GENERATION MEAN ANALYSIS IN YARD LONG BEAN (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) FOR YIELD AND QUALITY

by

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(2016-12-004)

THESIS

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DECLARATION

I, hereby declare that this thesis entitled **"GENERATION MEAN ANALYSIS IN YARD LONG BEAN (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) FOR YIELD AND QUALITY"** is a bonafide record of research work done by me during the course of research and that the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar title, of any other University or Society.

Vellayani,

Date: 8.06.2018

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CERTIFICATE

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LIST OF ABBREVIATIONS

%	Per cent
m^2	Square metre
KAU	Kerala Agricultural University
cm	Centimeter
$Plant^{-1}$	Per plant
g	Grams
Pod^{-1}	Per pod
et al	And others
ml	millilitre
L	Litre
N	Normality
mg	milligram
mg/ g	milligram per gram
nm	nanometre
i.e.,	That is
g^{-1}	Per gram
$year^{-1}$	Per year
% weight loss	Per cent weight loss
Fig.	Figure
F_1	First filial generation
F_2	Second filial generation
g $plant^{-1}$	Gram per plant
viz.	Namely
SE	Standard Error
t ha^{-1}	Tonnes per hectare
Kg	Kilo gram

Introduction

1. INTRODUCTION

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt; 2n=24), a distinct form of cowpea, is one of the most important leguminous vegetable crops originated from Central Africa and widely distributed in India, Indonesia, Philippines and Srilanka. It is an annual food legume belonging to the family Fabaceae and the genus *Vigna*, which comprises of about 80 species. According to Verdcourt (1970), *Vigna unguiculata* is sub divided into four subspecies namely *V. unguiculata* subsp. *cylindrica* (grain cowpea), *V. unguiculata* subsp. *unguiculata* (bush cowpea), *V. unguiculata* subsp. *sesquipedalis* (yard long bean) and *V. unguiculata* subsp. *dekindtiana* (black eyed pea). Yard long bean developed from common cowpea, which is considered to have the centre of genetic diversity in South East Asia. It is called as 'vegetable meat', being a rich and inexpensive source of vegetable protein (3.5 g), calcium (72 mg), iron (2.5 mg), riboflavin (0.09 mg), phosphorus (59 mg) and vitamin A (564 mg 100 g^{-1} of edible pod) (Yamaguchi, 1983). Cowpea is widely grown in China, South and South East Asia. Because of its quick growth habit and enrichment of soil fertility by fixing atmospheric nitrogen (70 – 240 kg ha^{-1} of nitrogen $year^{-1}$), it has become an essential component of sustainable agriculture.

Trailing type of vegetable cowpea or yard long bean, vernacularly known as 'Achingapayar', 'Kurutholapayar', 'Vallipayar', 'Pathinettumaniyan' etc., is one of the most popular and remunerative vegetable crop traditionally grown in Kerala, evenly distributed and preferred in all the 14 districts. It is cultivated mainly for crisp and tender pods which are consumed in cooked form. It is one of the most favourite vegetable crop as it ensures a stable market throughout the year.

Cultivar improvement in self-pollinated species, such as yard long bean, is accomplished by inducing genetic variability and then selectively recombining

desirable genotypes. Yield components that have significant association with yield could be used as a selection criteria to increase yield of a crop, particularly cowpea. Singh and Dabas (1992) opined that green pod yield and protein content in vegetable cowpea are complex traits governed by polygenic inheritance, affected by environment. In general, exploitation of heterosis in vegetable cowpea is difficult because of poor crossing success and less number of seeds per pod. However, homozygous lines equal to or better than F_1 hybrids revealing transgression from highly heterotic crosses of self-pollinated cowpea can be developed.

Prerequisite for the effective choice of breeding methodology for developing elite varieties is the understanding of the mode of inheritance of the yield components. Appropriate breeding procedure can be used for the improvement of the trait based on the gene action involved in the expression of the trait. Generation mean analysis, which provide the estimates of main gene effects (additive and dominance) along with their digenic interactions (additive × additive, additive × dominance and dominance × dominance) helps to understand the nature of gene effects involved in different traits of concern and accordingly the breeding procedure could be applied in developing superior populations. Experiments carried out in the Department of Vegetable Science, College of Agriculture, Vellayani have identified promising crosses with better yield and quality in yard long bean. With this background, the present project was undertaken to study the inheritance of yield and quality and to understand the gene action controlling these traits in order to suggest the proper breeding method for improving these traits. Therefore, the present experiment was undertaken with the following objectives:

1. Estimation of genetic variability among the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two crosses (VS 50 x VS 34 and VS 50 x VS 26).

2. To investigate the genetic basis and inheritance pattern of vegetative, flowering, yield and quality characters of the generations in two elite cowpea crosses.

3. To estimate the gene effects controlling yield and quality components using six parameter model.

4. To identify the most suitable breeding methods for improving the traits.

Review of literature

2. REVIEW OF LITERATURE

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) is one of the most popular and remunerative vegetable crop traditionally grown in Kerala. It is a trailing crop grown for crisp and tender pods and is an inexpensive source of vegetable protein, consumed in cooked form. It is widely grown in China, South and South East Asia. In general, exploitation of heterosis in vegetable cowpea is difficult because of poor crossing success and less number of seeds pod^{-1}. However, homozygous lines equal to or better than F_1 hybrids revealing transgression from highly heterotic crosses of self-pollinated cowpea can be developed (Singh and Dabas, 1992).

The present study has been undertaken to estimate the gene effects controlling yield and quality components using six parameter model. The literature available for generation mean analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and quality are reviewed and presented under the following headings -

2.1 Gene Action

2.2 Generation Mean Analysis

2.3 Variability studies in cowpea

2.1 GENE ACTION

Gene action refers to the way in which certain genes exert their effects on the plant system. They could be dominant, or recessive, or they could be sex-linked or be involved in chromosomal aberrations. A combination of such gene actions results in the observable phenotype of an organism. Gene action is the mode of expression of genes in a genetic population. It is of two types, additive and non - additive gene

action. Additive gene action included additive genetic variance and additive x additive type of epistatic variance whereas dominance genetic variance, additive x dominance and dominance x dominance types of epistatic variance comes under non - additive gene action.

Quantitative characters controlled by gene action can be measured using gene models. The first model suggested by Fisher (1918) included dominance at a single locus where the model by Fisher *et al.* (1932) describe gene action of any number of genes on a character. Gene models were also suggested to evaluate the additive and dominance gene effects by Comstock and Robinson (1948) and Mather (1949). Models developed by Anderson and Kempthorne (1954), Hayman (1958) and Gamble (1962) described the importance of epistatic effects for quantitative characters.

A comparative study was conducted by Pornsuriya (1994) on genetic inheritance of pod quality and yield in crosses between yardlong bean and cowpea. Using the three parental lines, KU8 (yardlong bean), B1 and IT86D - 325 (cowpea), the F_1, F_2 progenies and backcrosses were obtained. B_1 gave the highest fresh and frozen pod firmness but low yield, KU8 gave high yield but rather low pod firmness, while IT86D - 325 was the lowest in both yield and pod firmness. The results showed that variation due to additive gene action was found on all characters whereas dominant gene action was significant in some characters only.

Umaharan *et al.* (1997) studied the gene action involved in the pod quality characteristics in vegetable cowpea using a 6 x 6 diallel mating design and reported that for all pod characteristics both the gene action was observed while for pod seediness the additive gene action was high. The non-additive gene action for pod wall thickness was unidirectional, in the direction of the thin walled parent. The study showed that the improvement of characters can be done after the careful selection of parents for hybridization.

In 10 x 10 diallel analysis of cowpea, Sobha and Vahab (1998) observed the predominance of both additive and non-additive gene action for plant height, primary branches, days to flowering, pod length, pod weight, pods plant^{-1}, seeds pod^{-1}, 100-seed weight and yield plant^{-1}. Among the parents and hybrids used Arka Garima, VU-18, Selection 263, Pusa Komal and Kanakamoni, VU-18 x Arka Garima and Selection 2-1 x VS 389 were found superior for yield and yield attributes.

Kumar *et al.* (1998a) reported the predominance of additive gene actions for most of the characters under study except green pod yield plant^{-1} in an 8 x 8 diallel cross of cowpea excluding reciprocals. The parents, var. 263, Sel.2-2, IHR Sel.11, Pusa Komal and BC-244002 were selected as promising ones for number of characters including pod yield plant^{-1} while the crosses Sel.2-2 x Arka Garima, Sel.2-2 x IHR Sel.16, var. 263 x Sel.2-2, var. 263 x Arka Garima and IHR Sel.11 x IHR Sel. 16 for earliness and other desirable characters including pod yield plant^{-1}.

Kumar *et al.* (1998b) studied the genetics of green pod yield in cowpea for two seasons and reported both additive and non-additive gene action. The presence of additive (D) component indicated the presence of dominance in the expression of green pod yield. Combining ability and component analysis suggested non-additive gene action for controlling the green pod yield plant^{-1} whereas graphical analysis revealed over dominance.

Combining ability analysis for yield and different quality traits in vegetable cowpea conducted by Manivannan and Sekar (2005) and found that in the line IC 201099, additive variance is significant for characters such as green pod yield plant^{-1}, number of pods plant^{-1}, pod length, pod weight, number of branches plant^{-1}, protein content and crude fibre. Arka Garima, the tester, showed the highest additive variance for days to first flowering, pod weight, pod length, green pod yield, protein content

and crude fibre. The two hybrids, IC 201099 x Arka Garima and IC 201099 x Co-2 were identified for heterosis breeding.

Kumar and Sangwan (2005) reported the predominance of non-additive gene action for the expression of characters such as cluster plant^{-1}, pods cluster^{-1}, 100-seed weight, seed yield plant^{-1}, seeds pod^{-1} and pods plant^{-1} in cowpea. Pusa Phalguni x GC-3 was selected as a promising hybrid based on the characters.

Venugopal and Goud (2005) studied the inheritance of anthocyanin and chlorophyll pigmentation in the cowpea cross, P -737-2 x V-23. Monogenic ratio, duplicate ratio and tri-genic duplicate ratio was obtained for different pod characters. Pigmentation on peduncle surface, stipules and unripe pod colour showed pleiotropy and differential gene action.

The study conducted by Patil and Navale (2006) using line x tester analysis in cowpea reported the predominance of non-additive gene action for days to maturity, number of branches plant^{-1}, seeds pod^{-1} and seed yield plant^{-1} while additive gene action for 50 per cent flowering, plant height, plant spread, pods plant^{-1}, pod length and test weight.

Combining ability in cowpea was studied by Valarmathi *et al.* (2007) for yield and yield traits and reported the predominant role of non-additive gene action on twelve quantitative traits studied *viz.* days to 50% flowering, days to maturity, plant height, number of branches plant^{-1}, clusters plant^{-1}, pods cluster^{-1}, pod length, seed pod weight, green pod yield, seeds pod^{-1}, hundred seed weight and seed yield. For the trait green pod yield, parents belonging to *Vigna unguiculata* ssp. *unguiculata*, - GP1024, GP1238 and GP739 and *Vigna unguiculata* ssp. *sesquipedalis*, - Vyjayanthi and VS 33 were identified as promising while the hybrids GP 1231 x VS 33, GP1024 x Vyjayanthi, GP 739 x Vyjayanthi and GP 1126 x Lola were found to be superior ones.

Romanus *et al.* (2008) studied the combining ability among crosses derived from seven selected cowpea lines and reported the predominance of additive gene action for governing yield and yield attributes. Additive gene action was important for eight characters namely, days to flowering, grain filling period, number of nodules, pods plant^{-1}, pod length, seeds pod^{-1}, and 100-seed weight.

Patel *et al.* (2008) conducted genetic analysis of pod yield and its component characters in vegetable cowpea and reported the predominance of both additive variance and non-additive variance for characters like pod yield plant^{-1}, leaf area, branches plant^{-1}, plant height, pods plant^{-1} and protein content.

An experiment was conducted to study genetic variance and heterosis from a cross of landraces and cultivar parents of cowpea using four generations, F_1, F_2, BC_1 and BC_2 (Aremu and Adewale, 2010). Characters like flowering, maturity period, branching *etc.*, showed partial dominance recording higher additive components over dominant.

Genetic variability studies in F_2 and F_3 generations of cowpea cross, V-1188x Goa local was conducted by Shashidhar *et al.* (2010) and found that most of the characters *viz.,* plant height, braches plant^{-1}, canopy spread and 100 seed weight were controlled by additive gene action. Wide variation was observed in segregating generation for all the yield attributing traits studied and concluded that most productive genotypes in segregating generation could be identified after stabilization and evaluation.

In a line x tester analysis, Meena *et al.* (2010) studied combining ability in vegetable cowpea using 10 diverse lines and 4 testers and observed the prevalence of additive gene action for characters like number of pods plant^{-1}, 10 pod weight and pods cluster^{-1}, while for remaining characters including pod yield plant^{-1}, the non – additive gene action was prominent.

Combining ability for seed yield and related traits in cowpea was studied by Ushakumari *et al.* (2010). Non- additive gene action was reported for the traits *viz.* plant height, pods plant^{-1}, clusters plant^{-1}, pod length, 50 per cent flowering, number of seed pod^{-1} and yield plant^{-1}. TC 49-1, Lola, and VBN 1 were identified as promising parents for plant height, days to 50 per cent flowering, pods plant^{-1}, clusters plant^{-1}, pod length and seeds plant^{-1}.

Yadav *et al.* (2010) studied heterosis and inbreeding depression in 8 x 8 diallel mating system in cowpea and found that heterosis for green pod yield was due to the heterosis of yield components such as dry matter in pod, pod cluster^{-1} and pods plant^{-1}. The expression of the character was controlled by non- additive gene action. It was inferred that for rapid fixation of dominant genes and to break undesirable linkages, inter-mating in F_2 and resulting generation will be advantageous to improve the green pod yield in cowpea.

Gene action in dual purpose cowpea (*Vigna unguiculata* (L.) Walp.) for leaf yield and quality attributes was studied by Noubissie *et al.* (2011). All the characters were controlled by additive gene action except the crude protein content of the leaf, which indicated that the cross having maximum positive *gca* effect will give the best progeny. Predominance of non-additive gene action was observed for leaf protein, which could be improved through heterosis breeding.

According to Vaughan *et al.* (2011), for a systematic crop improvement programme, the nature and degree of gene action involved in the expression of earliness is essential. The inheritance and genetic control of earliness in cowpea was studied using diallel analysis and for the traits days to flowering and days to maturity, presence of additive and non –additive gene action was reported.

Combining ability for seed yield and its components of eight genetically divergent parental strains of cowpea was studied by Chaudhari *et al.* (2013) using

diallel analysis and revealed the significance of both additive and non-additive variances for seed yield plant^{-1} and its related traits. Higher magnitude of non-additive variance for seed yield plant^{-1} and its contributing traits indicated the predominant role of non-additive gene action in the inheritance of the traits.

Gene action in *Vigna unguiculata* was studied by Subbiah *et al.* (2013) and reported the presence of additive effect for traits such as days to flowering, number of branches plant^{-1}, number of pods plant^{-1}, pod length, pod weight, crude fibre content of the pods and green pod yield plant^{-1}, both additive as well as dominant gene action for plant height and dominant gene action for crude protein content.

Idahosa and Alika (2013) evaluated six agronomic characters in *Vigna unguiculata* genotypes and reported the predominance of both the gene actions (additive and non-additive) for all the characters studied. *Ekp-br* was found promising for pod length, *325* for seed weight and *ILCA-12648* for days to flowering and seeds pod^{-1}.

Sharma *et al.* (2013) studied the genetics of pod character in vegetable cowpea using line x tester analysis and reported that additive gene action controlled both the pod length and pod weight whereas non-additive gene action controlled number of pods cluster^{-1} and number of pods plant^{-1}.

Patel *et al.* (2013) studied the gene action of seed yield and related attributes in cowpea (*Vigna unguiculata* (L.) Walp.) using six generations. Presence of different gene effects for the inheritance of the same trait in different crosses and for different traits in the same cross was observed. Importance of both additive and non-additive gene action suggested that breeding methods involving high volume crossing like biparental, recurrent and diallel selective mating design were found to be more promising for the improvement of various characters studied.

Patel *et al.* (2013) conducted combining ability analysis in a half diallel mating system in cowpea using 9 parents and revealed that different characters studied in most of the high yielding hybrids were controlled by non-additive gene action. GC-4 and CGD-381 were found to be promising parents for seed yield and its related traits. Out of the hybrids, GC-4 x CGD-84, GC-4 x CGD-16 and CGD-1 x CGD-381 were selected as superior ones.

Eight cowpea (*Vigna unguiculata* (L.) Walp.) genotypes were used to study the inheritance pattern of leaf shape, pod shape, pod colour and seed coat colour (Emeka, 2014). Leaflet shape was found to be monogenically controlled with the lanceolate leaflet shape dominant over the ovoid. Coiled pods were dominant over straight pods and the F_2 generation segregated in a 3:1 ratio. Purple pods were dominant to brown pods while all the seed coat colours were monogenically controlled.

Khanpara *et al.* (2015) evaluated sixty diverse genotypes of vegetable cowpea and observed that additive gene action governed green pod yield plant^{-1}, plant height, pod length, pod width, number of seeds pod^{-1}, number of pods plant^{-1}, ten pod weight, number of pods cluster^{-1} and hundred fresh seed weight and non-additive gene action governed 50 per cent flowering, days to first green pod picking and number of seeds pod^{-1}.

Genetic analysis of fodder yield and associated traits in fodder cowpea [*Vigna unguiculata* (L.) Walp.] was done by Sanjeev *et al.* (2015) using line x tester analysis. They confirmed the predominance of non-additive gene action for all the characters studied. CPD-31, MFC-09-09 and EC-458505 were identified as promising lines while NBC-2, IC-1071 and EC-170578-1-1 were the promising testers.

Patel *et al.* (2016) conducted genetic analysis in three crosses of cowpea for seed related attributes. Single gene inheritance was found for traits *viz.,* flower colour,

seed surface, pod beak colour and calyx pigmentation while two gene interactions with supplementary gene action for seed colour and pod colour at maturity. Predominance of dominance gene action in different characters suggested its suitability as a good marker for different breeding activities.

In a line x tester analysis of cowpea, Pethe *et al.* (2018) reported the preponderance of non -additive gene action for all characters *viz.* days to first flowering, days to 50 per cent flowering, days to maturity, numbers of flowers plant^{-1}, number of pods plant^{-1}, number of branches plant^{-1}, number of pods cluster^{-1}, grain yield plant^{-1}, biological yield plant^{-1}, seed protein content, tryptophan content and harvest index. The lines CPD-83 and tester GS- 9240 were found promising for grain yield plant^{-1} and most of the yield related traits. Importance of non-additive gene action was observed in the inheritance of the traits studied.

2.2 GENERATION MEAN ANALYSIS

The biometrical method, generation mean analysis was developed by Mather and Jinks (1982) for determining the gene effects for polygenic traits. The analysis is based on the six generations of the cross used *i.e.*, P_1 and P_2 (parents), F_1, F_2 and their backcrosses (BC_1 and BC_2). For the estimation of gene effects, the mean values over the replication is used. Generation mean analysis, which provides the estimates of main gene effects (additive and dominance) along with their digenic interactions (additive x additive, additive x dominance and dominance x dominance) helps in understanding the nature of gene effects involved in different traits of concern and accordingly the breeding procedure could be applied in developing superior populations. It helps in deciding the most convenient breeding method for the enhancement of various quantitative characters.

Umaharan *et al.* (1997) evaluated the pod yield and its components among the F_2 and backcrosses of a cross between two vegetable cowpea (*Vigna unguiculata* (L.)

Walp.) varieties to understand the genetic basis of these characters. The additive, dominance and additive x additive genetic components were estimated for pod yield and clusters plant^{-1} using four-parameter model and found that additive and additive x additive effects were positive and larger than the dominance component. The relatively large additive and the predominantly positive dominant effects suggest that selection will be more effective. The study suggested that vegetable cowpea improvement programmes should focus on selecting for clusters plant^{-1} and average pod weight in the early generations, while selection for dry pod yield could be delayed to later generations.

Inheritance of yield and yield contributing characters investigated by Rahman and Saad (2000) using generation mean analysis in four crosses of *Vigna sesquipedalis* revealed the presence of dominance (h) gene action compared to additive (d) gene action for pod yield plant^{-1} and pods plant^{-1} in the crosses KU 7 x KU 8 and L 30 x CSL 19. Different crosses exhibited positive significance of additive gene action for the traits *viz.*, pod yield plant^{-1}, pods plant^{-1}, pod weight and seed weight. Role of dominance gene action in the inheritance was indicated by the lower F_2 means than their corresponding F_1 means, with a few exception in majority of yield components. In case of pod yield plant^{-1} and pods plant^{-1}, predominance of additive x additive and dominance x dominance type of digenic epistatic interactions was observed. Pedigree selection and heterosis breeding is suggested to exploit the fixable and non-fixable components of variation respectively in *Vigna sesquipedalis*.

Genetic analysis was done for yield and yield related traits in mungbean (*Vigna radiata* (L.) Wilczek) in two sets of crosses by Khattak *et al.* (2004) using generation mean analysis. Additive (d) and dominant (h) components of genetic variation were significant for all the traits in both the crosses, except for branches plant^{-1} and 1000 seed weight in the cross ML-5 x NM 54 and for pod bearing nodes on main stem in the cross 6601 x NM 92, dominant (h) being predominant.

Complementary type of epistasis was found for seed yield plant^{-1} in both the crosses whereas duplicate type of epistasis for pod cluster plant^{-1} and 1000 seed weight in cross 6601 x NM 92, and 1000 seed weight in cross ML-5 x NM 54. Biparental hybridization between recombinants in F_2 generation could be used for the production of better genetic combination.

Philip (2004) observed the predominance of one or more multiple epistatic interactions in all characters in cowpea through generation mean analysis. In most of the characters such as days to 50 per cent flowering, number of pods inflorescence^{-1}, number of seeds pod^{-1}, 100 seed weight, plant height and crude fibre content, additive gene action was significant. Dominance effect and dominance x dominance interaction suggested the presence of non-allelic duplicate gene action in the expression of all characters expect peduncle length whereas complimentary gene action plays the important role in case of peduncle length.

Genetic analysis of yield and mosaic resistance in yard long bean was conducted by Lovely (2005) and reported the presence of all the three digenic interactions for pods plant^{-1} and pod yield plant^{-1}. The presence of non- allelic duplicate gene action was suggested for pod weight, pod breadth, pods cluster^{-1}, seeds pod^{-1}, root weight plant^{-1} and days to first harvest by the direction of dominance effect and dominance x dominance interaction.

Genetic analysis of traits related to drought resistance in cowpea was conducted by Chozin *et al.* (2006) using generation mean analysis by crossing two genotypes having contrasting drought resistance. Generation mean analysis of traits, which were good discriminators for drought resistance *viz.,* stem diameter, delayed leaf senescence and leaf temperature, was done and the presence of additive effect in controlling these traits was suggested. The presence of dominance, additive-additive and additive-dominance effects were found significant for stem diameter, whereas additive-dominance effect was the only additional effect for leaf temperature.

Heritability and gene effects was studied by Aliyu (2007) using generation mean analysis for incorporating pubescence from *V. rhomboidea* into cowpea (*Vigna unguiculata* (L.) Walp.) using a cowpea variety and two accessions of *Vigna rhomboidea*. Inheritance of pubescence was found to be governed by one and two genes and the additive gene action was observed to be higher than the dominance gene action for all the traits in both the crosses (IT82D716 x TVnu 515 and IT82D716 x TVnu 1473). High heritability and significant and higher additive gene effects suggested the suitability of backcross selection method for the development of pubescent cowpea lines. Studies showed the predominance of additive gene action for incorporating pubescence into cowpea whereas dominant and epistatic gene action also had significant effect.

A study was conducted by Mittal and Bhardwaj (2008) to estimate gene effects in cowpea genotypes by generation mean analysis. Joint scaling tests revealed the presence of epistasis for pod length, pods plant^{-1}, pods cluster^{-1}, days to flowering, days to maturity, 100-seed weight and seed yield plant^{-1}.

