GENETIC STUDIES ON EDIBLE POD YIELD IN F_2 DIALLEL POPULATION OF LABLAB BEAN (*Lablab purpureus* L.)

A Thesis

Submitted to the Department of Genetics and Plant Breeding
Bangladesh Agricultural University, Mymensingh
in partial fulfilment of the requirements
for the degree of

MASTER OF SCIENCE (M.S.)
IN
GENETICS AND PLANT BREEDING

By

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Semester : July – December, 2002

Department of Genetics and Plant Breeding
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November, 2002


DEDICATED TO
MY
BELOVED PARENTS

ACKNOWLEDGEMENTS

All praises are for Almighty Allah, the great, gracious and merciful, whose blessing enabled the author to complete this research work.

The author expresses his deepest sense of gratitude and immense indebtedness to his supervisor, Professor Dr. M.A. Newaz, Department of Genetics and Plant Breeding, Bangladesh Agricultural University, Mymensingh for his inspiration, valuable suggestions, constant guidance and continuous intensive supervision throughout the period of his study and preparation of this thesis.

The author expresses his sincere gratitude and appreciation to Prof. Dr. Lutful Hassan and Prof. Dr. M. Wazuddin, present and previous Head of Department, Genetics and Plant Breeding, BAU, Mymensingh, respectively, for valuable suggestions, and provisions of facilities needed to undertake this research work.

The author humbly desires to acknowledge his heartiest appreciation and cordial thanks to his respected course teachers of the Department: Prof. Dr. Lutfur Rahman, Prof. Dr. Q.N. Ahmad, Prof. Dr. M.A. Islam, Prof. Dr. A.K. Patwary, Prof. Dr. M.S. Alam, Prof. M.A. Quddus and Prof. Dr. A.K.M. Shamsuddin for their valuable teaching, kind cooperation, encouragement and time to time advice during the period of his study. The author also thankfuly acknowledges the help extended by Mr. Ashraful Haque and Mr. Ujjal Kumar Nath, Lecturers of this department.

The author would like to express his thanks to senior brother Partha, Pavel, Hamid, Alam and Pallab for their helpful suggestion and inspiration. It is also a pleasure for the author to remember his friends Mamun, Ripon, Mizan, Rana, Ahasan, Sayid, Selim, Shamim and well wishers for their constant encouragement and moral support.

Thanks are also due to all field Laboratory and Office staff of the Department of Genetics and Plant Breeding, BAU, who directly or indirectly helped in this study. The author also wishes to thank Md. Nazrul Islam, Tutul bhai and Ashraf uncle for helping with the computer composition and printing of this thesis manuscript.

Last but not least, the author expresses his supreme gratitude and profound feelings to his beloved father, mother, uncle, aunt, grand father, grand mother and loving younger brother Saidur and sister Farida who have been constant source of inspiration, blessing and good wishes for his higher studies.

BAU, Mymensingh

The Author

SYMBOLS AND ABBREVIATIONS

a	=	additive genetic effect
ANOVA, anova	=	analysis of variance
b	=	i) regression coefficient (Wr on Vr)
		ii) dominance effect
b_1	=	mean dominance
b_2	=	dominance due to array
b_3	=	residual dominance
cf.	=	compare
cm	=	centimeter, centimetre
D	=	variation due to additive effect
d.f.	=	degrees of freedom
E	=	expected environmental component of variation
Env.	=	environmental
F	=	the mean of fr values over the arrays
g	=	gram
GCA, gca	=	general combining ability
H_1	=	component of variation due to the dominance effect of the genes
H_2	=	proportion of positive and negative genes in the parents
h^2	=	dominance effect
h^2_n	=	narrow sense heritability
ha	=	hectare
kg	=	kilogram
mt	=	metric ton
m	=	meter, metre
Me	=	mean square due to error
Mg	=	mean square due to gca
Ms	=	mean square due to sca
MS	=	mean square
RCBD	=	randomized complete block design
Rep.	=	replication
SE	=	standard error
SCA, sca	=	specific combining ability
Vr	=	variance
Wr	=	co-variance
Wt.	=	weight
>	=	greater than
<	=	smaller than

ABSTRACT

A 6 × 6 F_2 diallel experiment (without reciprocal) on Lablab bean (*Lablab purpureus* L.) was conducted to study combining ability and inheritance in some selected genotypes for pod yield and other related characters such as flowering, pod setting, no. of inflorescences per plant, no. of flowers per inflorescence, no. of pods per inflorescence, inflorescence length, pod length, pod width, 10-pod weight and 20-seed weight.

There were significant variations among the genotypes for all the characters studied. Variances for general combining ability (gca) and specific combining ability (sca) were significant for ten out of eleven characters including pod yield per plant, suggesting the presence of both additive and non-additive components in the genetic systems of these characters. For days to 1st flowering and 1st pod setting, the genetic system was predominantly of non-additive gene action. The parental genotype DS-52 was found to be the best general combiner for early flowering, pod setting and 20-seed weight. The parent DSN-26 was the best general combiner for inflorescences per plant, pod length, pod width, 10-pod weight and also for pod yield per plant. For sca effect the cross DS-52 × DS-161 and DS-30 × DSN-26 were the best specific combiners for early flowering and early pod setting. For 10-pod weight and pod yield per plant the cross DSN-26 × KBS-3 and DS-30 × KBS-2 were the best specific combiners.

Vr-Wr analysis relating to graphical presentation of major genetic features were done for all the eleven characters. Complete dominance was observed for pod yield per plant, partial dominance for no. of flowers per inflorescence, pod length, 10-pod weight, and 20-seed weight. While overdominance was recorded for days to 1st flowering, days to 1st pod setting, no. of inflorescences per plant, no. of pods per inflorescence, inflorescence length and pod width.

Components of variation and various genetic parameters such as degree of dominance, dominance ratio, narrow sense heritability etc. were estimated. Results showed that positive and negative alleles were in unequal proportion among the parents for all characters. The dominant alleles were in excess for all characters except pod length, pod width and 20-seed weight. Dominant and recessive genes were unequally distributed in the parents for all characters. High narrow sense heritability was observed for pod yield per plant and 10-pod weight, whereas for the others it was moderate to poor.

