, Veni, Sumeena,** and **Ajai** for their help and support throughout the study period.*

*I shall remain lifelong indebted to my dear friends **Vivek, Dilja** and **Pooja chechi** for their help, constant moral support, everlasting patience and valuable suggestions.*

*I am thankful to **Kerala Agricultural University** for their technical and financial assistance for carrying out my study and research work, I would like to express thanks to **Librarian** and **library staffs** of COA, Vellayani, for their support and assistance during the study period.*

*Words cannot express my deep sense of gratitude and indebtness to my beloved father **Sajeevdas**, my beloved mother **Bindu**, my beloved sister **Lekshmi** and my beloved brother **Binil** for their unconditional love, sacrifices, encouragement and faith rendered to me throughout my career.*

Finally I thank all those who extended helped and support to me in one way or another in the successful completion of this thesis work.

Reshma S. Nair

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LIST OF ABBREVIATIONS AND SYMBOLS USED

ANOVA	Analysis of Variance
%	Per cent
cm	Centimeter
RBD	Randomized Block Design
et al.	Co-authors/And others
Fig.	Figure
Mbp	Mega base pairs
g	Gram
/g	Per gram
mg/g	Milligram per gram
kg	Kilo gram
/ha	Per hectare
KAU	Kerala Agricultural University
DMSO	Dimethyl Sulfoxide
kg/ ha	Kilogram per hectare
/plant	Per plant
/day	Per day
m^2	Square meter
via	Through
No.	Number
Sl.	Serial
sp. or spp.	Species (Singular or Plural)

viz.	Namely
d.f	Degrees of freedom
S.E	Standard Error
C.D	Critical difference
PCV	Phenotypic Coefficient of Variation
GCV	Genotypic Coefficient of variation
&	And
GA	Genetic Advance
H^2	Heritability
GAM	Genetic Advance as per cent of Mean
NBPGR	National Bureau of Plant Genetic Resources
ARS	Agricultural Research Station
UAHS	University of Agricultural and Horticultural Sciences
TNAU	Tamil Nadu Agricultural University

Introduction

1. INTRODUCTION

Green gram (*Vigna radiata* (L.) Wilczek) is an important food legume in tropical, subtropical and temperate regions of Asia and East Africa. It is also called golden gram, mung bean, greensoy or moong. Among the twelve cultivated grain legumes, green gram occupies third position succeeding chickpea and red gram in India covering an area of about 34.4 lakh hectares with an annual production and productivity of 14 lakh tonnes and 407 kg/ha, respectively (Vir and Singh, 2015).

As an edible crop, mung is an excellent source of protein, carbohydrate and dietary fibres and contributes several minerals like iron, zinc, calcium, potassium and folate to the diet (Schafleitner *et al*., 2015). Sprouted beans are rich in beta carotene, thiamine, riboflavin and ascorbic acid. Green gram is referred to as the best pulse for humans in Ayurvedic treatises as it contains easily digestible protein with least flatulence causing factors compared to other pulses. Consumption of mung bean helps to improve eyesight. It can also be used in infant foods and for convalescing patients.

Green gram is inevitable in several preparations of Asian cuisine, especially in a vegetarian diet. Being a cheap source of vegetable protein, it is commonly used as a supplement to the normal diet of many people, particularly with low income. Mung can be used as dry seeds, immature pods and fresh sprouts. Also, the bean can be frozen, canned or grounded into flour for later use. Beyond the consumption purpose, green gram flour is an excellent substitute for soap, improves complexion and leaves the skin soft and smooth.

The photo-insensitive nature with a short duration makes green gram highly suitable for multiple cropping systems. Generally it is cultivated throughout the year either as a sole crop, in rotation with paddy and wheat or intercropped with other crops. The crop grows well in a wide range of soil types with low input requirements. The crop is well known for its drought tolerance and ability to improve soil fertility through atmospheric nitrogen fixation. The plant can also be used for forage, green manure or as a cover crop.

In Kerala, the cultivation of green gram mainly limits to a few pockets of northern districts despite its high demand and consumption. Since land is a highly limiting factor in the state, inter-cropping is the best alternative to boost the income of the farmers' in the state and to improve the fertility status of the soil. The upland gardens with increasing areas are the potential areas where we can intervene green gram cultivation in the state.

The global average productivity of the crop is 0.73 tonnes per hectare which is low as compared to other pulses (AVRDC, 2016). The dearth of genetic variability, absence of suitable ideotypes suited for different cropping systems, poor harvest index, poor management and susceptibility to disease are the major constraints in achieving a higher yield in mung bean. This may be due to the utilization of only a few selected cultivars and underutilization of the gene pool of the Indian subcontinent.

Breeding programmes to improve seed yield can be a breakthrough in green gram production. The success of any breeding programme depends much on the extent of variability present in the base population. Hence a survey of genetic variability in the experimental population is the base of any improvement strategy. The genetic variability assessed using different genetic parameters such as phenotypic and genotypic coefficient of variation, heritability along with genetic advance is absolutely necessary to accomplish a successful crop improvement programme. Association analysis provides a clear idea of the nature and extent of interrelation among yield and its attributing traits which is further utilized in the improvement of the genotype.

Keeping these aspects in view, the present study entitled "Genetic analysis in green gram (*Vigna radiata* (L.) Wilczek)" has been taken up with the following objectives:

- To assess the variability parameters in different genotypes of green gram
- To evaluate the performance of the genotypes under open and partially shaded conditions
- To identify the best genotype in terms of yield and protein content

Review of Literature

2. REVIEW OF LITERATURE

2.1. Origin and Distribution

Green gram popularly known as mung or moong bean is the third major pulse crop in India after Bengal gram and red gram. Its origin and domestication occurred in Indian subcontinent and then spread to other countries especially Asian countries. The progenitor of moong is believed to be *Vigna subloabata* which grows wild in our country (Nene, 2006). Now, green gram is cultivated in many countries like India, Myanmar, Srilanka, Pakistan, China, Fiji, Queens land, Africa and USA. Medicinal properties and storage practices of the crop has been mentioned in ancient literatures proving that the crop was in cultivation in India since pre historic times.

India is a major producer of green gram contributing 30 per cent of total world production (AVRDC, 2016). In India, major states cultivating mung bean are Odisha, Maharashtra, Andhra Pradesh, Gujarat, Rajasthan and Bihar.

2.2. Taxonomy

Green gram belongs to the family Fabaceae under order Fabales. Latin name of the crop is *Vigna radiata* (L.) Wilczek (Adsule, 1986). Green gram has 22 chromosomes with a genome size of 579 Mbp (Arumuganath and Earle, 1991). The crop is mentioned as munda in Sanskrit from which the word ‘mung’ has been originated. A variety of common names have been given to this grain legume in different parts of India (Nene, 2006).

Genus *Vigna* is a large group comprising a wide variety of legumes out of which ten species has been domesticated. The domesticated crops are classified under three subgenera *viz., Vigna, Plectrotropis* and *Ceratotropis*. Subgenus *Ceratotropis* is referred to as Asian *Vigna* as the members of this group are generally distributed in Asia which includes green gram and black gram (Takahashi *et al*., 2015).

V. radiata var. sublobata (Roxburgh) Verdcourt is the closest wild relative of cultivated green gram and is distributed widely in the Western Ghats and sporadically in Rajasthan, Madhya Pradesh and Northwestern Himalayas. Whereas, *V. radiata var. setulosa* (Dalzell) Ohwi and Ohashi is closely related to *V. radiata* and occurs sporadically in Western and Eastern Ghats (Bisht *et al*., 2005).

2.3. Variability

The crucial element that determines the success of a crop improvement programme is the presence of adequate variability and its effective utilization. Several studies have been carried out in green gram and other pulses to assess the variability using coefficients of variation as it provides a better estimate of total existing variability in the population. Along with the coefficient of variation, other genetic parameters such as heritability and genetic advance also serve as measures of variability within the population. Some of the reviewed studies are given below:

2.3.1. GCV and PCV

The values of GCV and PCV give an overall idea about the extent of variability for a particular trait among the genotypes studied. If the genotypic coefficient of variation is greater for a character, the effect of environment on the expression will be negligible and direct selection is effective. The available literature pertaining to green gram and black gram are listed below:

Fifteen landraces of green gram were assessed for diversity by Karuppanapandian *et al.* (2006). They observed existence of diversity for seed size (38.20-56.10mg), seed coat colour, surface luster and hypocotyl colour among the genotypes studied.

According to Makeen *et al.* (2007), seed yield exhibited higher phenotypic and genotypic coefficient of variation followed by pods per plant and pods per cluster in mung genotypes. They also observed minimum magnitudinal differences between PCV and GCV for three traits *viz.,* days to maturity, 50 per cent blooming and pod length.

A study conducted by Das *et al*. (2010) using 23 green gram genotypes revealed higher GCV for seed yield per plant (38.54) followed by seeds per pod

(30.01) and pods per plant (29.27). At the same time total plant yield showed high phenotypic coefficient of variation.

Variability in ten mung bean genotypes was studied by Tabasum *et al*. (2010). They reported adequate variability for traits like plant height, pod number, seed yield and total plant weight. Characters like clusters per plant, 100 seed weight, and harvest index showed moderate while number of branches, pods per cluster and pod length exhibited low variability. They observed higher magnitude of PCV for all the characters under study. Clusters per plant and single plant yield showed high GCV which were 21.05 and 17.12 per cent respectively.

Genetic variability studies in forty diverse green gram genotypes by Garje *et al.* (2013) revealed high values of PCV and GCV for seed yield, pod length, number of pods, pod clusters and secondary branches per plant.

Twenty two green gram genotypes including a check were evaluated for ten quantitative characters during kharif season by Mehandi *et al.* (2013), to ascertain variability. It was observed that, the magnitudinal difference between phenotypic and genotypic variation was lowest for number of pods per plant while, primary branches per plant recorded the maximum. The estimates of coefficients were highest for pods per plant followed by number of primary branches.

Nand and Anuradha (2013) evaluated fifty genotypes in mung to assess genetic variability. High GCV and PCV were reported for pods per plant, seeds per pod and incidence of pest and diseases. Days to first and 50 per cent flowering exhibited low values for coefficient of variation.

Seed yield in green gram showed high range of variation for all eight characters studied by Prasad and Prasad (2013). The study concluded that the highest magnitude of GCV was reported for pods per plant (23.74) followed by grain yield (20.61).

Genetic analysis conducted by Ahmad *et al*. (2014) in green gram observed high GCV for pod number followed by days to maturity and pods per cluster. Characters like pods per plant, plant height, days to 50 per cent blooming, number of days to maturity and 100 grain weight exhibited very low difference between coefficients of variation at genotypic and phenotypic levels indicating the genetic contribution of these traits in character expression therefore scope for direct selection.

Dafega *et al.* (2014) reported low estimates of GCV and PCV for characters like days for first flowering, days to maturity and plant height in the genetic variability assessment of thirteen genotypes of green gram under two different locations. Lowest measure of difference between phenotypic and genotypic coefficients of variation was noticed for days to maturity under both environments revealing high extend of genetic contribution.

A study conducted by Patel (2014) in mung revealed less influence of environment on characters like days for 50 per cent flowering, plant height (cm), number of primary branches, clusters per plant, number of pods per cluster, pod length, total number of pods, seed per pod, 100 seed weight, protein content and single plant yield as they showed close values of VG and VP. High PCV and GCV were recorded for seed yield.

Das and Barua (2015) studied variability in twenty three genotypes and reported high magnitude coefficients of variation for single plant yield followed by seeds per pod. Moderate range of GCV was exhibited by the character 100 seed weight.

The extent of variability between eleven quantitative characters in F_2 and F_3 progenies of cross BL-865 x Chinamung was assessed by Muralidhara *et al.* (2015). Highest GCV was observed for pods per plant in F_2 progenies, while seed yield recorded high value in F_3. Estimate of PCV also showed a similar trend in both generations.

Thirty genotypes comprising 22 mutant lines, parents, two checks and four landraces were assessed for twelve quantitative characters by Baisakh *et al.* (2016). The lowest estimates of phenotypic and genotypic coefficient of variation were noticed for number of days for fifty per cent blooming then pod length.

Gowsalya *et al.* (2016) conducted a genetic variability analysis in black gram using eighty genotypes. They reported the presence of considerable amount of variability for all eleven characters under study. Estimates of phenotypic and genotypic coefficient of variation were highest for number of branches per plant while the values were low for days to maturity.

Evaluation of 50 genotypes of green gram for eleven quantitative characters conducted by Rasal and Parhe (2017) revealed that three characters *viz.*, clusters per plant, seed yield and pods per plant showed high values for genotypic and phenotypic coefficient of variation.

According to Choudhary *et al.* (2017), characters like biological yield, number of primary branches and plant height showed high genotypic and phenotypic coefficient of variation in a genetic analysis using eighteen F_5 progenies and their parents. 100 grain weight (5.46, 7.66) and days to maturity (7.80, 8.21) showed low values of GCV and PCV.

A total of thirty green gram genotypes evaluated by Garg *et al.* (2017) revealed high values of PCV over GCV for all characters. Small difference between PCV and GCV for traits other than days to maturity and number of branches reflected the minimal environmental influence in the phenotypic expression. Grain yield per plant recorded the highest value of PCV (42.95) and GCV (42.27).

In black gram, high values of genotypic and phenotypic coefficient of variation were observed for harvest index and pod number in a study conducted by Hemalatha and Lal (2017). Plant height exhibited a high difference between PCV and GCV reflecting the influence of environment on stature.

Keerthiga *et al.* (2017) evaluated thirty F_4 progenies of Meha x GJM-1006 and Meha x GJM-1008. The study revealed presence of ample variability in the segregating population as the estimate of variance was high for most of the traits. In the segregating populations, high magnitudes of genotypic and phenotypic coefficient of variation were observed for number of pods and grain yield per plant. The lowest estimate was reported for days to 50 per cent blooming in progenies of Meha x GJM-1006 whereas days to maturity in the second population.

An experimental study conducted using thirteen green gram genotypes by Reddy (2017) reported high values of PCV and GCV for all 13 characters under study. The highest GCV estimate was recorded for yield per plant (30.92) and harvest index (28.06). Number of secondary branches and pod length exhibited highest magnitudinal difference between genotypic and phenotypic coefficients of variation, whereas the difference was least for days to 50 per cent flowering.

Fifteen different genotypes were evaluated for thirteen characters by Blessy *et al.* (2018) in randomized block design. The study revealed high values of coefficients for primary branches per plant and pod number both at phenotypic and genotypic levels. Magnitudinal difference between PCV and GCV was mere for biological yield indicating high genetic contribution to total variability for this trait.

Govardhan *et al.* (2018) studied 58 green gram genotypes and observed higher values of PCV and GCV for pods per cluster and specific leaf area under irrigated and 100 grain weight under moisture stress conditions. Branch number per plant showed high values under both the experimental conditions. Moderate estimates of GCV and PCV were reported for characters like number of pods, plant height and yield per plant and harvest index. While days to maturity, 50 per cent flowering and water content showed low values.

In green gram, Ramakrishnan *et al.* (2018) reported that the coefficient of genetic variation was the lowest for 50 per cent flowering. 100 seed weight scored the highest coefficients both at phenotypic and genotypic level followed by single plant yield.

According to Sandhiya and Saravanan (2018), the magnitudinal difference between phenotypic and genotypic coefficients was small for all characters except plant height (6.09). Pod length scored the lowest values of PCV (18.40) and GCV (17.84). The results indicate the minimal environmental influence on expression of most of the traits under study.

Experimental studies in thirty two black gram genotypes for variation by Sushmitharaj *et al.* (2018) revealed moderate to high variability for all characters studied. High values of GCV were recorded for yield per plant (41.14) and pod number (30.47). Low genotypic coefficient of variation was observed for the character pod length followed by seeds per pod.

Muthuswamy *et al*. (2019) assessed hundred green gram genotypes for ten characters in a randomized block design. They reported small magnitudinal difference between phenotypic and genotypic coefficient of variation revealing high genetic contribution of variance for all characters under study. The highest and lowest values of coefficients were reported for number of pods and seeds per plant, respectively.

Hundred and ten indigenous green gram genotypes were evaluated by Sneha *et al*. (2019). They reported that pods per plant, single plant yield and 100 grain weight exhibited high magnitude of coefficient of variation at genotypic and phenotypic levels. Whereas, the values were moderate for traits *viz.,* primary branches per plant, number of days for 50 per cent flowering, number of clusters and plant height. Low estimate of GCV and PCV was reported for seeds per pod and pod length.

2.3.2. Heritability and Genetic Advance

The estimate of heritability provides information about the heritable part of variance therefore useful for breeders. Range of heritability was classified into high (above 60 per cent), medium (30 per cent – 60 per cent) and low (below 30 per cent) (Johnson *et al.,* 1955). Genetic gain measures the expected genetic gain achieved by selecting a genotype. A combination of these two gives a reliable indication of gene action than heritability thus helps in the adoption of effective selection strategy.

Moderate values for broad sense heritability and high genetic advance were reported for protein content and test weight by Makeen *et al.* (2007) in green gram. The study states that, selection based on parameters pods per cluster, pods per plant, plant height and yield would be effective.

Twenty three genotypes of green gram were evaluated for six characters by Das *et al.* (2010). They noticed that heritability values were high for all characters under study. Among all the traits, yield per plant and number of seeds per pod showed high heritability estimate coupled with high genetic advance.

According to Tabasum *et al*. (2010), all traits except number of primary branches (57.18) exhibited high heritability. Moderate heritability coupled low genetic advance (0.09) was noticed for number of primary branches per plant showing the presence of non additive gene action.

A study conducted by Gadakh *et al.* (2013) using 50 green gram genotypes reported high heritability along with high GA for traits like plant height and single plant biological yield making them suitable for crop improvement under certain amount of selection pressure.

High broad sense heritability was scored by pod number and grain yield in a study conducted by Garje *et al*. (2013) using 40 genotypes. Pods per plant and plant height showed a combination of high heritability with high genetic advance.

Variability analysis conducted by Kumar *et al.* (2013) observed high broad sense heritability coupled with high genetic advance for 100 seed weight and stated the possibility of transfer of the trait in successive generations due to additive gene action.

Mehandi *et al*. (2013) conducted an experiment to evaluate 22 genotypes of green gram including Samrat as a check in kharif season. High broad sense heritability coupled with GAM was observed for pods per plant, plant height and clusters per plant. Days to maturity, seed yield and 100 seed weight showed high heritability and moderate genetic advance. They also stated the effectiveness of selection from the experimental population by indicating the presence of additive gene action for these traits.

Low heritability coupled with low genetic advance was recorded for characters like pod length, hundred seed weight, days to 50 per cent flowering and 50 per cent pod formation in a study conducted by Nand and Anuradha (2013). The values of heritability were high for percentage disease incidence followed by number of pods.

Genetic analysis of 32 green gram genotypes was conducted by Prasad and Prasad (2013). Two advanced breeding lines MGG 295 and MGG 348 were used as the check in this study. They concluded that days to 50 per cent flowering and maturity exhibited high heritability but low genetic advance. High heritability coupled with moderate genetic advance was observed for 100 seed weight.

Dafega *et al*. (2014) evaluated thirteen green gram genotypes to study the available genetic variability in the population. Two experiments were conducted at different locations to understand the impact of the environment on phenotypic expression. Seed number showed high estimates of heritability and high GAM at one location while the values were low for the second site.

According to Patel (2014), high heritability was recorded for all the twelve characters under a study conducted with 40 genotypes. All characters except days to 50 per cent blooming, maturity and protein content showed high heritability along with high values of GAM indicating increased scope for direct selection.

Evaluation of twenty three genotypes of green gram in summer season by Das and Barua (2015) revealed that, characters like grain yield, plant height, pod length, number of pods, seeds per pod and 100 seed weight showed high estimate of heritability with high genetic advance. A combination of high heritability with moderate GA for days to 50 per cent blooming and percentage of pod filling indicated that non additive gene action for these traits.

Progenies of cross BL-865 x Chinamung along with parents and checks were evaluated for eleven different characters in two segregating populations by Muralidhara *et al.* (2015). It was reported that, high estimates of heritability was noticed for all traits other than number of branches in F_2 and days to initial flowering in F_3 generation. The lowest GA was recorded for number of days to first flowering in both F_2 and F_3 generation with values 8.02 and 5.95, respectively.

Baisakh *et al.* (2016) reported high heritability for all twelve characters based on the work in thirty green gram genotypes. The association with high genetic advance was observed for characters other than number of days for 50 per cent flowering and pod length which exhibited low and moderate genetic advance respectively.

Seeds per pod and test weight recorded moderate heritability coupled with moderate GAM in a genetic analysis of eighty black gram genotypes by Gowsalya *et al.* (2016). They noticed high heritability and genetic advance for branch number, plant height, yield and pod number.

Heritability analysis in ten black gram genotypes was conducted by Sohel *et al.* (2016). They reported high estimates of heritability for all characters except number of seed per pod (53.10).

High heritability coupled with high GAM was recorded for all characters except days to maturity, 100 seed weight and pod length in a study conducted by Choudhary *et al.* (2017). 100 seed yield showed moderate range of heritability coupled with low GAM reflecting additive and non additive gene action making it less preferable for direct selection.

According to Garg *et al.* (2017), characters except days to 50 per cent flowering exhibited high heritability with moderate to high genetic advance. Days to maturity scored high heritability (90.10) with moderate genetic advance (14.53).

Hemalatha *et al.* (2017) evaluated twenty six black gram genotypes for twelve quantitative characters. Low heritability coupled with low genetic advance as per cent of mean was recorded for seed index. High heritability and low GAM of days to maturity indicates preponderance of non additive gene action.

A total of thirty F_4 progenies derived from two crosses Meha x GJM-1006 and Meha x GJM-1008 were evaluated by Keerthiga *et al.* (2017). Estimate of heritability was high for plant height, number of days to maturity and pod number in the first set progenies while days to 50 per cent flowering scored the maximum in the second population. Pods number and seed yield recorded high genetic advance coupled with high to moderate heritability.

Rasal and Parhe (2017) reported high heritability in broad sense for all characters studied ranging from 66.00 to 95.70. Characters exhibited a wide range of genetic advance. The value was highest for plant height, while test weight had the lowest magnitude.