Omo-Ikerodah *et al.* (2008) studied the gene action of resistance to flower bud thrips (FTh) in cowpea. Two FTh-susceptible and resistant lines were crossed in all possible combinations for resistance evaluation. Six generations, P_1, P_2, F_1, F_2, BCP_1, and BCP_2, for each cross were produced in the greenhouse. Estimates of the six parameters using generation mean analysis showed significance of both the additive and dominance gene effects for the inheritance of desirable traits studied. Among the various gene effects, dominance gene effects were higher than the additive gene effects. Inheritance of resistance to thrips was found to be controlled by additive x additive and dominance x dominance gene effects.

Generation mean analysis was conducted by Adeyanju (2009) to study the genetics of harvest and leaf-yield indices in cowpea (*Vigna unguiculata* (L.) Walp). Three cultivars IAR-00-1074 (good fodder yield) and IT93K-499-35 and

IT93K-452-1 (high grain yield) were used to understand and identify the appropriate breeding method based on the gene action controlling the two traits. The predominance of dominance effects along with low heritability and genetic advance suggested that selection could not be used in the traits, harvest index and leaf -yield index for the early-segregating generations. The appropriate method to utilize non-additive gene action was multiple crossing followed by selective mating of early generations plants.

Jithesh (2009) conducted generation mean analysis in yard long bean to study the genetic basis and inheritance pattern of important quantitative and qualitative characters for resistance to pod borers and yield. For characters such as days to 50 per cent flowering, days to first harvest and primary branches plant^{-1}, the presence of non-allelic interaction was observed. The presence of dominance and dominance x dominance interaction suggested the occurrence of non-allelic duplicate gene action for characters such as crop duration, main stem length, pod clusters plant^{-1}, pod weight and pod breadth. Additive x dominance gene action was significant for peduncle length whereas additive gene effect found to be significant for crude fibre content of pods.

Ojo *et al.* (2009) studied the inheritance of seed yield, yield related characters, their correlation and the number of genes controlling each trait in six generations of cowpea and observed that there was significant difference for all the traits evaluated. A positive mid-parent heterosis was observed for seed yield, number of seeds and number of pods plant^{-1} in addition to transgressive segregation for seed yield plant^{-1} in the F_2 generation and convergence of genes on the recurrent parent. The number of pods and seed yield plant^{-1}, which showed relatively high narrow sense heritability estimates, were adjudged the best predictors for seed yield among the four yield related characters evaluated.

Gene effects of grain and fodder productivity in dual purpose cowpea was estimated using generation mean analysis by Adeyanju *et al.* (2012) using two crosses. In the first cross, presence of dominance gene action was found for all the traits except for plant height and seed weight, whereas dominance x dominance gene effect in case of second cross. Presence of both additive and non-additive gene effects were found for fodder yield plant^{-1}. Predominance of duplicate type of gene action was observed in the inheritance of traits *viz.,* plant height, leaf weight and branch weight whereas complementary type of gene action for grain yield. Reciprocal recurrent selection was suggested as the most effective approach for the improvement of fodder and grain yield.

Generation mean analysis was performed to understand the gene actions of seed size in cowpea by Egbadzor *et al.* (2013) using CB27 (large seeded) and Gh3710 (small seeded) parents. It was concluded that eight genes control 100 seed weight in cowpea and that small seed size showed partial dominance over the large one. Except additive – additive interaction, additive and non-additive gene effects along with their interactions were found to be significant. Single seed descent and backcross methods followed by selection was found to be the appropriate method to improve the seed size of cowpea.

Generation mean analysis followed by scaling test was conducted by Singh (2014) to study the gene action for yield and yield contributing traits in cowpea (*Vigna unguiculata* (L.) Walp.) using three families, PGCP-12 x PGCP-14 (Family 1), Pant Lobia-1x PGCP- 14 (Family 2), Pant Lobia-1x Pant Lobia-3 (Family 3). For most of the quantitative characters in all the three families, estimates of additive [d] and dominance [h] effects as well as all three epistasis were found to be significant. For seed yield and related traits, additive and non-additive gene actions were involved. The additive gene action found in the traits showed that a part of the heterosis can be fixed in subsequent generations to take advantage in further

selection. The preponderance of non-additive gene action brought out that heterosis component could be explained in hybrid development in cowpea.

The study conducted by Behra (2015) to determine the gene effects and interaction of genes in various generations of soybean cross, JS 97-52 × JS 93-05, revealed that additive and dominance gene effects were predominant for yield traits. For traits *viz.,* days to 50% flowering, days to physiological maturity, number of primary branches plant^{-1}, plant height, number of pods plant^{-1}, number of seeds plant^{-1}, hundred seed weight, seed yield plant^{-1}, biological yield plant^{-1} and harvest index, both the additive and dominance gene affects were important whereas for number of pods plant^{-1}, number of seeds plant^{-1} and seed yield plant^{-1}, additive × additive and dominance × dominance were found be important. Type of gene interaction was found to be different in traits. Complimentary type of interaction found in days to 50% flowering, number of pods plant^{-1} and number of seeds plant^{-1} while non allelic duplicate type of interaction was predominant for days to physiological maturity, plant height, primary branches plant^{-1}, hundred seed weight, seed yield, biological yield plant^{-1} and harvest index.

Generation mean analysis conducted by Kaur (2017) for studying the genetic analysis for studying the gene effects for dual purpose traits in cowpea (*Vigna* unguiculata (L.) Walp.). Additive gene effects were found for traits such as plant height, green fodder yield, acid detergent fibre and neutral detergent fibre in the cross CL367 x GC89, for plant height and vine length in GC89 x C88 and for plant height and number of leaves in GC88 x CL400. Presence of high magnitude of non- allelic interactions (additive x additive, additive x dominance and dominance x dominance) were observed for characters plant height, vine length and green fodder in GC 89 x CL367, for characters vine length and green fodder yield plant^{-1} in GC89 x C88 and for green fodder yield plant^{-1}, vine length and number of leaves in

GC89 x CL400 and pedigree method was found to be the best breeding procedure for development of dual purpose cultivars in cowpea.

Generation mean analysis was undertaken to understand the gene action in the inheritance of yield and yield related attributes of cowpea (Gupta *et al.*, 2017). Six basic generations of five crosses, namely Pant lobia-1 x BRDCP-11 (cross I), Pant lobia-2 x GC-3 (cross II), Waghi local x W-203-1 (cross III), KM-5 x GC-3 (cross IV) and GC-3 x CDP-107 (cross V) were used for the study. Higher significance of dominant gene action along with duplicate type was observed than additive gene action for all the traits studied *viz.*, days to 50 % flowering, number of pods plant^{-1}, days to maturity, number of seeds pod^{-1}, 100 seed weight (g), seed yield plant^{-1} in most of the cases. In the inheritance of quantitative characters in cowpea, both the gene actions (additive and non-additive) was found to contribute significantly.

2.3 VARIABILITY STUDIES

Fresh pod yield and pod related traits was studied by Peksen (2004) using eight local genotypes and two registered cowpea cultivars, observed highest fresh pod yield plant^{-1} of 110.23 g plant^{-1} (G10). Plant height varied from 62.80 cm (Kirazlikz) to 120.90 cm (G10). G10 recorded highest average pod weight, pod length, pod width, pod thickness and no of branches plant^{-1}. Considering pod setting, G18 (57.03 days) was the earliest whereas Doganca (73.33 days) was the late. Shortest duration of pod harvest was observed in Duragan (59.00 days). Karagoz-86 recorded the highest number of pods plant^{-1}.

Resmi *et al.* (2005) studied the genetic divergence among yard long bean genotypes using Mahalanobis D^2 statistic. Broad variability was observed for traits *viz.*, vine length (249.00 to 439.48 cm), number of primary branches (3.43 to 4.07), petiole length (11.24 to 9.66 cm), length and breadth of lateral leaflet (13.63 to 12.58 cm and 6.62 to 8.33 cm respectively) and days to flowering (48.50 to 51.93 days).

Pod length, pod girth, pods kg^{-1}, pods $plant^{-1}$ and pod yield $plant^{-1}$ varied significantly (41.75 to 48.49 cm, 24.64 to 28.98 mm, 39.50 to 54.98, 39.50 to 54.98, 60.88 to 92.00 and 1.39 to 2.31 kg respectively).

Padi and Marfo (2005) studied the growth characteristics on which selection for seed yield could be based on early maturing cowpea. Significant differences between the fourteen early maturing cowpea genotypes and between locations (Damongo, Manga, Nyankpala and Wa) could be observed for all the traits studied except for genotypic differences in biological yield. Days to flowering and reproductive duration varied from 40 to 46 days and 21 to 26 days (Damongo), 44 to 53 days and 16 to 25 days (Manga), 42-49 days and 19 to 23 days (Nyankpala) and 35 to 46 days and 23 to 28 days (Wa) respectively.

Significant variability for pods $cluster^{-1}$, yield $plant^{-1}$, pod weight, number of pods $plant^{-1}$ and clusters $plant^{-1}$ in the range of 0.42 (VS 21) to 4.78 (VS 19), 21.03 g (VS 8) to 406.06 g (VS 41), 3.27 g (VS 7) to 26.49 g (VS 20), 3.09 (VS 21) to 45.41 (VS 30) and 3.12 (VS 20) to 22.32 (VS 14) respectively respectively was reported among fifty genotypes of cowpea by Lovely (2005).

Dhanasekar and Pandey (2005) reported that among the 40 cowpea genotypes including the fifteen mutants of cultivar VS-130 evaluated, plant height ranged from 19 cm to 135.4 cm, no of branches from 1.5 to 5.8 and leaf area from 2843.9 mm^2 to 9340.5 mm^2. Pod length, pods $plant^{-1}$ and yield $plant^{-1}$ varied significantly between 5.0 - 28.3 cm, 7.3 - 18 cm and 5.2 - 29.7 kg. Seeds pod^{-1} ranged from 6.0 - 16.1 and 100 seed weight from 7.5 g - 22.9 g. Days to first flowering and days to maturity exhibited significant variability with range of 32.0 – 47.0 days and 58.0 – 92.0 days respectively.

Characterization of vegetable cowpea was done by Manju (2006) and observed highest yield (1136.89 g) and pods $plant^{-1}$ (102.59) for VS 8 (CHCP-l), and extremely long pods (76.08 cm), pod girth (4.43 cm), vine length (6.17 m), 100- seed

weight (20.77 g), and seed length (13.03 mm) for VS 19 (Aryanad, Thiruvananthapuram). The highest pod weight (43.60 g) and highest number of seeds pod^{-1} (21.34) was recorded for VS 4 (Kanjikuzhi payar).

Twenty two cowpea genotypes were characterized using morphological characters and chemical tests by Swami (2007). High variability was also observed for biological yield and seed yield in different locations. Among the twenty four traits studied, terminal leaflet shape, leaf surface, plant habit, stem colour, flower colour, pod shape, number of pods plant^{-1}, days to 50 per cent flowering, seed shape, seed crowding and eye pattern were found to be the most important diagnostic characters for the identification of cowpea genotypes.

Halemani (2009) assessed the extent of genetic diversity among 40 cowpea genotypes. Plant height was in the range of 18.60 cm to 37.20 cm with a mean of 24.24 cm. Number of primary branches plant^{-1}, pod length, number of seeds pod^{-1} and hundred seed weight was maximum in DCG-1 (4.50, 20.22 cm, 15.90 and 23.25 g respectively) and minimum in DCG-20 (1.70, 11.79 cm, 8.90 and 8.45 g respectively). Number of pods plant^{-1} varied from 4.10 in DCG-36 to 19.70 in DCG-1 and protein content from 12.69 per cent (DCG-26) to 24.39 per cent (DCG-40).

Jithesh (2009) assessed the genetic variability among fifty genotypes of yard long bean and reported wide range of genetic variability for pod length (12.88 to 52.72 cm), pod weight (8.20 to 27.73 g), pods plant plant^{-1} (5.73 to 14.33), pod clusters plant^{-1} (4.07 to 9.13), pod yield plant^{-1} (170.33 to 415.33 g) and hundred seed weight (7.33 to 19.73 g).

Mishra and Dash (2009) conducted genetic variability studies in thirty three genotypes of yard long bean and observed wide variation in vine length (271.67 to 504.40 cm), branches plant^{-1} (2.23 to 5.08) and nodes branch^{-1} (24.36 to 48.69). Yield parameters varied significantly *viz*., green pods plant^{-1} (23.96 to 60.86), green pod

length (35.20 to 57.31 cm), green pod weight (11.31 to 27.30 g), 100-seed weight (9.88 to 19.68 g), protein content of green pod (5.19 to 6.50 per cent) and green pod yield plant^{-1} (0.33 to 1.40 kg). Days to first flowering ranged from 45.67 to 73.33 days and inflorescences plant^{-1} from 15.05 to 34.52.

Wide range of genetic variability for pod yield (4 to 11 t ha^{-1}), number of pods m^{-2} (70 to 261), number of pods plant^{-1} (21.83 to 37.51), pod length (14.42 to 23.30 cm), pod width (2.15 to 3.21 cm) and 100 seed weight (8 g to 16 g) was observed by Nwofia (2012) in nine vegetable cowpea cultivars on an ultisol.

Genetic variability studies by Manggoel *et al.* (2012) in ten cowpea accessions revealed that all the character studied were significantly different. Fifty per cent flowering ranged from 43.87 to 62.45 days and flowers plant^{-1} from 65.55 to 74.56. Pods plant^{-1}, seeds pod^{-1}, pod length and hundred seed weight varied significantly between 42.78 to 50.54, 9.58 to 14.88, 15.75 to 19.58 cm and 13.68 to 18.65 g respectively.

Peksen and Peksen (2012) evaluated twelve cowpea lines developed from twenty seven local genotypes. Days to first flowering varied between 52.42 days in Karagöz-86 and 64.25 days in L9. Karagöz-86, L12, Akkız-86, L13, L3 and L14 recorded early pod setting. The tallest genotypes were L2 and L3, while the shortest were L4 and Akkız-86. L13 and L2 produced significantly more numbers of pods plant^{-1} and the mean ranged between 10.82 and 19.92. L3 recorded maximum pod length which ranged from 11.40 to 14.11 cm for the genotypes. Fresh pod yield ranged from 18.0 t ha^{-1} (L3) and 4.48 t ha^{-1} (L1).

Fifty six accessions of yard long bean were evaluated by Hossain *et al.* (2013) to understand the extent of genetic diversity. Wide variability was observed for traits such as days to first flowering which ranged from 36.11 to 41.67 days, and days to pod maturity from 44.33 to 51.89 days. Pods plant^{-1}, pod length and pod girth showed a

range of 12.22 to 37.35, 9.32 to 91.87 cm and 1.52 to 3.68 cm respectively. Seeds pod^{-1}, hundred seed weight and yield plant^{-1} exhibited significant variability with a range of 8.33 to 19.33, 8.50 to 22.33 g, 66.78 to 957.60 g respectively.

Makanur *et al.* (2013) in a study to understand the extend of genetic diversity in thirty five genotypes of cowpea, observed wide variability for traits like days to first flowering (45.33 to 55.67 days), plant height (9.93 cm to 29.88 cm), branching ability (3.67 to 7.17), number of clusters plant^{-1} (17.67 to 69.83), number of pods peduncle^{-1} (1.33 to 3.00), number of pods plant^{-1} (23.47 to 107.00), days to maturity (82.33 to 97.33 days) and pod length (12.53 cm to 25.77). Seeds pod^{-1} ranged from 9.53 to 20.08. The seed yield plant^{-1} ranged from 20.94 g (Mumbai local) to 110.01 g (IC253181) with a mean of 57.69 g, while seed yield per hectare from 564.1 kg (Mumbai local) to 3194.4 kg (IC202881), with an average yield of 1405.4 kg.

Significant variability was reported by Sahai *et al.* (2013), in a study to evaluate morphological and yield attributes among 168 cowpea genotypes, for traits such as early plant vigour, number of primary branches, number of leaves plant^{-1}, biomass plant^{-1}, days to flower initiation, 100 seed weight, pod length, number of pods plant^{-1} *etc.*

Fourty four diverse genotypes of yard long bean (*Vigna unguiculata* (L.) Walp) were evaluated by Sivakumar (2012) and recorded highest yield (1125.52 g) and maximum number of pods per plant (87.09) in VS 29. Pod length (91.67 cm), pod girth (4.63 cm) and pod weight (67.07 g) were maximum in VS 45, with less number of pods per plant. Significant difference was observed among the genotypes with respect to yield and related characters. Protein content varied significantly from 9.22 per cent (VS 29) to 3.17 per cent (VS 32). Keeping quality was maximum in VS 5 (5.17 days) and minimum in VS 12 (3.07 days).

Hinge *et al.* (2015) conducted studies on genetic divergence in nine yard long bean genotypes grown under Konkan agro climatic conditions of Maharashtra. DPL-YLB-8 showed the highest values for number of pods plant^{-1} (120.67), number of pickings (11.33), harvesting duration (47.00 days), pod length (56.84 cm), number of seeds pod^{-1} (18.73), weight of flesh pod^{-1} (12.71 g), pod yield plant^{-1} (1.69 kg), pod yield plot^{-1} (16.93 kg) and pod yield hectare^{-1} (23.52 t) and protein content (4.40 %) with lowest number of days from anthesis to horticultural maturity (10.00 days). Highest total leaf area (16751.88 cm), leaf area index (2.33), earliness for first flowering (61.70 days after sowing), fifty per cent flowering (64.00 days after sowing), earliness for harvest (71.00 days after sowing), highest pod girth (3.09 cm), weight of tender green pod (17.65 g), weight of grains pod^{-1} (5.95 g) and moisture content (90.00 %) was recorded in the genotype DPL-YLB-5. Highest vine length was recorded by the genotype DPL-YLB-3 (450.33 cm), while the highest number of primary branches plant^{-1} by DPL-YLB-4 (25.60). Less variation was observed for protein content (2.64 to 4.40 per cent) and fibre content (11.34 to 16.47 per cent).

Evaluation of one hundred and thirty four accessions of cowpea from eight geographical origins of Ghana and selection of accessions with desirable qualitative and quantitative characters was done by Cobbinah *et al.* (2015). Majority of the accessions studied flowered within 39 to 44 days. At Pokuase and Bunso, mean terminal leaflet length (100.4 mm and 99.94 mm), terminal leaflet width (69.71 mm and 64.21 mm), peduncle length (294.20mm and 250.11mm), mean 100 seed weight (11.44g and 14.32g), yield plant^{-1} (20.04g and 23.53g), pod length (153.70 mm and 157.72 mm), no of pods plant^{-1} (22.74 and 26.37) and seeds plant^{-1} (20.04 and 23.53) were recorded.

Meena *et al.* (2015) investigated 72 cowpea [*Vigna unguiculata* (L.) Walp.] germplasm to study the extent of genetic diversity through ten quantitative characters and reported significant variability among the characters with respect to seed yield and its components traits.

In yard long bean, days to 50% flowering varied from 45.33 to 59.67 with a mean of 52.37 days, days to first green pod picking from 57.00 - 79.00 days with a mean of 67.27 days, green pod yield plant^{-1} from 11.21 to 233.20 g with a mean of 105.87 g, number of primary branches plant^{-1} from 2.85 - 7.85 with a mean of 4.70, plant height from 28.65 - 74.5 cm with a mean of 44.21 cm, pod length from 10.30 - 21.40 with a mean of 14.99 cm, pod weight from 19.54 - 97.42 g with a mean of 43.15 g and pod width from 0.56 - 0.92 cm with a mean of 0.69 cm. Green pod yield plant^{-1} ranged from 11.21 to 233.20 with a mean of 105.87 g. Number of seeds pod^{-1} ranged from 9.00 - 14.40 with an average of 11.26 and hundred fresh seed weight from 13.30 - 39.12 g with an average of 25.37 g (Khanpara *et al.*, 2015).

Genetic vaiability studied by Litty (2015) in 30 yard long bean accessions, including 18 landraces, three KAU varieties and nine hybrids/ varieties collected from private seed firms revealed that variety Rani was the earliest for flowering (30.41 days) and harvest (40.65 days) under poly house. Anad Local had the highest yield (1627.12 g). Highest pod length (85.07 cm) and pod weight (64.77 g) was observed in the variety, Super Green. Neyyattinkara Local recorded highest number of pods plant^{-1} whereas highest pod girth was for NS -634. Primary branches plant^{-1} and petiole length significantly varied from 3.95 to 6.57 and 14.27 cm to 21.27 cm respectively. The protein content varied significantly from 4.82 (VS 34) to 8.46 per cent (VS 50) and keeping quality ranged from 3.41 (VS 44) to 4.77 days (VS 42).

Morphological characterization of forty one genotypes of yard long bean was done by Rambabu *et al.* (2016) as per minimal descriptors of NBPGR developed for cowpea and noticed that maximum plant height was recorded by IC-582889 and minimum by Bhagya Lakshmi. Days to 95 per cent pod maturity was maximum in IC582827, IC-5828435, IC-582839, and IC-582875 (65.00 days) and minimum in IC-582862 (56.66 days). Pod length was maximum for IC-582850, whereas IC-582859 recorded maximum pod girth. Both pod length and pod girth was observed minimum for Bhagya Lakshmi. 100 seed weight was maximum for IC-582872 (19.61g) and the

check, Bhagya Lakshmi recorded the minimum (8.83g). Seed protein significantly varied with maximum content in IC-582861 and minimum in the genotype IC-582844. IC-582859 (2495.00 g) recorded the maximum pod yield plant^{-1} while Bhagya Lakshmi (904.87 g) recorded the minimum.

Khandait *et al.* (2016) reported that plant height varied from 11.18 to 14.06 cm, 25.88 to 33.57 cm and 44.72 to 62.88 cm at 30, 60 and 90 DAS respectively among fifteen genotypes of vegetable cowpea. Number of branches plant^{-1} ranged from 1.40 to 2.73, 2.53 to 4.26 and 6.25 to 7.80 respectively at 30, 60 and 90 DAS. Wide range of genetic variability was observed among the genotypes, pod yield plant^{-1} (153– 240 g), followed by pod yield ha^{-1} (85.13–134.39 q), number of pods plant^{-1} (29.33–77.0), number of flower clusters plant^{-1} (11.90–49.66), pod weight (28.33–63.0 g), pod length (14.87–33.28 cm), plant height at 90 DAS (44.72–62.88 cm), days to first picking (80.00–90.67 days), plant height at 60 DAS (25.88–33.57 cm), days to 50% flowering (64.00–70.00 days), days to first flowering (55.33–59.33 days), pod yield plot^{-1} (6.13–9.68 kg), number of flowers cluster^{-1} (2.93–5.53), plant height at 30 DAS (11.18–14.06 cm), number of pods cluster^{-1} (1.53–3.46), number of branches at 60 DAS (2.53–4.26), number of branches at 90 DAS (6.26–7.80) and number of branches at 30 DAS (1.40–2.73)

A study was conducted by Rajput (2016) to estimate the genetic variability, heritability and genetic advance for yield and its attributing characters in cowpea and to identify suitable and better performing genotypes for central zone of India. Mean number of days to first flowering was 38.97 days with a range of 34.33 to 43.00 days. The earliest for 50 cent flowering (46.67 days) was recorded in genotype 2014/COPBVAR-5 while the maximum was for Gomti and Shalini (54.00 days). Wide variability was observed in number of flowers cluster^{-1} and number of flower clusters plant^{-1} which ranged from 2.73 (Lobia Banarsi) to 5.07 (2014/COPBVAR-1) and 34.0 (2014/COPBVAR-1) to 12.73 (Lobia Banarsi) respectively. Mean value for number of pods cluster^{-1}, number of pods plant^{-1}, pod length, pod width, pod weight,

number of seeds pod^{-1}, pod yield plant^{-1}, pod yield plot^{-1} and pod yield ha^{-1} were 2.77, 25.13, 27.08 cm, 0.76 cm, 5.58 g, 10.68, 139.86 g, 5.57 kg , 77.38 q ha^{-1} respectively.

Chandrakar *et al.* (2016) conducted studies for genetic divergence in twenty one genotypes of vegetable cowpea and reported that 50% flowering ranged from 69.42 to 46.37 days with an average mean of 54.37. Plant height was observed from 221.72 to 99.033 cm with mean of 181.62 cm. Number of flowers plant^{-1} and number of pods plant^{-1} ranged from 29.73 to 17.56 and 14.89 to 7.41 respectively. Wide variation was observed for pod length and pod weight from 33.49 cm to 10.19 cm and 18.59 g to 10.88 g respectively. Green pod yield ranged from 114.71 g to 67.51 g.