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CHAPTER 1

INTRODUCTION

INTRODUCTION

Lablab bean (*Lablab purporeus* (L.) Sweet; hitherto *Dolichos lablab*) is one of the popular winter vegetables. In Bangladesh it is commonly called country bean, but it has got a variety of names at different regions of the country like Sheem, Chhoi, Uri, Ushi, Deshi Sheem etc. Internationally also the crop has various other names e.g. hyacinth bean, bonavist bean, Dolichos bean, Indian bean, Egyptian kidney bean, Kerara (Indonesia), Pegyi (Myanmar), Kana-kara, Kekara (Malaysia), Tua pab (Thailand), Itab (Philippines), Pintak (China), Parda (Sudan), Tonga bean (Australia), etc. (Taylor, 1961; Rashid, 1976; Bose and Som, 1986; Jadhav *et al.*, 1987 and Tindall, 1988).

Lablab bean is a perennial legume crop with twining, creeping or bushy habit, but it is generally cultivated as an annual or biennial crop. In Bangladesh many types and forms of Lablab bean are grown; but Chittagong and coastal areas are especially reputed for its commercial cultivation (CFLIP, 1988). It is also commercially cultivated in Sylhet and Jessore regions.

Lablab bean plays an important role in the agora-economy and national health of Bangladesh. The crop has multipurpose usage. Its young pods and tender beans are consumed as vegetables (Purseglove, 1968). The ripe and dried seeds are used as a split pulse (dhal) and in various curry preparation. In the southern part of Bangladesh shelled matured and green seeds are cooked with lobster to make a popular local dish called "Khasha" or "Khaishara". Lablab bean is also a popular fodder crop. Its foliar portion is used to produce "hay and silage" as animal feed. It has got a unique ability to fix atmospheric nitrogen to the soil through rhizobial symbiosis at root zone and can enhance soil fertility as a green manure crop. Its mature dried stems are also used as a source of fuel and provide more or less an opportunity to combat fuel crisis. It has good digestibility and free from flatulent effects. Its green pods and mature seeds are rich source (25%) of protein (on dry basis), vitamins (e.g. vitamin A, vitamin C, riboflavin etc.) and mineral such as

magnesium, calcium, phosphorus, potassium, iron, sulfur and sodium (Deka and Sarker, 1990; Newaz, 1992). Thus it is an important source of cash income as well as alleviating malnutrition and sickness caused by dietary deficiencies.

Lablab bean is held in high esteem in Bangladesh due to its easier cooking quality, better taste and comparatively low market price. According to BBS (2001 & 2002), Lablab bean occupies an area of 26045 acres with an annual production of 49140 thousand metric tons and give an yield of 4.7 t/ha which is very low in respect of other bean yield (10 t/ha) in global context. This drawback is due to lack of prescribe production practices and lack of high potential varieties. According to available statistics bean production is highest in Chittagong district with annual production of 6375 mt with area coverage 2120 acres (BBS, 2001 & 2002). In Bangladesh only creeping type and photoperiod sensitive Lablab bean are grown. For field scale cultivation of the crops, it is necessary to develop the bushy, short and erect plant type requiring no trailing support. But the research works in this direction in Bangladesh are limited (Rahman, 1989; Khondker, 1995).

Yield is a polygenic character resulting from the interaction of yield contributing characters influenced by environmental fluctuations. Selection is the important tool in a crop improvement programme. But it is difficult to make improvement through direct selection on the basis of phenotypic performance only. The value of selected progeny plants would largely depend upon the relative contribution of the heritable (due to gene) and non-heritable (due to environment) components. Selection also depends upon the nature and magnitude of gene effects involving in the inheritance of the traits. Studies on the inheritance of yield and yield contributing characters suggest that these are controlled by both additive and non-additive gene actions (Paroda and Joshi, 1970; Singh and Singh, 1992). Breeding programme differs in exploiting additive gene action than that of non-additive gene action. In case of hybrid breeding programme, selection of suitable parents for hybridization is one of the most important steps. But, selection of parents on the basis of phenotypic performance alone is not a sound procedure

since phenotypically superior lines may yield poor recombination in the segregation generation. It is, therefore, essential that parents should be chosen on the basis of their genetic value.

Diallel analysis provides an effective means of obtaining rapid features of the inheritance of genes in homozygous lines. According to Crumpacker and Allard (1962), diallel analysis could successfully unravel the major features of a genetic system and predict the outcome of selection in early generations. The analysis allows for every conceivable variation in experimental design, including presence or absence of parental lines and reciprocal crosses (Yates, 1947; Hayman, 1954a; Griffing, 1956; Jones, 1965) and varying degree of replication of diagonal (parents) and off-diagonal (F_1's or F_2's) entries in the diallel table (Jones, 1965). Thus diallel analysis provides a more systematic approach to study the inheritance of continuously varying characters and to select parents having suitable combining ability (both general and specific) for hybrid breeding programme.

1.1 Objectives

The present research work was undertaken with the view to studying the following genetic aspects of Lablab bean having an intimate and direct plant breeding implication:

a) To study the combining ability in the reference population for yield and yield contributing characters.

b) To study the nature and action of genes governing pod yield and component characters.

c) To study components of variation and genetic parameters through vr-wr analysis.

d) To select and isolate desired genotypes for use in relevant breeding programmes.

CHAPTER 2

REVIEW OF LITERATURE

REVIEW OF LITERATURE

2.1 Origin and distribution

Lablab bean (*Lablab purpureus* L.) is considered as one of the oldest cultivated crops in the world (Bullivant, 1963). There are different opinions about the origin of Lablab bean. It is believed that the main center of origin of cultivated Lablab bean is India and the secondary center Abyssinia. Some believes that the crop originated in the African center of diversity. But the fact is that out of total 242 species of Lablab, 161 are endemic to Africa and only 23 species are native to India, suggesting Africa to be more probable as its main center and India the Sub-center of origin (Dana, 1976). Now Lablab bean has been widely cultivated in the Indian sub-continent, Malaysia, Indonesia, the Philippines, Papua New Guinea, China, Japan, Australia, North Africa, South and East Africa, the Caribbean, South and Central America (Bailey, 1942; Rashid, 1976 and Tindall, 1988).