According to Reddy (2017), high heritability with genetic advance was reported for harvest index. Most of the traits exhibited high heritability in broad sense but with low genetic advance showing non additive nature of character expression.

Evaluation of black gram genotypes for thirteen quantitative characters during kharif season by Blessy *et al.* (2018) revealed a high level of heritability for all characters studied. However, estimate of high heritability along with genetic advance was noticed for seed index, number of clusters and pods per plant. The study concluded that selection based on these traits will be rewarding on which the phenotype could be relied upon.

Genetic analysis in 58 genotypes of green gram under irrigated and moisture stress condition was carried out by Govardhan *et al*. (2018). Out of the fifteen traits studied, low heritability was observed for water content under irrigated condition. Traits like harvest index, clusters per plant, seed yield, chlorophyll stability exhibited different values of heritability under two different experimental conditions thus proving environmental influence on the character expression.

Studies in twenty one varieties of green gram by Ramakrishnan *et al*. (2018) revealed that characters like days to 50 per cent flowering, plant height, pods per plant, threshing percentage, days to harvest, pod length, grain yield, seed number per pod, number of branches, clusters per plant and pod yield per plant exhibited high heritability associated with high GAM.

Sandhiya and Saravanan (2018) noticed high heritability coupled with genetic advance for characters like days to 50 per cent flowering, pods per plant, seeds per pod, pod length, number of primary branches, plant height and hundred grain weight.

Variability parameters for yield were determined by Sushmitharaj *et al.* (2018) using thirty two genotypes of black gram. They noticed high GAM for single plant yield, number of pods, clusters per plant and plant height. According to them, selection based on pod length would be ineffective as it exhibits low heritability (16.00) coupled with low genetic advance (4.54).

A study conducted by Muthuswamy *et al.* (2019) in green gram reported high heritability coupled with high GAM for all characters except number of seeds per plant which exhibited moderate GAM.

High heritability coupled with high genetic gain was recorded for characters *viz.*, days for 50 per cent blooming, plant height, number of pods and seed yield in green gram by Sneha *et al*. (2019). Number of primary branches, pod length and pods per cluster recorded moderate range for both parameters. High heritability with moderate GA was noticed for seeds per pod whereas, test weight recorded moderate heritability and high GA.

Evaluation of thirty green gram genotypes including seven parents and twenty one cross combinations conducted by Sopan *et al.* (2019) disclosed moderate to high heritability for all eleven traits. Characters days to maturity and protein content recorded high heritability with low GAM indicating non additive gene action. An association of moderate heritability with high genetic advance was reported for number of branches per plant.

2.4. Correlation Studies

Correlation coefficient measures the strength and direction of association between characters. An estimate of interrelation between yield and yield attributing traits will facilitate effective selection. Path coefficient divides the correlation coefficient into direct and indirect effects and gives information about the influence of one variable upon another (Dewey and Lu, 1959). Both these statistical measures provide an idea for selection.

Based on a correlation study, Makeen *et al.* (2007) disclosed that there exists a significant positive phenotypic and genotypic correlation of grain yield with pods per plant and plant height.

Correlation analysis performed by Tabasum *et al.* (2010) reported negative non significant correlation coefficient for number of primary and secondary branches, hundred seed weight and pod length on yield. Association of plant height with seed yield was significant and positive (0.507) at the phenotypic level. The greater genotypic correlation over phenotypic correlation reflects the predominance of the genetic component of variation in character expression.

A significant positive correlation of plant height with number of clusters per plant, primary branches and pods per plant in mung bean was reported by Kumar *et al.* (2013).

In a study, Nand and Anuradha (2013) observed positive correlation of days to first and 50 per cent flowering, number of branches, pods per plant, seeds per plant, days to full maturity, hundred seed weight, Pod length and 50 per cent pod formation with yield. But the association of per cent disease incidence on yield was negative.

Patel (2014) reported that single plant yield exhibits a significant positive correlation with plant height, number of primary branches, number of clusters, number of pods per cluster and plant, seeds per pod, test weight and protein content. Existence of a significant but negative correlation of yield with days to flowering, maturity and pod length was also reported in his study.

According to Das and Barua (2015), grain yield was positively correlated with the other seven characters. The highest correlation coefficient at phenotypic (0.673) and genotypic (0.673) level was observed for test weight.

Association of yield with other characters in segregating populations of cross BL 865 x Chinamung studied by Muralidhara *et al.* (2015) reported the existence of a significant positive correlation of seed yield with plant height, primary branches per plant, clusters per plant, pod number, pods per cluster, pod yield per plant and threshing percentage.

A strong positive correlation of grain yield both at phenotypic and genotypic levels with plant height, clusters per plant, pod length, pod number and seeds per pod in green gram was reported from a study using 30 genotypes including 22 mutant cultures by Baisakh *et al.* (2016). Days to 50 per cent flowering showed a non-significant negative correlation at the phenotypic level whereas the correlation was non-significant and positive at the genotypic level.

Correlation coefficient studies in black gram by Gowsalya *et al.* (2016) indicated that characters other than days to 50 per cent flowering and maturity have a significant positive correlation with yield. Number of pods (0.874) exhibited the highest genotypic correlation coefficient.

In a study comprising ten genotypes of urd bean by Sohel *et al.* (2016), it was noticed that seed yield was positively correlated to characters like harvest index, pod number, 100 grain weight, pod length, seeds per pod and pod weight, whereas it is negatively correlated to plant height, fresh and dry weight.

Choudhary *et al.* (2017) observed a strong positive correlation of biological yield per plant (0.615) and number of primary branches (0.120) on grain yield indicating the potential of bushy plants with more pods for high yield. While plant height showed a non-significant negative contribution to grain yield.

Evaluation of thirty genotypes of green gram by Garg *et al.* (2017) disclosed a significant association of yield with all characters except test weight. Days to flowering and maturity exhibited a negative correlation with single plant yield at phenotypic and genotypic levels. The study concluded that, selection of short duration varieties based on characters like number of pods, biological yield are harvest index will contribute positively towards yield.

According to Hemalatha *et al.* (2017), in black gram, pods per plant and harvest index had a significant positive association with seed yield, whereas the correlation of days to 50 per cent flowering was significant but negative. The study states the existence of a strong association between harvest index and seed yield with a genotypic correlation coefficient of 0.926.

A study conducted by Reddy (2017) revealed the existence of a significant positive correlation of seed yield with pod length (0.790), seeds per pod (0.780), pods per plant (0.770) and harvest index (0.740). But the correlation was negative for 50 per cent flowering (-0.670) and maturity (-0.660). He also concluded that the relation between yield and characters like pods per plant, harvest index, and cluster of pods per plant was positive and significant.

In green gram, a positive correlation between yield and characters like 50 per cent flowering, plant height, primary branches per plant, pods per plant and test weight was recorded by Keerthiga *et al.* (2018) from their study using 30 F_4 progenies and 3 parents of green gram.

Correlation analysis in 108 recombinant inbred lines derived from the interspecific cross between *V. radiata* and *V. umbellata* conducted by Mathivathana *et al.* (2018) reported maximum positive correlation pod number (0.770) on yield. They also observed a significant positive association of plant height with 100 grain weight.

It was reported by Parihar *et al.* (2018) that grain yield exhibited a significant negative correlation with plant height and days to maturity whereas days to 50 per cent flowering showed a negative and non-significant correlation with yield per plant. The highest positive correlation coefficient was recorded for the association between days to 50 per cent flowering and maturity.

On the basis of correlation analysis in green gram, Ramakrishnan *et al*. (2018) reported that there exists a significant positive correlation of seed yield with pod yield per plant, number of pods per plant, clusters per plant and threshing percentage. Number of clusters and pod length showed significant negative association with plant height.

According to Sandhiya and Saravanan (2018), number of pods per plant exhibited the highest positive correlation (0.597) with seed yield. Pod length showed a significant positive association with seeds per pod (0.495) and hundred grain weight (0.585). They noticed the presence of non-significant negative correlation of days to 50 per cent flowering and plant height with seed yield.

Based on an association analysis in black gram, Sushmitharaj *et al.* (2018) reported that, there exists a significant positive association of seed yield with plant height, pods per plant and number of pod clusters. They also observed an absence of correlation between yield and seeds per pod. Pod length was found to be non-significant but negatively correlated to single plant yield. Based on the inter-correlation studies, they reported a significantly positive association of days to 50 per cent flowering with these three characters.

In a study comprising of hundred genotypes of green gram by Muthuswamy *et al.* (2019), it was observed that seed yield was positively associated with characters like height, number of branches, clusters per plant, pods per plant, number of pods per cluster and plant. The highest estimate of correlation was showed by pod number (0.908) on grain yield.

Genetic analysis of 110 genotypes of green gram was conducted by Sneha *et al*. (2019) and reported that nine quantitative characters like days for 50 per cent blooming, plant height, number of primary branches, pods per cluster and plants, seeds per plant, test weight and pod length exhibited significant correlation with single plant yield. Among all nine, the highest positive correlation was shown by number of pods with values 0.850, 0.810 at five and one per cent level of significance respectively followed by number of clusters and test weight. Number of days for 50 per cent flowering displayed a negative correlation with single plant yield.

2.5. Path Coefficient Analysis

Makeen *et al*. (2007) reported positive direct effect for traits number of pods, test weight and content of protein on yield among which pods per plant recorded the maximum whereas, low to moderate effects were observed for days to 50 per cent flowering, plant height and seeds per single pod.

Highest positive direct on seed yield was recorded for pods per plant in a study conducted by Tabasum *et al.* (2010). Number of primary branches exhibited positive direct and indirect effect on single plant yield via secondary branches, plant height, number of clusters per plant, pods per cluster, pod length and 100 grain weight.

Kumar *et al.* (2013) disclosed positive direct effect of yield with number of secondary branches, bunches per plant, pod number, seeds per pod, pod length and

100 seed weight. They observed a residual effect of less than 0.5000 in the analysis and suggested the influence of some more traits other than those included in their study.

In green gram, the existence of high positive direct effect on yield per plant by characters like seeds per pod, pod length, 50 per cent pod formation and 100 seed weight was observed by Nand and Anuradha (2013).

In a study, Patel (2014) reported the highest path coefficient for grains per pod (0.6420) followed by pods per cluster (0.4320) positive direct on yield. Plant height and protein content had a negative direct effect on yield.

According to Das and Barua (2015), a positive direct effect was recorded for seed per pod (0.6920) on yield followed by 100 seed weight (0.6780).

Path coefficient analysis of highly correlated characters performed by Muralidhara *et al.* (2015) in segregating populations of cross BL 865 x Chinamung revealed the highest positive direct effect on yield by pod yield per plant followed by number of pods and threshing percentage. Indirect effect on seed yield was highest for plant height via per plant pod yield.

Path analysis by Baisakh *et al.* (2016) indicated that pod per plant (0.5947) has the high direct positive effect on seed whereas the effect was negative for days to 50 per cent flowering at phenotypic level. The study conducted states that, major parameters influencing yield has been covered as the residual effect was low in magnitude.

According to Gowsalya *et al.* (2016), pods per plant showed the highest positive direct effect (0.6841) on yield followed by seeds per pod in black gram. Days to maturity and number of clusters exhibited a negative direct effect on yield. They suggested that for the selection of genotypes, emphasis should be given for traits like pods per plant and seed per pod.

Sohel *et al.* (2016) reported that plant height and test weight exhibit negative direct on seed yield in black gram. The positive direct effect on grain yield was observed for biomass, pod number and seeds per plant.

The highest positive direct effect of biological yield per plant on grain yield followed by harvest index, number of pods per plant and plant height was reported by Choudhary *et al.* (2017) in a path coefficient analysis using eighteen F_5 progenies and their parents.

Path coefficient analysis of thirty green gram genotypes by Garg *et al.* (2017) revealed that, harvest index (0.6741) showed maximum positive direct effect on yield followed by biological yield per plant. It also exhibited positive indirect effect through pod number, number of branches, 100 seed weight and pod length on seed yield. The direct effect of plant height was negative on yield.

Reddy (2017) reported that, pods per clusters (0.2800) showed the high positive direct effect on yield followed by harvest index (0.2760) and test weight (0.2710). High magnitude of negative direct effect on yield was recorded by number of secondary branches and days to maturity.

Keerthiga *et al.* (2018) performed path coefficient analysis in two segregating population and concluded that two quantitative characters *viz.*, plant height and 100 seed weight possess high positive and direct association with seed yield in the cross Meha x GJM 1008. Whereas, in the cross, Meha x GJM 1006 plant height and seeds per pod exhibited high positive direct correlation on yield.

Low direct contribution of days to 50 per cent flowering (0.1250) and test weight (0.1320) on seed yield was reported by Mathivathana *et al*. (2018) based on the experiment in 108 recombinant lines derived from an interspecific cross of *Vigna radiata* x *Vigna umbellata*. Plant height exhibited a positive low indirect effect (0.1070) through pods per plant on grain yield.

Parihar *et al.* (2018) reported that characters like days to 50 per cent flowering, number of primary and secondary branches, 100 seed weight and seeds per pod showed a positive direct effect on seed yield, whereas plant height, number of pods and days to maturity had direct and negative effects.

According to Ramakrishnan *et al*. (2018), path analysis in green gram genotypes revealed strong positive direct association of grain yield per plant with pod yield, pods per plant, threshing percentage and clusters per plant.

Muthuswamy *et al.* (2019) conducted a path coefficient analysis in hundred green gram genotypes. They reported that positive direct effect on seed yield was contributed by pods per plant and test weight. Characters like number of clusters and pods per cluster showed positive but indirect effect via number of pods per plant on yield. The association of number of branches was negative with grain yield and may cause ineffective selection as per the results.

The path coefficients of 110 indigenous genotypes were studied by Sneha *et al*. (2019) and concluded that pod number showed a high positive and direct effect on seed yield among all the characters while number of seeds per pod had a moderate direct effect.

2.6. Effect of Shade

In green gram, optimum leaf area growth was observed under 50 per cent light condition by Nomoto *et al.* (1961). A reduction in leaf area was noticed with increase in shade level. The study revealed a reduction in relative growth rate, plant weight and leaf dry weight with a decrease in light intensity whereas leaf area ratio tends to increase with shade level.

An increment in plant height, chlorophyll content, dry matter content and leaf area index with shade was observed in black gram by Lakshmamma and Rao (1996). They also noticed a hike in nitrogen and protein content in urd seeds but the increase was non-significant. The seed yield showed a steady decrease with increase in shade levels.

An experiment to assess the effect of shade on phenology conducted by Singh and Alam (2010) revealed that plants under open and different shade regimes showed successful germination ranging from 93.00 to 100.00 per cent and the process was faster under shade condition. They observed a mere delay in flowering with increase in shade intensity.

Araki *et al.* (2014) studied the impact of shading on growth and photosynthetic efficiency in green gram. They reported that plants under shade treatment showed an increased amount of chlorophyll content per unit leaf area than those under control in a majority of genotypes. Values of specific leaf area also showed a similar trend while it was reverse for total dry weight.

Yield and leaf characteristics under 25.00, 50.00 per cent shade and completely open condition were assessed by Hossain *et al.* (2017) in four varieties of green gram. The study states that, a constant increment in plant height and seeds per pod was observed with reduced light intensities irrespective of the genotype. Leaf area exhibited a similar trend forty days after sowing. The impact of shade on yield, test weight and specific dry weight was not uniform with varietal differences while treatment BU Mug-4 showed reduction for all the three traits with falling light intensities. They also recorded a drop in leaf thickness, number of leaves and pods per plant with increasing shade levels.

According to Bhusara *et al.* (2018), the performance of green gram in terms of growth and reproductive parameters such as plant height, number of branches, leaves, flowers and pods were low under intercropping in a *Melia composita* plantation than open condition. They could observe an increase in yield with wider spacing suggesting a scope for intercropping and crop intensification.

A significant effect of shade on different morphological characters was observed by Masaku *et al.* (2018) in the evaluation of four green gram genotypes under short and long rainy seasons. An increment in plant height and pod length was exhibited by accessions under long rain condition while seed number per pod was high in short rain condition.

Materials and Methods

3. MATERIALS AND METHODS

The present investigation entitled "Genetic analysis in green gram (*Vigna radiata* (L.) Wilczek)" was carried out at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2018-2020. The study was aimed to assess the existing genetic variability among different genotypes and their performance under open and partially shaded condition to identify the best genotype in terms of yield and protein content.

3.1. MATERIALS

The experimental material comprised of 30 different green gram (*Vigna radiata* (L.) Wilczek) genotypes (Table 1) procured from University of Agriculture and Horticulture Sciences, Shivamogga, Agricultural Research Station, Amadalavalasa, Srikakulam, Andhra Pradesh, Tamil Nadu Agricultural University, Coimbatore and National Bureau of Plant Generic Resources, New Delhi. Individual genotypes were considered as different treatments.

3.2. METHODS

3.2.1. Location

The experiments were conducted at College of Agriculture, Vellayani located 29m above the mean sea level with 8˚5' N latitude and 76˚9'E longitude. Vellayani series red loam which is texturally classified as the sandy clay loam was the major soil type in the experimental area.

3.2.2. Season

Two simultaneous field experiments were conducted under open and partially shaded condition from September 2019 to January 2020.

3.2.3. Planting material

Seeds were used as the planting material. Seeds were dibbled on raised beds at a spacing of 30 cm between rows and 15 cm between plants.

Table 1. List of green gram (*Vigna radiata* (L.) Wilczek) genotypes used for the study

Treatment	Genotype	Location
T1	K1	UAHS, Shivamogga
T2	K4	UAHS, Shivamogga
T3	K7	UAHS, Shivamogga
T4	K6	UAHS, Shivamogga
T5	K13	UAHS, Shivamogga
T6	KKM-3	UAHS, Shivamogga
T7	MLS	UAHS, Shivamogga
T8	BGS -9	UAHS, Shivamogga
T9	K10	UAHS, Shivamogga
T10	Km-17-195	ARS, Andhra Pradesh
T11	Km-17-199	ARS, Andhra Pradesh
T12	Km-17-176	ARS, Andhra Pradesh
T13	Km-17-193	ARS, Andhra Pradesh
T14	Km-17-200	ARS, Andhra Pradesh
T15	Km-17-205	ARS, Andhra Pradesh
T16	LGG 644	ARS, Andhra Pradesh
T17	LGG 607	ARS, Andhra Pradesh
T18	LGG 630	ARS, Andhra Pradesh
T19	LGG 460	ARS, Andhra Pradesh
T20	LGG 450	ARS, Andhra Pradesh
T21	WGG 42	ARS, Andhra Pradesh
T22	GGG 1	ARS, Andhra Pradesh
T23	Ipm 2-14	ARS, Andhra Pradesh
T24	Tm 96-2	ARS, Andhra Pradesh
T25	CO 8	TNAU, Coimbatore
T26	MH 421	NBPGR, New Delhi
T27	EC 396399	NBPGR, New Delhi
T28	IC 282124	NBPGR, New Delhi
T29	IC 488841	NBPGR, New Delhi
T30	EC 398900	NBPGR, New Delhi

3.2.4. Layout of the experiment

Experiment I: Under open condition.

Season : August - October, 2019
Design : RBD
Treatments : 30
Replications : 3
Spacing : 30 cm X 15 cm
Plot size : (1.5 X 1.5) m^2

Experiment II: Under partially shaded condition.

The field experiment was conducted in a coconut garden with 57 per cent shade.

Season : August - October, 2019
Design : RBD
Treatments : 30
Replications : 3
Spacing : 30 cm X 15 cm
Plot size : (1.5 X 1.5) m^2

A population of forty-five plants was maintained in the individual experimental plot. The plants were grown by following the management practices as per the package of practices of Kerala Agricultural University.

3.3. Main items of observations

Five competitive plants were selected at random from each experimental plot and tagged as observation plants to take biometrical observations. The mean value was worked out for further statistical analysis.

3.3.1. Biometrical observations

3.3.1.1. Emergence percentage

The ratio of emerged seeds to the total number of seeds sown per plot was calculated and recorded.

3.3.1.2. Number of primary branches/ plant

The number of branches on the main stem from ground level was counted for individual plant at maturity and expressed in numbers.

3.3.1.3. Number of secondary branches /plant

The number of secondary branches on the primary branches was counted for individual plant at maturity and expressed in numbers.

3.3.1.4. Number of days for blooming

Total number of days taken from sowing to the appearance of the first flower in the plot was recorded.

3.3.1.5. Days to 50% flowering

Total number of days from sowing to blooming in 50 per cent plants in the plot was observed and recorded.

3.3.1.6. Days to maturity

The total number of days taken from the date of sowing to physiological maturity was recorded.

3.3.1.7. Number of pods /plant

Total number of matured pods harvested from the observational plants was counted and the mean value was recorded.

3.3.1.8. Number of seeds /pod

Five pods were selected at random and shelled to count the number of seeds and the mean value was calculated.

3.3.1.9. Number of abnormal, unfilled pods /plant

Total number of shrunken, unfilled and damaged pods from the observational plants was counted and calculated the mean value.

3.3.1.10. Pod length (cm)

Five pods were selected at random to measure the length and the mean value was calculated and expressed in centimeter.

3.3.1.11. Yield/ plant (g)

Total grain yield from the observation plants was weighed and the mean value was recorded.

3.3.1.12. 100 seed weight (g)

Hundred well dried seeds were counted at random, weighed and the weight was recorded in grams.

3.3.1.13. Plant height (cm)

The plant height was measured from the base to the tip using a meter scale at the time of the final harvest.

3.3.1.14. Harvest Index

$$\mathrm{HI}=\frac{\text{Economic yield}}{\text{Biological yield}}$$

Harvest index was calculated as the ratio of economic yield to the total biomass produced per plant.

3.3.1.15. Number of harvest

The total number of harvests from experimental plot was counted and recorded.

3.3.1.16. Incidence of pest and diseases

Very few pests and pathogen attack was observed in the field for which control measures were taken up.

3.3.1.17. Protein content (%)

The Nitrogen content in the seed samples was estimated by conventional Kjeldahl method (Mckenzie and Wallace, 1954) and the protein content was calculated by multiplying it with factor 6.25.

3.3.1.18. Specific leaf area (cm^2/g)

Specific leaf area was calculated as the ratio of leaf area to the dry weight. The leaf area was measured by the graphical method.