Genetic variability analysis for yield and yield related traits in 28 F_1 hybrids, 8 parents and a check of yard long bean was done by Lakshmi (2016). The highest yield (848.74 g plant^{-1}) and pods plant^{-1} (56.67) was observed in VS 29 among the eight parents. VS 50 recorded the highest pod weight (27 g) and pod length (66.28 cm). Maximum pod protein was recorded in VS 16 (6.44 per cent) while VS 38 had the best keeping quality. The highest yield was recorded in the hybrid VS 34 x VS 50 (1414.55 g per plant). Maximum number of pods plant^{-1} (107.17) and pod protein (7.01 per cent) was observed in VS 34 x VS 13. VS 50 x VS 16 (30.67 g) recorded highest pod weight whereas VS 54 x VS 26 had the maximum pod length (71.27 cm). VS 13 x VS 38 exhibited highest keeping quality.

Evaluation of ten hybrids along with a standard check variety (NS 634) in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) was done under rainshelter and open conditions by Feba (2017). Both in open field (1058.20 g plant^{-1}) and under rainshelter (689.67 g plant^{-1}) highest yield plant^{-1} was recorded in VS 34 x VS 50 followed by VS 50 x VS 26. Maximum pod length and girth in open field (69.36 cm and 3.34 cm respectively) as well as under rainshelter (68.42cm and 3.24 cm respectively) was recorded for VS 54 x VS 26. VS 50 x VS 13 recorded In both open field and rainshelter, VS 50 x VS 13 recorded the highest pods per plant

(72.27 and 55.67 respectively), fruit set percentage (66.55 per cent and 56.80 per cent respectively) and pollen viability (94.35 per cent and 90.70 per cent respectively).

Materials and Methods

3. MATERIALS AND METHODS

The experiment entitled "Generation mean analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and quality" was conducted at the Department of Vegetable Science, College of Agriculture, Vellayani, Thiruvananthapuram, Kerala, during 2017-2018. The objective was to study the inheritance and gene action of yield and quality in yard long bean using generation mean analysis.

The study was conducted as three parts:

Part-1 - Production of F_1 hybrids

Part-2 - Production of F_2 progenies and back crosses

Part-3 - Generation mean analysis

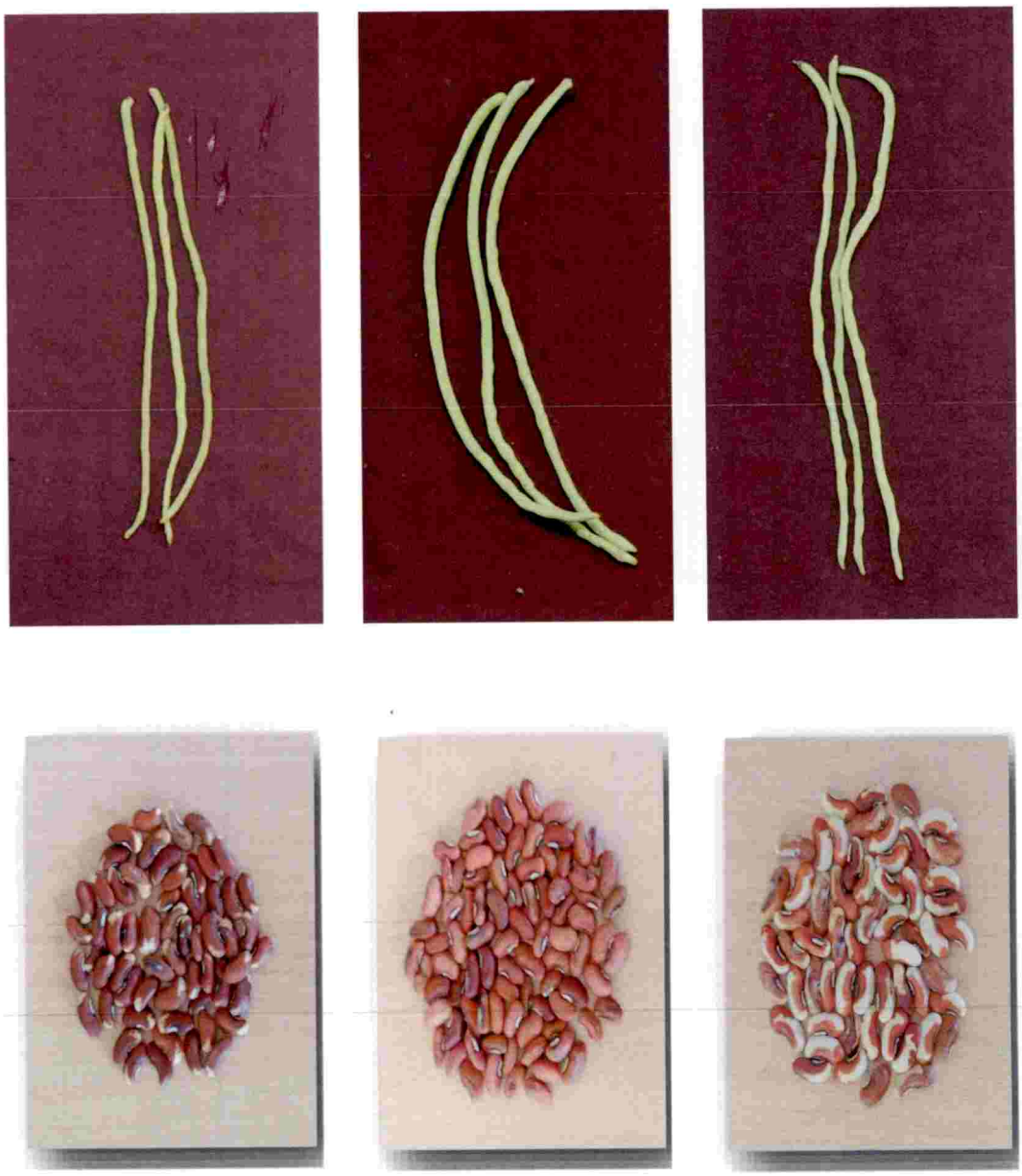
3.1 EXPERIMENTAL SITE

The experimental site was located at 8.5^0 30' North latitude and 76.9^0 54' East longitude, at an altitude of 29 m above mean sea level. Predominant soil type of the experimental site was red loam of Vellayani series, texturally classified as sandy clay loam.

3.2 PART-I PRODUCTION OF F_1 HYBRIDS

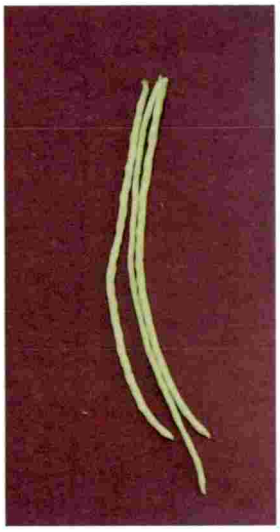
3.2.1 Materials

The materials for the study comprised of 12 treatments (P_1, P_2, F_1, F_2, BC_1 and BC_2 of two hybrids) using the parents, VS 50 (Kakkamoola Local), VS 34 (Githika), and VS 26 (Vellayani Jyothika). The details of genotypes used as parents are given in Table 1 and Plate 1. Two superior F_1 hybrids of yard long bean with high yield and quality characters *viz.* VS 50 x VS 34 (Kakkamoola Local x Githika) and VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) were selected based on specific

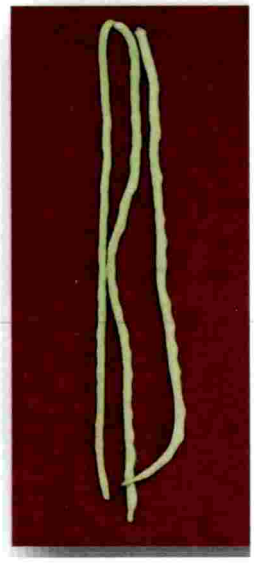


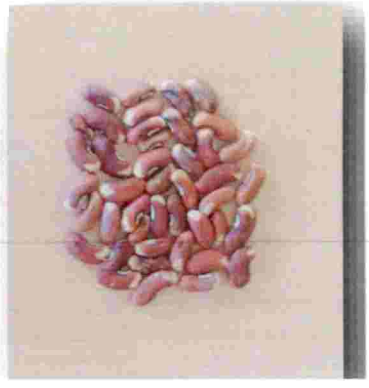
VS 50 VS 34 VS 26

Plate 1. Pods and seeds of parents used



VS 50 x VS 34





VS 50 x VS 26

Plate 2. Pods and seeds of hybrids used

Plate 3. Crossing Block I

combining ability and *per se* performance from the previous M.Sc. (Hort.) programme "Development of hybrids in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt)". The seeds of the two hybrids were produced in a crossing block during April 2017 – June 2017 (Plate 2).

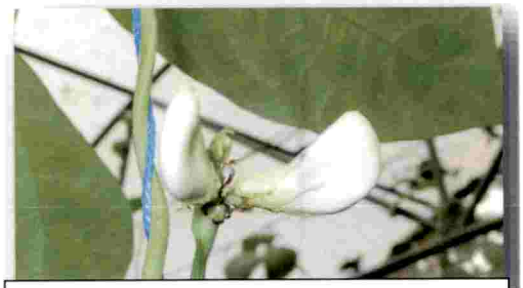
Table 1. Yard long bean accessions used as parental lines in crossing block 1

Sl.No.	Accession No.	Accession Name	Source
1	VS 50	Kakkamoola Local	Kakkamoola, Thiruvananthapuram
2	VS 26	Vellayani Jyothika	College of Agriculture, Vellayani
3	VS 34	Githika	College of Agriculture, Vellayani

3.2.2 Crossing Techniques

Yard long bean is highly self-pollinated, because of the cleistogamous flower structure, simultaneous pollen shedding and stigma receptivity. Self-pollinated nature is due to hermaphrodite sex form, homogamy and dehiscence of anther much earlier than anthesis. Stamens and pistil in opened flower remain enveloped together inside the tube like structure of joined petals called as keel, leading to cleistogamous nature. Stigma become receptive and pollen become fertile on the day of anthesis.

In the first crossing block, hand pollination was done using VS 50 as female parent and VS 34 and VS 26 as male parents (Plate 3). Flower bud due to open the next day, was selected in the female parent (VS 50). Emasculation was done in the afternoon hours by removing the keel petal. Hence butter paper bag was used to cover the bud and to prevent drying out of emasculated bud. Pollen was collected next day morning from a freshly opened flower. Pollination was done early in the morning between 6.30 am and 9.00 am. The standard petal and wing petal from the intended male parent (VS 34 and VS 26) was removed and by slight depression of the keel petal, the stigma covered with the pollen grains that protrudes was used as brush for pollination. It was brushed on the stigmatic surface of the emasculated flower. The



Mature female flower bud

Opened male flower bud

Emasculation

Pollination

Emasculation

Rebgging and tagging

Bagging

Fruit set

Plate 4. Crossing techniques

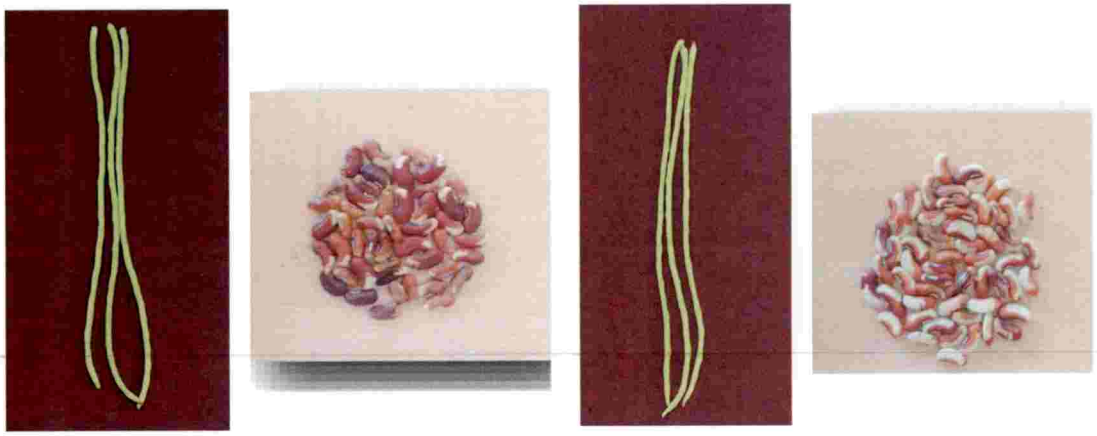
VS 50 x VS 34 (F_2)

(VS 50 x VS 34) x VS 50 (BC_1)

(VS 50 x VS 34) x VS 34 (BC_2)

Plate 5. Generations of cross VS 50 x VS 34

VS 50 x VS 26 (F_2)



(VS 50 x VS 26) x VS 50 (BC_1)

(VS 50 x VS 26) x VS 26 (BC_2)

Plate 6. Generations of cross VS 50 x VS 26

crossed flowers were covered and labeled to produce F_1 hybrids (Plate 4). At maturity stage, the seeds of both parents and hybrids were collected from the labeled pods separately. Percentage of pod set in the cross VS 50 x VS 26 is depicted in table 2.

Table 2. Percentage of pod set in the cross VS 50 x VS 26

Days of pollination	Total number of crosses made	No of pod set	Percentage of pod set (%)
1	12	3	25.00
2	9	3	33.33
3	15	5	33.33
4	13	5	38.46
5	12	4	33.33
6	11	5	45.45
7	8	2	25.00
Mean			33.41

3.3 PART-II PRODUCTION OF F_2 PROGENIES AND BACK CROSSES

3.3.1 Materials

The two F_1 hybrids VS 50 x VS 34 (Kakkamoola Local x Githika) and VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika), were selfed to produce F_2 progenies during June 2017 – August 2017. Simultaneously, the F_1 hybrids were backcrossed with female parent to produce BC_1 generation and male parent to produce BC_2 generations (Table 3 and Plate 5, 6).

Table 3. List of hybrids and back crosses

List of hybrids		
	Parents	Hybrids
Cross 1	$P_1 \times P_2$	VS 50 x VS 34
Cross 2	$P_1 \times P_3$	VS 50 x VS 26

Plate 7. Crossing Block II

List of back crosses		
	Cross 1	Cross 2
BC_1	(VS 50 x VS 34) x VS 50	(VS 50 x VS 26) x VS 50
BC_2	(VS 50 x VS 34) x VS 34	(VS 50 x VS 26) x VS 26

3.3.2 Selfing and Crossing Techniques

Both selfing and crossing techniques were involved in crossing block 2 (Plate 7). The two F_1 hybrids VS 50 x VS 34 and VS 50 x VS 26 were selfed. Flower bud due to open the next day was selected and bagging was done using butter paper bag without emasculation to prevent outcrossing in both the hybrids to produce F_2 progenies.

Backcrosses were produced by using hybrids VS 50 x VS 34 and VS 50 x VS 26 as the female parents and VS 50, VS 34 and VS 26 as male parents. Emasculation was done in the mature flower bud of female parent VS 50 x VS 34, which is due to open on the next day morning and pollination was done using VS 50 and VS 34 male parents. Similarly in the hybrid VS 50 x VS 26, VS 50 and VS 26 were used as male parents to produce backcrosses.

3.4 PART – III GENERATION MEAN ANALYSIS

3.4.1 Materials

The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two hybrids using the parents, VS 50 (Kakkamoola Local), VS 34 (Githika), and VS 26 (Vellayani Jyothika) were evaluated in a replicated field experiment using generation mean analysis.

Plate 8 a. Seedlings

Plate 8 b. Land preparation

Plate 8 c. Planting

Plate 8 d. Field view

Plate 8 d. Field view

3.4.2 Methods

3.4.2.1 Design and Layout

The experiment was laid out in randomized block design with 12 treatments (P_1, P_2, F_1, F_2, BC_1 and BC_2 of two hybrids) using the parents, VS 50 (Kakkamoola Local), VS 34 (Githika), and VS 26 (Vellayani Jyothika) from September- December 2017 (Rabi 2017).

One replication consisted of one row of parents, F_1, two rows of the back cross generations BC_1 and BC_2 and four rows of F_2. Each row consisted of 10 plants.

3.4.2.2 Field Preparation and Planting

Seedlings of six generations of the two hybrids were raised in protrays (Plate 8 a) filled with coirpeat and vermicompost (1:1 by ratio). Germinated seedlings were fertigated with 19:19:19 water soluble fertilizer @ 0.2%. Adequate irrigation was provided to maintain moisture content in the protray which is necessary for proper germination and growth of seedling. Twenty days old seedlings at 3-4 leaf stage were transplanted in the field.

The main field was prepared by thorough ploughing using power tiller and removal of weeds and stubbles (Plate 8 b). Furrows were made one metre apart and seedlings were transplanted one metre apart in the furrows. The treatments were allotted at random with three replications and 10 plants were planted in each plot of size 6.75 m^2. Transplanted seedlings were provided temporary shade for three days and net trellis for trailing (Plate 8 c). The crop was raised according to the Package of Practices Recommendations (KAU, 2016). Field view of the experiment is given in Plate 8 d.

3.4.3 Main Observations Recorded

Five plants from each treatment in the experimental field were randomly selected and tagged. The following observations were taken and the average of these five plants was worked out in each replication for statistical analysis.

3.4.3.1 Vegetative and Flowering Characters

3.4.3.1.1 Vine Length at Final Harvest (cm)

Vine length was recorded at the time of final harvest from the ground level to the top most leaf of the plants and presented in centimeters.

3.4.3.1.2 Primary Branches Plant[1]

Number of branches arising from the main stem from all the observational plants at the peak harvest stage was recorded and average was worked out.

3.4.3.1.3 Length and Breadth of Leaflets (cm)

Fifth leaf from the top of the observational plants (45 days after planting) was taken for measuring length and breadth of leaflets. Length of both terminal and lateral leaflets was measured as the distance from the base of the petiole to the leaf tip and expressed in centimeters. Breadth of leaflets was measured at the region of maximum width from the same leaflets used for measuring length and expressed in centimeters.

3.4.3.1.4 Days to First Flowering

Number of days from the date of sowing to the first flowering of observational plants was recorded and the average obtained.

3.4.3.2 Yield Characters

3.4.3.2.1 Pod Length (cm)

Five pods were selected at random from each observational plant at peak harvest period. Pod length was measured using a twine and scale as distance from the point of pedicel attachment to the apex of the pod and average worked out and expressed in centimeters.

3.4.3.2.2 Pod Girth (cm)

Pod girth was measured at the centre (using a twine and scale) from the same pods used for recording pod length, average taken and recorded in centimeters.

3.4.3.2.3 Pod Weight (g)

Pod weight taken from the same pods used for recording pod length, average taken and recorded in grams.

3.4.3.2.4 Pods Plant^{-1}

Total number of pods produced per plant till the last harvest was counted from each observational plant and average was recorded.

3.4.3.2.5 Seeds Pod^{-1}

Seeds extracted from the dried pod from the peak harvest were counted and average was worked out.

3.4.3.2.6 Hundred Seed Weight (g)

The dry weight of hundred seeds was noted using an electronic balance and was expressed in grams.

3.4.3.2.7 Yield (g plant^{-1})

Average weight of all pods harvested from the observational plants were taken and expressed in grams plant^{-1}.

3.4.3.2.8 Days to Harvest

Number of days from the date of sowing to the first harvest of the observational plants were counted and the average was taken.

3.4.3.2.9 Crop Duration

Number of days from the date of sowing to the drying of the vines of the observational plants were counted and average was taken.

3.4.3.3 Quality Characters

3.4.3.3.1 Pod Protein (%)

Pod Protein was estimated by Lowry method, developed by Lowry *et al.* (1951).

Materials

1. 2% sodium carbonate in 0.1 N sodium hydroxide (Reagent A)
2. 0.5% copper sulphate (CuS_2O_4 .$5H_2O$) in 1% sodium potassium tartrate solution (Reagent B)
3. Alkaline copper solution: Mixture of 50 ml of reagent A and 1 ml of reagent B prepared just before use (Reagent C)
4. Folin- ciaocalteau reagent (Reagent D): Straw- yellow coloured reagent was purchased commercially and stored in amber coloured bottles under refrigerated condition.
5. Protein Solution (stock standard):

The stock was prepared by dissolving 50 mg of bovine albumin serum in distilled water and made up to 50 ml in a standard flask.

6. Working standard:
   Working standard was prepared by diluting 10 ml of the stock solution in 40 ml distilled water in a standard flask. One ml working standard contains 200 micro gram protein.

Procedure

Extraction of protein from sample

500 mg of the sample was ground well using a pestle and mortar in 5-10 ml of water. The mixture was centrifuged and the supernatant was used for protein estimation.

Estimation of Protein

0.2, 0.4, 0.6, 0.8 and 1 ml of the working standard solution was pipetted out into series of test tubes while 0.1 ml and 0.2 ml of sample extract was pipetted out into two other test tubes. The volume was made upto 1 ml with water in all the tubes and the tube with 1 ml was the blank for the experiment. 5 ml of reagent C was added to all the tubes including blank and allowed to stand for 10 minutes after proper mixing. The content was mixed well after adding 5ml of reagent D and incubated at room temperature for the development of blue colour in dark for 30 minutes. The reading was taken at 660 nm. The amount of protein in the sample was calculated from the standard graph and expressed as mg g^{-1} or 100 g sample.

3.4.3.3.2 Keeping Quality

Keeping quality was determined to study the shelf life and number of days the pods remained fresh for consumption without loss of colour and glossiness. It is estimated in terms of physiological loss of weight *i.e.,* loss of weight that occur every

day was calculated and average was taken. Weight of harvested pods of all treatments kept under ordinary room condition was taken every day at a fixed time for five consecutive days.

$$\text{Physiological loss of weight} = \frac{\text{Initial weight} - \text{Final weight}}{\text{Initial weight}} \times 100$$

3.4.3.4 Incidence of Pests and Diseases

The crop was monitored for the incidence of major pests and diseases.

3.5 STATISTICAL ANALYSIS

3.5.1 Generation Mean Analysis

Components of genetic variance was done using generation mean analysis (Hayman, 1958) following scaling test (Mather, 1949). The biometrical analysis consists of two main steps, *viz.*, (i) testing for epistasis, and (ii) estimation of gene effects and variances.

3.5.1.1 Development of Scales

In generation mean analysis, the test which determine the presence or absence of non-allelic interactions and their type is known as scaling test. Additive (D) and dominance (H) components of genetic variance were estimated using mean and variance of six generations: P_1, P_2, F_1, F_2, BC_1 and BC_2. Mather (1949) has given four types of scaling tests, *viz.*, A, B, C and D as given below:

$$A = 2\overline{BC}_1 - \overline{P}_1 - \overline{F}_1$$

$$VA = 4V(\overline{BC}_1) + V(\overline{P}_1) + V(\overline{F}_1)$$

$$B = 2\overline{BC}_2 - \overline{P}_2 - \overline{F}_1$$

$$VB = 4V(\overline{BC}_2) + V(\overline{P}_1) + V(\overline{F}_1)$$

$$C = 4\,\bar{F}_2 - \bar{F}_1 - \bar{P}_1 - \bar{P}_2$$

$$VC = 16V(\bar{F}_2) + 4V(\bar{F}_1) + V(\bar{P}_2)$$

$$D = 2\bar{F}_2 - \overline{BC}_1 - \overline{BC}_2$$

$$VD = 4V(\bar{F}_2) + V(\overline{BC}_1) + V(\overline{BC}_2)$$

Here, P_1, P_2, F_1, F_2, BC_1 and BC_2 are the means over all the replications of various generations and the respective variance are represented by V ($\bar{P}_1$), V ($\bar{P}_2$), V ($\bar{F}_1$), ($\bar{F}_2$), V ($\overline{BC}_1$) and V ($\overline{BC}_2$).

The standard error of A, B, C and D is worked out by taking the square root of the respective variances, i.e., VA, VB, VC and VD.

$$\text{S.E. (A)} = \sqrt{V(A)}$$

$$\text{S.E. (B)} = \sqrt{V(B)}$$

$$\text{S.E. (C)} = \sqrt{V(C)}$$

$$\text{S.E. (D)} = \sqrt{V(D)}$$

3.5.1.2 Testing of Epistasis

The significance of any of the four scales indicates the presence of epistasis and inadequacy of additive-dominance model. The *t* values were calculated by dividing the effects of A, B, C and D by their respective standard error.

$$t\,(A) = \frac{|A|}{\sqrt{V(A)}}$$

$$t\,(B) = \frac{|B|}{\sqrt{V(B)}}$$

$$t\,(C) = \frac{|C|}{\sqrt{V(C)}}$$

$$t\,(D) = \frac{|D|}{\sqrt{V(D)}}$$

The calculated t values of the four tests are compared against the table value of t at 5 % level of significance. If the calculated values of these scales are higher than 1.96, it is considered significant and *vice versa*.