2.2 Taxonomy, Nomenclature and Cytology

Lablab bean is a dicotyledonous species. It belongs to :

Class -	Dicotyledon
Subclass-	Polypetalae
Group-	Calyciflorae
Order-	Rosales
Family-	Leguminosae
Sub-family-	Papilionaceae
Genus-	*Lablab*
Species-	*purpureus*

(cf. Darlington, 1955 and Benson, 1957)

Botanical name of Lablab bean is *Lablab purpureus* (Linn.) Sweet [Syn. *Lablab niger* Medik, *Dolichos lablab* L., *Dolichos purpureus* L.] (Gosh and Misra, 1973; Ali, 1977; Huq, 1986). Dolichos is a Greek word, meaning long pod

and Lablab an Arabic or Egyptian word, meaning dull rattle of the seed inside the dry pod (Choudhury, 1972). Two cultivated types of *Lablab purpureus* have been recognized namely var. *typicus* and *lignosus* (Shivashankar *et al.*, 1971*). Typicus* is garden type and cultivated for its soft and edible pod and *lignosus* is known as field bean and cultivated for dry seed or pulse. However, according to Tindall (1988), two botanical varieties of Lablab bean have been recognized namely var. *lablab* with long, tapering pods, and var. *lignosus* (L.) Parin with short pods.

Cytologically, Lablab bean is diploid in nature and contains 11 or 12 pair of chromosomes i.e. n =11, 12; 2n = 22; 24 (Darlington, 1955). For having an uncertain basic chromosome number (x = 11 or 12) it shares curiously with the related genera *Phaseolus* and *Pueraria* (Smith, 1976).

2.3 Floral Characteristics and Pollination Behavior

The mode of reproduction of Lablab bean is complete self-pollination due to its special floral characteristics. The cleistogamous nature and post pollination blooming ascertains its complete self-pollination. Like other legumes, Lablab bean produces numerous flowers, but small portion of them give rise to mature pods due to higher percentage (40-95%) of floral abscission or abortion (Fakir *et al.*, 2000). As a result, much of the reproductive potential is lost creating a serious problem limiting pod yield and reproductivity (Weibold *et at.*, 1981 and Fakir, 1997). Jadhav *et al.*, (1987) reported that the application of triacontanol reduced the flower drop and improved partitioning of assimilates towards sink, thereby increasing filled fruits per plant and harvest index. They found that application of triacontanol increased yield by 8-13% over control.

2.4 Diallel Analysis : Concept, Methodology and Application

Diallel analysis is a widely used genetic technique in the study of the inheritance of quantitative characters and assessing general and specific combining abilities of parents and their crosses. Schmidt (1919) first introduced the method of diallel crossing system. It implies all possible crosses between each of a group of

male and female individuals. Sprague and Tatum (1942) analysed diallel cross with statistical technique first.

Diallel analysis provides for obtaining a rapid picture of the genetic control of quantitative characters. Crumpacker and Allard (1962) stated that diallel analysis could successfully reveal the major features of a genetic system and predict the outcome of selection in early generations. It allows for every conceivable variation in experimental design, including presence or absence of parental lines and reciprocal crosses (Yates, 1947; Hayman, 1954a; Griffing, 1956; Jones, 1965) and varying degrees of replication of diagonal (parents) and off-diagonal (F_1's or F_2's) entries in diallel table (Jones, 1965).

Jinks (1954) defined the relationship between the parent-offspring array variance (Vr) and covariance between offspring and non-recurrent parent (Wr). The regression of Wr on Vr would give rise to a straight line of unit slope, provided the genes are independent in action. Hayman devised a graph almost similar to the one developed by Jinks (1954) which provides information about the adequacy of additive-dominance model, the average degree of dominance and characterizes parent containing proportion of the dominants and recessive genes. The effect of non-allelic interaction on the Vr-Wr graph has been described by Mather and Jinks (1987). They have shown that if the complementary kind of non-allelic interaction is present, the regression line is concave upward. If with duplicate type of non-allelic interaction, the regression line is concave downward. Jinks and Hayman (1953) also proposed numerical approach to estimate genetic parameters based on Mather's notation. They outlined four components viz. D, H_1, H_2 and F assuming additive and dominance effects of genes but no epistasis or non-allelic interaction. Hayman (1954b) presented in detail the theory and algebraic basis of analysis and added two more statistics h_2 and Fr to those suggested by Jinks and Hayman (1953).

The main feature of diallel analysis is combining ability. The term combining ability introduced by Sprague and Tatum (1942). They used general combining ability (gca) to designate "average performance of a line in hybrid combination" and specific combining ability (sca) as "those crosses in which certain combination that do relatively better or worse than would be expected on the basis of average performance of the lines involved".

The statistical concept of general and specific combining ability effects and variance using diallel crosses was presented by Griffing (1956a,b). Four methods were suggested by Griffing (1956) depending upon inclusion or exclusion of parents and the reciprocal crosses in the analysis. The methods are as follows:

Methods	Materials involved
1	Parents +one set of F_1's +reciprocals
2	Parents +one set of F_1's
3	One set of F_1's + reciprocals
4	Only one set of F_1's

The last two models, where the parents are not involved, Griffing termed them as "modified model".

Griffing (1956) has describe the method of analysis for combining ability considering Eisenhart's model-I (fixed effect) and model-II (random effect).

i. Model-I (Fixed effect model)-where the parental materials are selected and the results obtained are applicable to the material investigated. Here the main interest lies in the estimation of combining ability effects.

ii. Model-II (Random effect model)- where the parents are random sample from the population about which the inferences are to be drawn. Here interests lie in the estimation of genetic and environmental components of the population variance.

The contribution of each parent to general combining ability was measured by the estimates of gca effects (g_i) and the contribution of each parent to hybrids was given by estimates of sca effects (s_{ij}).

Arunachalam (1976) reviewed the genetic models employed in graphical analysis of Jinks and Hayman and combining ability analysis of Griffing. He concluded that methods given by Griffing alone provide all the information that a plant breeder needs from a diallel cross, in preference to the graphical analysis of Jinks and Hayman.

2.5 Genetic Analysis in Lablab Bean

Little genetic research has been carried out in Lablab bean for improvement of the crop, especially through diallel mating system. Relevant information available on Lablab bean is presented here.

Chikkadevaiah *et al.* (1979) investigated the mode of inheritance and segregation pattern in F_1 and F_2 generations of a lablab bean cross. They found that traits twining habit and flowers in axillary clusters and flat, green pods were dominant. They also suggested that pod colour was conditioned by three duplicate genes.

Singh and Gupta (1980), using a diallel experiment involving five varieties of *Lablab purpureus*, reported that four crosses showed heterosis over the better parent for leaf size. General combining ability variance was seven times higher than specific combining ability variance. The variety KT2 was a good general combiner and had the highest number of dominant genes. Additive gene effect was more important than non-additive gene effects.

In a 5 × 5 diallel study with Lablab bean Singh and Singh (1981) found that in the F_1 and F_2 pod length was principally affected by additive gene action. The

other characters were by and large affected by non-additive gene action, with the exception of pod width and days to flowering in the F_2.