3.3.1.19. Light intensity ($\mu molm^{-2}s^{-1}$)

The light intensity was recorded at random points in the field using a light meter at 12 pm. The average was worked out and recorded.

3.3.1.20. Chlorophyll content (mg/g)

Chlorophyll content was estimated by DMSO- acetone extraction method. 500mg fresh leaf sample was taken and cut into small pieces. 10ml 1:1 DMSO: 80 per cent acetone mixture was added to this and incubated overnight. Absorbance was measured using a spectrophotometer at 645, 663nm. The third leaf from the top was used for the estimation at the flowering stage.

$$\text{Total chlorophyll} = [(8.02 \times A_{663}) + (20.2 \times A_{645})] \times \frac{V}{1000 \times W}$$

Where, A_{663}, A_{645}- absorbance at 663, 645 nm respectively, V- volume, W- weight of leaf sample

3.4. STATISTICAL ANALYSIS

The analysis of variance for each character was calculated for both experiments. A pooled analysis was also conducted to compare the performance of genotypes for each character in open and partially shaded conditions.

3.4.1. Analysis of Variance

Replicated data was used to perform the analysis of variance to identify variations occurring within and between the genotypes. As reported by Panse and Sukhatme in 1967, Critical Difference (CD) values were calculated using “per replication mean value” of each treatment which is used to assess the difference between genotypes.

Sources of variation	**d.f**	**Sum of squares**	**Mean squares**	**F ratio**
Treatment	t-1	SSR	MSR	MSR/MSE
Replications	r-1	SST	MST	MST/MSE
Error	(t-1)(r-1)	SSE	MSE	
Total	rt-1			

Where,

r = number of replications

t = number of treatments

SSR= sum of squares for replication

SST= sum of squares for treatments

SSE= sum of squares for error

Critical Difference, $CD= t\alpha\sqrt{\frac{2MSE}{r}}$

Where, tα is students’ t table value distribution at error d.f with level of significance α (5% or 1%).

3.4.2. Estimation of Genetic Parameters

a. Components of Variance

The components of variance *viz.* genotypic, phenotypic and environmental components were determined by equating the expected mean square values with components of respective variance as suggested by Jain (1982) for each trait.

Genotypic Variance (VG) = $\frac{\text{MST-MSE}}{r}$

Environmental Variance (VE) = MSE

Phenotypic Variance (VP) = VG + VE

b. Coefficient of Variation

Genotypic, phenotypic and environmental components of variation were used to estimate the respective coefficient of variation for each character and expressed in percentage.

i. Genotypic coefficient of variation, GCV $= \frac{\sqrt{VG}}{X} \times 100$

ii. Phenotypic coefficient of variation, PCV $= \frac{\sqrt{VP}}{X} \times 100$

iii. Environmental coefficient of variation, ECV $= \frac{\sqrt{VE}}{X} \times 100$

Where, X = Grand mean

Classification of range of variation according to the scale made by Sivasubramanian and Menon (1973):

Category	**Range**
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

c. Heritability (broad sense)

Heritability in the broad sense can be estimated using the formula given by Burton (1952) and Johnson *et al*. (1955) as the ratio of genotypic variance to the phenotypic variance and expressed in per cent. It indicates the genetic contribution to the total phenotypic expression of a character.

$$H^2 = \frac{VG}{VP} \times 100$$

Classification of range of Heritability estimation as reported by Johnson *et al*. (1955)

Category	**Range**
Low	0-30%
Medium	30-60%
High	More than 60%

d. Genetic Advance

Genetic advance gives a measure of expected genetic gain or improvement that can be achieved in the succeeding generation by selecting a superior genotype. Genetic advance was computed by using the formula proposed by Johnson *et al*. (1955).

$$GA = KH^2\sqrt{V_p}$$

Where, K= selection differential, at 5% selection intensity

K = 2.06

H^2 = Heritability

Vp = Phenotypic variance

e. Genetic Advance as Percent of Mean

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

Where, GA= Genetic Advance

X= Grand Mean

Classification of the ranges of genetic advance as suggested by Johnson *et al.* (1955).

Category	**Range**
Low	Less than 10%
Medium	10-20%
High	More than 20%

3.4.3. Estimation of Correlation

Correlation coefficient is the statistical measure which indicates the degree and direction of association between two variables. Phenotypic, genotypic and environmental coefficients of correlation were calculated using the formula proposed by Falconer (1964) following analysis of covariance with all possible paired combinations among the characters.

Genotypic coefficient of correlation (r_g) $= r(xi.xj)_g = \dfrac{Cov(xi.xj)g}{\sqrt{v(xi)g.v(xj)g}}$

Phenotypic coefficient of correlation (r_p) $= r(xi.xj)_p = \dfrac{Cov(xi.xj)p}{\sqrt{v(xi)p.v(xj)p}}$

Error coefficient of correlation (r_e) $= r(xi.xj)_e = \dfrac{Cov(xi.xj)e}{\sqrt{v(xi)e.v(xj)e}}$

3.4.4. Path Coefficient Analysis

Path coefficient is a standardized partial regression coefficient that separates the correlation coefficients into direct and indirect effects (Dewey and Lu, 1959). It measures the cause of the association between two characters. Hence can be used to compute the direct and indirect effects of component characters on yield as suggested by Wright (1954).

$$r_{1y} = P_{1y}\, r_{11}+P_{2y}r_{12}+P_{3y}r_{13}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{1n}$$

$$r_{2y} = P_{2y}\, r_{21}+P_{2y}r_{22}+P_{3y}r_{23}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{2n}$$

$$r_{ny} = P_{1y}\, r_{n1}+P_{2y}r_{n2}+P_{3y}r_{n3}\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots+P_{ny}r_{nn}$$

Where,

1, 2…………..n = independent variables

y = dependent variable

r_{1y}, r_{2y}………r_{ny} = coefficient of correlation between independent variables 1 to n on dependent variable y.

P_{1y}, P_{2y}…….P_{ny} = direct effect of character 1 to n on character y.

In the matrix form

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ \vdots \\ \vdots \\ \vdots \\ r_{ny} \end{bmatrix} \begin{bmatrix} 1 & r_{12} & r_{13} & \cdots & \cdots & r_{1n} \\ r_{21} & 1 & r_{23} & \cdots & \cdots & r_{2n} \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ r_{n1} & r_{n2} & r_{n3} & \cdots & \cdots & 1 \end{bmatrix} \begin{bmatrix} p_{1y} \\ p_{2y} \\ \vdots \\ \vdots \\ \vdots \\ p_{ny} \end{bmatrix}$$

Then B=C^{-1}A, where C^{-1}= $\begin{bmatrix} C_{11} & C_{12} & C_{13} & \cdots & \cdots & C_{1n} \\ C_{21} & C_{22} & C_{23} & \cdots & \cdots & C_{2n} \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ \vdots & \cdots & \cdots & \cdots & \cdots & \vdots \\ C_{n1} & C_{n2} & C_{n3} & \cdots & \cdots & C_{nn} \end{bmatrix}$

Direct effects:

$P_{1i}= \sum_{i=1}^{k} C_{1i}.r_{iy}$

$P_{2i}= \sum_{i=1}^{k} C_{2i}.r_{iy}$

$P_{ni}= \sum_{i=1}^{k} C_{ni}.r_{iy}$

Residual effect, PRy= $\sqrt{1-r^2}$

Where,

$r^2 = (P_{1y}r_{1y}+ P_{2y}r_{2y}+P_{3y}r_{3y}……………………+P_{ny}r_{ny})$

P_{iy}= direct effect of x_i on y

r_{iy}= correlation coefficient of x_i on y

i = 1, 2, 3…..n

The direct and indirect effects were classified as per Lenka and Mishra (1973) given below,

Path coefficient	**Category**
0.00-0.09	Negligible
0.10-0.19	Low
0.20-0.29	Moderate
0.30-1.00	High
> 1.0	Very high

Results

4. RESULTS

The results obtained from statistical analysis of data of various morphological, biometrical and biochemical traits obtained from the research work entitled "Genetic analysis in green gram [*Vigna radiata* (L.) Wilczek] " are presented below:

4.1. EVALUATION OF GREEN GRAM GENOTYPES

4.1.1. Light intensity

The average value of light intensity in the partially shaded experimental field was 3.28 μmolm^{-2}s^{-1}.

4.1.2. Variability

Evaluation of thirty genotypes of green gram was carried out for different characters under open and partially shaded conditions. The data collected for each trait was analyzed using analysis of variance technique. A pooled analysis was also carried out to compare the performance of the genotypes under both growing conditions.

4.1.2.1. Variability in Emergence Percentage:

The data on emergence percentage of green gram genotypes under open and partially shaded conditions are presented in Table 2.

Under open condition, highest emergence percentage was recorded for the genotype T21 (98.52) which was on par with T18 (97.04), T23 (96.67), T22 (94.07), T6 (93.85), T13 (93.19), T5 (91.85) and T7 (91.85). The least value for emergence percentage was registered for T11 (81.67) and which was on par with all other Genotypes. Under partially shaded condition, emergence percentage was non-significant and recorded from 85.88 to 98.48 per cent for all thirty genotypes. In pooled analysis, Genotypes T18 (97.65) exhibited the highest emergence percentage which was on par with other genotypes like T23 (97.51), T21 (97.20), T22 (96.37), T13 (94.46), T14 (93.94), T5 (93.42), T3 (93.19), T7 (93.05), T25 (92.87), T6 (92.70), T24 (92.63), T12 (92.41), T28 (92.09) and T16 (91.67) whereas, the value was least for T2 (84.63). The results also showed that there was no significant interaction between the genotypes and condition for emergence percentage. The genotypes showed higher emergence under partial shade than open condition.

4.1.2.2. Variability in number of primary branches/ plant:

From Table 3 it is evident that, the highest number of primary branches/plant was recorded by genotype T5 in partially shaded condition as well as in pooled analysis. Under open condition, the performance of the genotype T4 (6.40) was on par with T5 (6.31) whereas T26, T21 and T12 produced the least number of primary branches (2.17) and which was on par with other genotypes like T7 (2.20), T2 (2.23), T9 (2.26), T27 (2.33), T25 (2.33), T14 (2.5), T13 (2.50), T10 (2.62), T16 (2.67), T29 (2.74), T11 (2.98), T20 (3.03), T17 (3.10), T1 (3.10) and T22 (3.17).

Under partially shaded condition, T5 (4.11) was on par with T4 (3.89) and T15 (3.61) and the number of primary branches was least for T22 (1.55) which was on par with genotypesT28 (1.62), T29 (1.67), T21 (1.78), T25 (1.88), T24 (1.92), T30 (2.00), T10, T7, T3, T20 (2.02), T13 (2.03) and T12 (2.03). In pooled analysis, T5 (5.21) exhibited the highest number and was significantly different from other genotypes except T4 (5.15) while, less number of primary branches was produced by T21 (1.98) which was on par with all other genotypes.

The genotypes exhibited significant difference in their performance over both conditions and the branch number was more in open than partially shaded condition. The interaction between genotypes and condition was significant for number of primary branches.

4.1.2.3. Variability in number of secondary branches/ plant:

Variability in number of secondary branches in green gram genotypes under open and partially shaded conditions is presented in Table 4. Highest number of secondary branches was produced by genotype T10 in open condition as well as in pooled analysis.

1a. Open condition

1b. Partial shade condition

Plate 1: General field view

While genotypes T4, T24 and T27 produced less secondary branching under both conditions and in pooled analysis. The interaction between genotypes with condition was also significant for the character.

Under open condition, most number of secondary branches was noticed in the genotype T10 (3.11) followed by T8 (2.33) which was on par with T5 (2.23), T20 (2.19) and T25 (1.83). The genotype T20 (1.65) produced the highest number of secondary branches under partially shaded condition which was on par with T8 (1.61) and T10 (1.58). In pooled analysis, performance of genotype T10 (2.35) with highest number of secondary branches was on par with T8 (1.97), T20 (1.92) and T5 (1.74), whereas the least number was observed for T4 (1.00), T24 (1.00) and T27 (1.00) which were on par with all other genotypes.

4.1.2.4. Variability in Number of Days for Blooming:

The observations on number of days taken for blooming in green gram genotypes are depicted in Table 5.

Number of days for blooming showed significant difference under open and partially shaded conditions and the interaction between genotypes and the conditions was significant. Genotypes T21 (36.00) and T30 (36.00) took less number of days for blooming while T4 (42.33) took more days to produce flowers under open condition and was on par with T17 (41.33) and T14 (40.33). Under partially shaded condition, the early flowering was observed in the genotype T26 (33.00) which was on par with T11 (35.00), T16 (35.33) and T22 (35.67) likewise, T2 (43.33) was in blooming. Flowering in genotypes T1 (43.00), T24 (43.00), T4 (42.67), T7 (42.33), T3 (42.00), T14 (42.00) and T29 (41.33) were on par with T2.

In pooled analysis, the genotype T26 (34.67) produced flowers at earliest and blooming was most delayed in T4 (42.50). In general, the plants showed a delay in flowering under partially shaded condition compared to open in most of the genotypes.

4.1.2.5. Variability in days to fifty per cent flowering:

There was significant difference among genotypes under the two different conditions in the duration taken to flower (Table 6). Under open condition, the genotype T19 took least number of days for blooming in fifty per cent plants (39.33) and which was on par with other genotypes like T10 (40.33), T12 (41.00), T12 (41.33), T15 (41.33), T11 (41.33), T6 (41.33), T22 (41.67), T26 (42.00), T24 (42.00) and T13 (42.00), whereas genotype T4 (47.67) recorded more days for attaining 50 per cent flowering on par with genotypes T5 (46.67), T2 (46.00), T17 (45.33).

Under partially shaded condition, the genotype T26 (37.67) took least days for 50 per cent flowering which was on par with T13 (38.00), T23 (40.67) and T6 (41.00), whereas more days for T30 (51.00). From the Table 6 it is clear that, most of the genotypes took more days to attain 50 per cent flowering in partially shaded condition than open condition. Results of pooled analysis revealed the existence of a significant interaction between genotypes and growing conditions for days to fifty per cent flowering.

4.1.2.6. Variability in days to maturity:

The result showing variation in days to maturity is presented in Table 7. Number of days to maturity exhibited a significant difference under open and partially shaded conditions but there was no significant interaction between the genotype and the conditions. Under open condition, the genotype T6 (68.33) took less days to attain maturity on par with T13 (68.67), T12 (69.33), T26 (70.33), T14 (71.00), T17 (71.33), T7 (72.33), T27 (72.33) and T15 (74.33), while early maturity was observed for the genotype T13 (65.33 and 67, respectively) under partially shaded condition as well as in pooled analysis. More number of days to maturity was exhibited by genotype T23 (94.67) under open condition and by genotype T22 (92.33) under shaded conditions. In pooled analysis, T22 (92.00) took highest number of days to attain maturity which was on par with genotypes like T20 (91.50), T23 (91.33), T5 (90.17) and T21 (88.50).

Table 2. Emergence percentage (%) of thirty green gram genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	88.28 (70.24)	91.66 (73.67)	89.97 (71.95)
T2	82.51 (65.28)	87.00 (68.94)	84.76 (67.11)
T3	89.08 (73.13)	96.57 (80.45)	92.83 (76.79)
T4	90.74 (72.38)	94.08 (76.31)	92.41 (74.34)
T5	91.85 (75.69)	93.46 (78.08)	92.66 (76.88)
T6	93.85 (77.61)	92.99 (74.72)	93.42 (76.17)
T7	91.85 (75.46)	94.53 (77.11)	93.19 (76.29)
T8	88.52 (70.26)	93.87 (77.40)	91.19 (73.83)
T9	88.15 (69.95)	91.49 (73.18)	89.82 (71.57)
T10	82.22 (65.17)	87.97 (69.85)	85.10 (67.51)
T11	81.67 (64.79)	92.22 (74.25)	86.95 (69.52)
T12	85.56 (67.73)	97.59 (82.99)	91.57 (75.36)
T13	93.19 (77.08)	95.74 (78.56)	94.46 (77.82)
T14	90.78 (72.80)	96.92 (82.27)	93.85 (77.54)
T15	82.96 (65.74)	86.29 (68.54)	84.63 (67.14)
T16	88.35 (70.11)	94.15 (79.86)	91.25 (74.98)
T17	83.97 (66.78)	89.26 (71.61)	86.62 (69.20)
T18	97.04 (82.20)	97.80 (83.24)	97.42 (82.72)
T19	87.49 (71.91)	92.39 (76.85)	89.94 (74.38)
T20	86.89 (69.94)	92.92 (75.69)	89.91 (72.82)
T21	98.52 (83.92)	96.69 (80.56)	97.61 (82.24)
T22	94.07 (77.51)	98.48 (84.13)	96.28 (80.82)
T23	96.67 (81.83)	97.55 (82.94)	97.11 (82.39)
T24	87.37 (69.48)	96.63 (81.97)	92.00 (75.73)
T25	89.07 (70.75)	96.10 (81.75)	92.59 (76.25)
T26	84.90 (67.15)	87.52 (69.57)	86.21 (68.36)
T27	86.87 (68.87)	85.88 (68.10)	86.37 (68.49)
T28	91.35 (72.90)	94.75 (77.82)	93.05 (75.36)
T29	87.78 (69.60)	88.27 (70.50)	88.03 (70.05)
T30	83.58 (66.16)	93.78 (75.66)	88.68 (70.91)
Mean	88.84 (71.75)	93.15 (76.55)	90.99 (74.15)
SE (m)	3.72	3.93	2.71
CD Genotype	10.56	NS	8.11
CD Open X Shade	2.46		
CD Genotype X Condition	NS		

- (Transformed data)

4.1.2.7. Variability in number of pods/ plant:

The observations on number of pods produced by green gram genotypes under open and partially shaded condition are presented in the Table 8.

The genotypes differed significantly under open and partially shaded conditions for this trait and there existed a significant interaction between genotypes and conditions. The number of pods per plant was highest for the genotype T28 (39.90) under open conditions and this was significantly different from all other genotypes followed by genotypes T30 (34.04). Under partially shaded conditions, genotype T19 (40.62) produced more number of pods per plant followed by genotypes T28 (33.85) and this was on par with T9 (30.46) and T8 (30.09), whereas minimum number of pods were produced by T1 (13.03).

The genotype T28 (36.88) produced the highest number of pods in the pooled analysis which was on par with T19 (35.06), T8 (30.96), T9 (29.56), T30 (28.5), T3 (26.98) and T23 (26.58), whereas the less production was observed in T27 (12.94) which was on par with other genotypes except T21 (24.35).

4.1.2.8. Variability in number of seeds/ pod:

According to Table 9, the character showed significant difference in both conditions along with a significant interaction. The number of seeds per pod was noticed to be high for genotype T6 both open (12.70) and partially shaded (13.28) conditions. Likewise, minimum number of seeds per pod was exhibited by the genotype T2 (10.2) under open condition and this was on par with T25 (10.37), T14 (10.70), T5 (10.73), T28 (11.10), T27 (11.27), T3 (11.27), T16 (11.30), T4 (11.40) and T8 (11.5), whereas less seeds per pod in partially shaded condition was recorded for T24 (8.68). The performance of genotypes T27 (8.82), T7 (9.61), T26 (9.65) and T15 (10.04) were on par with T24.

4.1.2.9. Variability in number of abnormal, unfilled pods / plant:

The genotype T27 (1.15) recorded least number of abnormal pods under open condition and its performance was on par with other genotypes like T21 (2.01), T2 (1.95), T29 (1.92), T6 (1.82), T24 (1.80), T15 (1.77), T22 (1.72), T9 (1.67), T23 (1.55) and T11 (1.22). Number of abnormal pods was more in T14 (4.01) which was on par with genotypes like T20 (3.66), T13 (3.5), T18 (3.45), T25 (3.29) and T28 (3.09). Under shaded condition, the least value for abnormal pod formation was observed for T26 (1.27) and was on par with other five genotypes *viz.*, T16 (1.28), T8 (1.36), T13 (1.77), T10 (2.02) and T27 (2.03). The highest number was recorded for T20 (4.87). T23 (4.77), T18 (4.72), T3 (4.59), T5 (4.07), T12 (4.05), T9 (3.97) and T15 (3.97) were on par with T20 in their performance.

The pooled analysis revealed the existence of a significant interaction between genotypes and condition for number of abnormal pods per plant even though the performance of genotypes was non-significant (Table 10). Overall, it was noticed that number of abnormal, unfilled pods per plant under shaded condition was more than open condition.

4.1.2.10. Variability in pod length:

The results of pooled analysis in Table 11 showed that there was no significant interaction between the genotypes and condition for the length. The longest pod was observed for T8 under both growing conditions as well as in pooled analysis.

Under open condition, highest pod length was recorded for the genotype T8 (9.39) which was on par with T19 (8.67), T11 (8.58), T21 (8.37), T10 (8.36), T15 (8.18) and T20 (8.12), whereas the pod length was least for T25 (6.08). The same genotype, T8 (9.39) produced longer pods under partially shaded condition which significantly differed from genotypes other than T21 (8.75), T10 (8.65) and T5 (8.37) while shorter pods were produced by the genotype T23 (5.82).