The type of epistasis is revealed by the significance of specific scale as given in Table 4.

Table 4. Significance of specific scales

Sl. No	*Scales*	*Significance*
1	A, B or both scales	Presence of all three types of epistasis, *viz.*,A x A, A x D and D x D
2	C scale	Dominance x Dominance type of epistasis (*l*)
3	D scale	Additive x Additive type of epistasis (*i*)
4	C and D scales	Additive x Additive (*i*) and Dominance x Dominance (*l*)

3.5.1.3 Analysis of Variance

The biometric observation recorded were subjected to ANOVA for the estimation of six generations used.

Source	Degrees of freedom	Sum of squares	Mean squares	F
Replication	(r-1)	SS_R	MSR	MSR/MSE
Error	(n-r)	SS_E	MSE	
Total	(n-1)	SS_T		

r - Number of replications n - Total number of observation

Error mean sum of squares (MSE) is the estimate of variance

Estimate of variance of mean = $\frac{MSE}{r}$

Standard error of mean $= \sqrt{\frac{MSE}{r}}$

3.5.1.4 Estimation of Genetic Components

A digenic interaction was assumed, when the scales A, B, C and D were significantly different from zero. Hayman (1958) and Jinks and Jones (1958) suggested a six parameter model for the estimation of various genetic components from generation means. This model provides information about all the types of non-allelic interaction, *i.e., i, j and l.*

In this model, various gene effects and variances are estimated as follows.

m = mean effects = $\bar{F}_2$

d = additive effects = $\overline{BC}_1 - \overline{BC}_2$

h = dominance effects = $\bar{F}_1 - 4\,\bar{F}_2 - \frac{1}{2}\,\bar{P}_1 - \frac{1}{2}\,\bar{P}_2 + 2\overline{BC}_1 + 2\overline{BC}_2$

i = additive x additive gene interaction = $2\,\overline{BC}_1 - 2\,\overline{BC}_2 - 4\,\bar{F}_2$

j = additive x dominance gene interaction = $\overline{BC}_1 - \frac{1}{2}\,\bar{P}_1 - \overline{BC}_2 + \frac{1}{2}\,\bar{P}_2$

l = dominance x dominance gene interaction = $\bar{P}_1 + \bar{P}_2 + 2\,\bar{F}_1 + 4\,\bar{F}_2 - 4\,\overline{BC}_1 - 4\,\overline{BC}_2$

where, $\bar{P}_1$, $\bar{P}_2$, $\bar{F}_1$, $\bar{F}_2$, $\overline{BC}_1$ and $\overline{BC}_2$ are the mean values over replication for the character in P_1 , P_2 , F_1 , F_2 , BC_1 and BC_2 population, respectively. The variance for the above gene effects are obtained as follows:

$Vm = V\,\bar{F}_1$

$Vd = V\,\overline{BC}_1 + V\,\overline{BC}_2$

$Vh = V\,\bar{F}_1 + 16\,V\,\bar{F}_2 + \frac{1}{4}\,V\,\bar{P}_1 + \frac{1}{4}\,V\,\bar{P}_2 + 4\,V\,\overline{BC}_1 + 4\,V\,\overline{BC}_2$

$Vi = 4\,V\,\overline{BC}_1 + \frac{1}{4}\,V\,\overline{BC}_2 + 16\,V\,\bar{F}_2$

$Vj = V\,\overline{BC}_1 + \frac{1}{4}\,V\,\bar{P}_1 + V\,\overline{BC}_2 + \frac{1}{4}\,V\,\bar{P}_2$

$Vl = V\,\bar{P}_1 + V\,\bar{P}_2 + 4\,V\,\bar{F}_1 + 16\,\bar{F}_2 + 16\,V\,\overline{BC}_1 + 16\,V\,\overline{BC}_2$

In the absence of epistasis (non-allelic interactions) three parameter model suggested by Jinks and Jones (1958) was used. The gene effects for three parameters, *viz.,* m, *d* and *h* were estimated using the following formulae

$$m = \tfrac{1}{2}\,\bar{P}_1 + \tfrac{1}{2}\,\bar{P}_2 + 4\,\bar{F}_2 - 2\,\overline{BC}_1 - 2\,\overline{BC}_2$$

$$d = \tfrac{1}{2}\,\bar{P}_1 - \tfrac{1}{2}\,\bar{P}_2$$

$$h = 6\,\overline{BC}_1 + 6\,\overline{BC}_2 - 8\,\bar{F}_2 - \bar{F}_1 - 3/2\,\bar{P}_1 - 3/2\,\bar{P}_2$$

The variance for these estimates are calculated as follows:

$$Vm = \tfrac{1}{4}\,V\,\bar{P}_1 + \tfrac{1}{4}\,V\,\bar{P}_2 + 4\,V\,\overline{BC}_1 + 4\,V\,\overline{BC}_2 + 16\,V\,\bar{F}_2$$

$$Vd = \tfrac{1}{4}\,V\,\bar{P}_1 + \tfrac{1}{4}\,V\,\bar{P}_2$$

$$Vh = 36\,V\,\overline{BC}_1 + 36\,V\,\overline{BC}_2 + 64\,V\,\bar{F}_2 + V\,\bar{F}_1 + 9/4\,V\,\bar{P}_1 + 9/4\,V\,\bar{P}_2$$

The three parameter model is done when epistasis is absent and unnecessary calculation for non-allelic interactions were avoided.

Results

4. RESULTS

4.1 GENERATION MEAN ANALYSIS

The experiment entitled "Generation mean analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and quality" was conducted in the Department of Vegetable Science, College of Agriculture, Vellayani, during 2017-2018. The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two superior crosses of yard long bean with high yield and quality characters *viz.* Cross 1 - VS 50 x VS 34 (Kakkamoola Local x Githika) and Cross 2 - VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) were evaluated for vegetative and flowering characters, yield and yield attributes and quality characters. The observations were analyzed statistically using generation mean analysis (Hayman, 1958) followed by scaling test (Mather, 1949) and the result obtained from the present study are given below. The results of generation mean analysis for the characters are presented from tables 5 to 13.

4.1.1 Vegetative and Flowering Characters

4.1.1.1 Vine Length at Final Harvest (cm)

Significant variation was observed among the generations for vine length at final harvest as shown by the significant value of 'm' in cross 2 (Table 5). Maximum vine length at final harvest was reported in P_2 (536.67 cm) and minimum in F_2 (367.33 cm) in cross 2.

Positive significance was observed for scale A in cross 1 while it was non-significant in cross 2, negative significance was observed for scale B in cross 2 while it was non-significant in cross 1 and scales C and D were significant and negative in both the crosses denoting the presence of all types of epistatic interactions.

Table 5. Generation means (±SE), Scale values (±SE), and estimates of genetic component (±SE) for vine length at final harvest (cm) and primary branches plant^{-1} in yard long bean

	Vine length at final harvest (cm)		Primary branches plant^{-1}	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	508.67 ± 4.84	508.67 ± 4.84	4.00 ± 0.10	4.00 ±0.10
P_2	481.67 ± 26.31	536.67 ± 18.78	5.00 ± 0.17	3.66 ± 0.10
F_1	386.33 ± 4.38	440.00 ± 14.43	4.55 ± 0.15	2.88 ± 0.20
F_2	310.67 ± 11.00	367.33 ± 15.45	3.55 ± 0.10	3.66 ± 0.13
BC_1	463.67 ± 7.25	479.00 ± 21.17	3.22 ± 0.08	3.66 ± 0.07
BC_2	414.67 ± 14.89	405.00 ± 3.57	5.22 ± 0.14	3.11 ± 0.10
Scale values				
A	32.33* ± 15.91	9.33 ± 44.99	-2.11* ± 0.23	0.45 ± 0.26
B	-38.67 ± 39.38	-166.67* ± 24.74	0.89* ± 0.35	-0.33 ± 0.30
C	-520.33* ± 52.23	-456.00* ± 70.90	-3.88* ± 0.53	1.23 ± 0.68
D	-257.00* ± 27.32	-149.33* ± 37.62	-1.33* ± 0.26	0.56 ± 0.30
Genetic components				
m	-18.83 ± 56.25	224.00* ± 75.87	1.83* ± 0.52	4.94* ± 0.58
d	13.50 ± 13.38	-14.00 ± 9.70	-0.50* ± 0.10	0.17* ± 0.07
h	912.83* ±137.18	357.33* ± 181.44	4.18* ± 1.28	-3.06* ± 1.31
i	514.00* ± 54.64	298.67* ± 75.24	2.67* ± 0.51	
j	71.00 ± 42.02	176.00* ± 47.12	-3.00* ± 0.37	
l	-507.67* ± 83.23	-141.33 ± 111.37	-1.45 ± 0.82	
Epistasis	D	D	D	

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34 Cross 2: VS 50 X VS 26

*Significant at 5% level

Dominance (h) effect was significant, positive and greater than all other genetic components in both the crosses, while additive effect (d) was non-significant.

Among the interactions, additive x additive (i) was positively significant in cross 1 and 2. Dominance x dominance (l) was significant and negative in cross 1 and non-significant in cross 2 whereas additive x dominance (j) was positively significant in cross 2 and non-significant in cross 1.

Presence of duplicate nature of epistasis was observed in both the crosses as indicated by opposite signs of dominance (h) and dominance x dominance (l) type of interaction.

4.1.1.2 Primary Branches Plant^{-1}

Significant 'm' denoted wide variation for primary branches plant^{-1} among the generations as given in Table 5. Highest number of primary branches plant^{-1} was observed in BC_2 (5.22) in cross 1 and P_1 (4.00) in cross 2. BC_1 (3.22) in cross 1 and F_1 (2.88) in cross 2 recorded the lowest number of primary branches plant^{-1}.

Significance was noticed for all the scales A, B, C and D in cross 1, which indicated the presence of all types of epistasis. Non- significance in cross 2 indicated the absence of epistasis and adequacy of additive- dominance model for explaining the gene effects. Hence the genetic components were estimated using three parameter model.

Additive (d) effect was significant and negative in cross 1 and positive in cross 2 whereas dominance (h) effect was significant and positive in cross 1 and negative in cross 2. Among interactions in cross 1, additive x additive (i) was significant and positive, additive x dominance (j) was significant and negative and dominance x dominance (l) was non-significant.

Table 6. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for length and breadth of leaflets (cm) in yard long bean

	Length and breadth of leaflets (cm)							
	Terminal leaf length (cm)		Lateral leaf length (cm)		Terminal leaf width (cm)		Lateral leaf width (cm)	
	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2	Cross 1	Cross 2
Generation means								
P_1	14.99 ± 0.47	14.99 ± 0.47	13.90 ± 0.83	13.90 ± 0.83	10.22 ± 0.59	10.22 ± 0.59	9.60 ± 0.48	9.60 ± 0.48
P_2	12.38 ± 0.27	13.93 ± 0.52	11.57 ± 0.15	14.52 ± 0.50	6.86 ± 0.11	9.78 ± 0.11	7.00 ± 0.04	9.50 ± 0.07
F_1	13.63 ± 0.10	16.27 ± 0.27	13.60 ± 0.10	15.24 ± 0.02	9.48 ± 0.30	12.27 ± 0.01	8.93 ± 0.09	10.57 ± 0.03
F_2	15.52 ± 0.10	18.50 ± 0.15	15.28 ± 0.05	16.92 ± 0.27	10.77 ± 0.04	13.09 ± 0.30	9.80 ± 0.06	10.64 ± 0.05
BC_1	15.89 ± 0.12	16.33 ± 0.25	16.94 ± 0.09	14.51 ± 0.24	10.05 ± 0.02	10.56 ± 0.11	9.48 ± 0.01	9.87 ± 0.10
BC_2	15.25 ± 0.33	14.87 ± 0.03	16.06 ± 0.27	14.53 ± 0.04	10.47 ± 0.19	9.33 ± 0.16	10.02 ± 0.14	9.76 ± 0.03
Scale values								
A	3.15* ± 0.53	1.41 ± 0.73	6.37* ± 0.85	-0.12 ± 0.96	0.39 ± 0.59	-1.37* ± 0.63	0.44 ± 0.49	-0.43 ± 0.52
B	4.48* ± 0.71	-0.45 ± 0.59	6.95* ± 0.56	-0.72 ± 0.50	4.60* ± 0.40	-3.40* ± 0.33	4.12* ± 0.29	-0.54* ± 0.10
C	7.45* ± 0.69	12.54* ± 1.10	8.46* ± 0.89	8.79* ± 1.45	7.02* ± 0.62	7.80* ± 1.33	4.75* ± 0.57	2.34* ± 0.52
D	-0.90 ± 0.40	5.79* ± 0.39	-2.43* ± 0.30	4.81* ± 0.60	1.01* ± 0.21	6.28* ± 0.63	0.09 ± 0.18	1.65* ± 0.14
Genetic components								
m	13.51* ± 0.84	26.05* ± 0.85	7.88* ± 0.73	23.83* ± 1.29	10.56* ± 0.52	22.57* ± 1.29	8.49* ± 0.44	12.85* ± 0.37
d	1.31* ± 0.27	0.53 ± 0.35	1.16* ± 0.42	-0.31 ± 0.48	1.68* ± 0.30	0.22 ± 0.30	1.30* ± 0.24	0.05 ± 0.24
h	7.94* ± 2.36	-20.41* ± 2.20	23.90* ± 2.13	-19.06* ± 3.00	1.90 ± 1.50	-27.63* ± 2.79	4.82* ± 1.20	-6.56* ± 1.02
i	0.18 ± 0.79	-11.59* ± 0.77	4.86* ± 0.59	-9.63* ± 1.19	-2.02* ± 0.42	-12.57* ± 1.25	-0.19 ± 0.36	-3.31* ± 0.27
j	-1.34 ± 0.88	1.86* ± 0.86	-0.57 ± 1.00	0.60 ± 1.08	-4.21* ± 0.71	2.03* ± 0.71	-3.68* ± 0.56	0.11 ± 0.53
l	-7.81* ± 1.54	10.63* ± 1.46	-18.18* ± 1.42	10.46* ± 1.75	-2.98* ± 0.99	17.34* ± 1.54	-4.38* ± 0.79	4.27* ± 0.66
E	D	D	D	D	D	D	D	D

E: Epistasis

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34

Cross 2: VS 50 X VS 26

*Significant at 5% level

Duplicate nature of epistasis was predominant in cross 1 which was indicated by opposite signs of dominance (h) and dominance x dominance (l) type of interaction.

4.1.1.3 Length and Breadth of Leaflets (cm)

Significant positive 'm' value for leaf area in terms of dimensions of terminal and lateral leaves denoted significant variation among the generations (Table 6). Maximum terminal and lateral leaf length was recorded in BC_1 (15.89 cm and 16.94 cm respectively) in cross 1 and F_2 (18.50 cm and 16.92 cm respectively) in cross 2. F_2 exhibited maximum terminal leaf width in cross 1 (10.77 cm) and cross 2 (13.09 cm). Maximum lateral leaf width was observed in BC_2 (10.02 cm) in cross 1 and F_2 (10.64 cm) in cross 2. P_2 recorded minimum terminal leaf length for both the crosses (12.38 cm and 13.93 cm respectively). Lowest lateral leaf length was reported for P_2 (11.57 cm) in cross 1 and P_1 (13.90 cm) in cross 2. P_2 showed the minimum terminal (6.86 cm) and lateral leaf width (7.00 cm) in cross 1 whereas BC_2 (9.33 cm) and P_2 (9.50 cm) for the same in cross 2.

Scales A, B and C were positively significant in cross 1 for terminal leaf length while scales C and D showed positive significance in cross 2, which indicated the presence of non-allelic interactions. Significance was noticed for all the scales A, B, C and D in cross 1 for lateral leaf length whereas for C and D only, in cross 2. Presence of all types of epistatic interactions was revealed by the significance of all the scales in cross 2 for terminal leaf width whereas scales B, C and D were significant in cross 1. In the case of lateral leaf width, scales B and C were significant and positive in cross 1, whereas scales C and D were significant and positive and B significant and negative in cross 2.

In the case of terminal leaf length and lateral leaf length, significance was observed for dominance (h) effect which was positive in cross 1 and negative in cross

2 whereas additive (d) effect was positively significant in cross 1 and non-significant in cross 2. Additive (d) effect was positively significant and dominance (h) was non-significant in cross 1 whereas dominance (h) effect was negatively significant and additive (d) non-significant in cross 2 for terminal leaf width. Both additive (d) and dominance (h) effect were significant and positive in cross 1 while dominance (h) effect was negatively significant and additive (d) effect non-significant in cross 2 for lateral leaf width.

Among the interactions, for terminal leaf length, dominance x dominance (l) was significant but negative in cross 1 and positive in cross 2, additive x additive (i) and additive x dominance (j) were significant but with negative and positive value respectively in cross 2 and was non-significant in cross 1. Additive x additive (i) interaction was significant and positive in cross 1 and negative in cross 2 whereas dominance x dominance (l) was significant and negative in cross 1 and positive in cross 2 in the case of lateral leaf length. Considering terminal leaf width, additive x additive (i), additive x dominance (j) and dominance x dominance (l) types of interactions were significant and negative in cross 1, while in cross 2, additive x additive (i) was negatively significant and additive x dominance (j) and dominance x dominance (l) were positively significant. In the case of lateral leaf width, dominance x dominance (l) interaction was significant and negative in cross 1 but positive in cross 2, additive x dominance (j) was significant and negative in cross 1 whereas non-significant in cross 2 and additive x additive (i) type of epistasis was significant and negative in cross 2 whereas non-significant in cross 1.

Opposite signs of dominance (h) and dominance x dominance (l) interactions indicated the presence of duplicate type of epistasis in both the crosses for terminal and lateral leaf length and width.

Table 7. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for days to first flowering in yard long bean

Days to first flowering		
	Cross 1	Cross 2
Generation means		
P_1	53.50 ± 0.17	53.50 ± 0.17
P_2	53.00 ± 0.10	54.00 ± 0.25
F_1	50.00 ± 0.19	49.50 ± 0.14
F_2	50.17 ± 0.21	50.17 ± 0.20
BC_1	50.60 ± 0.21	50.41 ± 0.13
BC_2	50.03 ± 0.21	49.92 ± 0.18
Scale values		
A	-2.29* ± 0.50	-2.17* ± 0.34
B	-2.94* ± 0.47	-3.66* ± 0.46
C	-5.82* ± 0.93	-5.83* ± 0.93
D	-2.93 ± 0.51	0.00 ± 0.00
Genetic components		
m	52.66* ± 1.02	53.75* ± 0.94
d	0.25* ± 0.10	-0.25 ± 0.15
h	-7.31* ± 2.44	-10.07* ± 2.15
i	0.59 ± 1.01	0.00 ± 0.93
j	0.65 ± 0.62	1.49* ± 0.53
l	4.65* ± 1.50	5.83* ± 1.26
Epistasis	D	D

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34 Cross 2: VS 50 X VS 26

*Significant at 5% level

4.1.1.4 Days to First Flowering

'm' was significant and greater than all other effects in both the crosses, denoting the significant variation between the treatments for days to first flowering as given in table 7. F_1 was earlier to flower in cross 1 (50.00) and 2 (49.50) while P_1 (53.50) in cross 1 and P_2 (54.00) in cross 2 were late.

Scales A, B and C were significant and negative in the two crosses indicating the presence of non-allelic interaction and inadequacy of additive- dominance model. Non significance could be observed for scale D in cross 1 while it was absent in the cross 2.

Additive effect (d) was positively significant in cross 1 while it was non-significant in cross 2. Cross 1 and 2 showed negatively significant values for dominance effect (h).

Of the interaction effects, dominance x dominance (l) was significant and positive in cross 1 and 2. Additive x additive (i) interaction was non-significant in both the crosses whereas additive x dominance (j) was positively significant in cross 2 and non-significant in cross 1.

Presence of duplicate nature of epistasis was observed in both the crosses as indicated by opposite signs of dominance (h) and dominance x dominance (l) type of interaction.

4.1.2 Yield Characters

4.1.2.1 Pod Length (cm)

Significant variation was observed among the generations for pod length as shown by the significant value of 'm' in both the crosses (Table 8). Pod length was

Table 8. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for pod length (cm) and pod girth (cm) in yard long bean

	Pod length (cm)		Pod girth (cm)	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	65.99 ± 0.04	65.99 ± 0.04	3.11 ± 0.03	3.11 ± 0.03
P_2	47.86 ± 0.39	60.58 ± 0.46	2.93 ± 0.02	3.01 ± 0.02
F_1	62.16 ± 0.48	68.56 ± 0.21	3.10 ± 0.08	3.57 ± 0.04
F_2	62.50 ± 0.30	68.44 ± 0.10	3.02 ± 0.03	3.49 ± 0.03
BC_1	63.91 ± 0.45	67.09 ± 0.30	3.04 ± 0.01	3.19 ± 0.04
BC_2	61.22 ± 0.21	64.01 ± 0.36	3.04 ± 0.01	3.33 ± 0.05
Scale values				
A	-0.34 ± 1.01	-0.37 ± 0.65	-0.12 ± 0.08	-0.31* ± 0.09
B	12.42* ± 0.75	-1.11 ± 0.88	0.05 ± 0.08	0.07 ± 0.11
C	11.82* ± 1.58	10.09* ± 0.75	-0.16 ± 0.19	0.68* ± 0.16
D	-0.13 ± 0.77	5.78* ± 0.51	-0.05 ± 0.05	0.46* ± 0.09
Genetic components				
m	56.66* ± 1.56	74.85* ± 1.05	2.93* ± 0.11	3.98* ± 0.18
d	9.07* ± 0.20	2.71* ± 0.23	0.09* ± 0.02	0.05* ± 0.02
h	17.85* ± 3.87	-19.34* ± 3.02	0.20 ± 0.24	-1.56* ± 0.46
i	0.27 ± 1.55	-11.57* ± 1.02		-0.92* ± 0.18
j	-12.76* ± 1.06	0.74 ± 1.05		-0.38* ± 0.13
l	-12.35* ± 2.53	13.05* ± 2.02		1.16* ± 0.30
Epistasis	D	D		D

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34 Cross 2: VS 50 X VS 26

*Significant at 5% level

Cross 1: VS 50

Cross 2: VS 50 x VS 26

Plate 9. Maximum pod length

highest for P_1 (65.99 cm) in cross 1 and F_1 (68.56 cm) in cross 2 (Plate 9). Lowest pod length was recorded for P_2 in crosses 1 and 2 (47.86 cm and 60.58 cm respectively).

Significance could be noticed for the scales B and C in cross 1 indicating the presence of all types of epistatic interactions, whereas in cross 2, significance of C and D scales indicated the presence of additive x additive (i) and dominance x dominance (l) type of interactions.

Additive (d) effect was significant and positive in both the crosses, whereas dominance (h) effect was significant and positive in cross 1 and significant and negative in cross 2.

Additive x additive (i) effect was negatively significant in cross 2 and non-significant in cross 1, additive x dominance (j) type of interaction was significant and negative in cross 1 and non-significant in cross 2 and dominance x dominance (l) was significant and negative in cross 1 while significant and positive in cross 2.

Opposite signs of dominance (h) and dominance x dominance (l) type of interaction indicated the presence of duplicate type of epistasis in both the crosses.

4.1.2.2 Pod Girth (cm)

All the generations were significantly different for pod girth in cross 1 and cross 2 as denoted by 'm' value (Table 8). Pod girth was maximum in P_1 (3.11 cm) in cross 1 and F_1 (3.57 cm) in cross 2. P_2 showed lowest pod girth in both the crosses (2.93 cm and 3.01 cm in 1 and 2 respectively).