Jacob (1983) analysed data on 14 traits obtained from the F_1-F_3 generations of a complete diallel involving 4 elite, genetically divergent Lablab bean genotypes covering a period of 2 years. Result showed that heterosis over better parent for seed yield ranged form 52.09 to 106.49% in 1977 and form -47 to 104.34% in 1979. L76 was the best general combiner for seed yield and other yield components. RW × CO8 exhibited the highest specific combining ability for seed yield. Most traits were predominantly under the control of additive genetic effects with partial dominance.

Roa (1983) studied a 9 × 9 complete diallel cross in Lablab bean (*Lablab purpureus)* and reported results of genetic components of variance for seed yield per plant and 13 other quantitative traits. Reciprocal recurrent selection was recommended for improvement of the traits studied.

Rathnaiah (1985) in a trial of 34 genotypes in field bean (*Lablab purpureus)* found high heritability for green pod yield per plant, number of pods per plant, number of inflorescences per plant and length of inflorescence and pod.

Raut and Patil (1985) observed in a study of segregation in the F_2 of a cross between *Dolichos lablab* cultivars Poona perennial and Poona Arevada that purple colour of stem, leaf margin and flower were dominant and under monogenic control while leaf vein colour was governed by digenic complementary factors. Joint segregation revealed close linkages between these colour controlling genes, with combination values ranging form 0.81-3.01%.

Singh *et al.* (1986a) estimated genetic variance of and combining ability for number of flowers, pods per raceme and flowering by analysis of data from a 5 × 5 half diallel cross in *Dolichos lablab (Lablab purpureus).* Non-additive gene action and overedominance were important for all the three traits. The cross Rajani × 7001

was the best specific combination in all the cases. Rajani and 6802 had the most recessive genes for the traits confirming that additive × additive gene interaction contributed to specific combining ability and to increase number of flowers and pods per raceme.

From a 5 parent F_2 diallel in Lablab bean Singh *et al.* (1986b) showed that additive and non-additive gene actions were both important in the inheritance of various traits, non-additive components being slightly more influential for all traits except days to flowering, pod length and pod width. The best general combiners were Kalianpur type 2, 6802 and Rajani.

Kabir and Sen (1987) evaluated seven traits of *Dolichos lablab* (*Lablab purpureus*), one strain of *D. biflorus* (*Nacrotyloma uniflorum*) and 28 F_1 plants (from all possible crosses excluding reciprocals) and reported significant genetic differences for days to flowering and six yield components.

Kabir and Sen (1990) from the F_1 of 8-parent half diallel cross involving seven varieties of *Lablab niger* Medik and one variety of *Dolichos uniflorus* Lam., estimated genetic parameters and combing ability of pod yield and five yield influencing traits. They found that the additive genetic variance was important for days to flowering, pod length, pod width and 100-seed weight. It was suggested that biparental mating between the selected recombinants and recurrent selection may prove most effective with a view to exploiting the additive and dominance components of variation.

Kumari (1991) observed 11 fodder characters in 6 *Lablab purpureus* genotypes and their 30 F_1 hybrids grown during 1984. The hybrids Co9 × Pondicherry and Co9 × DL 3196 were the best combiners for green fodder yield and dry matter production.

Ushakumari and Chandrasekharan (1992) estimated genetic variance and heritability from data on several qualitative and quantitative traits including yield in

the parents and hybrids of a 6 × 6 diallel cross of *L. purpureus*. Predominantly dominant gene action was found for plant height, total area, stem weight and green fodder yield.

Kabir and Sen (1995) studied inheritance of pod colour using F_1 and F_2 progenies of 10 crosses involving 8 varieties of *Lablab purpureus*. Segregation analysis indicated that the colour was controlled by two gene pairs with complete dominance at both pairs. One of the gene pairs had partial dominance for deviation of the suture colour.

Khondker (1995) carried out genetic analysis of eight characters in a 6 × 6 diallel population of Lablab bean (*L. purpureus*). Results showed predominant role of additive genetic action for days to flowering, pod width, seeds/pod and 20-pod weight. While inflorescences/plant, pods/inflorescence and pod yield/plant were mostly governed by non-additive genetic effects. For pod yield, parent DS-52 proved best general combiner and cross KBS-1 × DS-161 the best specific combiner.

Jayarani and Manju (1996) studied combining ability analysis using two lines, six testers and 12 hybrids of Lablab bean which revealed the importance of specific combining ability for all the characters except pod length and days to flowering.

Srinivasan and Das (1996) studied combining ability in 6 genotypes of fodder Lablab (*Lablab purpureus*) for 12 traits. Based on GCA effects among the parents, MS9495, CO1, CO2 and DL3196 were deemed good combiners. The GCA variance indicated a preponderance of additive gene action in all the traits.

Genetic analysis in a 6 parental F_2 diallel of Lablab bean without reciprocal was carried out in two cultural environments by Khanam (1997) who examined flowering date, flowers/inflorescence, pods/inflorescence, inflorescences/plant, pod length, pod width, 10-pod weight and pod yield per plant. Predominant additive

genetic action was observed in inflorescences/plant and pod yield/plant. While pods/Inflorescence was found to be governed by non-additive gene action.

Uddin and Newaz (1997) evaluated fifteen hyacinth bean genotypes for eight flower and pod characters. Highly significant differences were observed among the genotypes for all the characters studied. High heritability and high expected genetic advance were recorded for pod yield, number of pods and inflorescences/plant, pod weight and flowers per inflorescence.

Valu *et al.* (1999) from a 7 × 7 half diallel cross in *Lablab purpureus*, reported that both additive and non-additive gene actions were in operation in the inheritance of all the traits studied. Further dominance ratio indicated the presence of overdominance in all the characters. Heritability estimates were high for pod length and number of seeds per pod indicated the prospect of involving these traits through selection while it was moderate to low for days to first picking, number of branches per plant, number of pods per plant and pod yield per plant.

Sarker (2000) conducted an experiment on 6 × 6 half diallel in Lablab bean. The combining ability analysis suggested the importance of both additive and non additive components in the genetic system with the preponderance of additive part in expression of all the characters except pods/inflorescence. The Vr-Wr analysis and estimation of components of variation showed complete dominance for pod yield/plant. Partial dominance was noticed for flowers/inflorescence, inflorescence length, pod length, pod width, seeds/pod and 10-pod weight; while for days to 1st flowering, days to 1st pod setting, number of inflorescences/plant and pods/inflorescence overdominance was observed.