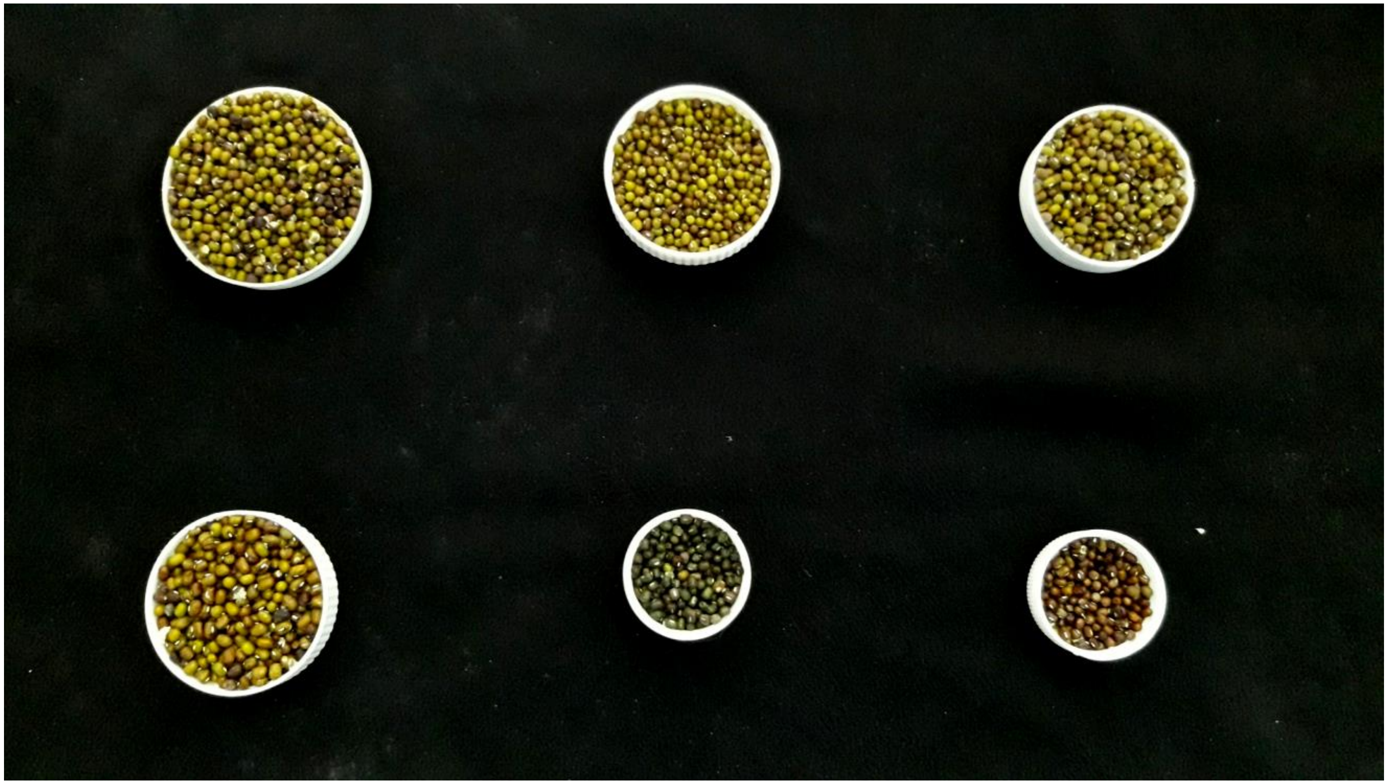


Plate 2. Variability in seed size and colour

Table 3. Number of primary branches of thirty green gram genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	3.10	2.58	2.84
T2	2.23	2.24	2.24
T3	4.83	2.00	3.42
T4	6.40	3.89	5.15
T5	6.31	4.11	5.21
T6	4.04	2.34	3.19
T7	2.20	2.00	2.10
T8	3.58	2.33	2.96
T9	2.26	2.26	2.26
T10	2.62	2.00	2.31
T11	2.98	2.67	2.82
T12	2.17	2.03	2.10
T13	2.50	2.03	2.27
T14	2.50	2.21	2.36
T15	3.33	3.61	3.47
T16	2.67	2.50	2.58
T17	3.10	2.49	2.80
T18	3.33	2.82	3.08
T19	3.28	2.33	2.81
T20	3.03	2.02	2.53
T21	2.17	1.78	1.98
T22	3.17	1.53	2.35
T23	3.39	3.02	3.21
T24	3.33	1.92	2.63
T25	2.33	1.88	2.11
T26	2.17	2.33	2.25
T27	2.33	2.67	2.50
T28	4.12	1.62	2.87
T29	2.74	1.67	2.20
T30	3.31	2.00	2.66
Mean	3.18	2.36	2.77
SE (m)	0.37	0.20	0.21
CD Genotype	1.05	0.56	1.60
CD Open X Shade	0.13		
CD Genotype X Condition	1.10		

Table 4. Number of secondary branches per plant of thirty green gram genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	1.76	1.07	1.42
T2	1.32	1.03	1.18
T3	1.40	1.20	1.30
T4	1.00	1.00	1.00
T5	2.23	1.26	1.74
T6	1.00	1.13	1.07
T7	1.52	1.36	1.44
T8	2.33	1.61	1.97
T9	1.29	1.03	1.16
T10	3.11	1.58	2.35
T11	1.30	1.06	1.18
T12	1.03	1.00	1.02
T13	1.57	1.12	1.34
T14	1.38	1.26	1.32
T15	1.27	1.20	1.24
T16	1.23	1.00	1.12
T17	1.07	1.08	1.08
T18	1.25	1.10	1.18
T19	1.33	1.00	1.17
T20	2.19	1.65	1.92
T21	1.50	1.22	1.36
T22	1.42	1.10	1.26
T23	1.40	1.09	1.25
T24	1.00	1.00	1.00
T25	1.83	1.09	1.46
T26	1.57	1.41	1.49
T27	1.00	1.00	1.00
T28	1.63	1.10	1.37
T29	1.43	1.07	1.25
T30	1.48	1.07	1.28
Mean	1.50	1.16	1.33
SE (m)	0.20	0.08	0.11
CD Genotype	0.56	0.23	0.63
CD Open X Shade	0.11		
CD Genotype X Condition	0.56		

Table 5. Number of days for blooming of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	39.67	43.00	41.33
T2	39.33	43.33	41.33
T3	37.00	42.00	39.50
T4	42.33	42.67	42.50
T5	36.67	39.00	37.83
T6	36.33	36.00	36.17
T7	36.67	42.33	39.50
T8	37.33	38.00	37.67
T9	38.00	39.33	38.67
T10	36.33	39.33	37.83
T11	37.00	35.00	36.00
T12	37.67	37.67	37.67
T13	36.33	37.33	36.83
T14	40.33	42.00	41.17
T15	36.33	36.33	36.33
T16	38.33	35.33	36.83
T17	41.33	42.33	41.83
T18	37.00	40.33	38.67
T19	36.33	38.33	37.33
T20	38.33	39.00	38.67
T21	36.00	36.00	36.00
T22	36.33	35.67	36.00
T23	37.00	36.67	36.83
T24	39.33	43.00	41.17
T25	39.00	39.67	39.33
T26	36.33	33.00	34.67
T27	37.00	38.67	37.83
T28	36.33	37.00	36.67
T29	39.67	41.33	40.50
T30	36.00	37.00	36.50
Mean	37.72	38.89	38.31
SE (m)	0.75	0.97	0.62
CD Genotype	2.14	2.76	3.86
CD Open X Shade	1.03		
CD Genotype X Condition	3.22		

Table 6. Days to fifty per cent flowering of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	43.67	48.33	46.00
T2	46.00	46.67	46.33
T3	44.00	44.67	44.33
T4	47.67	47.00	47.33
T5	46.67	42.67	44.67
T6	41.33	41.00	41.17
T7	44.00	48.00	46.00
T8	43.33	43.00	43.17
T9	44.00	45.00	44.50
T10	40.33	46.33	43.33
T11	41.33	50.33	45.83
T12	41.00	44.67	42.83
T13	42.00	38.00	40.00
T14	43.33	45.33	44.33
T15	41.33	47.00	44.17
T16	43.00	46.33	44.67
T17	45.33	50.67	48.00
T18	42.67	45.00	43.83
T19	39.33	45.67	42.50
T20	43.00	45.67	44.33
T21	43.33	47.33	45.33
T22	41.67	43.00	42.33
T23	43.00	40.67	41.83
T24	42.00	49.67	45.83
T25	43.67	45.67	44.67
T26	42.00	37.67	39.83
T27	43.00	42.33	42.67
T28	44.00	42.67	43.33
T29	43.67	47.67	45.67
T30	41.33	51.00	46.17
Mean	43.03	45.30	44.17
SE (m)	1.14	1.32	0.87
CD Genotype	3.24	3.74	NS
CD Open X Shade	1.10		
CD Genotype X Condition	4.57		

Table 7. Days to maturity of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	75.67	76.33	76.00
T2	80.00	79.33	79.67
T3	75.00	76.33	75.67
T4	82.67	84.67	83.67
T5	89.67	90.67	90.17
T6	68.33	68.33	68.33
T7	72.33	70.00	71.17
T8	75.00	72.67	73.83
T9	77.67	79.00	78.33
T10	80.00	81.67	80.83
T11	81.33	82.00	81.67
T12	69.33	70.67	70.00
T13	68.67	65.33	67.00
T14	71.00	73.33	72.17
T15	74.33	76.33	75.33
T16	79.00	80.00	79.50
T17	71.33	71.67	71.50
T18	79.67	81.67	80.67
T19	76.00	76.67	76.33
T20	91.33	91.67	91.50
T21	88.33	88.67	88.50
T22	91.67	92.33	92.00
T23	94.67	88.00	91.33
T24	86.33	87.00	86.67
T25	75.33	76.33	75.83
T26	70.33	69.67	70.00
T27	72.33	72.00	72.17
T28	85.00	88.00	86.50
T29	79.00	78.33	78.67
T30	87.67	88.33	88.00
Mean	78.97	79.23	79.10
SE (m)	2.19	2.28	1.58
CD Genotype	6.20	6.47	3.55
CD Open X Shade	NS		
CD Genotype X Condition	NS		

Plate 3. Variability in leaves

Table 8. Number of pods/ plant of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	14.33	13.03	13.68
T2	21.11	14.57	17.84
T3	29.95	24.02	26.98
T4	12.96	16.16	14.56
T5	19.45	18.99	19.22
T6	22.80	21.35	22.07
T7	21.72	20.09	20.91
T8	31.83	30.09	30.96
T9	28.67	30.46	29.56
T10	18.35	16.98	17.67
T11	12.80	17.97	15.39
T12	24.89	20.39	22.64
T13	20.47	17.80	19.14
T14	25.54	20.34	22.94
T15	30.14	15.27	22.71
T16	19.33	26.27	22.80
T17	29.18	15.42	22.30
T18	26.64	17.84	22.24
T19	29.49	40.62	35.06
T20	18.98	24.48	21.73
T21	23.52	25.19	24.35
T22	28.04	18.71	23.38
T23	24.28	28.89	26.58
T24	12.68	14.41	13.55
T25	17.00	14.11	15.55
T26	15.68	15.51	15.60
T27	11.13	14.74	12.94
T28	39.90	33.85	36.88
T29	20.68	18.88	19.78
T30	34.09	22.91	28.50
Mean	22.85	20.98	21.92
SE (m)	1.79	1.65	1.22
CD Genotype	5.08	4.67	11.24
CD Open X Shade	1.48		
CD Genotype X Condition	6.37		

In pooled analysis, the genotype T8 (9.39) recorded the highest pod length followed by genotypes T21 (8.56), T10 (8.50) and T20 (8.05). Minimum length of pod was exhibited by the genotype T25 (6.05).

4.1.2.11. Variability in yield per plant:

The results from Table 12 revealed the existence of significant difference in the performance of green gram genotypes between open and partially shaded conditions for yield per plant and the seed production was noticed to be high in open condition compared to partial shade.

Under open condition, the performance in terms of seed yield was highest for the genotype T8 (11.80) which significantly differed from all other genotypes except T28 (10.83) followed by T3 (10.58), T9 (9.64) and T6 (9.28). Yield per plant was least for T26 (2.42) which was on par with T2 (2.79), T11 (2.84), T16 (2.88), T1 (3.21), T14 (3.32) and T25 (3.46). Under partially shaded condition, highest yield was recorded for T3 (9.26) which was on par with T8 (9.15) and T28 (8.56), whereas lowest yield was given by genotype T16 (2.29). The performance of genotypes T1 (2.50), T13 (2.55), T26 (2.60) and T11 (2.79) were on par with T16. In pooled analysis also, the genotype T8 (10.48) gave the maximum single plant yield, which was on par with other genotypes like T3 (9.92), T28 (9.70), T9 (8.68), T6 (8.36), T30 (8.06), T20 (7.86) and T10 (7.57). Minimum value for yield per plant was exhibited by the genotype T26 (2.51). The results showed that there existed significant interaction between the genotypes and the condition for seed yield per plant.

4.1.2.12. Variability in 100 seed weight:

The observations on 100 seed weight of green gram genotypes are given in Table 13.

The genotype T8 recorded the highest test weight under both growing conditions. Under open condition, the genotype T8 (5.00) significantly differed from all other genotypes except T26 (4.59) and T15 (4.58), whereas the value for test weight by genotype T8 (5.17) was on par with T27 (4.37), T21 (4.31), T10 (4.15) and T11 (4.02). Likewise, the minimum 100 seed weight was observed for T17 (2.52) in open and T29 (2.67) in partially shaded conditions.

Pooled analysis of the genotypes under the two conditions revealed that high value for 100 seed weight was shown by the genotype T8 (5.09) which perform on par with other genotypes T21 (4.31), T10 (4.22), T27 (4.20) and T11 (4.11). The least value for 100 seed weight was recorded for the genotype T17 (2.73) and this was on par with most of the genotypes included in this study and the interaction was significant for the character.

4.1.2.13. Variability in plant height:

The result of variability in plant height is depicted in the Table 14.

The character exhibited significant difference under open and partially shaded conditions and showed a significant interaction between the genotype and the conditions. From Table 14 it is clear that the plants grow longer in partially shade than open condition.

The maximum plant height was recorded by genotype T17 in pooled analysis as well as in open and partially shaded conditions. Under open condition, T17 (49.36) was on par with other genotypes like T7 (49.13), T11 (49.02), T23 (47.64), T5 (46.84), T4 (44.92), T22 (44.40), T14 (44.06), T18 (41.01) and T21 (40.87), whereas the shorter plants were observed for T26 (20.50) which was significantly different from all other genotypes followed by T19 (30.05). Under partial shade, T17 (61.85) showed highest value for plant height that was on par with T24 (56.31) and T22 (55.58) followed by genotypes T18 (50.92) and T9 (49.10) while low value for plant height for genotype T6 (29.83). In pooled analysis, taller plants were observed in genotype T17 (55.61) while shorter for T26 (25.94).

Table 9. Number of seeds/ pod of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	12.50	11.24	11.87
T2	10.20	11.30	10.75
T3	11.27	11.97	11.62
T4	11.40	11.25	11.32
T5	10.73	12.56	11.65
T6	12.70	13.28	12.99
T7	12.07	9.61	10.84
T8	11.50	11.28	11.39
T9	11.60	11.87	11.73
T10	11.80	11.20	11.50
T11	11.60	12.51	12.05
T12	12.13	10.25	11.19
T13	12.50	12.18	12.34
T14	10.70	11.56	11.13
T15	12.40	10.04	11.22
T16	11.30	11.29	11.30
T17	11.60	11.26	11.43
T18	11.91	11.47	11.69
T19	12.40	13.16	12.78
T20	11.77	11.04	11.41
T21	11.80	11.67	11.74
T22	12.33	12.67	12.50
T23	12.20	12.19	12.19
T24	12.10	8.68	10.39
T25	10.37	10.48	10.42
T26	12.20	9.65	10.92
T27	11.27	8.82	10.04
T28	11.10	10.75	10.93
T29	12.00	10.51	11.26
T30	12.10	12.06	12.08
Mean	11.72	11.26	11.49
SE (m)	0.48	0.48	0.34
CD Genotype	1.37	1.37	NS
CD Open X Shade	0.30		
CD Genotype X Condition	1.78		

Table 10. Number of abnormal pods/ plant of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	2.25	2.83	2.54
T2	1.95	3.04	2.50
T3	2.81	4.59	3.70
T4	2.82	3.81	3.32
T5	2.17	4.07	3.12
T6	1.82	3.07	2.44
T7	3.00	3.01	3.01
T8	2.24	1.36	1.80
T9	1.67	3.97	2.82
T10	2.28	2.02	2.15
T11	1.22	3.40	2.31
T12	2.11	4.05	3.08
T13	3.50	1.77	2.63
T14	4.01	2.41	3.21
T15	1.77	3.97	2.87
T16	2.44	1.28	1.86
T17	2.78	2.98	2.88
T18	3.45	4.72	4.08
T19	2.33	2.33	2.33
T20	3.66	4.87	4.27
T21	2.01	2.89	2.45
T22	1.72	3.47	2.59
T23	1.55	4.77	3.16
T24	1.80	2.33	2.07
T25	3.29	2.92	3.11
T26	2.33	1.27	1.80
T27	1.15	2.03	1.59
T28	3.09	2.98	3.04
T29	1.92	3.06	2.49
T30	2.81	3.66	3.24
Mean	2.40	3.10	2.75
SE (m)	0.33	0.34	0.24
CD Genotype	0.93	0.97	NS
CD Open X Shade	0.16		
CD Genotype X Condition	1.24		

Table 11. Pod length (cm) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	7.14	6.68	6.91
T2	7.12	7.40	7.26
T3	7.25	7.07	7.16
T4	7.06	7.29	7.18
T5	7.36	8.37	7.87
T6	8.06	6.77	7.41
T7	7.48	6.84	7.16
T8	9.39	9.39	9.39
T9	7.14	7.10	7.12
T10	8.36	8.65	8.50
T11	8.58	7.03	7.81
T12	7.37	6.76	7.07
T13	7.78	6.61	7.19
T14	6.46	5.92	6.19
T15	8.18	7.30	7.74
T16	7.52	6.24	6.88
T17	6.64	6.69	6.67
T18	7.68	7.67	7.68
T19	8.67	6.92	7.80
T20	8.12	7.98	8.05
T21	8.37	8.75	8.56
T22	7.79	7.21	7.50
T23	7.33	5.82	6.57
T24	7.28	7.14	7.21
T25	6.08	6.01	6.05
T26	8.05	6.50	7.28
T27	7.83	7.04	7.44
T28	6.58	6.53	6.56
T29	6.92	5.91	6.41
T30	7.83	7.97	7.90
Mean	7.58	7.12	7.35
SE (m)	0.46	0.44	0.32
CD Genotype	1.31	1.25	1.29
CD Open X Shade	0.24		
CD Genotype X Condition	NS		

Fig 1. Mean performance of yield per plant (g) of green gram genotypes under open and partial shade conditions

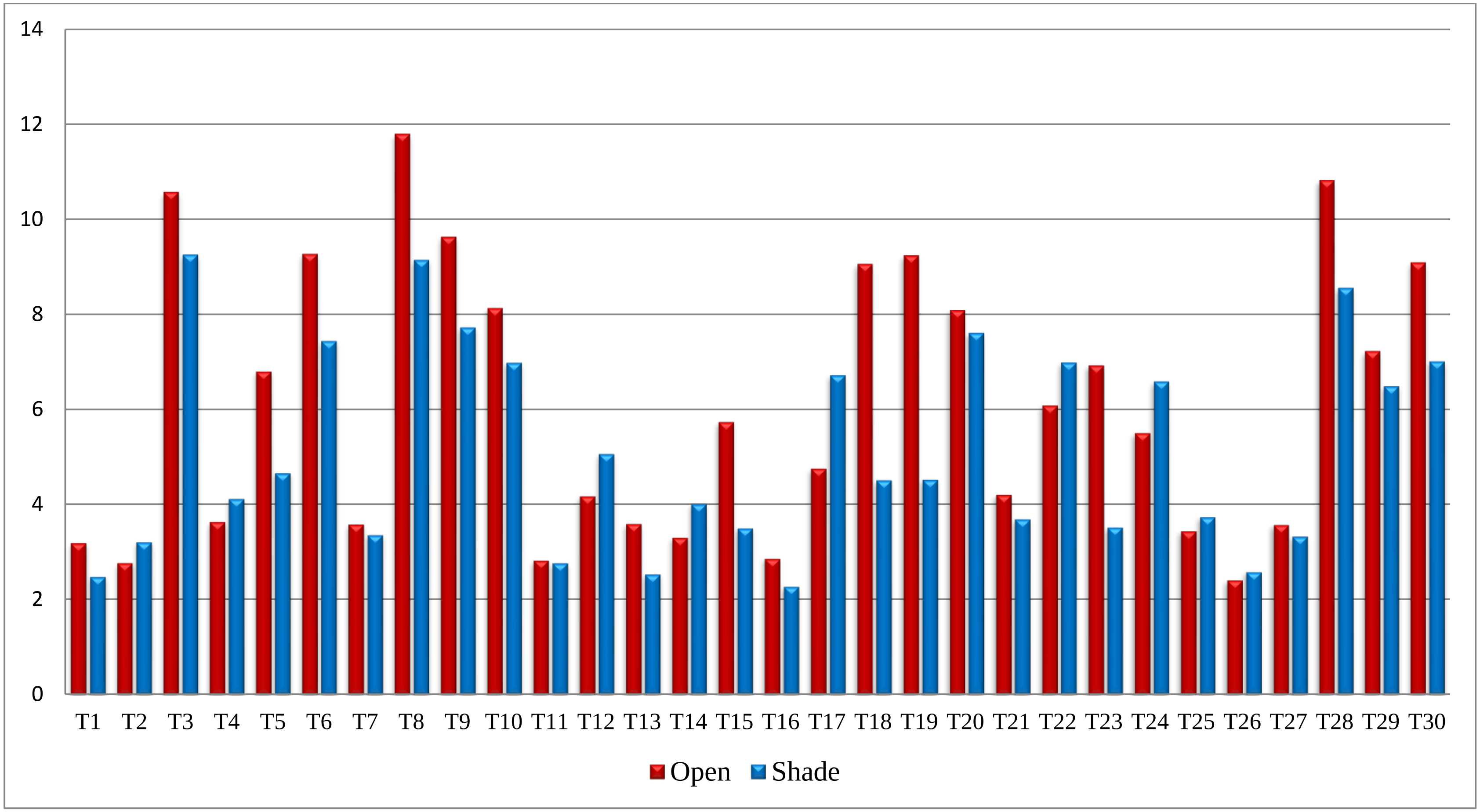


Table 12.Yield / plant (g) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	3.21	2.50	2.86
T2	2.79	3.23	3.01
T3	10.58	9.26	9.92
T4	3.65	4.14	3.90
T5	6.81	4.68	5.74
T6	9.28	7.45	8.36
T7	3.60	3.38	3.49
T8	11.80	9.15	10.48
T9	9.64	7.73	8.68
T10	8.14	6.99	7.57
T11	2.84	2.79	2.82
T12	4.19	5.08	4.64
T13	3.61	2.55	3.08
T14	3.32	4.03	3.67
T15	5.75	3.52	4.64
T16	2.88	2.29	2.58
T17	4.77	6.73	5.75
T18	9.07	4.53	6.80
T19	9.25	4.54	6.90
T20	8.10	7.62	7.86
T21	4.22	3.71	3.97
T22	6.10	7.00	6.55
T23	6.94	3.54	5.24
T24	5.52	6.60	6.06
T25	3.46	3.76	3.61
T26	2.42	2.60	2.51
T27	3.59	3.35	3.47
T28	10.83	8.56	9.70
T29	7.24	6.50	6.87
T30	9.10	7.02	8.06
Mean	6.09	5.16	5.63
SE (m)	0.39	0.31	0.25
CD Genotype	1.09	0.87	2.98
CD Open X Shade	0.23		
CD Genotype X Condition	1.29		