Negatively significant value of scale A and positively significant values of scales C and D in cross 2 indicated the presence of non- allelic interactions. The scales A, B, C and D were non-significant in cross 1 indicating that the additive-

Table 9. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for pod weight (g) and pods plant^{-1} in yard long bean

	Pod weight (g)		Pods plant^{-1}	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	35.33 ± 0.17	35.33 ± 0.17	32.67 ± 0.73	32.67 ± 0.73
P_2	27.33 ± 0.26	30.33 ± 0.10	45.67 ± 1.45	27.67 ± 0.44
F_1	37.89 ± 0.15	49.00 ± 0.39	84.00 ± 0.87	69.00 ± 0.58
F_2	42.22 ± 0.14	50.89 ± 0.17	75.67 ± 0.70	62.67 ± 0.30
BC_1	47.22 ± 0.14	46.22 ± 0.21	80.67 ± 0.41	66.00 ± 0.52
BC_2	45.66 ± 0.17	44.22 ± 0.36	78.67 ± 0.30	74.67 ± 0.70
Scale values				
A	21.22* ± 0.35	8.11* ± 0.60	44.67* ± 1.40	30.33* ± 1.40
B	26.11* ± 0.46	9.11* ± 0.83	27.67* ± 1.80	52.67* ± 1.57
C	30.44* ± 0.70	39.88* ± 1.03	56.33* ± 3.66	52.33* ± 1.88
D	-8.44* ± 0.35	11.33* ± 0.54	-8.00* ± 1.49	-15.33* ± 1.06
Genetic components				
m	14.45* ± 0.72	55.49* ± 1.08	23.17* ± 3.07	-0.50 ± 2.16
d	4.00* ± 0.15	2.50* ± 0.10	-6.50* ± 0.81	2.50* ± 0.43
h	87.66* ± 1.80	-11.93* ± 2.89	149.17* ± 6.86	183.17* ± 5.93
i	16.89* ± 0.71	-22.66* ± 1.07	16.00* ± 2.96	30.67* ± 2.12
j	-4.89* ± 0.54	-0.10 ± 0.86	17.00* ± 1.92	-22.33* ± 1.94
l	-64.22* ± 1.13	5.44* ± 1.98	-88.33* ± 4.19	-113.67* ± 3.96
Epistasis	D	D	D	D

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34

Cross 2: VS 50 X VS 26

*Significant at 5% level

Cross 1: VS 50 x VS 34

Cross 2: (VS 50 x VS 26) x VS 26

Plate 10. Highest number of pods plant^{-1}

dominance model is adequate, hence three parameter was applied for estimating gene effects.

Additive (d) effect was significant and positive in both the crosses 1 and 2 whereas dominance (h) effect was non-significant in cross 1 and negatively significant in cross 2. Among the interactions, additive x additive (i) and additive x dominance (j) type of epistasis were significant and negative while dominance x dominance (l) was significant and positive in cross 2.

Duplicate type of epistasis was observed for the trait in cross 2 which was evident from the opposite signs of dominance (h) and dominance x dominance (l) type of interaction.

4.1.2.3 Pod Weight (g)

Significance of 'm' denoted wide variation for pod weight among the generations as given in Table 9. The highest mean values for pod weight was recorded by BC_1 (47.22 g) and F_2 (50.89 g) in cross 1 and 2 respectively and the lowest values by P_2 in cross 1 (27.33 g) and cross 2 (30.33 g).

Scales A, B, C and D were significant and positive in both the crosses except scale D in cross 1, which was negatively significant. It revealed the presence of all types of epistatic interactions.

Additive (d) effect was significant and positive in crosses 1 and 2 whereas dominance (h) effect was significant and positive in cross 1 but negative in cross 2. Additive x additive (i) type of interaction was significant and positive in cross 1 but negative in cross 2. Additive x dominance (j) effect was negatively significant in cross 1 and non-significant in cross 2. Dominance x dominance (l) was significant and negative in cross 1 and significant and positive in cross 2.

In cross 1 and 2, duplicate type of epistasis was observed for the trait, which was evident from the opposite signs of dominance (h) and dominance x dominance (l) type of interaction.

4.1.2.4 Pods Plant^{-1}

The generations differed significantly for pods plant^{-1} in cross 1 as given by significant 'm' value in table 9. F_1 produced highest number of pods plant^{-1} (84.00), while P_1 (32.67) the lowest (Plate 10).

All the four scales displayed positive significance in both the crosses, except scale D which was negatively significant, indicating the presence of all type of epistasis.

Among the genetic components, dominance (h) effect was significant and positive in both the crosses, whereas additive (d) effect was significant and negative in cross 1 but positive in cross 2.

Additive x additive (i) interaction was positively significant for both the crosses. Additive x dominance (j) was significant and positive in cross 1 but negative in cross 2. Cross 1 and 2 displayed negatively significant values for dominance x dominance (l) effect.

Duplicate nature of epistasis was predominant in both the crosses which was indicated by opposite signs of dominance (h) and dominance x dominance (l) interaction.

4.1.2.5 Seeds Pod^{-1}

Wide variation was observed between the treatments for number of seeds pod^{-1} in both the crosses, 'm' value being significant (Table 10). Maximum number of seeds pod^{-1} was observed in F_1 (22.33) in cross 1 and BC_1 (20.33) in cross

Table 10. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for seeds pod^{-1} and hundred seed weight (g) in yard long bean

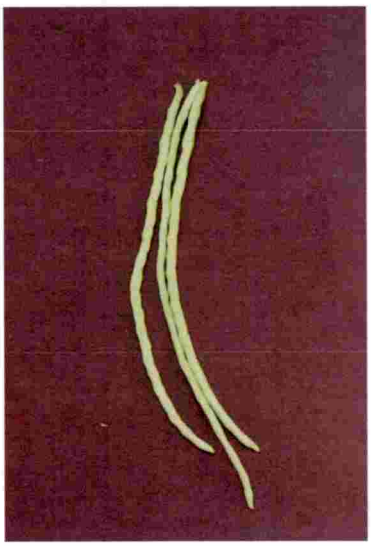
	Seeds pod^{-1}		Hundred seed weight (g)	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	19.17 ± 0.30	19.17 ± 0.30	16.17 ± 0.04	16.17 ± 0.04
P_2	20.33 ± 0.17	17.83 ± 0.22	13.03 ± 0.13	19.35 ± 0.08
F_1	22.33 ± 0.67	19.25 ± 0.19	17.05 ± 0.49	21.83 ± 0.06
F_2	21.67 ± 0.30	19.17 ± 0.25	17.02 ± 0.50	21.53 ± 0.21
BC_1	19.77 ± 0.27	20.33 ± 0.11	14.81 ± 0.04	18.80 ± 0.26
BC_2	20.00 ± 0.20	19.00 ± 0.20	14.87 ± 0.03	17.44 ± 0.17
Scale values				
A	-1.95* ± 0.91	2.25* ± 0.42	-3.59* ± 0.50	-0.40 ± 0.53
B	-2.67* ± 0.80	0.92 ± 0.49	-0.35 ± 0.51	-6.29* ± 0.36
C	2.50 ± 1.83	1.17 ± 1.13	4.76* ± 2.25	6.95* ± 0.85
D	3.56* ± 0.69	-1.00 ± 0.55	4.35* ± 1.00	6.82* ± 0.52
Genetic components				
m	26.86* ± 1.39	16.50* ± 1.11	23.31* ± 2.02	31.40* ± 1.05
d	-0.58* ± 0.17	0.67* ± 0.19	1.57* ± 0.07	-1.59* ± 0.05
h	-16.26* ± 3.25	7.92* ± 2.49	-18.91* ± 4.07	-29.91* ± 2.51
i	-7.11* ± 1.38	2.00 ± 1.10	-8.71* ± 2.02	-13.65* ± 1.04
j	0.72 ± 0.75	1.33* ± 0.59	-3.24* ± 0.17	5.89* ± 0.63
l	11.73* ± 2.27	-5.17* ± 1.45	12.65* ± 2.26	20.34* ± 1.51
Epistasis	D	D	D	D

D: Duplicate type of epistasis

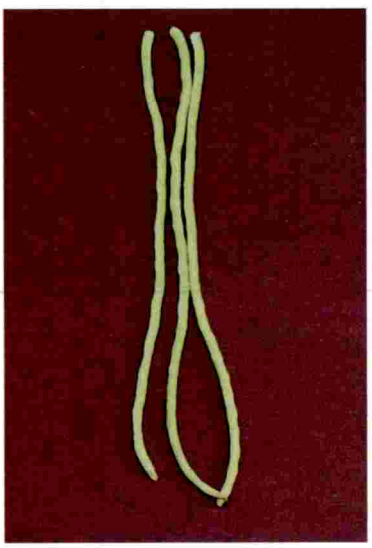
Cross 1: VS 50 X VS 34

Cross 2: VS 50 X VS 26

*Significant at 5% level



Cross 1: VS 50 x VS 34



Cross 2: (VS 50 x VS 26) x VS 50

Plate 11. Maximum number of seeds pod^{-1}

Cross 1: VS 50 x VS 34

Cross 2: VS 50 x VS 26

Plate 12: Maximum hundred seed weight

2 (Plate 11). In cross 1 and cross 2, least number of seeds pod^{-1} was recorded by parents P_1 (19.17) and P_2 (17.83) respectively.

Scales A, B and D exhibited significance in cross 1 and scale A in cross 2, indicating the presence of all types of epistatic interactions.

Additive (d) and dominance (h) effects were significant and negative in cross 1 and significant and positive in cross 2. Negative significant additive x additive (i) interaction was noticed in cross 1, while it was not significant in cross 2. Positively significant additive x dominance (j) interaction was noticed in cross 2, while it was not significant in cross 1. Dominance x dominance (l) type of epistasis was significant in both crosses, but positive in 1 and negative in 2.

Epistasis was revealed to be duplicate for both the crosses due to opposite signs of dominance (h) and dominance x dominance (l) interaction.

4.1.2.6 Hundred Seed Weight (g)

'm' was significant and greater than all other effects in both the crosses, denoting the significant variation between the treatments for hundred seed weight as given in table 10. Hundred seed weight was recorded maximum by F_1 in cross 1 (17.05 g) and cross 2 (21.83 g) (Plate 12). Minimum hundred seed weight was recorded by the parents P_2 (13.03 g) in cross 1 and P_1 (16.17 g) in cross 2.

Scale A was negative and significant in cross 1 but non-significant in cross 2 while scale B was negative and significant in cross 2 but non-significant in cross 1, indicating the presence of all the epistatic interactions. Significance was noticed for scales C and D in both the crosses.

Table 11. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for yield (g plant^{-1}) in yard long bean

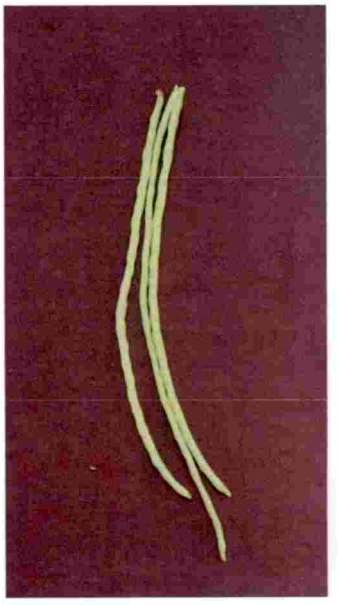
	Yield (g plant^{-1})	
	Cross 1	Cross 2
Generation means		
P_1	707.95 ± 2.62	707.95 ± 2.62
P_2	642.61 ± 14.22	584.00 ± 19.34
F_1	1210.51 ± 24.55	1116.83 ± 31.29
F_2	1018.46 ± 5.99	881.22 ± 24.80
BC_1	1071.52 ± 11.52	771.97 ± 10.32
BC_2	913.87 ± 1.48	818.38 ± 19.07
Scale values		
A	224.57* ± 33.77	-280.84* ± 37.57
B	-25.39 ± 28.53	-64.07 ± 52.99
C	302.27* ± 56.52	-0.73 ± 118.91
D	51.54* ± 16.69	172.09* ± 54.14
Genetic components		
m	778.36* ± 34.15	990.16* ± 108.71
d	32.67* ± 7.23	61.98* ± 9.76
h	528.25* ± 90.71	-562.41* ± 241.11
i	-103.08* ± 33.37	-344.18* ± 108.27
j	249.96* ± 27.37	-216.78* ± 47.56
l	-96.11 ± 73.17	689.09* ± 147.18
Epistasis	D	D

D: Duplicate type of epistasis

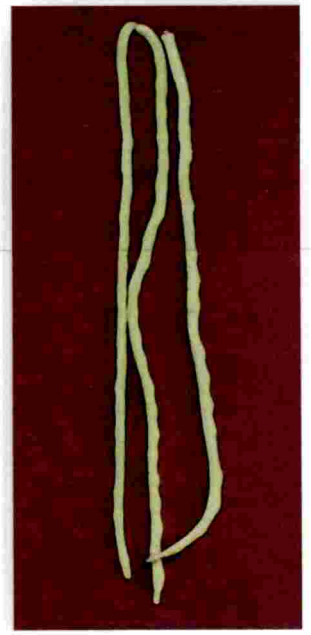
Cross 1: VS 50 X VS 34

Cross 2: VS 50 X VS 26

*Significant at 5% level



Cross 1: VS 50 x VS 34



Cross 2: VS 50 x VS 26

Plate 13: Highest yielder

Additive effect (d) was significant and positive in cross 1 but negative in cross 2. Cross 1 and 2 displayed negatively significant values for dominance (h) effect.

Considering the interaction effects, additive x additive (i) effect was significant and negative in cross 1 and 2 while additive x dominance (j) effect was significant but negative in cross 1 and positive in cross 2. Dominance x dominance (l) interaction was positively significant in both the crosses.

Epistasis was revealed to be duplicate for both the crosses as shown by the opposite signs of dominance (h) effect and dominance x dominance (l) interactions.

4.1.2.7 Yield (g plant^{-1})

Significant difference was observed among the six generations for pod yield plant^{-1}, since 'm' value was significant and greater than all other effects as given in table 11. Among the treatments, yield plant^{-1} was highest for F_1 in cross 1 (1210.51 g) and cross 2 (1116.83 g) (Plate 13). Lowest yield plant^{-1} was recorded by P_2 in cross 1 (642.61 g) and cross 2 (584.00 g).

Scales A and D were significant for both the crosses, which revealed the presence of all types of epistatic interactions. Scale C was significant in cross 1 while non-significant in cross 2.

Both the crosses exhibited positively significant additive (d) effect whereas dominance (h) effect was significant but positive in cross 1 and negative in cross 2.

All the interactions were significant in both crosses except dominance x dominance (l) interaction in cross 1. Additive x additive (i) effect was negatively significant in both crosses whereas additive x dominance (j) was significant but

Table 12. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for days to harvest and crop duration in yard long bean

	Days to harvest		Crop duration	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	64.00 ± 0.87	64.00 ± 0.87	111.00 ± 0.58	111.00 ± 0.58
P_2	64.00 ± 0.00	64.33 ± 0.17	120.33 ± 0.17	115.00 ± 0.76
F_1	61.00 ± 0.00	63.00 ± 0.50	122.33 ± 0.17	118.67 ± 0.93
F_2	62.00 ± 0.34	64.33 ± 0.61	123.33 ± 0.11	120.67 ± 0.64
BC_1	62.00 ± 0.34	63.00 ± 0.34	124.00 ± 0.00	121.33 ± 0.92
BC_2	61.00 ± 0.00	63.00 ± 0.34	125.67 ± 0.30	122.67 ± 0.98
Scale values				
A	-1.00 ± 1.11	-1.00 ± 1.21	14.67* ± 0.60	13.00* ± 2.13
B	-3.00 ± 0.00	-1.33 ± 0.87	8.67* ± 0.65	11.67* ± 2.29
C	-2.00 ± 1.62	3.00 ± 2.76	17.33* ± 0.83	19.33* ± 3.29
D	1.00 ± 0.77	2.67* ± 1.30	-3.00* ± 0.38	-2.67 ± 1.85
Genetic components				
m	66.00* ± 1.59	69.50* ± 2.64	109.67* ± 0.82	107.67* ± 3.73
d	0.00 ± 0.00	-0.17 ± 0.44	-4.67* ± 0.30	-2.00* ± 0.48
h	-11.00* ± 3.67	-14.17* ± 5.82	42.00* ± 2.23	41.00* ± 9.66
i		-5.33* ± 2.61	6.00* ± 0.76	5.33 ± 3.69
j		0.17 ± 0.66	3.00* ± 0.43	1.33 ± 2.84
l		7.67* ± 3.38	-29.33* ± 1.47	-30.00* ± 6.29
Epistasis		D	D	D

D: Duplicate type of epistasis

Cross 1: VS 50 X VS 34 Cross 2: VS 50 X VS 26

*Significant at 5% level

positive in cross 1 and negative in cross 2. Positive significance was observed for dominance x dominance (l) in cross 2 and non-significance in cross 1.

In both crosses, dominance (h) and dominance x dominance (l) effects with opposite sign showed duplicate nature of epistasis.

4.1.2.8 Days to Harvest

The treatments differed significantly for days to harvest in both the crosses as given by significant 'm' value in table 12. The generations F_1 and BC_2 (61.00) in cross 1 and F_1, BC_1 and BC_2 (63.00) in cross 2 were found earlier to harvest. P_1 and P_2 (64.00) in cross 1 and P_2 and F_2 (64.33) in cross 2 took maximum number of days to harvest.

All the scales were found to be non-significant for both the crosses except scale D which was positively significant in cross 2.

In cross 1 and 2, dominance (h) effect was negatively significant whereas additive (d) effect was non-significant. In cross 2, additive x additive (i) type of epistasis was negatively significant, dominance x dominance (l) positively significant and additive x dominance (j) non-significant.

In cross 2, dominance (h) and dominance x dominance (l) with opposite sign showed duplicate nature of epistasis.

4.1.2.9 Crop Duration

Significant positive 'm' value for crop duration denoted significant variation among the generations (Table 12). Crop duration was longest in BC_2 (125.67 and 122.67 respectively) and shortest in P_1 (111.00) in cross 1 and 2.

Table 13. Generation means (±SE), Scale values (±SE), and estimates of genetic components (±SE) for pod protein (%) and keeping quality (% weight loss) in yard long bean

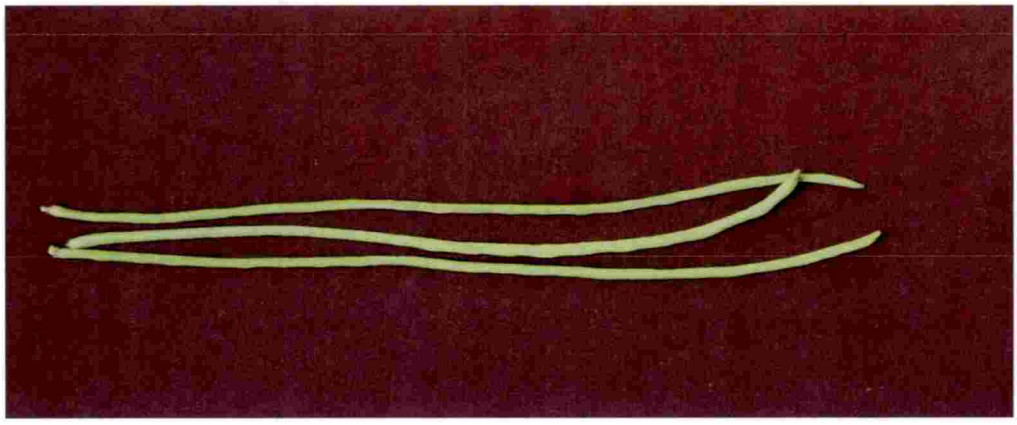
	Pod protein (%)		Keeping quality (% weight loss)	
	Cross 1	Cross 2	Cross 1	Cross 2
Generation means				
P_1	5.07 ± 0.004	5.07 ± 0.004	25.08 ± 0.29	25.08 ± 0.29
P_2	4.55 ± 0.03	4.43 ± 0.03	19.85 ± 0.19	21.87 ± 0.52
F_1	6.11 ± 0.03	6.19 ± 0.004	16.44 ± 0.12	17.82 ± 0.19
F_2	6.16 ± 0.02	6.19 ± 0.002	15.59 ± 0.23	17.72 ± 0.06
BC_1	6.23 ± 0.03	6.27 ± 0.02	14.37 ± 0.17	17.40 ± 0.12
BC_2	6.19 ± 0.02	6.18 ± 0.04	14.16 ± 0.04	16.88 ± 0.08
Scale values				
A	1.28* ± 0.06	1.27* ± 0.05	-12.77* ± 0.47	-8.10* ± 0.41
B	1.71* ± 0.06	1.75* ± 0.09	-7.97* ± 0.24	-5.93* ± 0.58
C	2.80* ± 0.09	2.89* ± 0.04	-15.47* ± 1.02	-11.70* ± 0.74
D	-0.10* ± 0.05	-0.07 ± 0.05	2.64* ± 0.50	1.17* ± 0.18
Genetic components				
m	4.61* ± 0.09	4.62* ± 0.10	27.74* ± 1.01	25.81* ± 0.46
d	0.26* ± 0.02	0.32* ± 0.02	2.61* ± 0.17	1.60* ± 0.30
h	4.69* ± 0.24	4.71* ± 0.29	-37.31* ± 2.21	-24.35* ± 1.31
i	0.20* ± 0.09	0.13 ± 0.09	-5.27* ± 0.10	-2.33* ± 0.35
j	-0.43* ± 0.08	-0.48* ± 0.10	-4.79* ± 0.49	2.16* ± 0.66
l	-3.19* ± 0.17	-3.15* ± 0.19	26.01* ± 1.25	16.36* ± 0.92
Epistasis	D	D	D	D

D: Duplicate type of epistasis

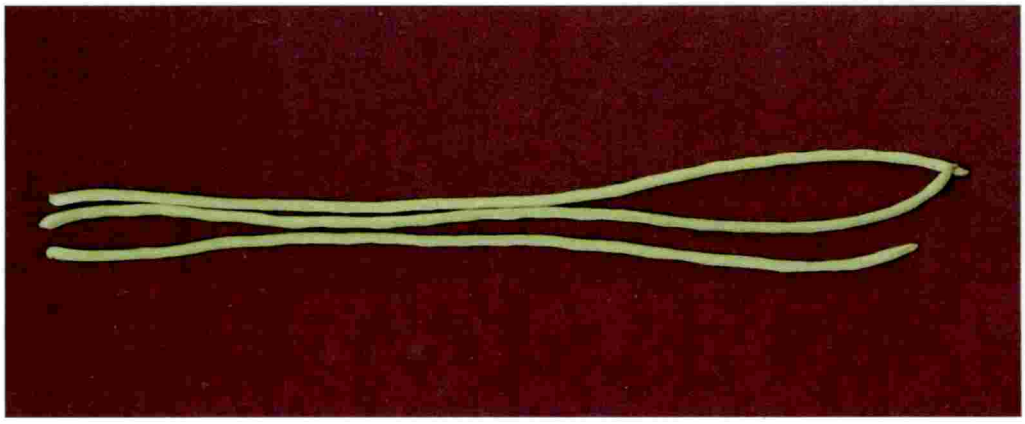
Cross 1: VS 50 X VS 34

Cross 2: VS 50 X VS 26

*Significant at 5% level



Cross 1: (VS 50 x VS 34) x VS 50



Cross 2: (VS 50 x VS 26) x VS 50

Plate 14: Maximum pod protein

Scales A, B and C were significant and positive in cross 1 and 2 denoting the presence of non-allelic interactions. Negative significance could be observed for scale D in cross 1 and non-significance in cross 2.

Additive (d) effect had negative significance whereas dominance (h) effect had positive significance in both the crosses.

Among the interactions, additive x additive (i) and additive x dominance (j) effect were positively significant for the first cross but non-significant for the other. Dominance x dominance interaction had negative significance in cross 1 and 2.

Prevalence of duplicate nature of epistasis in both the crosses was indicated by the opposite signs of dominance (h) and dominance x dominance (l) effects.