Alam (2002) studied a 6 × 6 F_2 half-diallel of Lablab bean in two growing seasons (S1 & S2) and observed that the predominat role of additive gene action in all characters in both the growing seasons. Vr-Wr analysis showed complete dominance for pod yield in S2, overdominance for days to first flowering,

inflorescences per plant and pod setting in both S1 and S2; and for 10-pod weight in S2 and for pod yield in S1. Partial dominance was noticed for number of flowers per inflorescence, pods per inflorescence and pod length in S2.

2.6 Genetic Analysis in other Legume Crops

Lal and Waldia (1980) studied an 8 × 8 diallel cross in urd bean (*Vigna mungo* L. hepper) and reported predominance of additive genetic variance for all the characters, except grain yield, in which dominance variance was found to be high.

Venkateswarlu and Singh (1981) evaluated the parents, F_1's and F_2's of 10 diverse cultivars of pea in diallel. They reported that both general and specific combining ability were important for all traits examined. However, additive effects were predominant in the inheritance of quantitative characters.

Venkateswarlu and Singh (1982) analysed data for combining ability of 10 diverse cultivers of pea (*Pisum sativum*) which indicated the importance of both general and specific combining abilities for pods/plant, pod length, seeds/pod, 100-seed weight and seed yield/plant.

Singh and Saini (1983) from a 7 × 7 diallel analysis of climbing and dwarf *Phaseolus vulgaris* reported predominance of additive gene effects for number of pods/plant and pod diameter. While non-additive genetic effects were more important for seed yield/plant.

Mitranov (1983) evaluated 6 varieties in a diallel crossing system with 15 crosses of *Phaseolus vulgaris* L. and reported the highest general combing ability for yield. Crosses Diamant × Progress and Stewben × Progress showed the highest specific combining ability.

Habib *et al.* (1985) in a twelve parent's diallel cross in peanuts found that both additive and non-additive effects were important for plant height, pod yield and days to maturity.

Singh *el at.* (1986) studied genetic variance and combining ability for yield and its components in a 5 × 5 half diallel cross in hyacinth bean. Results indicated that non-additive gene action and overdominance were important for the traits.

Singh and Saini (1986) in a diallel cross without reciprocals of 7 *Phaseolus vulgaris* studied yield/plant, 100-seed weight and protein content. They concluded that both general and specific combining ability (GCA and SCA) effects were significant for all the 3 characters. GCA effects predominated for seed yield and 100-seed weight.

From a study of 8 chickpea lines and their 28 F_1's Yadavendra and Kumar (1987) observed that non-additive type of gene action was predominant for number of branches, pods per plant, seeds per pod and grain yield per plant. However, for days to flowering, days to maturity, plant height and 100-grain weight additive type of gene action was important.

Rodrigues *et at.* (1988) evaluated pod number, seed number, pod length, pod diameter, fibre content and plant height in a diallel crosses of *Phaseolus vulgrais* L. They showed gca was significant for all characters and sca was significant for pod diameter, fibre content and plant height. BAC-06, A-794 and Alessa were considered superior genotypes for pods/plant, pod length and fibber content.

Sharma and Sharma (1988) analysed the data from 10 parental diallel cross progenies in soybean for seed yield and component characters and showed that pod cluster/plant, seeds/plant, harvest index and seed yield/plant were controlled mainly by additive genetic variance. Both additive and non-additive genetic variances were important for the remaining characters.

Rodriguez and Kuruvadi (1990) studied combining ability for different quantitative characters in *Phaseolus vulgaris* L. from 6 parents and their 15 hybrids. They showed that gca effects were predominant for internode number, pods/plant, seeds/pod, 100-seed weight and number of days to flowering and physiological maturity, while for seed yield/plant and plant height gca and sca effects contributed almost equally.

Przulj (1991) observed hybrids derived from crosses of 2 lines and 3 varieties, and reported that dominance and in one case overdominance occurred for long pods. Narrow pods were generally overdominant to wide ones but in one cross the value was intermediate between the parental ones. Thick pods were dominant in 2 crosses and recessive in one. Similarly thick seeds were dominant in 2 crosses and thin seeds were dominant in one, with overdominance of thin seeds being seen in another.

Savithramma (1991) studied the nature of combining ability in cowpea in a set of diallel crosses of ten varieties and reported that both gca and sea variances were significant for all the characters except gca variance for seed yield.

Satpute *et at.* (1992) conducted a 6 × 6 combining ability analysis in pigeon pea and showed predominant role of non-additive gene action for seed yield per plant. But number of pods and seeds/plant had equal importance of both additive and non-additive gene effect.

Singh *et al.* (1992) studied combining ability for yield and its components in large seeded common bean (*Phaseolus vulgaris* L.). They measured gca effects for seed yield (kg/ha), pods per square meter, seeds per square meter, 100-seed weight and days to maturity and found positive gca effects for yield (19 parents), seed weight (6 of the 19), seeds per square meter (20), pods per square meter (19) and days to maturity (29). Negative gca effect was found for days to maturity (25 parents).

Halvankar and Patil (1993) investigated a 7 × 7 diallel cross (excluding reciporocals) of soybean (*Glycine max* L.) for seed yield and yield contributing characters. They found that both general and specific combining ability variances to be highly significant. Non-additive gene effects were relatively more important for yield and yield contributing characters except for days to flowering and 100-seed weight. The parental genotypes E.C. 95837, MACS-III and MACS-13 were the best general combiners while crosses Monetta × MACS-III, E.C. 95837 × MACS-13 and E.C. 95837 × MACS-III were the most promising in future breeding programme.

Harer and Deshmukh (1993) crossed seven diverse soybean genotypes in a half diallel fashion and the parents, F_1 and F_2 generations were evaluated for combining ability. The gca and sca were highly significant for all the ten characters in both the generations indicating the role of the additive and non-additive gene effects for expression of these characters.

Deshmukh and Patil (1995) estimated components of genetic variation for yield and some of the yield components in chickpea (*Cicer arietinum*) using a 5 × 5 diallel cross in F_1 and F_2 generations. Additive as well as dominance components were significant for 100-seed weight in both generations. Overdominance was observed for seed yield, pods/plant and seeds/pod but only partial dominance for seed weight. Analysis based on the parents and F_1's and parents and F_2's, particularly in respect of degree of dominance, showed good agreement.