Table 13. 100 seed weight (g) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	2.94	3.10	3.02
T2	3.47	3.51	3.49
T3	3.47	3.29	3.38
T4	3.39	2.95	3.17
T5	3.25	3.46	3.36
T6	3.96	3.45	3.71
T7	3.94	3.13	3.53
T8	5.00	5.17	5.09
T9	3.57	3.19	3.38
T10	4.28	4.15	4.22
T11	4.21	4.02	4.11
T12	3.78	3.42	3.60
T13	4.13	3.28	3.71
T14	3.40	2.97	3.19
T15	4.58	2.76	3.67
T16	3.52	2.87	3.19
T17	2.52	2.93	2.73
T18	3.78	3.45	3.61
T19	4.06	3.11	3.59
T20	3.50	3.38	3.44
T21	4.31	4.31	4.31
T22	3.76	3.37	3.57
T23	3.46	3.23	3.35
T24	3.02	3.05	3.04
T25	3.25	2.99	3.12
T26	4.59	3.45	4.02
T27	4.04	4.37	4.20
T28	3.62	3.34	3.48
T29	3.38	2.67	3.02
T30	3.84	3.15	3.49
Mean	3.73	3.38	3.56
SE (m)	0.22	0.17	0.14
CD Genotype	0.61	0.49	0.88
CD Open X Shade	0.15		
CD Genotype X Condition	0.72		

Table 14. Plant height (cm) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	33.54	34.98	34.26
T2	39.68	35.95	37.82
T3	35.06	47.21	41.14
T4	44.92	48.04	46.48
T5	46.84	44.74	45.79
T6	30.05	29.83	29.94
T7	49.13	42.55	45.84
T8	33.52	41.53	37.53
T9	39.82	49.10	44.46
T10	38.00	41.51	39.76
T11	49.02	42.20	45.61
T12	38.52	39.22	38.87
T13	40.46	46.75	43.61
T14	44.06	37.67	40.86
T15	36.19	40.96	38.58
T16	39.99	34.89	37.44
T17	49.36	61.85	55.61
T18	41.01	50.92	45.96
T19	30.37	35.86	33.12
T20	40.06	38.15	39.10
T21	40.87	43.84	42.35
T22	44.40	55.58	49.99
T23	47.64	43.08	45.36
T24	36.27	56.31	46.29
T25	40.32	38.17	39.24
T26	20.50	31.38	25.94
T27	38.61	35.96	37.28
T28	35.35	46.98	41.17
T29	35.46	37.66	36.56
T30	37.97	47.16	42.56
Mean	39.23	42.67	40.95
SE (m)	3.03	2.77	2.05
CD Genotype	8.61	7.85	12.89
CD Open X Shade	1.37		
CD Genotype X Condition	10.75		

4.1.2.14. Variability in harvest index:

According to Table 15, there was a significant difference in the performance of the genotype under the two conditions. Under open condition, highest harvest index was reported for the genotype T8 (0.83) followed by genotype T9 (0.69) which was on par with T19 (0.69), T6 (0.67), T10 (0.67), T3 (0.66), T28 (0.66) and T29 (0.62), whereas least harvest index was observed for the genotype T26 (0.30). Under partially shaded conditions, the genotype T28 (0.67) recorded the highest harvest index, while the lowest harvest index was noticed for the genotype T25 (0.33) which was on par with other genotypes such as T7 (0.38), T13 (0.41) and T4 (0.41).

From pooled analysis, highest harvest index was observed for the genotype T8 (0.74), which was on par with genotypes T28 (0.67), T3 (0.65), T6 (0.65), T9 (0.63), T10 (0.62), T19 (0.60), T15 (0.59), T30 (0.57), T21 (0.56) and T24 (0.56), whereas lowest value for harvest index was exhibited by the genotype T25 (0.35). The results also disclosed the existence of a significant interaction between the genotypes and the environmental condition for this character.

4.1.2.15. Variability in number of harvest:

Under open condition, highest number of harvest was recorded for T3 (3.67) which was significantly different from all other genotypes except T8 (3.33) whereas the picking was single for genotypes T7 and T13. The genotype T5 (3.00) exhibited the highest number of pickings under shaded condition and was on par with T17 (2.67) likewise, the value was least for T13 (1.00). The genotypes T1 (1.33), T7 (1.33) and T16 (1.33) performed on par with T13 for the number of harvest. In pooled analysis, the genotype T3 showed the highest number of harvest which was on par with genotypes except T1 (1.67), T16 (1.67), T11 (1.67), T7 (1.17), and T13 (1.00). Between the different genotypes studied and the two growing conditions there existed a significant interaction and the observations are depicted in Table 15.

Table 15. Harvest index of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	0.46	0.58	0.52
T2	0.47	0.46	0.46
T3	0.66	0.64	0.65
T4	0.47	0.41	0.44
T5	0.56	0.45	0.51
T6	0.67	0.62	0.65
T7	0.39	0.38	0.38
T8	0.83	0.66	0.74
T9	0.69	0.57	0.63
T10	0.67	0.57	0.62
T11	0.35	0.51	0.43
T12	0.46	0.57	0.51
T13	0.39	0.41	0.40
T14	0.49	0.48	0.48
T15	0.55	0.64	0.59
T16	0.36	0.46	0.41
T17	0.53	0.56	0.55
T18	0.56	0.46	0.51
T19	0.69	0.52	0.60
T20	0.57	0.50	0.54
T21	0.58	0.55	0.56
T22	0.49	0.56	0.52
T23	0.55	0.45	0.50
T24	0.57	0.56	0.56
T25	0.37	0.33	0.35
T26	0.30	0.50	0.40
T27	0.38	0.52	0.45
T28	0.66	0.67	0.67
T29	0.62	0.47	0.55
T30	0.58	0.56	0.57
Mean	0.53	0.52	0.52
SE (m)	0.03	0.04	0.03
CD Genotype	0.09	0.11	0.18
CD Open X Shade	NS		
CD Genotype X Condition	0.13		

Table 16. Number of harvest of thirty genotypes under open and partially shadedconditions.

Genotypes	Open	Shade	Pooled
T1	2.00	1.33	1.67
T2	2.00	2.00	2.00
T3	3.67	2.00	2.83
T4	2.00	2.00	2.00
T5	2.33	3.00	2.67
T6	2.00	2.00	2.00
T7	1.00	1.33	1.17
T8	3.33	2.00	2.67
T9	2.33	2.33	2.33
T10	2.00	2.00	2.00
T11	1.67	1.67	1.67
T12	2.00	2.00	2.00
T13	1.00	1.00	1.00
T14	2.00	2.00	2.00
T15	2.00	1.67	1.83
T16	2.00	1.33	1.67
T17	2.00	2.67	2.33
T18	3.00	2.00	2.50
T19	2.33	2.00	2.17
T20	2.33	2.33	2.33
T21	2.00	2.00	2.00
T22	2.67	2.00	2.33
T23	3.00	2.00	2.50
T24	2.00	2.33	2.17
T25	1.67	2.33	2.00
T26	2.33	1.67	2.00
T27	2.00	2.00	2.00
T28	2.67	2.00	2.33
T29	2.00	2.33	2.17
T30	2.33	2.00	2.17
Mean	2.19	1.98	2.08
SE (m)	0.21	0.21	0.15
CD Genotype	0.60	0.61	1.06
CD Open X Shade	0.08		
CD Genotype X Condition	0.79		

4.1.2.16. Variability in protein content

The results showing variability in protein content in green gram genotypes under open and partially shaded conditions are given in the Table 17.

There existed significant difference for protein content in the performance of genotypes between open and partially shaded conditions. Under open condition, highest protein content was recorded for genotype T9 (28.56) which was on par with T8 (28.52), T18 (28.31) and T10 (27.75), while the least protein content was noticed for T27. Performance of T27 (21.88) was significantly different from all other genotypes except T29 (22.14). Likewise, the genotype T5 (31.19) registered high value for protein content that was on par with T9 (30.62) and T25 (30.38) followed by T6 (29.38) and T19 (28.63) under partial shade, whereas the genotype T1 (21.43) showed the minimum protein content on par with T17 (21.88).

The pooled analysis disclosed the existence of a significant interaction between genotypes and growing conditions. The highest amount of protein was observed for T9 (29.59) while least for T1 (22.81). Overall, an increment in the amount of protein was visible for most of the genotypes grown under partial shade than those under open condition.

4.1.2.17 Variability in specific leaf area (SLA)

The data on variability in specific leaf area of genotypes is depicted in the Table 18.

The genotype T22 (572.73) showed the highest specific leaf area under open condition and was significantly different from all other genotypes followed by T23 (454.81), T17 (362.25) and T9 (354.45) whereas the performance of T23 and T9 was on par. The value of SLA was least for T26 (181.99) and was on par with the genotype T24 (180.07).

The specific leaf area was noticed to be high for T7 (523.88) under shaded condition followed by T23 (487.88), T2 (457.14) and T14 (446.77) likewise, Genotypes T12 (142.54) showed the least. The pooled analysis revealed the presence of an interaction effect between genotypes and condition for specific leaf area.

4.1.2.18. Variability in chlorophyll content:

The observations on chlorophyll content in green gram genotypes are depicted in the Table 19.

The character showed significant difference under open and partially shaded conditions. Under open condition, the highest value for total chlorophyll content was recorded for genotypeT2 (1.76) followed by T3 (1.73) and T6 (1.61) whereas, the amount was least for T27 (0.65) whose performance was significantly different from all other genotypes. Under shade condition, chlorophyll content was noticed to be high in the genotype T2 (1.58) which was on par with T6 (1.55), T22 (1.54), T1 (1.53), T12 (1.53), T19 (1.52), T30 (1.52), T10 (1.51), T11 (1.51) T17 (1.50) and T23 (1.50). Likewise, amount of chlorophyll content was low for the genotype T14 (1.35) and on par with other genotypes like T4 (1.40), T25 (1.41), T26 (1.42) and T15 (1.42). The interaction between genotypes and condition was significant for total chlorophyll content in green gram. An increase in the total chlorophyll content for genotypes under partial shade than those under open condition was clearly evident from the Table 19.

4.1.2.19. Incidence of pest and diseases:

Mild attack by leaf eating caterpillars was observed in the initial stage. At pod formation stage, no much incidence of pod borers and pod bug were observed. Infection of *Sclerotium* was noticed on a few pods.

Table 17. Protein content (%) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	24.19	21.43	22.81
T2	26.25	22.77	24.51
T3	25.63	24.25	24.94
T4	24.19	26.94	25.56
T5	26.25	31.19	28.72
T6	26.81	29.38	28.09
T7	26.25	24.25	25.25
T8	28.52	23.63	26.08
T9	28.56	30.62	29.59
T10	27.75	26.56	27.15
T11	24.81	24.81	24.81
T12	24.25	25.38	24.81
T13	26.25	26.25	26.25
T14	26.81	26.25	26.53
T15	26.27	25.69	25.98
T16	26.56	25.06	25.81
T17	25.63	21.88	23.75
T18	28.31	27.77	28.04
T19	27.13	28.63	27.88
T20	27.13	26.25	26.69
T21	24.85	27.77	26.31
T22	24.25	25.70	24.98
T23	26.25	27.13	26.69
T24	24.81	26.56	25.69
T25	23.38	30.38	26.88
T26	25.63	24.81	25.22
T27	21.88	25.38	23.63
T28	23.65	25.38	24.51
T29	22.14	26.25	24.20
T30	24.25	28.31	26.28
Mean	25.62	26.22	25.92
SE (m)	0.33	0.35	0.24
CD Genotype	0.93	0.98	NS
CD Open X Shade	0.27		
CD Genotype X Condition	1.25		

Table 18. Specific leaf area (cm^2/g) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	258.85	398.88	328.87
T2	343.08	457.38	400.23
T3	269.44	365.94	317.69
T4	329.07	439.33	384.20
T5	283.99	414.14	349.07
T6	271.70	364.39	318.04
T7	272.99	523.88	398.43
T8	310.83	207.59	259.21
T9	354.45	405.87	380.16
T10	248.71	183.05	215.88
T11	200.57	208.68	204.63
T12	221.95	142.54	182.24
T13	238.23	351.15	294.69
T14	312.55	446.77	379.66
T15	317.03	356.56	336.80
T16	247.45	246.64	247.04
T17	362.25	392.00	377.13
T18	267.86	412.39	340.12
T19	219.22	404.81	312.01
T20	236.83	306.67	271.75
T21	219.91	292.98	256.45
T22	572.73	294.98	433.85
T23	454.81	487.14	470.97
T24	180.07	426.52	303.30
T25	230.74	360.22	295.48
T26	181.99	323.68	252.83
T27	221.38	273.19	247.28
T28	305.57	293.43	299.50
T29	262.52	375.24	318.88
T30	212.77	327.68	270.22
Mean	280.32	349.46	314.89
SE (m)	5.04	3.86	3.17
CD Genotype	14.30	10.95	NS
CD Open X Shade	1.76		
CD Genotype X Condition	16.62		

BGS 9

K7

Plate 4. Superior genotypes

IC 282124

K10

Plate 4. Superior genotypes

K13

Plate 4. Superior genotypes

Table 19. Chlorophyll content (mg/g) of thirty genotypes under open and partially shaded conditions.

Genotypes	Open	Shade	Pooled
T1	1.18	1.53	1.36
T2	1.76	1.58	1.67
T3	1.73	1.46	1.59
T4	1.59	1.40	1.49
T5	1.48	1.45	1.46
T6	1.61	1.55	1.58
T7	1.35	1.46	1.41
T8	1.60	1.49	1.54
T9	1.40	1.47	1.44
T10	1.28	1.51	1.39
T11	1.28	1.51	1.39
T12	1.51	1.53	1.52
T13	1.49	1.35	1.42
T14	1.54	1.48	1.51
T15	1.52	1.42	1.47
T16	1.52	1.45	1.48
T17	1.45	1.50	1.47
T18	1.32	1.49	1.41
T19	1.33	1.52	1.42
T20	1.38	1.49	1.43
T21	1.35	1.48	1.41
T22	1.41	1.54	1.47
T23	1.42	1.50	1.46
T24	1.47	1.47	1.47
T25	1.54	1.41	1.47
T26	1.47	1.42	1.45
T27	0.65	1.46	1.06
T28	1.48	1.49	1.49
T29	1.10	1.46	1.28
T30	1.32	1.52	1.42
Mean	1.42	1.48	1.45
SE (m)	0.02	0.03	0.02
CD Genotype	0.06	0.08	NS
CD Open X Shade	0.01		
CD Genotype X Condition	0.09		

4.2. Genetic Parameters

The genetic parameters such as range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability and genetic advance as per cent of mean (GAM) for fourteen characters under open and partially shaded conditions are presented Table 20 and 21 and depicted in Figures 2 ,3,4 and 5, respectively.

4.2.1. Under open condition:

The results in the Table 20 revealed the existence of wide range of variation in the experimental population for all the characters studied. Under open condition, characters like plant height (20.50-49.36), number of pods per plant (11.13-39.90), days to maturity (68.33-94.67), harvest index (0.30-0.83) and yield per plant (2.42-11.80) exhibited wide range of variation, while the range was low for number of secondary branches per plant (1.00-3.11), number of seeds per pod (10.20-12.70) and chlorophyll content (0.65-1.76).

The PCV values were found to be higher than their corresponding GCV values for all the traits. High PCV and GCV were recorded for characters like yield per plant (47.94, 46.94) followed by number of primary branches per plant (37.71, 31.85), number of secondary branches, number of pods per plant and harvest index, whereas PCV and GCV were moderate for plant height, 100 seed weight and chlorophyll content. Number of days for blooming (5.29, 4.01), days to 50% flowering (5.65, 2.29), seeds per pod (7.99, 3.63) and protein content (6.96, 6.60) recorded low PCV and GCV. However, characters like days to maturity and pod length showed moderate PCV with low GCV (Fig.2).

High heritability was observed for most of the characters studied with highest value for chlorophyll content (97.21) followed by yield per plant (94.78), protein content (90.00), number of pods per plant (82.94), harvest index, days to maturity, number of primary branches, 100 seed weight and number of secondary branches per plant. Number of seeds per pod (20.70) recorded the lowest heritability, while others showed medium range.

Most of the characters showed high values for genetic advance expressed as the percentage of mean. Under open condition, yield per plant (93.60) recorded the highest value followed by number of pods per plant (56.08) and number of primary branches per plant (55.42). Genetic advance as percentage of mean was found to be moderate for days to maturity (16.58) and protein content (12.91), whereas it was low for number of seeds per pod (3.41), days to 50 per cent flowering (3.94), number of days for blooming (6.25) and pod length (8.65) (Fig.3).

High heritability coupled with high genetic advance was recorded for yield per plant, harvest index, number of primary branches, number of pods per plant, chlorophyll content, 100 seed weight and number of secondary branches per plant. From the results in Table 20 it is clear that, characters like yield per plant, harvest index, number of primary branches, number of pods and number of secondary branches per plant recorded high GCV, PCV, heritability and genetic advance which indicated their importance in further selection.

4.2.2. Under partial shade condition:

Under partially shaded condition, characters like plant height (29.83-61.85), days to maturity (65.33-92.33), number of pods per plant (13.03- 40.62) and harvest index (0.33-0.67) exhibited wide range of variation, whereas the range was noticed to be narrow for chlorophyll content (1.35-1.58) and number of secondary branches per plant (1.00-1.65).

The character yield per plant (42.78, 41. 78) exhibited the highest values for coefficient of variation both at phenotypic and genotypic levels followed by number of pods (33.42, 30.53) and number of primary branches per plant (28.90, 24.98). Moderate PCV and GCV were recorded for plant height (19.66, 16.14), harvest index (19.16, 14.44), number of secondary branches (18.72, 14.44), 100 seed weight (17.48, 15.07) and pod length (15.03, 10.56), while other characters showed low values for PCV and GCV. Characters like days to maturity and number of seeds per pod recorded moderate PCV with low GCV. The lowest PCV and GCV were registered for chlorophyll content (4.29, 2.55) under partially shaded condition (Fig.4).

The value for heritability was observed to be high for most of the characters among which yield per plant (94.27) scored the highest value followed by protein content (93.91) and number of pods per plant (83.45). Characters like number of secondary branches (59.45), harvest index (56.74), pod length (49.44) and chlorophyll content (35.25) exhibited moderate heritability. In general, all the fourteen characters showed medium to high heritability under partial shade condition.

Genetic advance expressed as percentage of mean was highest for yield per plant (83.09) followed by pods per plant (57.45), number of primary branches per plant (44.49), plant height, 100 seed weight, number of secondary branches and harvest index. The lowest record of genetic advance expressed as percentage of mean was observed for chlorophyll content (3.11), while other traits exhibited medium GAM under partial shade condition (Fig.5).

High heritability coupled with genetic advance was recorded for yield per plant, number of primary branches, number of pods per plant, 100 seed weight and plant height under partial shade. The three characters *viz,.* yield per plant, number of pods and number of primary branches per plant scored high GCV, PCV, heritability and genetic advance (Table 21).