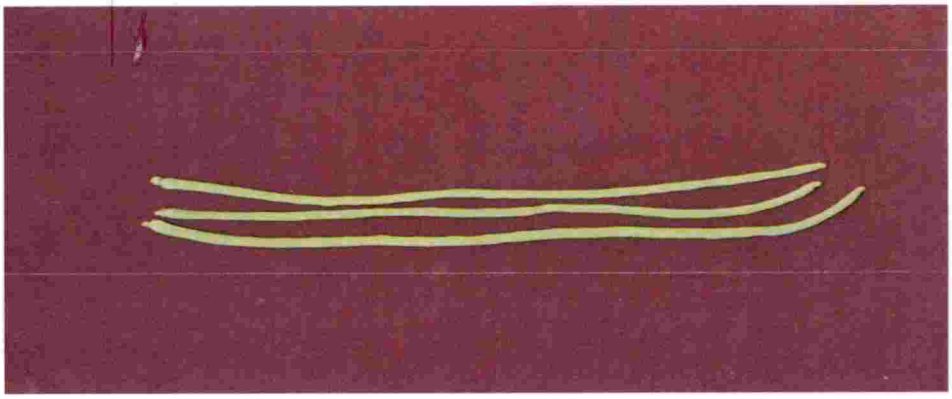
4.1.3 Quality Characters

4.1.3.1 Pod Protein (%)

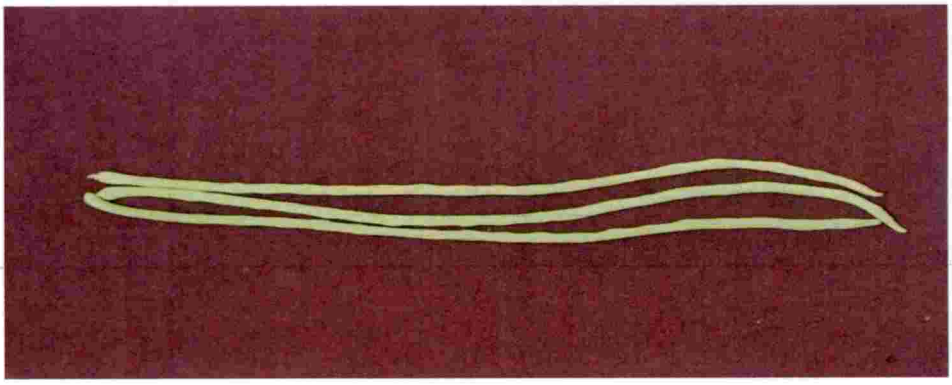
The effect of 'm' was positively significant in both the crosses, hence there was significant difference among the generations (Table 13). Pod protein content was maximum in BC_1 generation (6.23 % and 6.27 % respectively) for the cross 1 and 2, but minimum in P_2 (4.55 % and 4.43 % respectively) (Plate 14).

The cross 1 and 2 had positive significance for scales A, B and C values indicating the presence of all the type of epistatic interactions. Scale D was significant and negative in cross 1 and non-significant in cross 2.

Additive (d) and dominance (h) effect had positive significance for both the crosses. Additive x additive interaction was positively significant in cross 1 but non-significant in cross 2. Both the crosses had negative significance for additive x dominance (j) and dominance x dominance (l) type of epistatic interactions.



Cross 1: (VS 50 x VS 34) x VS 34



Cross 2: (VS 50 x VS 26) x VS 26

Plate 15: Best keeping quality

Prevalence of duplicate nature of epistasis in both the crosses was indicated by the opposite signs of dominance (h) and dominance x dominance (l) effects.

4.1.3.2 Keeping Quality (% weight loss)

Significant variation was observed among the generations for keeping quality as shown by the significant value of 'm' in both the crosses (Table 13). Best keeping quality was for BC_2 generation in cross 1 (14.16 %) and cross 2 (16.88 %) (Plate 15). Lowest keeping quality was observed in the common parent P_1 (25.08 %) in both the crosses.

Scales A, B and C were significant and negative for both the crosses whereas scale D was positively significant indicating the presence of all types of non-allelic interactions.

Additive (d) effect was positively significant for cross 1 and 2 whereas dominance (h) effect was negatively significant. In cross 1 and 2, additive x additive (i) type of interaction had negative significance whereas dominance x dominance (l) effect had positive significance. Additive x dominance (j) was significant and negative for cross 1 whereas significant and positive for the other.

Duplicate nature of epistasis was revealed in all the crosses from the opposite signs of dominance (h) and dominance x dominance (l) effects.

4.2 INCIDENCE OF PESTS AND DISEASES

Six generations of both the crosses VS 50 x VS 34 (Kakkamoola Local x Githika) and VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) were monitored for the incidence of pests and diseases during the entire cropping season. Major pest problem observed during the cropping period were spotted pod borer (*Maruca vitrata*), aphids (*Aphis craccivora*), leaf eating caterpillar (*Spodoptera*

Spotted pod borer (*Maruca vitrata*)

Aphids (*Aphis craccivora*)

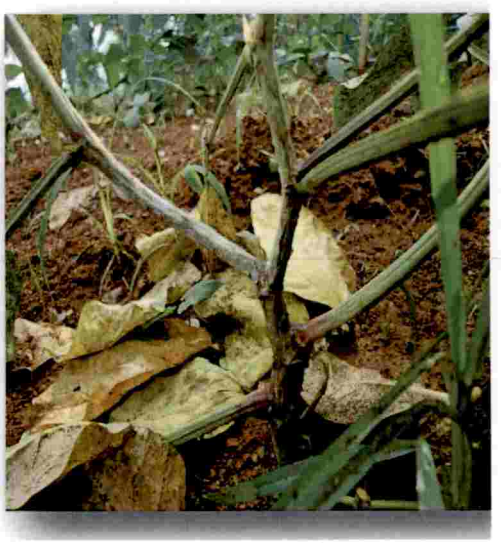
Plate 16. Pests observed during crop period

Leaf eating caterpillar (*Spodoptera litura*)

Pod bug (*Riptortus pedestris*)

Plate 16. Pests observed during crop period

Cowpea Aphid Borne Mosaic Virus (CABMV)



Fusarium wilt (*Fusarium oxysporum*)

Plate 17. Diseases observed during crop period

Cercospora leaf spot (*Cercospora* sp.)

Web blight and Collar rot (Rhizoctonia Solani)

Plate 17. Diseases observed during crop period

Rust (*Uromyces vignae*)

Plate 17. Diseases observed during crop period

litura) and pod bug (*Riptortus pedestris*) (Plate 16). Cowpea Aphid Borne Mosaic Virus (CABMV), fusarium wilt (*Fusarium oxysporum*), collar rot and web blight (*Rhizoctonia solani)*, cercospora leaf spot (*Cercospora sp.*) and rust (*Uromyces vignae*) were the main diseases observed in the field (Plate 17). No incidence of pythium rot, bacterial blight, ashy stem blight, anthracnose and powdery mildew were observed in the field during the entire growing period.

Discussion

5. DISCUSSION

Generation mean analysis is a statistical method having great importance in understanding the nature of inheritance as it reveals the information regarding the gene effects (additive and dominance) and epistasis (additive x additive, additive x dominance and dominance x dominance type of interactions). It is an important tool which helps us to choose a suitable breeding procedure for the development of a variety and also used to estimate heritability of a character and genetic advance under selection.

Generation mean analysis was done in two superior crosses of yard long bean to understand the inheritance and magnitude of gene action using the means of six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) for 15 yield and quality parameters. A brief discussion regarding the results obtained is furnished below.

5.1 VEGETATIVE AND FLOWERING CHARACTERS

5.1.1 Vine Length at Final Harvest (cm)

Length of the vine at final harvest is a major factor that determines the plant vigour. With respect to mean performance, P_2 was superior in cross 2. In both the crosses *viz.,* VS 50 x VS 34 and VS 50 x VS 26, mean value of F_1 was higher than that of F_2. Significance of all the scales except scale B in cross 1 and scale A in cross 2 suggested the inadequacy of additive-dominance model and presence of non-allelic interaction. F_1 was better than P_1 in cross 1, which was evident from the significance of scale A with highest magnitude.

In cross 1, dominance, additive x additive and dominance x dominance effects were significant, in which dominance effect was positive and greater than all other genetic components while dominance x dominance type of interaction was negative.

Even though non-additive gene action were significant, the relative assessment of magnitude indicated the predominance of dominance effect. Hence heterosis breeding can be suggested for improving the trait.

Detailed analysis in cross 2 showed the significance of dominance, additive x additive and additive x dominance in favorable positive direction, among which dominance gene action had the highest magnitude. The predominance of dominance gene action suggested the usefulness of heterosis breeding for improving this trait. Sawant (1994), Nagaraj *et al.* (2002), Subbiah *et al.* (2013) and Jithesh (2009) reported the presence of dominance effect in controlling the trait in cowpea and Behra (2015) in soyabean. Thiyagarajan *et al.* (1990), Valarmathi *et al.* (2007), Ushakumari *et al.* (2010) and Lakshmi (2016) suggested the role of non-additive gene action in plant height of cowpea. Duplicate nature of epistasis was present in both the crosses as indicated by opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

5.1.2 Primary Branches Plant^{-1}

Primary branches plant^{-1} is an important growth parameter which contributes to the plant vigour and total yield plant^{-1}. On the basis of mean performance, BC_2 in cross 1 was superior among the generations. In cross 1, mean value of F_1 was higher than that of F_2. During scaling test, significance was observed for all the scales of which scale B was positive which implies that F_1 is better than the second parent. All the genetic components were significant of which dominance and additive x additive were in the favourable positive direction. Predominance of dominance effect suggested that heterosis breeding would improve the trait primary branches plant^{-1}. These results are in agreement with the findings of Sawant (1994) and Lakshmi (2016). The predominance of non-additive gene action was also reported by Manivannan and Sekar (2005) and Patel *et al.* (2013). Duplicate nature of epistasis

was predominant in cross 1 which was indicated by opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

In cross 2, considering mean performance, P_1 was superior compared to the other generations. All the scales A, B, C and D were found to be non-significant which indicates the absence of non-allelic interaction and adequacy of additive-dominance model in accordance with earlier report of Lovely (2005). All the genetic components m, d and h were significant and dominance effect was in negative direction. Direct selection would improve the trait primary branches plant^{-1} in cross 2 since additive effect was predominant. Predominance of additive gene action for primary branches plant^{-1} was reported by Anbuselvam *et al.* (2000), Nagaraj *et al.* (2002), Philip (2004) and Romanus *et al.* (2008) in cowpea and Das *et al.* (2010) and Soumya (2015) in brinjal. Sobha and Vahab (1998) reported the significance of both additive and non-additive gene action for primary branches plant^{-1} in vegetable cowpea. Duplicate nature of epistasis was predominant in cross 1 which was indicated by opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

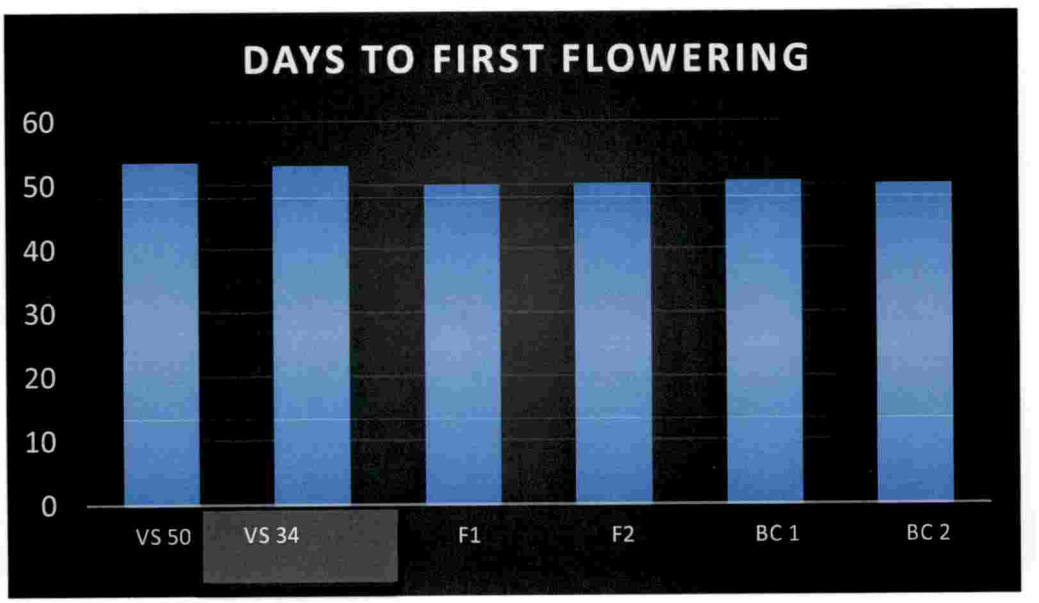
5.1.3 Length and Breadth of Leaflets (cm)

Length and breadth of leaflets plays an important role in the photosynthetic efficiency of the crop and thereby the biological yield. In terminal leaf length, positive significance was noticed in scales A, B and C in cross 1 and scales C and D in cross 2. Scale C had the highest magnitude in both the crosses which indicates that F_2 is better than the parents. Significant, positive and highest magnitude of dominance effect in cross 1 and dominance x dominance interaction in cross 2 was observed. Hence, heterosis breeding in cross 1 and hybridization followed by selection in cross 2 would improve the trait.

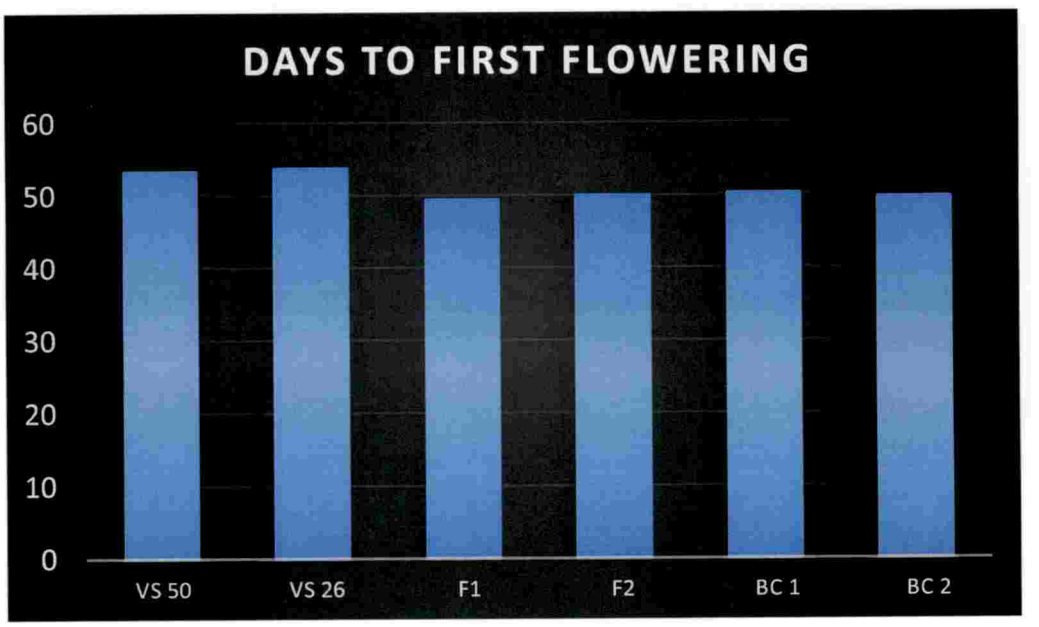
Significance was noticed for all scales in cross 1 and for scales C and D in cross 2 for lateral leaf length. The highest value of scale C implies the superiority of F_2 over the parents. Predominance of non-additive gene action was observed due to positive significance of dominance and dominance x dominance effect in crosses 1 and 2 respectively, which revealed that reliance should be placed on heterosis breeding in cross 1 and hybridization followed by selection in cross 2.

For the trait terminal leaf width, significance was observed for all the scales, except scale A in cross 1. Scale C had the highest positive value in both the crosses, which implies that F_2 is better than both the parents. Even though significance was observed for additive and all the three types of digenic interactions in cross 1, only additive effect was positive. Hence direct selection would improve the trait. Presence of additive genetic variance for leaf length and breadth in cowpea was also reported by Mittal *et al.* (2009). In cross 2, though dominance effect and digenic interactions were significant, dominance x dominance was positive and of highest magnitude. Predominance of dominance x dominance effect pointed out the suitability of hybridization followed by selection for the improvement of the trait.

In the character lateral leaf width, significance was observed for scales B and C in cross 1 and scales B, C and D in cross 2, among which highest value was observed in scale C which indicates that F_2 is superior than both the parents. Among the interactions, positive significance with highest magnitude was observed for dominance in cross 1 and dominance x dominance in cross 2. Hence, heterosis breeding could be resorted to in cross 1 and hybridization followed by selection in cross 2. This is in accordance with the reports of Prasanth and Ponnuswami (2008) in chilli and Sanjeev *et al.* (2015) in fodder cowpea. Duplicate nature of epistasis was present in both the crosses was indicated by opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.



CROSS 1



CROSS 2

Fig 1. Variability for days to first flowering among the generations in cross 1 and cross 2

5.1.4 Days to First Flowering

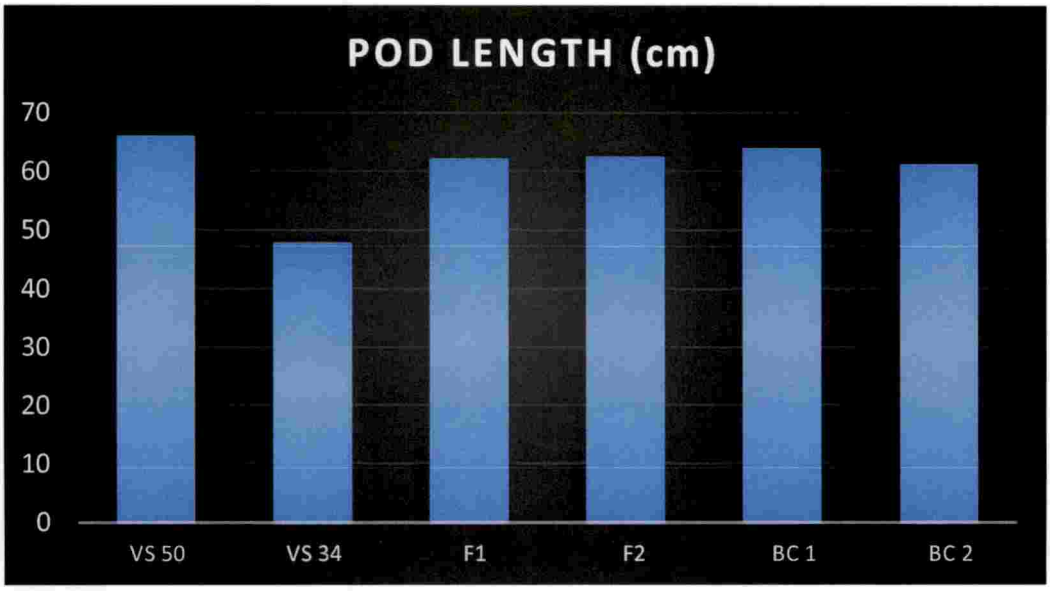
Early flowering is an important parameter which gives an indication of early yield which is preferred for commercial cultivation and considered for crop improvement.

Among the generations, early flowering was noticed in F_1 while flowering was delayed in P_1 in cross 1 (Fig. 1). Significance was observed for scales A, B and C and all were acting in the favourable negative direction. Superiority of F_2 over the parents was denoted by the significance with highest value of scale C over all other scales.

Significance was observed for additive, dominance and dominance x dominance. Dominance effect was acting in the favourable negative direction and had the highest magnitude. Hence heterosis breeding would improve the trait days to first flowering and restore early flowering types in cross 1.

In cross 2, F_1 recorded early flowering whereas P_2 late flowering. Scales A, B and C were significant and acting in favourable negative direction, among which value of scale C was the highest which implies the superiority of F_2 over the parents.

Dominance, additive x dominance and dominance x dominance were significant among which dominance effect had the highest negative value indicating the need for exploitation of heterosis in cross 2 to get early flowering types. Similar results of predominance of dominance gene effect was reported by Sawant (1994), Jithesh (2009) and Gupta *et al.* (2017). Philip (2004) and Lakshmi (2016) reported the predominance of non-additive gene action in controlling the trait. Duplicate type of epistasis was observed for the trait which was proved from the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.



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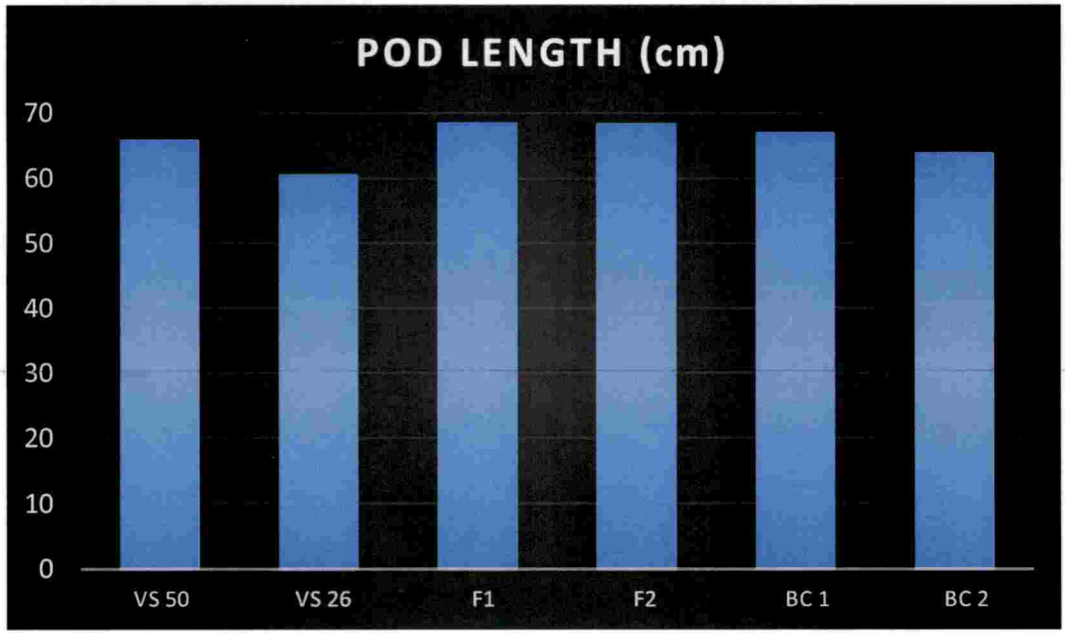


CROSS 2

Fig 2. Variability for pod length (cm) among the generations in cross 1 and cross 2

5.2 YIELD CHARACTERS

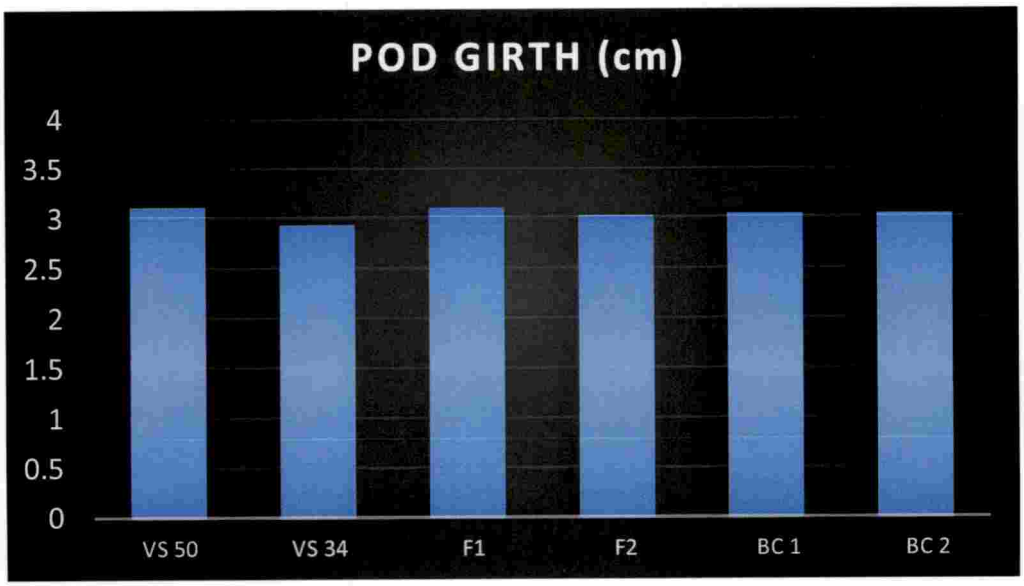
5.2.1 Pod Length (cm)

Consumers prefer long, crisp and tender yard long bean pods that are used in cooked form. P_1 in cross 1 and F_1 in cross 2 were superior for pod length based on mean performance over the generations studied (Fig 2).

In cross 1, significance was observed for scales B and C in favourable positive direction among which scale B had the highest magnitude, which implies that F_1 is better than the second parent. All the genetic components except additive x additive were significant among which additive x dominance and dominance x dominance were in negative direction and dominance gene action possessed the highest positive value. The predominance of dominance gene action revealed that reliance should be placed on heterosis breeding for the improvement of pod length in cross 1. The findings are in concurrence with Sawant (1994), Nagaraj (2002), Aliyu (2007) and Khodambashi *et al.* (2012) in cowpea and Prasad *et al.* (2010) in brinjal.