Aravindhan and Das (1996) showed predominance of sca variance over gca variance for all the traits in cowpea, suggesting greater role of non-additive gene action. Among the parental line UPC 1903, UPC 9201 and the tester Co5 were the best combiners.

Kaul and Vaid (1996) evaluated an 8 × 8 diallel of faba bean (*Vicia faba*) for combining ability. Both gca and sca were highly significant showing the existence of both additive and dominance effects on yield per plant and seed protein content.

Halkude *et al.* (1996) studied combining ability in an 8 × 8 half diallel set for seed yield and its component characters in green gram (*Vigna radiata).* The parent phule M-2 was the best general combiner for grain yield and most of the characters. ML-337 and MB-112 were the other two good general combiners for grain yield and some of its components. Most of the parents which showed good general combining ability for grain yield were poor general combines of 1000-grain weight except KDM-1. Chahardi local was observed to be the best general combiner for 1000-grain weight followed by KBM-1 and Russian Mung. Phule M-2 × Charhardi local, a combination of the best and the most poor general combiner proved to be the best specific combination for grain yield.

Singh and Mishra (1996) studied combining ability in a 6 × 6 diallel set of midseason peas. VP-7906 and VL-3 showed high gca effects for most of the characters. Bonneville × Rachna exhibited best for primary branches and pod yield.

Oliveira *et at.* (1997) evaluated 11 hybrids form unbalanced partical and circulating diallel crosses of 7 cultivars of dry bean (*Phaseolus vulgaris* L.) for 3 yield components viz. plant height, pods per plant and seed weight/plant. They found the unbalanced circulating system was more efficient and it provided (gca) information on 3 other parents by using only one additional hybrid combination. Estimates of mean squares (gca) effects were higher than that of (sca) for all traits.

Dasgupta *et al.* (1998) from combining ability analysis of a 6 × 6 half diallel in mung bean (*Vigna raidiata*) reported the role of both additive and non-additive components of variances in the control of plant height, days to 50% flowering, number of pods/plant and protein percentages. Additive gene effects were predominant for seed yield/plant, number of pods/cluster and harvest index.

Emygdio *et al.* (1998) studied combining ability for 4 yield related traits in an 11 × 11 F_2 diallel populations in Southern Brazil bean (*Phaseolus vulgaris* L.) cultivars. They found that both additive and non-additive genetic effects were important in the expression of each of the traits. Based on general combining ability and on specific combining ability, the most promising crosses for yield components were Macanudo × IAPARA, Macanudo × IAPR65 and IAPAR44 × Barrigaverde.

Carvalho *et al.*(1999) evaluated 8 agronomic characters in a diallel mating design without reciprocals of bush snap bean (*Phaseolus vulgaris*) cultivars. General combining ability (GCA) effects were significant for pod number, pod weight, pod length, pod diameter, days from sowing to flowering and plant height. Specific combining ability (SCA) effects were significant for all the 8 characters. They showed that dominance/epistatic effects were involved in the control of these characters.

Aher *et al.* (1999) found highly significant gca and sca variance for 13 traits in a 7 × 7 diallel analysis excluding reciprocals in mung bean (*Vigna radiata*) suggesting that both additive and non-additive components played role in the inheritance of these traits. The gca analysis showed that parents MP-2, E-65 and TARM-18 were the best general combiners making them suitable for further crop improvement research. The crosses BM- 4 × TLN-5 and Kopargaaon × TARM-18 showed significant sca effects for seed yield/plant and most of the yield contributing characters.

Oliveira *et al.* (1999) evaluated the properties of an F_3 generation of dry bean (*Phaseolus vulgaris*) based on F_1 generation data form diallel crosses for pods per plant and seed weight per plant. They showed general combining ability in the F_1 generation was more efficient than performance in the F_1 generation to predict F_3 segregant- hybrid combinations.

Sharma (1999) crossed nine diverse genotypes of garden pea (*Pisum sativum*) in diallel fashion to determine combining ability for 5 quantitative traits viz. days to flowering, pods/plant, pod length, grains/pod and green pod yield. Analysis of variance revealed highly significant differences for all the traits. Significant negative gca effects were found in early maturity which is desirable in crop breeding programme. For pods/plant four genotypes exhibited significant and positive gca effects. None of the hybrids indicated significant positive sca effects for the characters under study.

Islam and Newaz (2000) carried out a 7 × 7 diallel experiment on dry bean using F_2 populations in two cultural environments. Results suggest both additive and dominance genetic components were important in the genetic system controlling various yield related characters such as days to first flowering, days to first pod setting, days to maturity, plant height, pods/plant, pod length, seeds/pod, seeds/plant and 20-seed weight.

CHAPTER 3

MATERIALS AND METHODS

MATERIALS AND METHODS

3.1 Experimental Period and Experimental Site

In keeping with the objectives (section 1.1) the research work was carried out during July 2001 to March 2002 at the field Laboratory of the Department of Genetics and Plant Breeding, Bangladesh Agricultural University (BAU), Mymensingh.

3.2 Soil and Climate

The soil of the experimental area belongs to the Barhmaputra Alluvium Tract of Bangladesh (AEZ 9) with pH of 6.5 (Uddin, 1975). The land was of medium high and sandy loam soil texture. The nutrient status of the experimental soil as tested by the Humboldt Soil Testing Laboratory, Department of Soil Science, BAU, Mymensingh is as follows:

Soil Properties	Results
i) Organic Carbon	0.79%
ii) Total Nitrogen	0.06%
iii) Exchangeable Potassium	70-90 ppm
iv) Sulphur	14 ppm
v) Phosphorus	13 ppm
vi) pH	6.5

Wet summer and dry winter is the general climatic feature of the region. The rainfall at the beginning of the experimental period was very high. Temperature was also initially high. During the rabi season the rainfall generally is scant and temperature moderate with short day length. The weather data for the experimental period are provided in Appendix I.

3.3 Materials Used

Six genotypes of the Lablab bean viz. DS-30, DS-52, DS-161, DSN-26, KBS-2 and KBS-3 and their 15 F_2 population derived from half diallel cross were used in the experiment. The seeds of experimental materials were collected form Bean Research Programme of Genetics and Plant Breeding Department, BAU. The origin and important characteristic features of the parental genotypes are given in Table 1.