Fig.2 . GCV and PCV for 14 characters in green gram genotypes under open condition

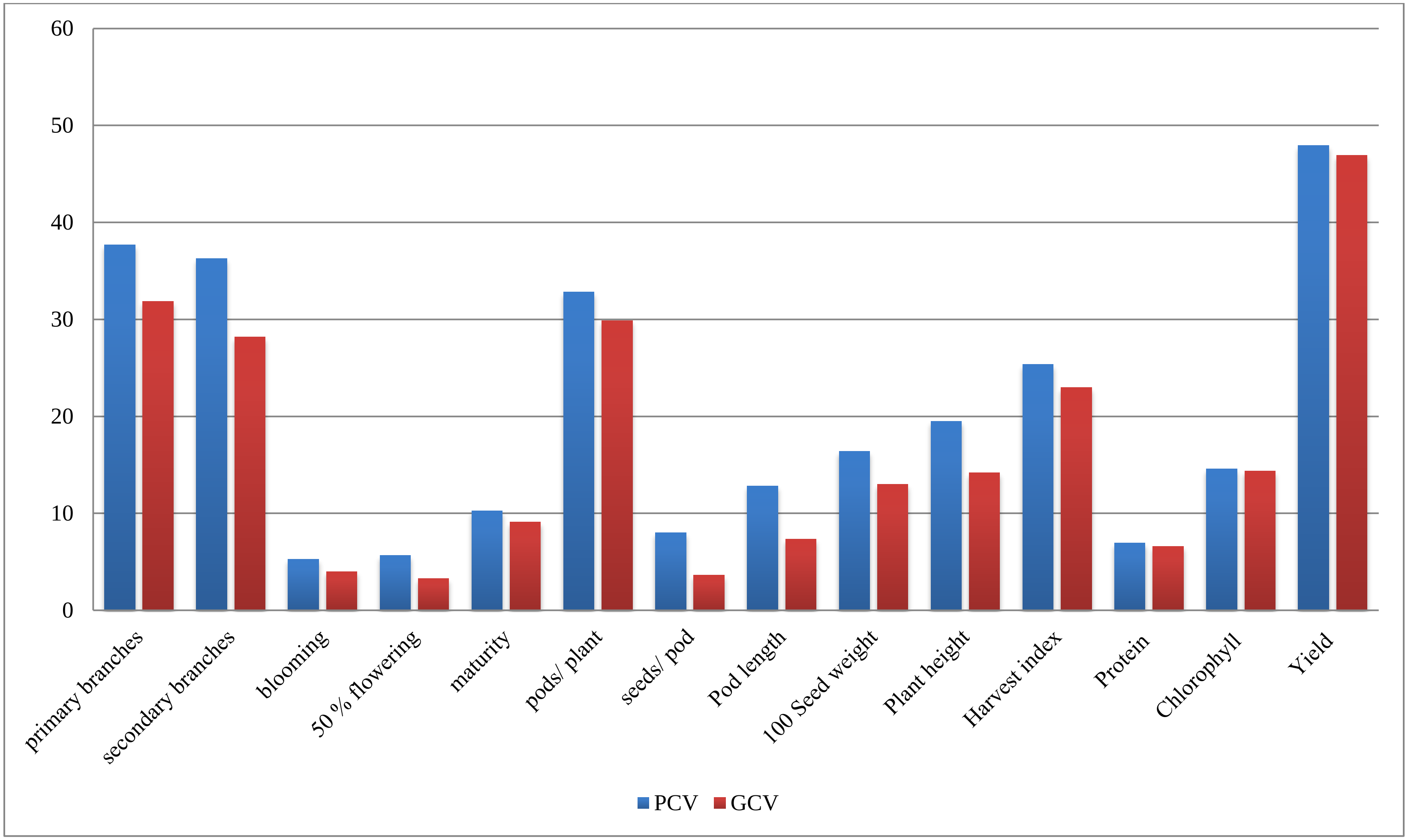


Fig.3. Heritability and genetic advance for 14 characters in green gram genotypes under open condition

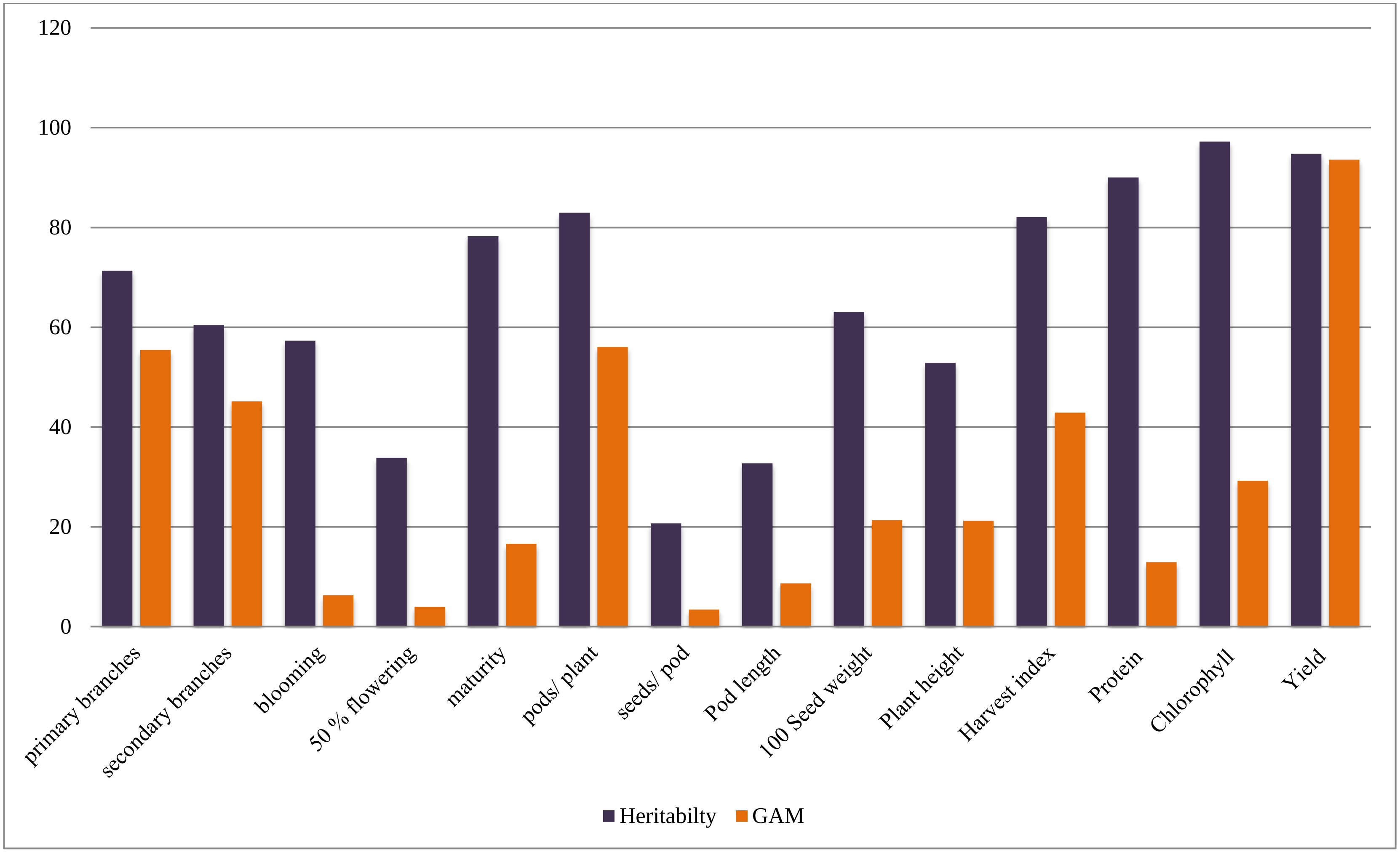


Table 20. Estimates of genetic parameters for yield and yield contributing characters of green gram genotypes under open condition

Character	Mean	Range	PCV	GCV	H^2	GAM
No. of primary branches/ plant	3.18	2.17-6.40	37.71	31.85	71.34	55.42
No. of secondary branches/ plant	1.50	1.00-3.11	36.26	28.18	60.42	45.13
No. of days for blooming	37.72	36.00-42.33	5.29	4.01	57.32	6.25
Days to 50 % flowering	43.03	39.33-47.67	5.65	3.29	33.82	3.94
Days to maturity	78.97	68.33-94.67	10.28	9.10	78.26	16.58
No. of pods/ plant	22.85	11.13-39.90	32.82	29.89	82.94	56.08
No. of seeds/ pod	11.72	10.20-12.70	7.99	3.63	20.70	3.41
Pod length	7.58	6.08-9.39	12.83	7.34	32.75	8.65
100 Seed weight	3.73	2.52-5.00	16.40	13.02	63.09	21.31
Plant height	39.23	20.50-49.36	19.51	14.19	52.88	21.25
Harvest index	0.53	0.30-0.83	25.36	22.98	82.07	42.88
Protein content	25.62	21.88-28.56	6.96	6.60	90.00	12.91
Chlorophyll content	1.42	0.65-1.76	14.59	14.38	97.21	29.21
Yield per plant	6.09	2.42-11.80	47.94	46.94	94.78	93.60

Table 21. Estimates of genetic parameters for yield and yield contributing characters of green gram genotypes under partially shaded condition

Character	Mean	Range	PCV	GCV	H^2	GAM
No. of primary branches/ plant	2.36	1.53-4.11	28.90	24.98	74.74	44.49
No. of secondary branches/ plant	1.16	1.00-1.65	18.72	14.44	59.45	22.93
No. of days for blooming	38.89	33.00-43.33	8.11	6.85	71.37	11.92
Days to 50 % flowering	45.30	37.67-51.00	8.49	6.83	64.76	11.32
Days to maturity	79.23	65.33-92.33	10.44	9.18	77.24	16.61
No. of pods/ plant	20.98	13.03-40.62	33.42	30.53	83.45	57.45
No. of seeds/ pod	11.26	8.68-13.28	11.87	9.27	60.98	14.91
Pod length	7.12	5.82-9.39	15.03	10.56	49.44	15.30
100 Seed weight	3.38	2.67-5.17	17.48	15.07	74.37	26.77
Plant height	42.67	29.83-61.85	19.66	16.14	67.41	27.30
Harvest index	0.52	0.33-0.67	19.16	14.44	56.74	22.40
Protein content	26.22	21.43-31.19	9.26	8.97	93.91	17.91
Chlorophyll content	1.48	1.35-1.58	4.29	2.55	35.25	3.11
Yield per plant	5.16	2.29-9.26	42.78	41.78	94.27	83.09

Fig.4. GCV and PCV for 14 characters in green gram genotypes under partially shaded condition

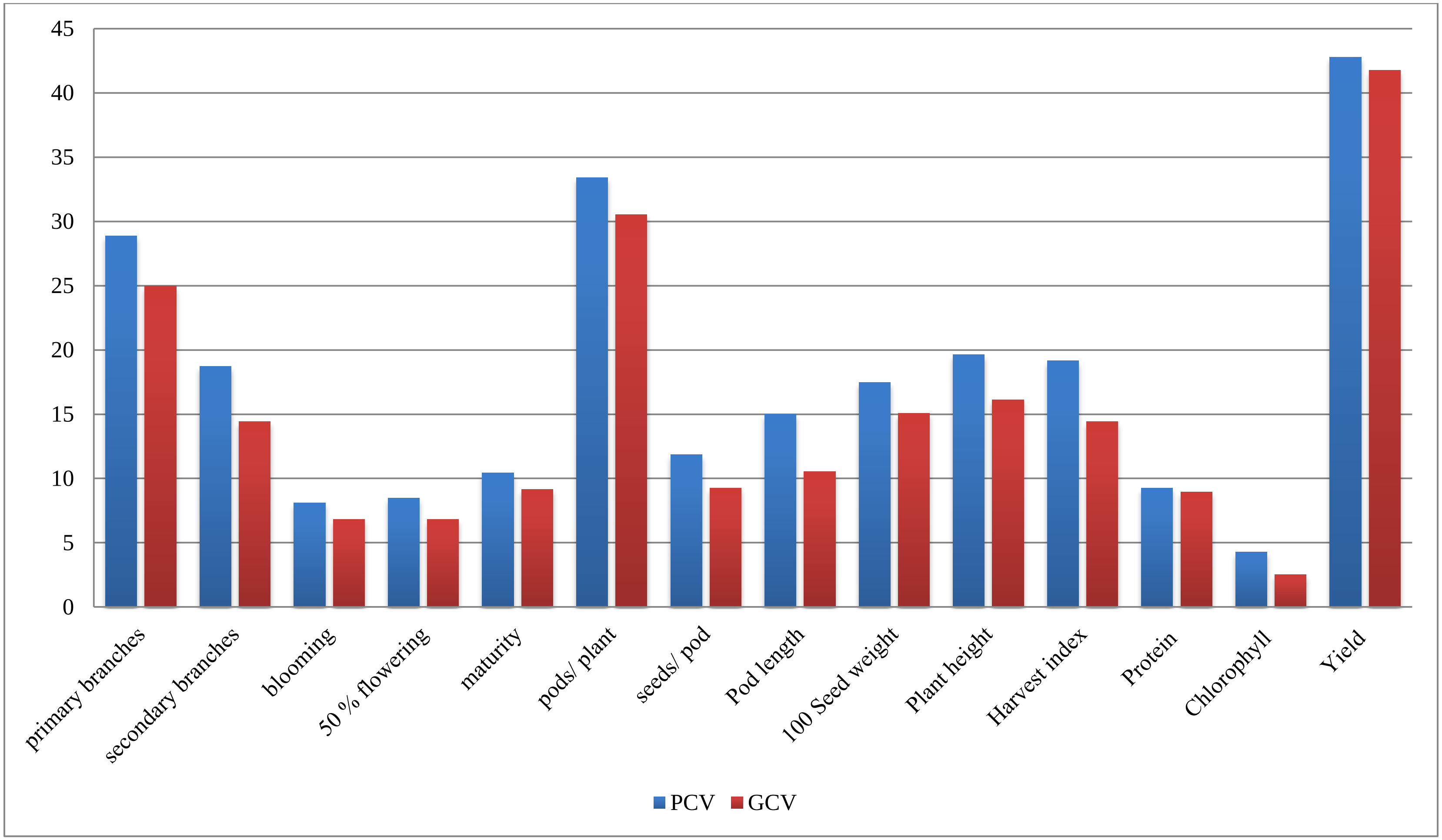
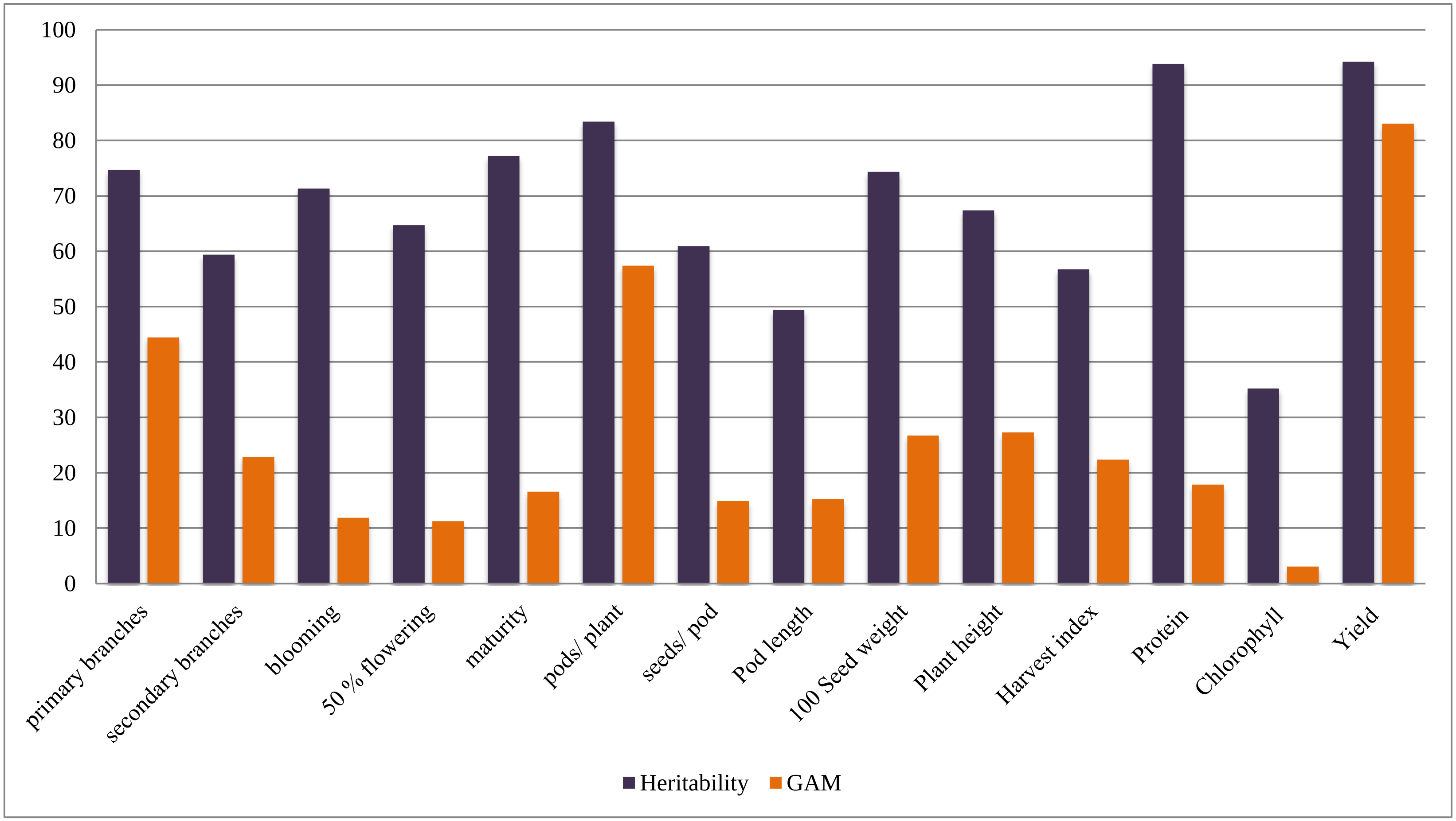


Fig.5. Heritability and genetic advance for 14 characters in green gram genotypes under partially shaded condition



4.3. Correlation studies

4.3.1. Under Open Condition:

The results of correlation analysis showing genotypic and phenotypic correlation coefficients of different characters with yield and inter-correlation among themselves are presented in the Table 22 and 23, respectively.

Genotypic correlation analysis revealed that, yield enjoys a strong positive highly significant correlation with harvest index (0.907) followed by pods per plant (0.666), protein content (0.372), number of primary branches per plant (0.366), number of secondary branches per plant (0.317), pod length (0.273) and days to maturity (0.212), whereas the association of yield per plant was negative with days for blooming (-0.379) and plant height (-0.278).

From the results of inter correlation studies it is clear that, the number of pods per plant exhibited a highly significant positive association with harvest index (0.584), chlorophyll content (0.328) and protein content (0.278).

Highly significant association of number of seeds per pod was noticed with pod length (0.637) and 100 seed weight (0.367), while chlorophyll content (-0.346) showed a negative correlation with seeds per pod.

Number of primary branches per plant showed positive association with days to 50 per cent flowering (0.607) followed by days to maturity (0.353), harvest index (0.352) and chlorophyll content (0.325), while the correlation with 100 seed weight (-0.296) and number of seeds per pod (-0.212).

Association of number of secondary branches was highly positive with pod length (0.377), protein content (0.370), harvest index (0.355), 100 seed weight (0.296) and days to maturity (0.274). However, characters like number of seeds per pod (-0.248) and days for blooming (-0.249) were found to negatively correlated with secondary branches per plant under open condition.

A strong significant positive correlation was observed between 100 seed weight and pod length (0.924). Association of pod length was significant and positive with harvest index (0.260), while the association was found to be negative with days to fifty per cent flowering (-0.869). 100 seed weight exhibited high negative correlation with days to 50 per cent flowering (-0.669) followed by days to maturity (-0.273).

Genotypic correlation of protein content was found be highly significant and positive with characters like pod length (0.478), chlorophyll content (0.430), harvest index (0.414) and 100 seed weight (0.288).

The character days to flowering showed negative correlation with other traits such as pod length (-0.790), 100 seed weight (-0.778), seeds per pod (-0.524), number of pods per plant (-0.352) and protein content (-0.214), but had high a positive association with days to 50 per cent flowering (0.779) followed by plant height (0.321).

Positive association was observed for days to fifty per cent flowering with chlorophyll content (0.289), while characters like seeds per pod (-0.990) and days to maturity (-0.213) showed a negative correlation with fifty per cent flowering.

A strong negative correlation was observed for plant height with number of seeds per pod (-0.461) followed by 100 seed weight (-0.415), pod length (-0.289) and harvest index (-0.215), while days to fifty per cent flowering (0.528) and days to maturity (0.475) showed positive correlation with plant height.

4.3.2. Under Partial Shade Condition:

The results of correlation studies showing genotypic and phenotypic correlation coefficients of different characters with seed yield and between themselves under partially shaded conditions are given in Tables 24 and 25.

Strong positive significant correlation of yield per plant with harvest index (0.671) followed by plant height (0.397), number of pods per plant (0.364), chlorophyll content (0.361), pod length (0.348), number of secondary branches per plant (0.346) and days to maturity (0.211) was observed under partial shade condition. Number of primary branches per plant (-0.386) was found to exhibit a negative correlation with seed yield per plant.

Number of pods per plant showed significant positive correlation with characters like number of seeds per pod (0.445), harvest index (0.292), protein content (0.269) and total chlorophyll (0.235), while days to flowering (-0.315) and fifty per cent flowering (-0.241) were negatively correlated with pods per plant.

Association of number of secondary branches with pod length (0.730) and 100 seed weight (0.523) was found to be positive and highly significant as opposed to days to 50 per cent flowering (-0.254) and harvest index (-0.242) which had negative correlation with secondary branches per plant.

Days to maturity was positively correlated to harvest index (0.405), pod length (0.314) protein content (0.307), chlorophyll content (0.270) and days to fifty per cent flowering (0.252).

A strong positive significant correlation was observed for harvest index with chlorophyll content (0.547) followed by pod length (0.316 and 100 seed weight (0.286), while it had negative correlation with protein content (-0.275) and number of days for blooming (-0.257).

Association of plant height with days to 50 per cent flowering (0.323), days to blooming (0.284) and pod length (0.208) was significant and positive. Characters like number of seeds per pod (0.765) and chlorophyll content (0.233) had high positive correlation with pod length.

Characters like number of seeds per pod (0.488), 100 seed weight (0.393) and days to fifty per cent flowering (0.327) were found to have a positive correlation with total chlorophyll content while number of primary branches (-0.316) and protein content (-0.281) gave negative correlation.