Cross 2 witnessed positive significance for scales C and D among which scale C had the highest magnitude which implies the superiority of F_2 over both the parents. Even though additive, dominance and all epistatic effects except additive x dominance interactions were significant, dominance x dominance gene action was in the favourable positive direction and had the highest magnitude which underlines the efficient utility of heterosis and selection for the improvement of pod length, as reported by Philip (2004) and Lovely (2005).

The predominance of non-additive gene action for pod length in cowpea was earlier reported by Ushakumari *et al.* (2010), Chaudhari *et al.* (2013) and Lakshmi (2016). Opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction indicated the presence of duplicate type of epistasis in both the crosses.



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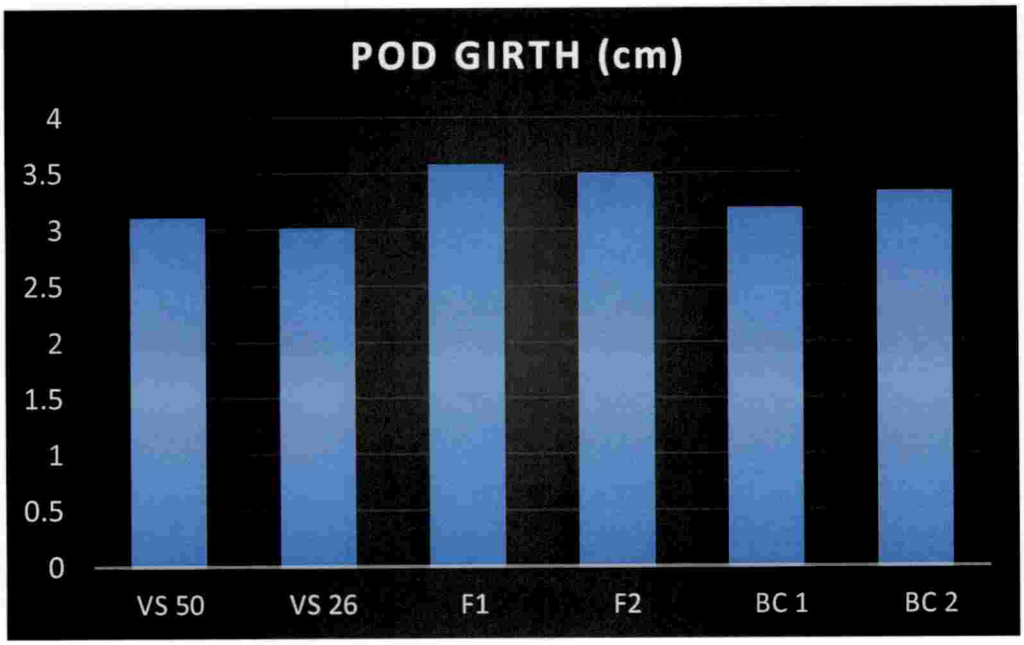

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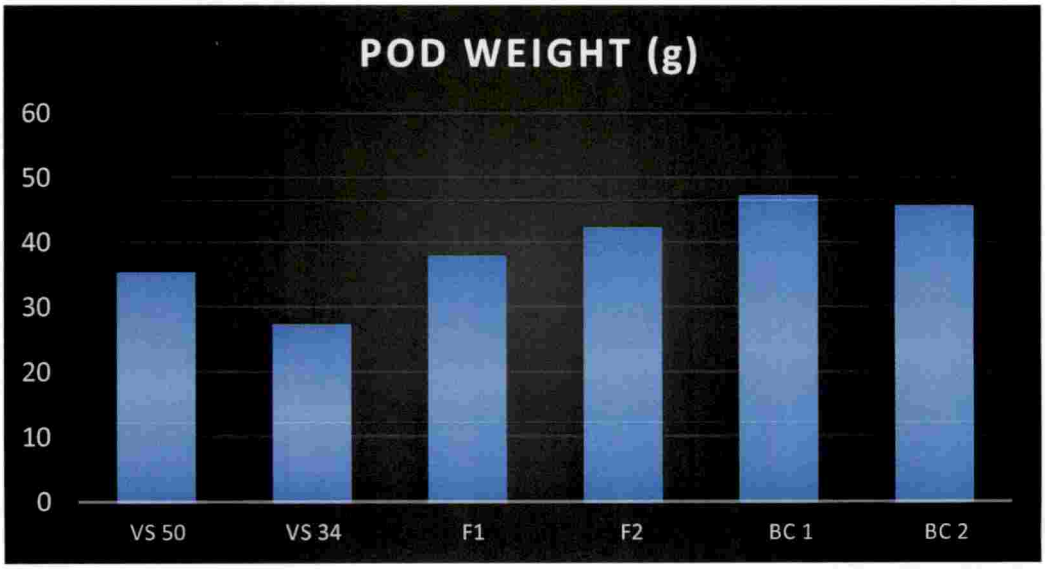
Fig 3. Variability for pod girth (cm) among the generations in cross 1 and cross 2



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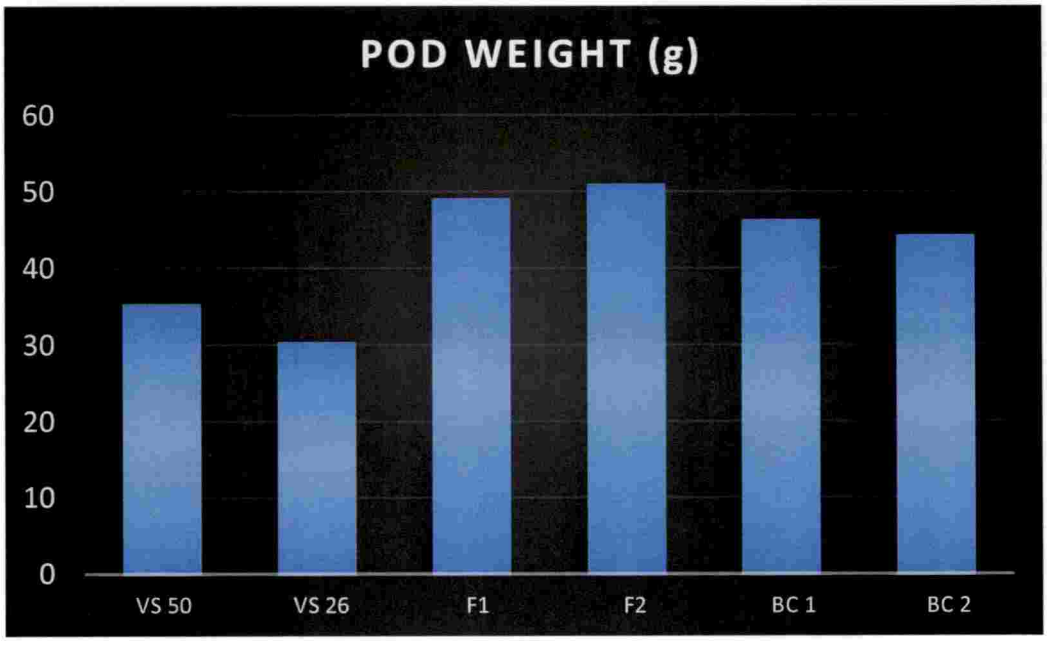

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Fig 4. Variability for pod weight (g) among the generations in cross 1 and cross 2

5.2.2 Pod Girth (cm)

Pod girth is also an important character as that of pod length, which contributes to consumer preference and yield. Considering the mean performance, P_1 in cross 1 and F_1 in cross 2 were superior for the character pod girth (Fig. 3).

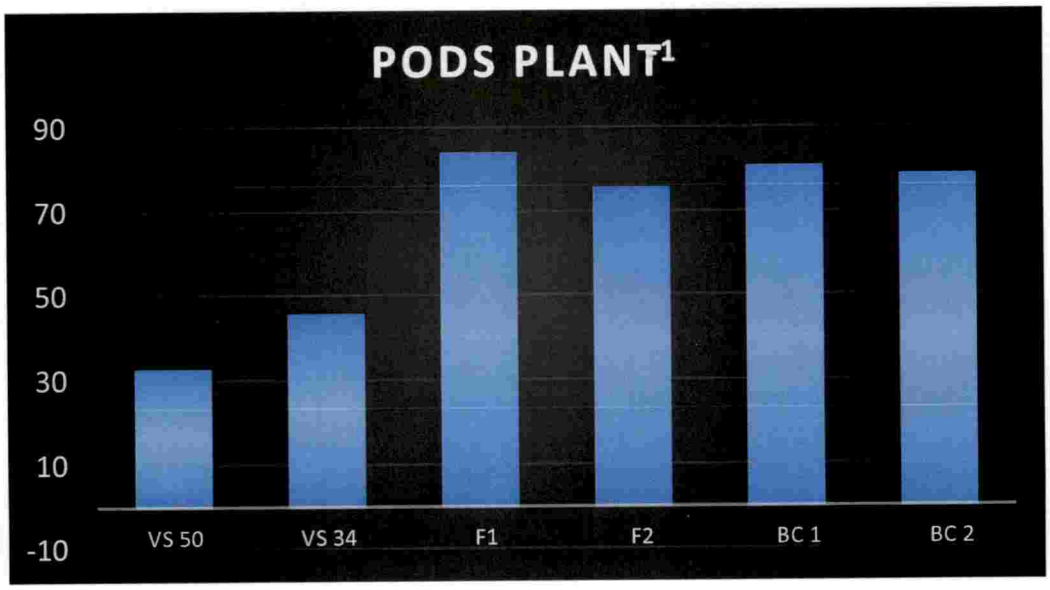
In cross 1, all the scales A, B, C and D were found to be non-significant, which indicates the absence of non-allelic interaction and that additive-dominance model was adequate. Among the genetic components, additive effect was in positive direction and had the highest magnitude. Hence direct selection could be used for the improvement of the trait, in accordance with earlier reports of Tamgadge *et al.* (2008) and Khanpara (2015) in cowpea and Kafytullah *et al.* (2011) and Soumya (2015) in brinjal.

Scales A, C and D were significant among which scale C was in positive direction with highest magnitude, which reveals the superiority of F_2 over both the parents in cross 2. Though all the genetic components were significant, additive and dominance x dominance effects were in favourable positive direction and dominance x dominance had the highest value, which pointed out the suitability of hybridization and selection for improving the trait. The predominance of non-additive gene action was reported by Jithesh (2009) and Lakshmi (2016). Duplicate nature of epistasis was prevalent in cross 2 while epistasis was absent in cross 1.

5.2.3 Pod Weight (g)

Pod weight is one of the component trait directly influencing the pod yield. The perusal of result based on the mean performance revealed that BC_1 in cross 1 and F_2 in cross 2 were superior for pod weight (Fig. 4).

In both the crosses, significance was observed for all the scales A, B, C and D in favourable positive direction except D in cross 1, which was negative. The highest



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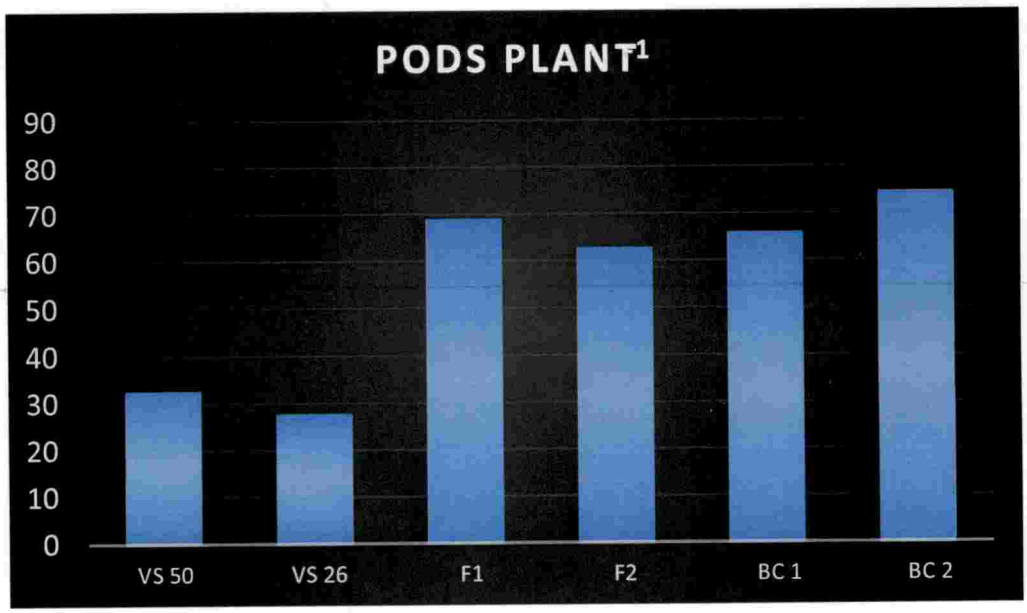

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Fig 5. Variability for pods plant $^{-1}$ among the generations in cross 1 and cross 2

magnitude of scale C denotes the betterment of F_2 over the parents. Significance was observed for all the genetic components in cross 1, among which additive, dominance, and additive x additive were positive while additive x dominance and dominance x dominance were in negative direction. Dominance gene action had the highest magnitude. Since dominance effect was predominant, heterosis breeding could be used for the improvement of the trait in accordance with Adeyanju (2009) and Jithesh (2009).

Further analysis in cross 2 showed positive significance in additive and dominance x dominance gene action and negative in dominance effect and additive x additive interaction. Hybridization followed by selection would be used for the improvement of the trait in cross 2 since dominance x dominance type of epistasis was predominant. The above result is in conformity with that of Lovely (2005) in vegetable cowpea. Predominance of non-additive gene action was suggested by Rahman and Saad (2000) and Manivannan and Sekar (2005). Duplicate type of epistasis was seen for the trait which was observed from the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

5.2.4 Pods Plant^{-1}

Pods plant^{-1} is an important parameter which contributes for yield in vegetable cowpea. In both the crosses, VS 50 x VS 34 and VS 50 x VS 26, mean value of F_1 was higher than that of F_2. Based on the mean performance, F_1 in cross 1 exhibited maximum number of pods plant^{-1} while BC_2 in cross 2 recorded maximum number of pods plant^{-1} (Fig. 5).

All the scales were significant in cross 1 among which scale C had the highest magnitude in positive direction indicating that F_2 is better than the parents. Though all the genetic components displayed significance, additive and dominance x dominance effect were negative while dominance, additive x additive and additive x dominance

were positive of which dominance effect had the highest value. Predominance of dominance effect suggested that heterosis breeding would improve the trait in cross 1.

In cross 2, highest magnitude and significance of scale B in favourable positive direction over the significance of all other scales reveals the superiority of F_1 over the second parent. All the types of epistatic interactions were significant among which dominance type of gene action had the highest positive value. Hence the improvement of the trait could be done by heterosis breeding. These results are in agreement with the findings of Smitha (1995), Valarmathi *et al.* (2007), Ushakumari *et al.* (2010), Yadav *et al.* (2010), Chaudhari *et al.* (2013), Lakshmi (2016) and Gupta *et al.* (2017) who suggested the presence of non-additive action for controlling the trait. Epistasis was revealed to be duplicate for both the crosses due to opposite signs of dominance (h) effect and dominance x dominance (l) interactions.

5.2.5 Seeds Pod^{-1}

Pods with more number of seeds are longer, which is preferred most by consumers. With regard to mean performance, maximum number of seeds pod^{-1} was observed in F_1 in cross 1 and BC_1 in cross 2.

Significance was observed for scales A, B and D in cross 1, among which scale D had the highest magnitude in favourable positive direction which implies the superiority of F_2 over the backcrosses BC_1 and BC_2. The analysis of genetic components revealed the significance of additive, dominance, additive x additive and dominance x dominance effects of which dominance x dominance type of epistasis was in favourable positive direction with highest value. Predominance of dominance x dominance effect indicated the suitability of hybridization and selection for the improvement of the trait in cross 1, which was in accordance with the earlier reports of non-additive gene actions in controlling the trait by Rahman and Saad (2000), Nagaraj *et al.* (2002), Singh *et al.* (2006) and Meena *et al.* (2010)

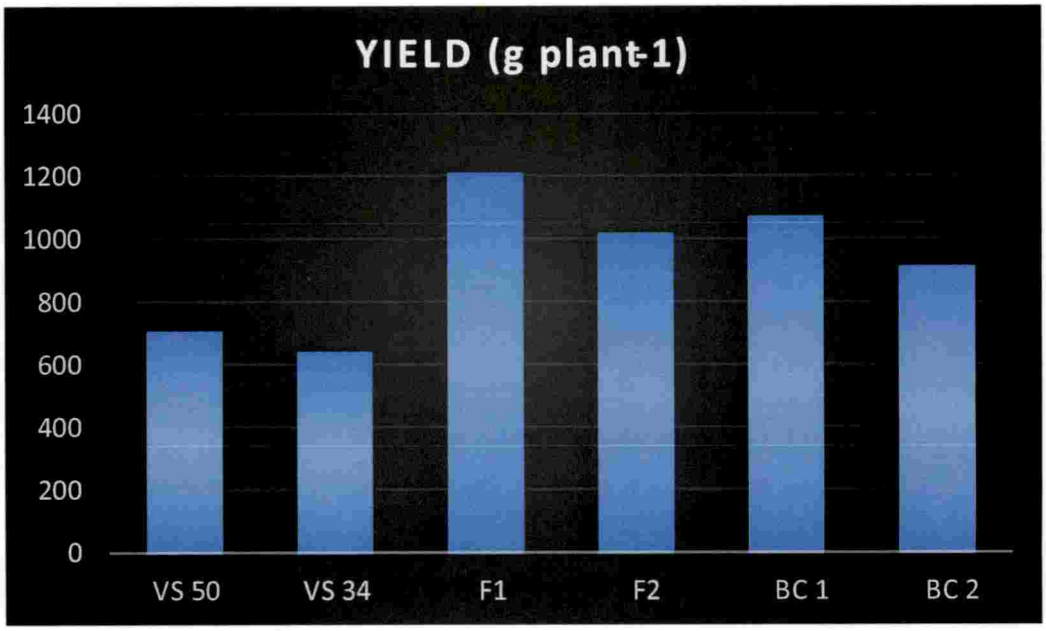
In cross 2, significance was observed for scale A in favourable positive direction, which implies the superiority of F_1 over the first parent. All the genetic components, except additive x additive type of interaction, were significant. Dominance type of gene action, being positive and exhibiting highest magnitude points out that heterosis breeding would improve the trait number of seeds pod^{-1} in cross 2. The above result satisfies the earlier reports of Sawant (1994), Lal *et al.* (2013), Behra (2015) and Gupta *et al.* (2017). Duplicate type of epistasis was observed in both the crosses.

5.2.6 Hundred Seed Weight (g)

Hundred seed weight is an important parameter considered for a good quality seed. Considering the mean performance, F_1 was superior over the generations considered for hundred seed weight in cross 1and cross 2.

Cross 1 witnessed significance for A, C and D, among which scale C was in positive direction and had the highest magnitude, which implies that the F_2 is better than both the parents. All the genetic components showed significance of which dominance effect, additive x additive and additive x dominance type of epistasis were in negative direction. Additive and dominance x dominance were positive, of which dominance x dominance effect had the highest magnitude which implies the usefulness of hybridization followed by selection for the improvement of the trait in cross 1.

Significance of B, C and D were observed in cross 2, of which scale C was positive and had the highest magnitude, which indicates the superiority of F_2 over the parents. Detailed analysis of genetic components displayed significance for all the components where additive, dominance and additive x additive were in negative direction while additive x dominance and dominance x dominance were positive, dominance x dominance type of epistasis having the highest magnitude. Hence



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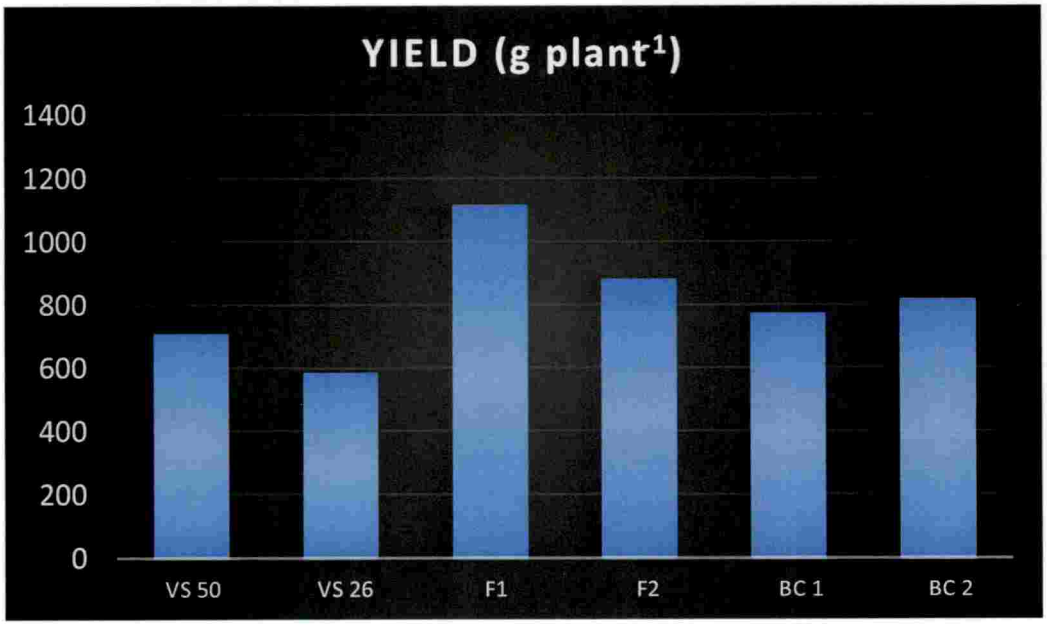


CROSS 2

Fig 6. Variability for yield (g plant^{-1}) among the generations in cross 1 and cross 2

hybridization followed by selection could be used for the improving the hundred seed weight. The result showed the importance of duplicate type of epistasis in controlling the character, in accordance with the earlier findings of Abd-Elkader (2006), Zaher (2016) and Gupta *et al.* (2017). The involvement of non-additive gene action was reported by Sobha and Vahab (1998), Rashwan (2010), Adeyanju *et al.* (2012) and Patel *et al.* (2013) for hundred seed weight. Epistasis was revealed to be duplicate for both the crosses due to opposite signs of dominance (h) effect and dominance x dominance (l) interactions.

5.2.7 Yield (g plant^{-1})

The main objective of any breeding programme is higher yield and in the present study it was recorded in terms of pod yield (g plant^{-1}). Based on mean performance, F_1 was superior over the generations for pod yield plant^{-1} in cross 1 and cross 2 (Fig. 6).

Positive significance was noticed for scales A, C and D, of which scale C had the highest magnitude, which implies the superiority of F_2 over both the parents. Further analysis of genetic components showed the significance of additive, dominance, additive x additive and additive x dominance of which dominance had the highest positive value. The predominance of dominance effect underlines the suitability of exploiting heterosis breeding for the improvement of the character, as observed in earlier studies of Adeyanju (2009), Patel *et al.* (2009), Kumar and Kumar (2013) and Behra (2015).