Table 1. Origin and some characteristic features of parental genotypes of Lablab bean used in the study

Genotypes	Origin	Characteristics
DS-30	Mymensingh	Purple green, wavy sickle shaped pods, moderately late flowering.
DS-52	Sitakundu, Chittagong	Flat, heavy and light green pods, moderately late flowering.
DS-161	Mymensingh	Long, slender, sickle shaped pods with moderately early flowering.
DSN-26	Mymensingh	Leafy but flashy pods with deep green colour. Locally termed as "pathaseem" due to the structure of the pod.
KBS-2	Local selection from a cross KBS-1 × DS-52 at BAU	Photoperiod neutral, early flowering, deep green pods with moderate width.
KBS-3	Local selection from a cross KBS-1 × DS-52 at BAU	Photoperiod neutral, early flowering, deep green pods which are wider than KBS-2

3.4 Land Preparation and Fertilization

The experimental plots were prepared by digging pits about one week ahead of sowing. The pits were spaced 2m both between rows and within rows. The size of each pit was approximately 30cm × 30cm × 30cm. For ensuring proper growth and development of the plant, each pit was fertilized with the following doses:

Fertilizers	Dose/Pit
Urea	10g
TSP	30g
MP	20g

After application, fertilizers were well mixed with the soil of the pits.

3.5 Date of Sowing and Intercultural Practices

Sowing of seeds for the experiment in pits was 1st August 2001. Three seeds were sown per pit. Seeds germinated in about 5-6 days. When the seedlings become one month old, they were thinned out keeping only one healthy plant in each pit. During thinning operation, weeding was done as well. There was an incidence of bean aphid infestation, which was controlled by spraying Malathion 57 EC @ 560 ml/ha (Ahad *et al.*, 1987). To check further infestation, the insecticide was sprayed two more days with 15 days intervals. A single bamboo pole, untrimmed with side shoots, was provided to support the growing plant in a pit. Other intercultural operations were done as an when necessary.

3.6 Experimental Design and Layout

The experiment was laid out in a Randomized Complete Block Design (RCBD) with 4 replications.

3.7 Care and Protection

Careful and continuous watch was ensured to protect the experiment for herbivorous animals (e.g. cows, sheep, goats) and from unauthorized plucking of pods. Fencing was also done around the experimental plots for the purpose.

3.8 Harvesting of Edible Pods and Mature Seeds

Harvesting of green edible pods was started in the second week of January, 2002 and continued up to last week of March, 2002. Both starting and completion of green pod harvest varied depending on the genotypes. Harvesting of mature

seeds was done during the first fifteen days of April 2002. The harvested matured seeds were sun dried appropriately to facilitate further data recording (eg. 20-seed wt.) and storage.

3.9 Data Collection

Data on eleven characters were recorded from each family of F_2 diallel populations covering all replications, as details below :

Days to 1st flowering : Counted in days from sowing to opening of the first flower.

Days to 1st pod setting : Counted in days from sowing to initiation of 1st pod formation.

No. of inflorescences per plant : Total number of inflorescences per plant counted on the mature plant by the floral stalks with edible pods having been harvested already.

No. of flowers per inflorescence : Counted and averaged from ten randomly selected inflorescences per plant.

No. of pods per inflorescence : Counted and averaged from ten randomly selected inflorescences per plant.

Inflorescence length (cm) : Measured and averaged from ten randomly selected inflorescences per plant.

Pod length (cm) : Measured and averaged from ten randomly selected green edible pods from each plant.

Pod width (cm) : Measured along the widest middle part of pod, from ten randomly selected green edible pods and averaged.

10-pod weight (g) : Ten randomly selected edible pods were harvested from each plant and weight was taken in gram.

20-seed weight (g) : Twenty randomly selected seeds from each plant were weighed in gram.

Pod yield per plant (kg) : The values of pod yield were derived in the following way in kilogram.

$$\text{Pod yield/plant (kg)} = \frac{(\text{Pods / Inflores.}) \times (\text{Inflores./ plant}) \times (10 - \text{pod wt. in g})}{(10 \times 1000)}$$

Among the above characters, no. of flowers per inflorescence, no. of pods per inflorescence, inflorescence length, pod length, pod width and 10-pod weight were estimated in the mid season of the crop while no. of inflorescences per plant, pod yield per plant and 20-seed weight were estimated in late into season.

3.10 Statistical Analysis of the Experimental Data

3.10.1 Genetic analysis of diallel population

The preliminary statistical analysis of the data was done according to standard texts and the subjects (Snedecor and Cochran, 1967; Clark, 1973). For the genetic analysis of daillel population, data were subjected to two main approaches viz. Griffing's approach and Hayman's approach. An understanding of general and specific combining ability, and the genetic system controlling important traits was thus attempted. The analytical methods and procedures of them, often quoted with worked out examples, may be found in several reference literature (Mather and Jinks, 1987; Singh and Chaudhary, 1985; Dabholkar, 1992; Narain, 1993 and Falconer and Mackay, 1996).

3.11 Combining Ability Analysis (Griffing's approach)

Griffing's (1956b) method-2, model-1(Fixed effect model) was used for combining ability analysis for each of the traits. In model 1 the experimental material is deliberately chosen and regarded as the population about which inferences are to be made; the general objectives are to compare combining abilities of the parents and, using parents as tester, to identify better cross combination (s).

The mathematical model for the combining ability analysis in model 1 is assumed to be as under :

$$X_{ij} = u + g_i + g_j + S_{ij} + \frac{1}{bc}\sum_{k}\sum_{l} e_{ij}kl$$

Where,

ij = 1 ---------- p
k = 1 ---------- b
l = 1 ---------- c
p = number of parents
b = number of blocks
c = number of observations in each plot

X_{ij} is the mean of x_{ij}th genotype over k and l; u is the population mean; g_i (g_j) is the gca effect. S_{ij} is the sca effect such that $S_{ij} = S_{ji}$ and $e_{ij}kl$ is the environmental effect particular to the ijklth individual observation.