Table 22. Genotypic correlation of yield and yield contributing characters of green gram under open condition

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
X1	1													
X2	0.366**	1												
X3	0.317**	0.032^{NS}	1											
X4	-0.379**	0.158^{NS}	-0.249*	1										
X5	-0.200^{NS}	0.607**	-0.157^{NS}	0.779**	1									
X6	0.212*	0.353**	0.274**	-0.095^{NS}	0.187^{NS}	1								
X7	0.666**	0.079^{NS}	0.027^{NS}	-0.352**	-0.142^{NS}	0.013^{NS}	1							
X8	0.168^{NS}	-0.212*	-0.248*	-0.524**	-0.990**	-0.213*	0.002^{NS}	1						
X9	0.293**	-0.073^{NS}	0.377**	-0.790**	-0.869**	-0.071^{NS}	-0.098^{NS}	0.637**	1					
X10	0.145^{NS}	-0.296**	0.296**	-0.778**	-0.669**	-0.273**	0.076^{NS}	0.367**	0.924**	1				
X11	-0.278**	0.132^{NS}	-0.102^{NS}	0.321**	0.528**	0.475**	-0.035^{NS}	-0.461**	-0.289**	-0.415**	1			
X12	0.907**	0.352**	0.355**	-0.143^{NS}	-0.067^{NS}	0.163^{NS}	0.584**	0.069^{NS}	0.260*	0.063^{NS}	-0.215*	1		
X13	0.372**	0.021^{NS}	0.370**	-0.214*	-0.154^{NS}	-0.074^{NS}	0.278**	0.123^{NS}	0.478**	0.288**	-0.020^{NS}	0.414**	1	
X14	0.109^{NS}	0.325**	0.001^{NS}	0.160^{NS}	0.289**	-0.047^{NS}	0.328**	-0.346**	-0.195^{NS}	-0.063^{NS}	-0.036^{NS}	0.164^{NS}	0.430**	1

* Significant at 5% level ** Significant at 1% level

X1	Yield per plant	**X8**	No. of seeds/ pod
X2	No. of primary branches	**X9**	Pod length
X3	No. of secondary branches	**X10**	100seed weight
X4	Days for blooming	**X11**	Plant height
X5	Days to 50% flowering	**X12**	Harvest index
X6	Days to maturity	**X13**	Protein content
X7	No. of pods/ plant	**X14**	Chlorophyll content

Table 23. Phenotypic correlation of yield and yield contributing characters of green gram under open condition

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
X1	1													
X2	0.311**	1												
X3	0.234*	0.033^{NS}	1											
X4	-0.315**	0.123^{NS}	-0.255*	1										
X5	-0.150^{NS}	0.322**	0.035^{NS}	0.433**	1									
X6	0.229*	0.247*	0.153^{NS}	-0.106^{NS}	0.118^{NS}	1								
X7	0.662**	0.061^{NS}	-0.004^{NS}	-0.269*	-0.111^{NS}	0.113^{NS}	1							
X8	0.140^{NS}	-0.055^{NS}	-0.078^{NS}	-0.261*	-0.377**	0.019^{NS}	0.101^{NS}	1						
X9	0.245*	-0.045^{NS}	0.187^{NS}	-0.406**	-0.304**	0.159^{NS}	0.138^{NS}	0.363**	1					
X10	0.198^{NS}	-0.105^{NS}	0.187^{NS}	-0.544**	-0.355**	-0.067^{NS}	0.218*	0.243*	0.705**	1				
X11	-0.232*	0.106^{NS}	-0.020^{NS}	0.197^{NS}	0.292**	0.159^{NS}	-0.115^{NS}	-0.198^{NS}	-0.275**	-0.340**	1			
X12	0.876**	0.251*	0.217*	-0.154^{NS}	-0.105^{NS}	0.241*	0.605**	0.146^{NS}	0.295**	0.189^{NS}	-0.224*	1		
X13	0.361**	-0.024^{NS}	0.236*	-0.145^{NS}	-0.100^{NS}	-0.065^{NS}	0.261*	0.039^{NS}	0.313**	0.242*	-0.005^{NS}	0.374**	1	
X14	0.104^{NS}	0.230*	-0.006^{NS}	0.097^{NS}	0.174^{NS}	-0.027^{NS}	0.294**	-0.150^{NS}	-0.098^{NS}	-0.052^{NS}	-0.029^{NS}	0.151^{NS}	0.412**	1

* Significant at 5% level ** Significant at 1% level

X1	Yield per plant	**X8**	No. of seeds/ pod
X2	No. of primary branches	**X9**	Pod length
X3	No. of secondary branches	**X10**	100seed weight
X4	Days for blooming	**X11**	Plant height
X5	Days to 50% flowering	**X12**	Harvest index
X6	Days to maturity	**X13**	Protein content
X7	No. of pods/ plant	**X14**	Chlorophyll content

Days to fifty per cent flowering exhibited a strong positive correlation with days for blooming (0.497), whereas the association of 100 seed weight (-0.295), seeds per pod (-0.224) and protein content (-0.215) was negative with 50 per cent flowering. Protein content was positively correlated with seeds per pod (0.349) but a negative association was noticed for days for blooming (-0.250) which had a negative correlation with number of seeds (-0.335) and 100 seed weight (-0.330).

2.4. Path Analysis

The correlation among various yield attributing characters was partitioned into direct and indirect effects using path analysis. Path coefficient analysis was carried out using the data from open condition.

2.4.1. Under open condition

The path analysis was done using nine characters which had significant correlation with yield. The direct and indirect effects of each of these characters on yield are presented in the Table 26.

2.4.1.2. Direct Effect:

The results of path analysis revealed that, harvest index (0.5735) exhibited highest positive direct effect on yield followed by number of pods per plant (0.3331) while, days to maturity (0.1882) pod length (0.1552) and number of primary branches per plant (0.1112) exhibited low positive direct effect on yield. Characters like plant height (-0.2046), number of secondary branches per plant (-0.0240), protein content (-0.0165) and number of days for blooming (-0.0013) had a negative direct effect on seed yield.

4.3.1.2. Indirect Effects:

High indirect effect was recorded for number of pods per plant (0.3347) on yield per plant followed by protein content (0.2377) though harvest index.

Table 24. Genotypic correlation of yield and yield contributing characters of green gram under partially shaded condition

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
X1	1													
X2	-0.386**	1												
X3	0.346**	-0.113^{NS}	1											
X4	0.110^{NS}	0.059^{NS}	-0.138^{NS}	1										
X5	0.013^{NS}	-0.058^{NS}	-0.254*	0.497**	1									
X6	0.211*	0.083^{NS}	0.059^{NS}	-0.079^{NS}	0.252*	1								
X7	0.364**	-0.206^{NS}	0.092^{NS}	-0.315**	-0.241*	0.159^{NS}	1							
X8	0.142^{NS}	0.123^{NS}	-0.078^{NS}	-0.335**	-0.224*	0.163^{NS}	0.445**	1						
X9	0.348**	0.154^{NS}	0.730**	-0.093^{NS}	0.036^{NS}	0.314**	0.029^{NS}	0.091^{NS}	1					
X10	0.164^{NS}	-0.081^{NS}	0.523**	-0.330**	-0.295**	-0.037^{NS}	0.113^{NS}	-0.007^{NS}	0.765**	1				
X11	0.397**	-0.058^{NS}	-0.242*	0.284**	0.323**	0.405**	-0.050^{NS}	0.027^{NS}	0.208*	-0.118^{NS}	1			
X12	0.671**	-0.177^{NS}	0.196^{NS}	-0.257*	-0.032^{NS}	-0.016^{NS}	0.292**	0.003^{NS}	0.316**	0.286**	0.123^{NS}	1		
X13	0.098^{NS}	0.160^{NS}	-0.106^{NS}	-0.250*	-0.215*	0.307**	0.269*	0.349**	0.090^{NS}	-0.109^{NS}	-0.022^{NS}	-0.275**	1	
X14	0.361**	-0.316**	-0.085^{NS}	0.142^{NS}	0.393**	0.270*	0.235*	0.488**	0.233*	0.327**	-0.082^{NS}	0.547**	-0.281**	1

* Significant at 5% level ** Significant at 1% level

X1 Yield per plant
X2 No. of primary branches
X3 No. of secondary branches
X4 Days for blooming
X5 Days to 50% flowering
X6 Days to maturity
X7 No. of pods/ plant
X8 No. of seeds/ pod
X9 Pod length
X10 100seed weight
X11 Plant height
X12 Harvest index
X13 Protein content
X14 Chlorophyll content

Table 25. Phenotypic correlation of yield and yield contributing characters of green gram under partially shaded condition

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**	**X10**	**X11**	**X12**	**X13**	**X14**
X1	1													
X2	-0.313**	1												
X3	0.214*	-0.069^{NS}	1											
X4	0.116^{NS}	-0.007^{NS}	-0.070^{NS}	1										
X5	0.102^{NS}	-0.019^{NS}	-0.130^{NS}	0.391**	1									
X6	0.243*	0.048^{NS}	-0.058^{NS}	-0.047^{NS}	0.272**	1								
X7	0.388**	-0.146^{NS}	0.013^{NS}	-0.249*	-0.059^{NS}	0.223*	1							
X8	0.171^{NS}	0.070^{NS}	-0.054^{NS}	-0.101^{NS}	0.018^{NS}	0.234*	0.397**	1						
X9	0.344**	0.081^{NS}	0.310**	-0.008^{NS}	0.241*	0.341**	0.155^{NS}	0.155^{NS}	1					
X10	0.184^{NS}	-0.070^{NS}	0.354**	-0.198^{NS}	-0.109^{NS}	0.028^{NS}	0.141^{NS}	0.079^{NS}	0.592**	1				
X11	0.319**	0.022^{NS}	-0.094^{NS}	0.218*	0.263*	0.286**	-0.071^{NS}	0.038^{NS}	0.143^{NS}	-0.105^{NS}	1			
X12	0.567**	-0.156^{NS}	0.036^{NS}	-0.109^{NS}	0.127^{NS}	0.108^{NS}	0.295**	0.154^{NS}	0.334**	0.314**	0.106^{NS}	1		
X13	0.106^{NS}	0.152^{NS}	-0.074^{NS}	-0.204^{NS}	-0.162^{NS}	0.263*	0.247*	0.264*	0.078^{NS}	-0.087^{NS}	-0.011^{NS}	-0.185^{NS}	1	
X14	0.212*	-0.188^{NS}	-0.015^{NS}	0.004^{NS}	0.168^{NS}	0.151^{NS}	0.133^{NS}	0.136^{NS}	0.141^{NS}	0.125^{NS}	-0.080^{NS}	0.289**	-0.132^{NS}	1

* Significant at 5% level ** Significant at 1% level

X1	Yield per plant	**X8**	No. of seeds/ pod
X2	No. of primary branches	**X9**	Pod length
X3	No. of secondary branches	**X10**	100seed weight
X4	Days for blooming	**X11**	Plant height
X5	Days to 50% flowering	**X12**	Harvest index
X6	Days to maturity	**X13**	Protein content
X7	No. of pods/ plant	**X14**	Chlorophyll content

Besides protein content, characters like number of primary branches (0.2020), secondary branches per plant (0.2036) showed moderate positive indirect effect on yield through harvest index, while number of pods per plant (0.1490) recorded a low positive indirect effect.

Harvest index (0.1944) showed a low positive indirect effect through number of pods per plant followed by plant height (0.0439) and pod length (0.0403) on yield.

Low negative indirect effect on yield per plant was observed for number of days for blooming (-0.1173, -0.1226) through pods per plant and pod length, respectively.

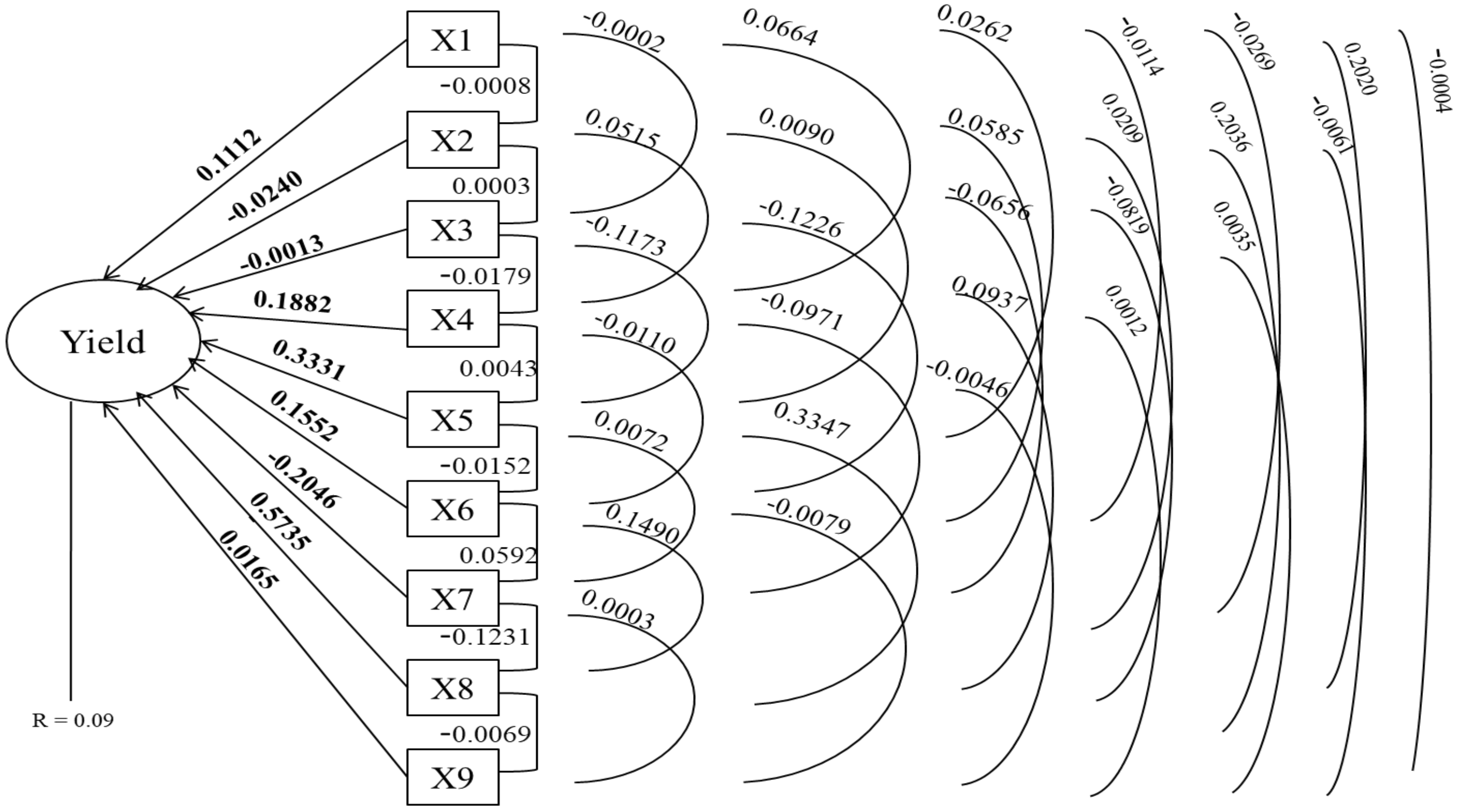
Table 26. Direct and indirect effects of different characters on yield under open condition

	X1	**X2**	**X3**	**X4**	**X5**	**X6**	**X7**	**X8**	**X9**
X1	**0.1112**	-0.0008	-0.0002	0.0664	0.0262	-0.0114	-0.0269	0.2020	-0.0004
X2	0.0036	**-0.0240**	0.0003	0.0515	0.0090	0.0585	0.0209	0.2036	-0.0061
X3	0.0176	0.0060	**-0.0013**	-0.0179	-0.1173	-0.1226	-0.0656	-0.0819	0.0035
X4	0.0393	-0.0066	0.0001	**0.1882**	0.0043	-0.0110	-0.0971	0.0937	0.0012
X5	0.0088	-0.0007	0.0005	0.0024	**0.3331**	-0.0152	0.0072	0.3347	-0.0046
X6	-0.0081	-0.0090	0.0011	-0.0133	-0.0327	**0.1552**	0.0592	0.1490	-0.0079
X7	0.0147	0.0025	-0.0004	0.0894	-0.0117	-0.0449	**-0.2046**	-0.1231	0.0003
X8	0.0392	-0.0085	0.0002	0.0307	0.1944	0.0403	0.0439	**0.5735**	-0.0069
X9	0.0024	-0.0089	0.0003	-0.0139	0.0926	0.0741	0.0042	0.2377	**-0.0165**

R = 0.09

X1	No. of primary branches	**X4**	Days to maturity	**X7**	Plant height
X2	No. of secondary branches	**X5**	No. of pods/ plant	**X8**	Harvest index
X3	Days for blooming	**X6**	Pod length	**X9**	Protein content

Fig.6. Path diagram showing direct and indirect effects of components of yield



X1	No. of primary branches	**X4**	Days to maturity	**X7**	Plant height
X2	No. of secondary branches	**X5**	No. of pods/ plant	**X8**	Harvest index
X3	Days for blooming	**X6**	Pod length	**X9**	Protein content

Discussion

5. DISCUSSION

Green gram (*Vigna radiata* (L.) Wilczek) is a major pulse crop of humid tropics to arid and semiarid regions, because of its short duration, its adaptability to different cropping systems and the low water requirement. Apart from being an excellent source of dietary protein and minerals, mung is favoured for consumption due to ease in digestion and low flatulence causing factors, which makes it a potential source to address the nutrition hunger. Since land is the limiting factor in Kerala, intercropping has the potential to increase farmers' income. Hence identification of genotypes that grows well in open and partial shade conditions is essential.

The present study titled "Genetic analysis in green gram (*Vigna radiata* (L.) Wilczek)" was conducted to evaluate the variability and performance of different green gram genotypes for yield and protein content under open and partially shaded conditions. The results obtained from the study are discussed under the following headings.

5.1. VAR IABILITY ANALYSIS

The success of any crop improvement programme aimed at higher yield, lies with the availability of variation in the experimental population. Information on the nature and magnitude of variation in the available germplasm and the part played by the environment in the expression of characters are important. Hence, the knowledge on the presence of genetic component of variability is of paramount importance for a breeder as it provides a basis for effective selection. The present investigation was undertaken to study genetic variability in 30 green gram genotypes and a wide range of variation was observed for all the characters studied.

5.1.1. Mean Performance

In the present investigation, eighteen characters including biometric, biochemical and physiological parameters were studied for thirty genotypes of green gram under open and partial shade conditions. Varietal differences were significant for all the characters studied under open condition, indicating the presence of a considerable amount of variation. Under partial shade, characters except emergence percentage showed significant difference in the performance of genotypes. Variability for different characters studied was previously reported by Makeen *et al.* (2007), Patel (2014) and Reddy (2017).

In green gram, emergence percentage ranged from 84.63 to 97.65 per cent in the pooled analysis. Similar variation with a higher range was earlier reported by Singh and Alam (2010). Emergence was more in partial shade due to ambient environment condition with adequate soil moisture for seed germination in coconut garden compared to open condition.

The results showed that the genotypes produced more number of branches under open condition compared to partial shade indicating the suitability of bushy plants under open condition. The number of primary branches per plant was higher in the open condition ranging between 2.17 and 6.40, whereas the branch number was slightly lower in partial shade (1.53-4.11). Similar findings were recorded by Sandhiya and Saravanan (2018) and Sneha *et al*. (2019). In pooled analysis, number of secondary branches per plant ranged from 1.00 to 2.35 with an average of 1.33. The characters exhibited significant difference in performance between open and partial shade conditions.

Green gram genotypes exhibited significant difference for number of days for blooming and days to 50 per cent flowering between the growing conditions. In open field, number of days for blooming was observed in the range from 36.00 to 42.33 days, while the character ranged between 33.00 and 43.33 days under partial shade. Similar range for days to flowering was earlier recorded by Rasal and Parhe (2017). The genotypes T21 (WGG 42) and T30 (EC 398900) took minimum days for blooming under open condition, whereas the genotype T26 (MH 421) showed early flowering under shade. Likewise, delayed flowering was observed for genotype T4 (K6) under open and T2 (K4) under partial shade conditions. Days to 50 per cent flowering ranged between 39.33 and 47.67 days under open condition with an average 43.03 days in accordance with the findings of Keerthiga *et al.* (2017), while it was between 37.67 and 51.00 days under partial condition with mean 45.30 days. Early flowering was noticed in most of the genotypes under open condition than those under partial shade. The delay in flowering under partial shade was due to the delay in reproductive stage caused by reduced light intensity and photosynthesis. The result was in accordance with the findings of Jiang (1993) in soybean and Singh and Alam (2010) in green gram.

Under open condition, genotypes took 68.33 to 94.67 days with an average of 78.97 days to attain full maturity, whereas the range was from 65.33 to 92.33 days with an average 79.23 days under partial shade. Similar variations in days to maturity, but with lower range were reported by Patel (2014) and Keerthiga *et al.* (2017).The results of the present study revealed that, the duration of green gram genotypes remained same under open and shade.

The highest variability was recorded for number of pods per plant. Under open condition, pod number ranged from 11.13 to 39.90 with an average of 22.85, while the range was between 13.03 and 40.62 with mean of 20.98 under partial shade. The range corresponds to the findings by Reddy (2017) and Sandhya and Saravanan (2018). The character showed a highly significant positive correlation with yield per plant which can be used as the selection criteria for crop improvement in green gram. However, in most of the genotypes, number of pods was more under open condition compared to partial shade. A similar reduction in pod formation under intercropped condition was earlier reported by Bhusara *et al.* (2018).

In the present investigation, harvest index was found to range from 0.30 to 0.83 under open condition and from 0.33 to 0.67 under partial shade. Similar variations were reported by Reddy (2017). Similar variation with lower range for harvest index was reported by Keerthiga *et al*. (2017) and Govardhan *et al*. (2018). Since the character showed a highly significant positive correlation with seed yield, an increasing trend for harvest index with an increase in single plant yield was observed in the study.

From the results of pooled analysis, it is evident that there existed no variation for characters like number of seeds per pod and abnormal, unfilled pods per plant under open and partially shaded conditions. Seeds per pod showed a range from 10.04 to 12.99 when averaged over both growing conditions. The narrow range may be due to the production of bold seeds with difference in seed filling and maturity. The number of abnormal, unfilled pods ranged between 1.15 and 3.66 under open condition, whereas the range was from 1.27 to 4.87 under partial shade condition. Similar variation was earlier reported by Rajeswari (1998). Number of harvests showed significant difference under both conditions. In pooled analysis, the genotype T15 recorded single plant yield of 4.64 g with least number of harvest and thus can be selected for cultivation.

There was significant variability for yield per plant among different genotypes under open and partially shaded conditions. Under open condition, seed yield ranged between 2.42 and 11.80 g, whereas the range was from 2.29 to 9.26 g under partial shade. The highest yield per plant was recorded for the genotype BGS 9 under open and K7 for partially shaded conditions. In general, the seed production was more in open condition when compared to partial shade and this may due to low photosynthetic efficiency and competition for nutrients under intercropping in coconut garden than sole cropping.

Pod length ranged from 6.08 to 9.39 cm under open condition, while it was from 5.82 to 9.39 cm under partial shade. The range was in accordance with the findings of Garje *et al.* (2013). Muthuswamy *et al.* (2019) reported a higher range between 5.84 and 12.27 cm for pod length in green gram.

The genotype T8 (BGS 9) recorded high 100 seed weight under (5.00 and 5.17 g) open and partially shaded conditions, respectively. The character showed significant difference in the performance under both growing conditions. In pooled analysis, the range for 100 seed weight was from 2.73 to 5.09 g and similar variation was recorded by Patel (2014), Govardhan *et al.* (2018) and Sandhya and Saravanan (2018).

Plant height ranged between 20.50 and 49.36 cm under open condition, while it was from 29.83 to 61.85 cm under partial shade condition. In general, genotypes exhibited more plant height under partial shade which may be due to lengthening of internodes under low light intensities to reach more sunlight (Sumner, 1922). Similar trend in plant height was earlier recorded by Lakshmamma and Rao (1996) in black gram, Hossain *et al.* (2017) and Masaku *et al.* (2018) in green gram. But, these results are in contradiction to the findings of Bhusara *et al*. (2018) who reported a reduction in plant height with shade. Moreover, the genotypes showed significant interaction with growing conditions for this trait.