Though scales A and D were significant in cross 2, A was negative and D positive, which implies that F_2 is better than the backcrosses. Detailed analysis of genetic components revealed the significance of additive, dominance and all the epistatic interactions, among which dominance x dominance gene action had the highest magnitude in positive direction. Hence hybridization followed by selection

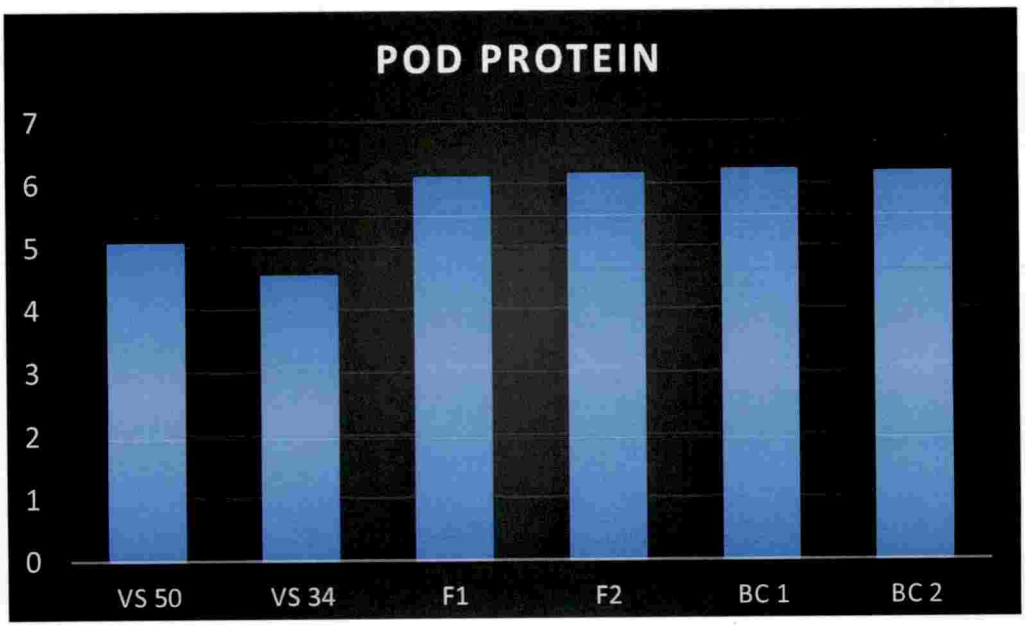
could be used for the improvement of the trait in accordance with the studies of Rahman and Saad (2000), Philip (2004), Lovely (2005), Manivannan and Sekar (2005), Jithesh (2009) and Meena *et al.* (2010). Duplicate type of epistasis was seen for the trait which was observed from the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

5.2.8 Days to Harvest

Early harvest is desirable as the yard long bean pods fetch a good market price. Among the generations, considering mean performance, P_1 and P_2 were superior in cross 1 and P_2 and F_2 in cross 2.

Non-significance was noticed in all the scales A, B, C and D which indicates the absence of non-allelic interaction and adequacy of additive-dominance model to study the trait in cross1. Among the genetic components, predominance of dominance gene action was observed in favourable negative direction, which implies the suitability of using heterosis breeding for the improvement of the character. The absence of epistasis for days to harvest was earlier observed by Singh *et al.* (1988), Rana and Gupta (1994), Nagaraj *et al.* (2002) and Lovely (2005).

In cross 2, highest positive significance was noticed in scale D, which indicates the superiority of F_2 over the backcrosses. Further analysis showed significance of dominance and additive x additive gene action in negative direction and dominance x dominance in positive direction. Dominance effect showed the highest magnitude in the favourable negative direction. This showed the possibility of getting early harvesting varieties through heterosis breeding. The predominance of non-additive gene action in controlling the trait was observed in the studies of Vaghasiya *et al.* (2000), Bendale *et al.* (2005), Pal *et al.* (2007) and Uma and Kalubowila (2010). Epistasis was revealed to be duplicate in cross 2 due to opposite signs of dominance (h) effect and dominance x dominance (l) interactions.



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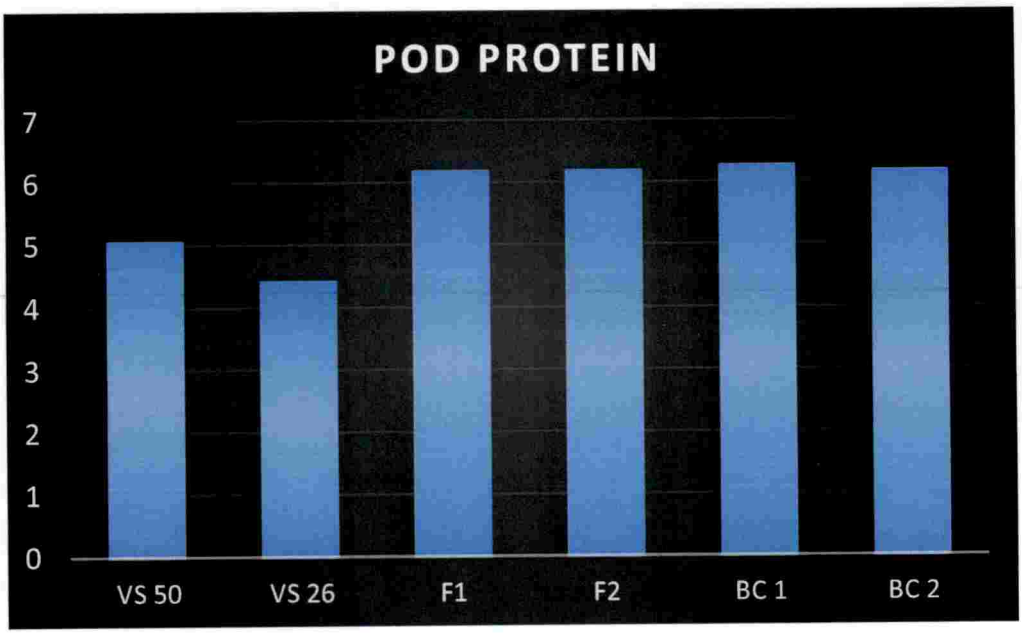

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Fig 7. Variability for pod protein (%) among the generations in cross 1 and cross 2

5.2.9 Crop Duration

Crop duration is an important growth parameter to understand how long the crop remains in its yielding period. Among the generations for mean performance, BC_2 was superior in both the crosses for crop duration.

Positive significance was observed in all the scales in both the crosses except scale D in cross 2. Scale D was significant but negative in cross 1 while non-significant in cross 2. Scale C had the highest magnitude in cross 1 and 2, which implies the superiority of F_2 over the parents. Significance was observed in all genetic components of which dominance effect had the highest positive value in cross 1. Hence heterosis breeding would be used to improve the trait crop duration.

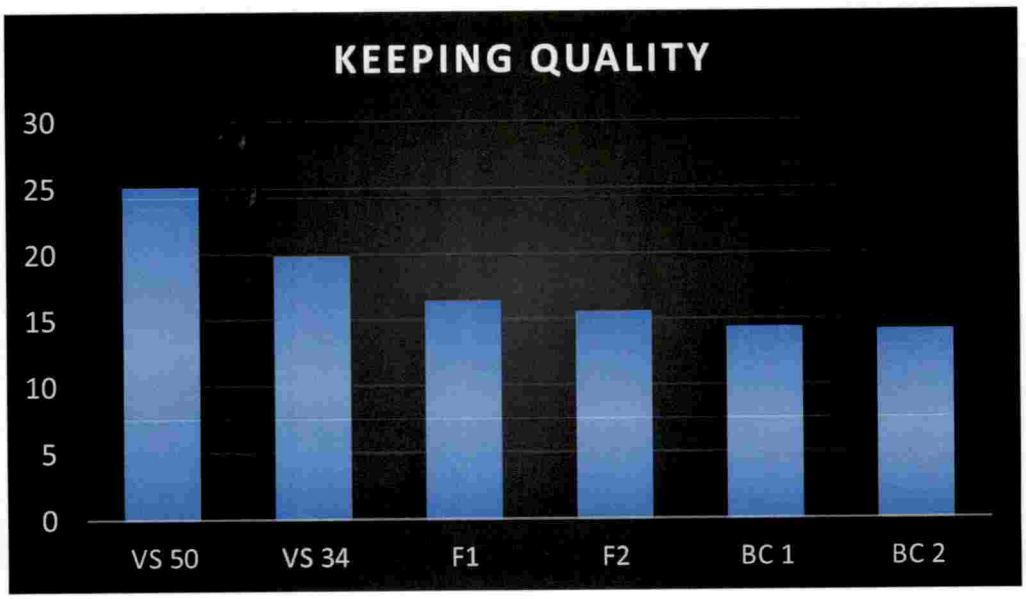
In cross 2, significance was observed for dominance gene action in favorable positive direction while for additive and dominance x dominance effect negative. Predominance of dominance gene action was observed which pointed out the suitability of using heterosis breeding for improvement of the trait crop duration. Presence of duplicate nature of epistasis was present in both the crosses as indicated by opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

5.3 QUALITY CHARACTERS

5.3.1 Pod Protein (%)

Yard long bean is a rich and inexpensive source of vegetable protein and hence pod protein (%) is an important quality parameter. On the basis of mean performance, BC_1 was superior among generations in both the crosses (Fig. 7).

Significance was observed for all scales during scaling test except scale D in cross 2, among which scales A, B and C were acting in favourable positive direction



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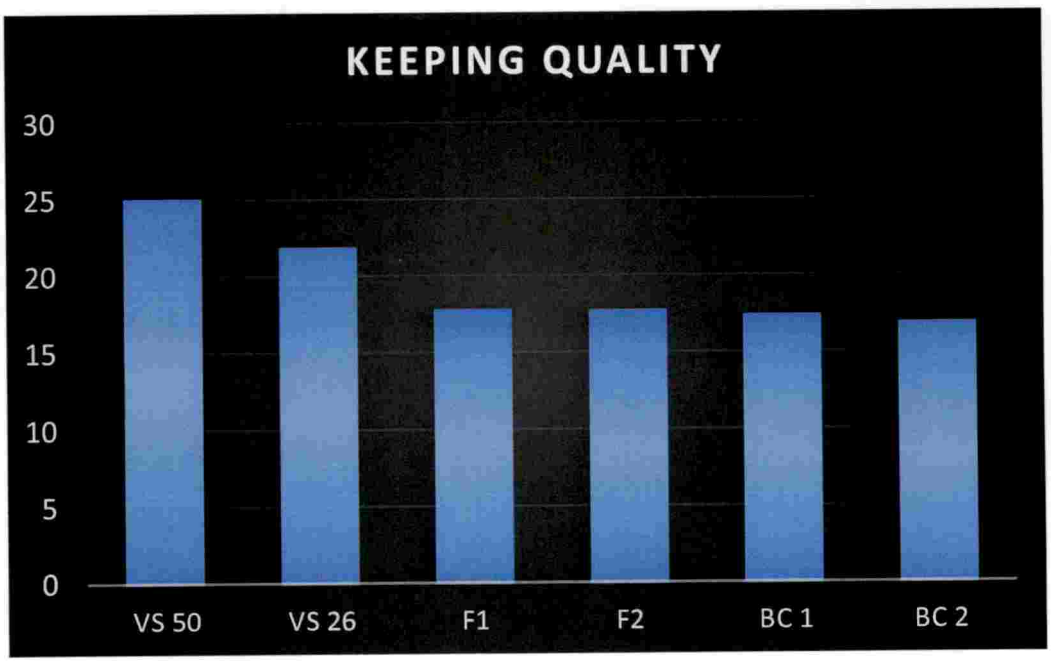

CROSS 2

Fig 8. Variability for keeping quality (% loss weight) among the generations in cross 1 and cross 2

and scale C having the highest magnitude which indicates the superiority of F_2 over the parents in cross 1 and 2. Detailed analysis of genetic components showed positive significance of additive x additive in cross 1 and non-significance in cross 2. Positive significance of additive and dominance and negative significance of additive x dominance and dominance x dominance type of epistasis was observed, of which dominance possessed the highest positive value in both the crosses, which indicates the improvement of the trait through heterosis breeding.

Dominance variance component was positively significant for pod protein content. Preponderance of non-additive gene action for pod protein content was observed in accordance with earlier reports of Malarvizhi (2002), Noubissie *et al.* (2011) and Subbaih *et al.* (2013). Duplicate type of epistasis was present in both crosses indicated by the presence of opposite signs of dominance (h) effect and dominance x dominance (l) type of non-allelic interactions.

5.3.2 Keeping Quality (% weight loss)

Cultivation of yard long bean for commercial market requires pods having longer keeping quality, without losing the freshness and tenderness. So keeping quality measured in terms of percentage weight loss is an important quality parameter considered for crop improvement. Best keeping quality was for BC_2 in both the crosses (Fig. 8).

Scales A, B and C were significant and negative in both the crosses, whereas scale D was positively significant. Scale C had the highest magnitude in the favourable negative direction, which implies the superiority of F_2 over the parents. Detailed study of genetic components showed significance in negative direction in dominance, additive x additive and additive x dominance while additive and dominance x dominance had positive significance. Dominance effect had the highest

magnitude in the favourable negative direction, which suggested heterosis breeding for the improvement of the trait in cross 1.

In cross 2, significance was observed for all the genetic components of which dominance and additive x additive interactions were in the favourable negative direction and dominance had the highest magnitude. Hence heterosis breeding can be utilized for the improvement of keeping quality of pods in cross 2. Garg *et al.* (2008) in tomato and Lakshmi (2016) in vegetable cowpea attributed the predominance of non-additive gene action for inheritance of keeping quality of pods. Duplicate type of epistasis was present in both crosses indicated by the presence of opposite signs of dominance (h) effect and dominance x dominance (l) type of non-allelic interactions.

Summary

6. SUMMARY

Yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Walp.) a distinct form of cowpea, is a major leguminous vegetable crop which originated from Central Africa. It is one of the most popular and remunerative vegetable, traditionally grown in Kerala for crisp and tender pods, which are consumed in cooked form. An understanding of the mode of inheritance of the yield components is a prerequisite for the effective choice of breeding methodology for developing elite varieties. The type of gene action involved in the expression of a trait is helpful in deciding the appropriate breeding procedures to be used for the improvement of the trait. So detailed investigation of both gene action and genetic variability is essential for the improvement of the desirable trait.

The present investigation on "Generation mean analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and quality" was conducted at the Department of Vegetable Science, College of Agriculture, Vellayani during 2017-2018, to study the inheritance and gene action of yield and quality in yard long bean using generation mean analysis. The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two superior crosses of yard long bean with high yield and quality characters *viz.* Cross 1 - VS 50 x VS 34 (Kakkamoola Local x Githika) and Cross 2 - VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) were used for the study.

The experiment was carried out in three parts. In part I, two superior crosses of yard long bean with high yield and quality characters, selected based on specific combining ability and *per se* performance from the previous M.Sc. (Hort.) programme, were used. The seeds of the two hybrids were produced in a crossing block. In part II, the two F_1 hybrids were selfed to produce F_2 progenies. Simultaneously, the F_1 hybrids were backcrossed with the female parent to produce

BC_1 generation and the male parent to produce BC_2 generation. In part III, the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two hybrids were evaluated in a replicated field experiment for fifteen yield and quality components in randomized block design using generation mean analysis.

Mean performance and gene action were studied for the vegetative and flowering characters *viz.,* vine length at final harvest (cm), primary branches plant^{-1}, length and breadth of leaflets (cm) and days to first flowering, yield characters like pod length (cm), pod girth (cm), pod weight (g), pods plant^{-1}, seeds pod^{-1}, 100 seed weight (g), yield (g plant^{-1}), days to harvest, crop duration and quality characters like pod protein (%) and keeping quality (% weight loss). The salient observations of the present investigation are summarized as follows.

Analysis of variance showed significant differences among the generations of the two crosses VS 50 x VS 34 (Kakkamoola Local x Githika) and VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) for most of the characters studied. Maximum vine length at final harvest was reported in P_2 (536.67 cm) and minimum in F_2 (367.33 cm) in cross 2. Highest number of primary branches plant^{-1} was observed in BC_2 (5.22) in cross 1 and P_1 (4.00) in cross 2. BC_1 in cross 1 and F_1 in cross 2 recorded the lowest number of primary branches plant^{-1} (3.22 and 2.88 respectively). Among the generations, maximum leaf area was recorded for BC_1 in cross 1 and F_2 in cross 2. Earliest flowering was observed in F_1 in both the crosses (50.00 days and 49.50 days in cross 1 and 2 respectively) while P_1 (53.50) in cross 1 and P_2 (54.00) in cross 2 were late.

Pod length was highest for P_1 (65.99 cm) in cross 1 and F_1 (68.56 cm) in cross 2. Lowest pod length was recorded for P_2 in crosses 1 and 2 (47.86 cm and 60.58 cm respectively). Pod girth was maximum in P_1 (3.11 cm) in cross 1 and F_1 (3.57 cm) in cross 2. P_2 showed lowest pod girth in both the crosses (2.93 cm and 3.01 cm in 1 and 2 respectively). The highest mean values for pod weight was recorded by BC_1 (47.22

g) and F_2 (50.89 g) in cross 1 and 2 respectively and the lowest values by P_2 in cross 1 (27.33 g) and cross 2 (30.33 g). F_1 produced highest number of pods plant^{-1} (84.00), while P_1 (32.67) the lowest in cross 1.

Maximum number of seeds pod^{-1} was observed in F_1 (22.33) in cross 1 and BC_1 (20.33) in cross 2. In cross 1 and cross 2, least number of seeds pod^{-1} was recorded by parents P_1 (19.17) and P_2 (17.83) respectively. . Hundred seed weight was recorded maximum by F_1 in cross 1 (17.05 g) and cross 2 (21.83 g). Minimum hundred seed weight was recorded by the parents P_2 (13.03 g) in cross 1 and P_1 (16.17 g) in cross 2.

Significant difference was observed between the treatments for yield plant^{-1}. Among the treatments, yield plant^{-1} was highest for F_1 in cross 1 (1210.51 g) and cross 2 (1116.83 g). Lowest yield plant^{-1} was recorded by P_2 in cross 1 (642.61 g) and cross 2 (584.00 g).

The generations F_1 and BC_2 (61.00) in cross 1 and F_1, BC_1 and BC_2 (63.00) in cross 2 were found earlier to harvest. P_1 and P_2 (64.00) in cross 1 and P_2 and F_2 (64.33) in cross 2 took maximum number of days for harvest. Crop duration was longest in BC_2 (125.67 and 122.67 respectively) and shortest in P_1 (111.00) in cross 1 and 2.

Among quality characters, highest pod protein content was recorded by BC_1 in both the crosses (6.23 % and 6.27 % in cross 1 and 2 respectively) and keeping quality by BC_2 in both the crosses (14.16 % weight loss and 16.88 % weight loss in cross 1 and 2 respectively).

Using generation mean analysis, various gene effects and interactions controlling different characters were studied. Predominance of dominance gene action was observed for most of the characters in cross 1 (VS 50 x VS 34) *viz.,* vine length at final harvest, primary branches plant^{-1}, terminal and lateral leaf length,

lateral leaf width, days to first flowering, pod length, pod weight, pods plant^{-1}, yield, days to harvest, crop duration, pod protein and keeping quality and in cross 2 (VS 50 x VS 26) *viz.,* vine length at final harvest, days to first flowering, pods plant^{-1}, seeds pod^{-1}, days to harvest, crop duration, pod protein and keeping quality. Predominance of dominance gene action pointed out the suitability of resorting to heterosis breeding for the improvement of the trait.

Presence of dominance x dominance interaction for the characters such as seeds pod^{-1} and hundred seed weight in cross 1 (VS 50 x VS 34) and terminal and lateral leaf length and width, pod length, pod girth, pod weight, hundred seed weight and yield in cross 2 (VS 50 x VS 26) suggested the use of hybridization followed by selection as the appropriate breeding method for the improvement of the above mentioned traits in their respective crosses.

Terminal leaf width and pod girth in cross 1 (VS 50 x VS 34) and primary branches plant^{-1} in cross 2 (VS 50 x VS 26) were controlled by additive gene effect. Simple selection procedure would be more rewarding for improving the characters governed by additive type of gene effects.

Heterosis breeding and hybridization followed by selection could be the appropriate breeding methods for both the crosses since predominance of dominance and dominance x dominance interaction was observed for most of the characters. Duplicate type of epistasis was observed for most of the traits studied, as shown by the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.

Major pest problem observed during the cropping period were spotted pod borer (*Maruca vitrata*), aphids (*Aphis craccivora*), leaf eating capertillar (*Spodoptera litura*) and pod bug (*Riptortus pedestris*) while cowpea aphid borne mosaic virus (CABMV), fusarium wilt (*Fusarium oxysporum*), collar rot and web blight

(*Rhizoctonia solani*), cercospora leaf spot (*Cercospora sp.*) and rust (*Uromyces vignae*) were the main diseases observed in the field.

FUTURE LINE OF WORK:

- Effective breeding methodology can be adopted for developing elite varieties with respect to gene action prevalent for each character needed for improvement.
- Two superior hybrids (VS 50 x VS 34 and VS 50 x VS 26) can be advanced to farm trials and multi-locational trials to confirm their outstanding performance in different locations before the release of elite hybrids.
- From the segregating populations, superior genotypes can be selected for further breeding programmes.

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Abstract

GENERATION MEAN ANALYSIS IN YARD LONG BEAN (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) FOR YIELD AND QUALITY

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Abstract of the thesis

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ABSTRACT

The project entitled "Generation mean analysis in yard long bean (*Vigna unguiculata* subsp. *sesquipedalis* (L.) Verdcourt) for yield and quality" was carried out at the Department of Vegetable Science, College of Agriculture, Vellayani, during 2017-2018, to study the inheritance and gene action of yield and quality in yard long bean using generation mean analysis.

The six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of two superior crosses of yard long bean with high yield and quality characters *viz.* Cross 1 - VS 50 x VS 34 (Kakkamoola Local x Githika) and Cross 2 - VS 50 x VS 26 (Kakkamoola Local x Vellayani Jyothika) were used for the study. The experiment was carried out in three parts. In part I, two superior crosses of yard long bean with high yield and quality characters, selected based on specific combining ability and *per se* performance from the previous M.Sc. (Hort.) programme, were used. The seeds of the two hybrids were produced in a crossing block. In part II, the two F_1 hybrids were selfed to produce F_2 progenies. Simultaneously, the F_1 hybrids were backcrossed with the female parent to produce BC_1 generation and the male parent to produce BC_2 generation. In part III, the six generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) of the two hybrids were evaluated in a replicated field experiment using generation mean analysis.

The six generations of the two crosses were evaluated for vegetative and flowering characters, yield and yield attributes and quality characters. Significant difference was observed among the generations for most of the traits studied. Earliest flowering was observed in F_1 in both the crosses (50.00 days and 49.50 days in cross 1 and 2 respectively). Pod length and pod girth was maximum for P_1 (65.99 cm and 3.11 cm respectively) in cross 1 and F_1 (68.56 cm and 3.57 cm respectively) in cross 2. The highest pod weight was recorded by BC_1 (47.22 g) and F_2 (50.89 g) in cross 1 and 2 respectively. Maximum number of pods plant^{-1} was recorded in F_1 (84.00) in

cross 1 and BC_2 (74.67) in cross 2. Highest number of seeds pod^{-1} was observed in F_1 (22.33) in cross 1 and BC_1 (20.33) in cross 2. Hundred seed weight was maximum for F_1 in both the crosses (17.05 g and 21.83 g in cross 1 and 2 respectively). The highest yield was recorded by F_1 in both the crosses (1210.51 g plant^{-1} and 1116.83 g plant^{-1} in cross 1 and 2 respectively). Among quality characters, highest pod protein content was recorded by BC_1 in both the crosses (6.23 % and 6.27 % in cross 1 and 2 respectively) and keeping quality by BC_2 in both the crosses (14.16 % weight loss and 16.88 % weight loss in cross 1 and 2 respectively).

Predominance of dominance gene action was observed for most of the characters in cross 1 (VS 50 x VS 34) *viz.,* vine length at final harvest, primary branches plant^{-1}, terminal and lateral leaf length, lateral leaf width, days to first flowering, pod length, pod weight, pods plant^{-1}, yield, days to harvest, crop duration, pod protein and keeping quality. Terminal leaf width and pod girth were controlled by additive gene action whereas seeds pod^{-1} and hundred seed weight by dominance x dominance interaction. In cross 2 (VS 50 x VS 26), characters such as terminal and lateral leaf length and width, pod length, pod girth, pod weight, hundred seed weight and yield were governed by dominance x dominance, vine length at final harvest, days to first flowering, pods plant^{-1}, seeds pod^{-1}, days to harvest, crop duration, pod protein and keeping quality by dominance and primary branches plant^{-1} by additive gene actions. Incidence of spotted pod borer, aphids, leaf eating caterpillar, pod bug were observed during the cropping period. Cowpea Aphid Borne Mosaic Virus (CABMV), fusarium wilt, collar rot and web blight, cercospora leaf spot and rust were the diseases observed.

Predominance of dominance gene action pointed out the suitability of resorting to heterosis breeding for the improvement of the trait. Presence of dominance x dominance interaction suggested the use of hybridization followed by selection as the appropriate breeding method. Simple selection procedure would be

more rewarding for improving the characters governed by additive type of gene effects. Duplicate type of epistasis was observed for most of the traits studied, as shown by the opposite signs of dominance (h) effect and dominance x dominance (l) type of interaction.