There were significant differences among the performance of genotypes for protein content under the growing conditions. The amount of seed protein ranged from 21.88 to 28.56 per cent under open and 21.43 to 31.19 per cent under partial shade conditions. The value was highest for the genotype T9 (K10) under open condition, while it was highest for genotype T5 (K13) under partially shaded condition. Overall, an increase in the amount of protein was visible for most of the genotypes grown under partial shade than those under open condition and the result corresponds to the finding of Lakshmamma and Rao (1996) in black gram.

The performance of genotypes for characters like specific leaf area and chlorophyll content differed significantly under both conditions. Total chlorophyll showed a narrow range along with a visible increment in the amount under partial shade condition than open condition. The specific leaf area ranged from 180.07 to 572.73 cm^2/g under open and from 142.54 to 523.88 cm^2/g under shaded conditions. In most of the genotypes, an increment in specific leaf area under partial shade was observed when compared to those under open condition. Araki *et al.* (2014) recorded similar results in green gram, but a reduction in leaf area under more than 50 per cent shade was reported by Nomoto *et al.* (1961). Increase in leaf area helps for more light interception, whereas the increased chlorophyll content will increase the rate of photosynthesis.

5.1.2. GCV and PCV

Genotypic and phenotypic coefficient of variation measures the extent of variation present in the population. Estimate of PCV is an indication of total variability, while GCV provides a valid basis for assessment and comparison of the genetic variability for the traits studied. Small magnitudinal difference between genotypic and phenotypic coefficients of variation indicates a low environmental influence on character expression therefore the reliability of selection based on phenotypic performance for that character.

In the present study, the PCV values were higher than GCV for all the characters indicating variable environmental influence on phenotypic expression under open and partial shade conditions (Table 20 and 21). High GCV and PCV values were recorded for characters like yield per plant, number of primary branches and pod number under open and partially shaded conditions. Similar result for seed yield, pod number and number of branches per plant was obtained by Muthuswamy *et al.* (2019). Sneha *et al.* (2019) reported high GCV and PCV values for seed yield and pods per plant, while the values were moderate for number of primary branches. Under open condition, two more characters *viz.,* secondary branches per plant and harvest index showed high range of genotypic and phenotypic coefficients. The magntidinal difference between GCV and PCV was narrow for characters like protein content, yield per plant, days for blooming, days to maturity and number of pods per plant under both conditions.

Estimates of GCV ranged from 3.29 to 46.94 under open and from 2.55 to 41.78 under partial shade conditions. The highest GCV was recorded for yield per plant followed by number of pods per plant. Highest GCV for seed yield was earlier reported by Garg *et al.* (2017), Keerthiga *et al.* (2017) and Sneha *et al.* (2019). Current study showed a higher contribution of yield per plant and number of pods towards variability suggesting that selection of parents based on these traits can be utilized in crop improvement programmes to get good segregants.

100 seed weight and plant height recorded moderate GCV under both conditions and this was in accordance with findings by Garg *et al.* (2017) in green gram. Besides, total chlorophyll content exhibited moderate GCV under open condition, while characters like number of secondary branches, pod length and harvest index showed moderate range in partial shade. Lowest value for GCV was recorded for number of seeds per pod and chlorophyll content under open and shade conditions, respectively.

5.1.3. Heritability and Genetic Advance

The genetic variability in terms of coefficients of variation alone is not sufficient for the determination of the amount of heritable variability. Heritability measures the extent of contribution of genotype to the total phenotypic variation in a population and provides information about the transmission of traits from parents to progeny. Therefore, estimation of heritability and genetic advance as per cent of mean is also needed to assess the heritable portion of total variation and to predict the extent of genetic gain expected under selection.

In the present investigation, the heritability values ranged from 20.70 to 97.21 per cent under open condition. High heritability was observed for most of the characters except days to flowering and pod length which exhibited moderate range, while number of seeds per pod recorded low value for heritability. Total chlorophyll content (97.21 per cent) recorded the highest heritability followed by yield per plant (94.78 per cent) and number of pods (82.94 per cent). High heritability estimates for yield per plant, pod number, number of days for blooming and plant height was reported by Govardhan *et al.* (2018) and Sneha *et al.* (2019).

Under partial shade, all the characters showed moderate to high range of heritability. High heritability was recorded for yield per plant (94.27 per cent) followed by protein content (93.91), number of pods per plant (83.45), days to maturity (77.24) and number of primary branches per plant (74.74). Four characters *viz.,* number of secondary branches (59.45 per cent), harvest index (56.74), pod length (49.44) and chlorophyll content (35.25) showed moderate heritability. Ramakrishnan *et al.* (2018) earlier reported similar results for yield, 100 seed weight and number of seeds per pod, but they recorded moderate heritability for pod number along with a high estimate of heritability for pod length.

Genetic advance as per cent of mean was high for yield per plant, number of pods per plant, harvest index, 100 seed weight and number of primary and secondary branches per plant under both open and partial shade conditions, which indicates additive gene action for these characters. The results were in accordance with the findings of Sneha *et al.* (2019) except for number of primary branches which recorded a medium GAM. Low estimates of GAM was observed for days for blooming, 50 per cent flowering, seed number and pod length under open condition, while total chlorophyll content showed a low value under partial shade. Keerthiga *et al.* (2018) earlier reported low estimates of GAM for days to fifty per cent flowering and seed number.

High heritability coupled with high genetic advance was recorded for yield per plant, harvest index, number of primary branches, number of pods per plant, chlorophyll content, 100 seed weight and number of secondary branches per plant under open condition, whereas characters like yield per plant, number of primary branches, number of pods per plant, 100 seed weight and plant height showed high heritability coupled with high genetic advance under partial shade indicate their importance in further selection. Similar findings were earlier reported by Garg *et al.* (2017).

The results of the present investigation reveal that direct selection based on characters like yield per plant, harvest index, number of primary branches, number of pods and number of secondary branches per plant will be rewarding under open condition as they scored high GCV and heritability coupled with GAM. Whereas high estimates of genetic parameters were recorded for three characters *viz.,* yield per plant, number of pods and number of primary branches per plant under partial shade reflecting the scope for selection based on them.

5.1.4. Correlation Studies

The knowledge about the association between yield and its contributing characters is needed for an efficient selection strategy. Correlation coefficient measures the nature and magnitude of the relationship between yield and other attributing traits. It also provides information on inter-relation among them. Selection based on a particular trait of interest will lead to the simultaneous improvement of other correlated characters in the same direction of selection.

Correlation analysis of fourteen quantitative characters was carried out under open and partial shade conditions in green gram. The values of genotypic correlation coefficients were higher than the corresponding phenotypic correlation coefficients for all characters studied which indicate a strong association between these traits genetically.

Yield per plant highly significant positive correlation with characters like harvest index, pods per plant, protein content, number of primary and secondary branches per plant, whereas the association of yield per plant was negative with days for blooming and plant height. Pod length and days to maturity showed a significant positive association with seed yield under open condition. A significant positive correlation of number of pods, pod length with single plant yield was earlier reported by Sneha *et al*. (2019) where plant height showed a positive association with yield. Strong positive correlation between 100 seed weight and pod length indicates the possibility of simultaneous improvement of these characters. The result was in accordance with findings obtained by Muthuswamy *et al*. (2019).

Under partial shade condition, association of yield per plant was positive and highly significant with characters like harvest index, plant height, number of pods per plant, chlorophyll content, pod length, number of secondary branches per plant and days to maturity. Nand and Anuradha (2013) reported a positive correlation of yield with pods per plant, pod length and days to maturity. The number of primary branches per plant exhibited a negative correlation with seed yield per plant. The result was in contradiction with the findings of Sandhya and Saravanan (2019). A highly significant positive correlation between pods per plant and seed number implies that selection based on pod number simultaneously improve number of seeds per pod.

5.1.5. Path Analysis

Correlation analysis does not reveal the exact picture on the relative significance of individual characters towards yield. Path coefficient analysis is a powerful statistical tool for selection as it partitions the correlation coefficients into direct and indirect effects of characters on seed yield.

In this study, yield per plant was taken as the dependent variable, whereas characters like number of primary branches, secondary branches per plant, number of days for blooming, days to maturity, pod per plant, pod length, plant height, harvest index and protein content were considered as independent variables.

Under open condition, high direct effect on seed yield was recorded for harvest index followed by number of pods per plant. Characters like days to maturity, pod length and number of primary branches per plant exhibited low positive direct effect, while plant height and days for blooming showed a negative direct effect on yield. The findings were in contradiction to the results obtained by Nand and Anuradha (2013) who reported negative direct effect of branch number and pod number with yield. However, the result was in agreement with findings recorded by Sneha *et al.* (2019) except for pod length.

High indirect effect was recorded for number of pods per plant and protein content though harvest index on yield per plant. A low residual effect (0.09) was found in the study, which implies the contribution of the traits towards variability. The results of path analysis along with other genetic parameters suggest that direct selection of early flowering, bushy plants with high harvest index, seed yield and number of pods per plant will be rewarding for future crop improvement programmes in green gram.

Summary

6. SUMMARY

Green gram is one of the leading annual food legumes of tropical and subtropical regions of the world. It is an important kharif and summer crop in India and grown in rotation with wheat and rice or intercropped with other crops. As an edible crop, mung is highly preferred for consumption as it contains dietary protein, fibre along with minerals and complement staple rice diet. On account of its low input requirement, photo insensitivity and dense canopy, green gram assumes special significance in crop intensification, diversification and sustainability of production systems.

The present investigation entitled "Genetics analysis in green gram (*Vigna radiata* (L.) Wilczek)" was conducted at Department of Plant Breeding and Genetics, College of Agriculture, Vellayani, during 2018-20 to study the variability parameters and performance of green gram genotypes collected from different regions under open and partially shaded conditions, for yield and protein content.

Two simultaneous field experiments were undertaken to assess the performance of 30 genotypes of green gram under open and partial shade conditions. Intercropping is done in coconut garden with an average of 57 per cent shade in order to provide required partial shade. The genotypes procured from NBPGR and nearby State Agricultural Universities were evaluated in randomized block design with three replications. The seeds were dibbled on raised beds at a spacing of 30 x 15 cm in September, 2019. Each genotype was considered as a treatment and observations were taken from five randomly selected plants from each plot.

Analysis of variance using mean values of the data disclosed significant difference among the genotypes for all the characters studied. A pooled analysis was also conducted to compare the performance of genotypes under open and partially shaded conditions. Characters like emergence percentage, number of primary branches, secondary branches per plant, days for blooming, pods per plant, pod length, 100 seed weight, yield per plant, chlorophyll content, plant height, number of harvest, abnormal, unfilled pods per plant and specific leaf area showed significant difference in performance between open and partial shade conditions.

Under open and partially shaded conditions, PCV values were found to be higher than their corresponding GCV values for all the traits studied indicating variable influence of environment in character expression. The highest genotypic coefficient of variation (GCV) was observed for yield per plant (46.94, 41.78) under open and partially shaded conditions, respectively followed by number of primary branches per plant (31.85, 24.98) and number of pods per plant (29.89, 30.53). Seed yield per plant, number of primary branches and pods per plant exhibited high PCV. The estimate of heritability was high for most of the characters studied under growing conditions. High heritability coupled with high genetic advance was recorded for yield per plant, number of primary branches, number of pods per plant and 100 seed weight under both conditions whereas, under open conditions, two more characters such as number of secondary branches per plant and chlorophyll content also showed high heritability with high genetic gain.

Correlation coefficient measures the strength and direction of association between two or more variables. The character yield per plant was found to be highly significant and positively correlated with harvest index, number of pods per plant, number of secondary branches per plant and pod length both at genotypic and phenotypic levels under open and partially shaded conditions indicating their importance in yield enhancement. Path coefficient analysis was conducted using yield as the dependent variable and other characters as independent variables. The study revealed that, harvest index and number of pods per plant had a high positive direct effect on seed yield per plant, followed by days to maturity, pod length and number of primary branches per plant. Number of pods per plant reported high positive indirect effect on yield per plant through harvest index. The results of path analysis along with other genetic parameters suggest that, direct selection of early flowering, bushy plants with high harvest index, seed yield and number of pods per plant will be rewarding for future crop improvement programmes in green gram.

The results of the present study revealed the existence of a considerable amount of variation among the thirty green gram genotypes under open and partially shaded conditions. The genotype BGS 9 was found to be superior in yield performance under open condition which was on par with the genotype IC 282124 followed by the genotype K7. Under partially shaded condition, the genotype K7 recorded the highest yield and was on par with the genotype BGS 9 and IC 282124. In terms of protein content, the highest value was recorded for genotype K10 (28.56 per cent) under open condition and genotype K13 (31.19 per cent) under partial shade condition. The superior genotypes identified in the study can be utilized as such after further trials or as parents for crop improvement programmes to develop superior varieties.

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GENETIC ANALYSIS IN GREEN GRAM
(*Vigna radiata* (L.) Wilczek)

by

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(2018-11-020)

ABSTRACT

Submitted in partial fulfilment of the
requirement for the degree of

MASTER OF SCIENCE IN AGRICULTURE

Faculty of Agriculture
Kerala Agricultural University

DEPARTMENT OF PLANT BREEDING AND GENETICS

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KERALA, INDIA

2020

ABSTRACT

The study entitled “Genetic analysis in green gram (*Vigna radiata* (L.) Wilczek)” was conducted at the Department of Plant Breeding and Genetics, College of Agriculture, Vellayani during 2018-2020. The study was carried out to assess the existing genetic variability and performance of different genotypes of green gram under open and partially shaded conditions and to identify the best genotype in terms of yield and protein content.

Two simultaneous field experiments under open and partially shaded conditions were conducted during 2019-2020. Intercropping is done in coconut garden with an average of 57 per cent shade in order to provide required partial shade. Thirty green gram genotypes procured from NBPGR, New Delhi and nearby State Agricultural Universities were assessed in a randomized block design, replicated thrice. The seeds were dibbled on raised beds in the field at a spacing of 30 cm x 15cm and each genotype was considered as individual treatment. Very few pests and pathogen attack was observed in the field for which control measures were taken up.

The thirty genotypes were evaluated for eighteen characters and their mean values were recorded. Analysis of variance, estimation of genetic parameters such as genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability and genetic advance, correlation analysis and path coefficient analysis were carried out. A pooled analysis was also conducted to compare the performance of genotypes for each character in open and partially shaded conditions.

Variability analysis revealed the existence of a considerable amount of variability for yield per plant, plant height, number of pods per plant, harvest index and days to maturity under both open and partially shaded conditions, whereas number of secondary branches and chlorophyll content showed narrow range of variation. Emergence percentage was more under partial shade than open condition. Likewise, plant height, specific leaf area and chlorophyll content exhibited an increase under partial shade compared to those under open condition.

Estimates of phenotypic coefficient of variation were higher than corresponding genotypic coefficient of variation for all the characters studied. The highest GCV was recorded for yield per plant under both open and partially shaded conditions, respectively followed by number of primary branches per plant and number of pods per plant. High heritability was recorded for most of the characters studied under both growing conditions. High heritability coupled with high genetic advance as per cent of mean was recorded for yield per plant, number of primary branches, number of pods per plant and 100 seed weight under both conditions, whereas under open condition, two more characters such as number of secondary branches per plant and chlorophyll content also showed high heritability with high genetic gain.

The character yield per plant was found to be highly significant and positively correlated with harvest index, number of pods per plant, number of secondary branches per plant and pod length both at genotypic and phenotypic levels under open and partially shaded conditions indicating their importance in yield enhancement. Path analysis was carried out using yield per plant as the dependent variable and other characters as independent variables. The study revealed that, harvest index and number of pods per plant had high positive direct effect on seed yield per plant, followed by days to maturity, pod length and number of primary branches per plant. High indirect effect was recorded for number of pods per plant on yield per plant through harvest index.

The results of the present study revealed the presence of ample variability among the thirty green gram genotypes under open and partially shaded conditions. The genotype BGS 9 was found to be superior in yield performance under open condition which was on par with the genotype IC 282124. Under partially shaded condition, the genotype K7 recorded the highest yield and was on par with the genotypes BGS 9 and IC 282124. When protein content was assessed, maximum value was recorded for genotype K10 under open condition and genotype K13 under partially shaded condition. The superior genotypes identified in the present study can be utilized as such after further trials or as parents for crop improvement programmes to develop superior varieties.

സംഗ്രഹം

“ചെറുപയറിലെ ജനിതകവിശകലനം” എന്ന വിഷയത്തിൽ ഒരു പഠനം വെള്ളായണി കാർഷിക കോളേജിലെ ഇൻസ്ട്രക്ഷണൽ ഫാർമിൽ നടത്തുകയുണ്ടായി. വിവിധ ചെറുപയർ ഇനങ്ങളിലെ ലഭ്യമായ ജനിതക വൈവിധ്യം മനസിലാക്കുക, തനിവിളയായും ഇടവിളയായും കൃഷി ചെയ്യുമ്പോൾ വിളവിലും പ്രോട്ടീൻ സാന്നിധ്യത്തിലും മികച്ച ഇനങ്ങളെ കണ്ടെത്തുക എന്നിവയായിരുന്നു പഠനത്തിന്റെ ലക്ഷ്യങ്ങൾ.

വിവിധ സംസ്ഥാന കാർഷിക സർവ്വകലാശാലകൾ, നാഷണൽ ബ്യൂറോ ഓഫ് പ്ലാന്റ് ജനറ്റിക് റിസോഴ്സസ് എന്നീ സ്ഥാപങ്ങളിൽ നിന്നും ശേഖരിച്ച 30 ചെറുപയർ ഇനങ്ങളാണ് പഠനത്തിനായി ഉപയോഗിച്ചത്. സെപ്തംബർ, 2019 – ജനുവരി, 2020 മാസങ്ങളിൽ, 30 ട്രീറ്റ്മെന്റുകളും മൂന്നു തവണ ആവർത്തിച്ചു റാൻഡമൈസ്ഡ് ബ്ലോക്ക് ഡിസൈൻ എന്ന രീതിയിലാണ് പഠനം നടത്തിയത്. ഓരോ ജനിതക ഇനങ്ങളും ഓരോ ട്രീറ്റ്മെന്റുകളായി കണക്കാക്കി. ഒരേ സമയം, തുറസ്സായ സ്ഥലത്ത് തനിവിളയായും ചോല ലഭിക്കുന്ന തെങ്ങിൻ തോപ്പിൽ ഇടവിളയായും കൃഷി ചെയ്ത് വിശകലനം നടത്തുകയുണ്ടായി.

ജനിതക ഇനങ്ങളിലെ വൈവിധ്യത്തിന്റെ വ്യാപ്തി അറിയാൻ വിവിധ സ്റ്റാറ്റിസ്റ്റിക്കൽ രീതികൾ അവലംബിച്ചു. തനിവിളയായും ഇടവിളയായി നടുമ്പോഴും ഉള്ള താരതമ്യ പഠനത്തിനായി പൂൾഡ് വിശകലന രീതിയും അവലംബിക്കുകയുണ്ടായി. വിളവ്, ചെടിയുടെ ഉയരം, കായ്കളുടെ എണ്ണം, ഹാർവെസ്റ്റ് ഇൻഡക്സ്, പൂർണ വളർച്ച

എത്താൻ എടുക്കുന്ന സമയം എന്നിവ കൂടിയ അളവിൽ വൈവിധ്യം രേഖപ്പെടുത്തി. തെങ്ങിൻ തോപ്പുകളിൽ ഇടവിളയായി നടുമ്പോൾ എമെർജൻസ് പെർസെന്റേജ്, ചെടിയുടെ ഉയരം, സ്പെസിഫിക് ലീഫ് ഏരിയ, ഹരിതകത്തിന്റെ അളവ് തുടങ്ങിയവയിൽ വർദ്ധനവ് ഉണ്ടായതായി മനസിലാക്കാൻ സാധിച്ചു.

വിളവ്, പ്രാഥമീയ ശാഖകളുടെ എണ്ണം, കായ്കളുടെ എണ്ണം, 100 വിത്തുകളുടെ തൂക്കം തുടങ്ങിയവയിൽ ഉയർന്ന ഹെറിറ്റബിലിറ്റിയോടൊപ്പം ഉയർന്ന ജനറ്റിക് അഡ്വാൻസും രേഖപ്പെടുത്തി. കൂടാതെ, ചെറുപയറിലെ വിളവ് ഹാർവെസ്റ്റ് ഇൻഡക്സ്, കായ്കളുടെ എണ്ണം, പൂർണവളർച്ച എത്താനെടുക്കുന്ന സമയം, പ്രാഥമിക, ദ്വിതീയ ശാഖകളുടെ എണ്ണം, കായയുടെ നീളം എന്നിവയുമായി നേരിട്ട് ബന്ധപ്പെട്ടിരിക്കുന്നുവെന്നും മനസിലാക്കാൻ സാധിച്ചു.

ഈ പഠനത്തിന്റെ പ്രധാന കണ്ടെത്തലുകൾ ഇവയാണ്. പഠനത്തിനായി തിരഞ്ഞെടുത്ത 30 ജനിതക ഇനങ്ങൾ നിരീക്ഷിച്ച എല്ലാ സ്വഭാവങ്ങളിലും വ്യതാസങ്ങൾ കാണിക്കുന്നു. തനിവിളയായി നടുമ്പോൾ, BGS-9 എന്ന ജനിതക ഇനവും ഇടവിളയായി നടുമ്പോൾ K7 എന്ന ഇനവും മികച്ച വിളവ് നൽകി. തനിവിളയായും ഇടവിളയായും നടുമ്പോൾ ഏറ്റവും കൂടുതൽ പ്രോട്ടീൻ രേഖപ്പെടുത്തിയത് യഥാക്രമം K10, K13 എന്നീ ഇനങ്ങളാണ്. ഈ പഠനത്തിലെ കണ്ടെത്തലുകൾ ചെറുപയറിലെ തുടർ പഠനങ്ങൾക്ക് വിനിയോഗിക്കാവുന്നതാണ്.