The restrictions imposed are :

$$\sum_i g_i = 0 \text{ and } \sum s_{ij} + S_{ii} = 0 \text{ (for each i)}$$

The analysis of variance for combining ability was carried out using block mean of each entry (diallel family) as follows:

Item	d.f.	Sum of squares	Mean squares
gca	n-1	$\frac{1}{n+2}\sum_i (X_{i.} + X_{ii})^2 - \frac{4}{n}X^2_{..}$	Mg
sca	n(n-1)/2	$\sum_i \sum_j X^2_{ij} - \frac{1}{n+2}\sum (X_{i.} + X_{ii})^2 + \frac{2}{(n+1)(n+2)}Y^2_{..}$	Ms
Error	(r-1)(t-1)	SSE	Me

Where,

gca = general combining ability
sca = specific combining ability
n = number of parents
r = number of replications
t = number of treatments
$X_{i.}$ = Array total of the i^{th} parent
X_{ii} = Mean value of the i^{th} parent
X.. = Grand total of the ½ [n (n-1)] crosses and parental lines
X_{ij} = Progeny mean values in the diallel table
SSE = Sum of square due to error (obtained from preliminary anova after dividing by the number of replications)

The gca and sca effects of each character may be calculated as follows:

$g_i = 1/(n+2)\ \Sigma\ (x_{i.} + x_{ii}) - (2/n)\ X..$

$s_{ij} = X_{ij} - 1/(n+2)\ (x_{i.} + x_{ii} + x_{.j} + x_{ij}) + 2/(n+1)\ (n+2)\ Y..$

Standard error (S.E.) of an estimate was calculated as the square root of the variance of concerned estimate e.g. $\sqrt{var(g_i)}$ and $\sqrt{var(s_{ij})}$

$$var(g_i) = \frac{n-1}{n(n+2)}\sigma_e^2$$

$$var(s_{ij}) = \frac{n(n-1)}{(n+1)(n+2)}\sigma_e^2$$

3.12 The Vr-Wr Analysis and Graphical Presentation (Hayman's approach)

The Vr-Wr analysis with graphical presentation facilitates study of major genetic features of the quantitative characters, subject to fulfilment of certain assumptions as listed by Hayman (1954):

(i) Diploid segregation
(ii) Only environmental difference between reciprocal crosses
(iii) Independent action of non-allelic genes
(iv) No multiple allelism
(v) Homozygosity of parental lines
(vi) Independent distribution of genes

Vr-Wr Graph: By calculating array variance (Vr) and parent-offspring covariance (Wr) and regressing Wr on Vr, it is possible to test the adequacy of the simple additive-dominance genetic model, to discern the relative proportion of dominant to recessive genes present in the common parents of the arrays and to find the average level of dominance.

In the Vr-Wr graph, the parabola $Wr=\sqrt{Vp\ Vr}$ delimits the area in which the co-ordinate (Vr . Wr) array data may occur and the Wr intercept is an indicator of

the average degree of dominance, being positive with partial dominance and negative with overdominance. If there is no dominance all the points on the Vr-Wr graph are estimates of single point ($\overline{Wr}$, $\overline{Vr}$) with Wr=2Vr and there is no regression and the line is tangent to the limiting parabola. While with complete dominance, the regression line is of unit slope and passes through the origin.

The position of the array points along the regression line depends on the relative proportion of dominant and recessive alleles present in the common parent of each array.

Parents with a preponderance of dominant alleles will have low Vr and Wr values will be near the origin, while highly recessive parents have large Vr and Wr values will be farthest from the origin.

3.13 Morley Jones' Modification for Diallel Analysis Without Reciprocal

The analysis of variance for the complete diallel table was given by Hayman (1954a), developing in one direction that of Yates (1947). Frequently, however, reciprocal differences are assumed absent, and only one of each pair of reciprocal crosses is raised. For such situation Morely Jones (1965) brought some modification of Hayman's approach. In this modification using the same model as Hayman, the determination of the sum of squares corresponding to additive effects (a), and on the assumption of no epistasis to mean dominance (b_1), to additional dominance effects that can be accounted for by genes having one allele present in only one line (b_2) and to residual dominance effects (b_3), is in essence a straight forward application of fitting constants by least squares.

The analysis of variance following Morely Jones' (1965) modification for diallel without reciprocal using mean value of diallel fashion may be outlined as under:

Item	d.f.	Sum of squares	Mean squares
a	n-1	$\frac{1}{n+2}$ dev²ur	MSa
b_1	1	$\frac{1}{n(n^2-1)}[2X.. - (n+1)X.]^2$	MSb_1
b_2	n-1	$\frac{1}{n^2-4}$ dev² tr	MSb_2
b_3	n(n-3)/2	Total SS –(a ss + b_1 ss + b_2 ss)	MSb_3
b	n(n-1)/2	b_1 ss + b_2 ss + b_3 ss	MSb
Error	(r-1)(t-1)	SSE	MSe

Where,

a = Additive effects

b_1 = Mean dominance

b_2 = Additional dominance effects that can be accounted for by genes having one allele present in only line the remaining n-1 lines being assumed to carry the same alternative allele (=dominance deviation due to arrays).

b_3 = Residual dominance effects

dev^2 = Sum of square of deviations from the mean

ur = $X_i + X_{ii}$

tr = $2(X_i + X_{ii}) - (n+2)X_{ii}$

3.14 Components of Genetic Variation and Genetic Parameters in F_2

Based on the Hayman's (1954) estimation of the components of genetic variation and genetic parameters, Jinks (1956) demonstrated the estimation of the components of variation of F_2 as follows (Sing and Chaudhary, 1985):

D = V_0L_0-E = Variation due to additive effect

F = 4 V_0L_0-8 W_0L_{02}-4 (n-2) E_2/n = The mean of 'Fr' values over the arrays

H_1 = 16 V_1L_2-16 W_0L_{02} + 4 V_0L_0-4 (5n-4)E_2/n = Component of variation due to the dominance effect of the gences

H_2 = 16V_1L_2-16 V_0L_2-16 (n-1) E_2/n = proportion of positive genes u and proportion of negative genes v in the parents

h^2 = (4 ML_2 – 4ML_0)^2-16 (n-1) E_2/n = Dominance effect

Where,

E = Error

= (Error sum of square + replication sum of square)/no. of replication.

= The expected environmental component of variation.

E_2	= VE/r = Me' of F_2
n	= Number of parents
V_0L_0	= Variance of parents
V_1L_2	= Mean of variance between the parents and the arrays
W_0L_{02}	= Mean of covariance of arrays
V_0L_2	= The variance of the mean of arrays
(ML_2-ML_0)^2	= The difference between the mean of the parents and the mean of their n^2 progeny.

The significance of the estimates of variance components are tested by calculating their corresponding standard errors (SE). The standard errors are the square root of the products of common multiplier and specific multipliers calculated from the formulae as follows:

Common multiplier or variance (S^2) is calculated from the formula :

S^2 = ½ [var (Wr – Vr)]

Specific multipliers of various components are calculated from the following formulae:

For, D; $\frac{(n^5 + n^4)}{n^5}$

H_1; $\frac{(16n^5 + 656n^4 - 192n^3 + 64n^2)}{n^5}$

H_2; $\frac{576n^4}{n^5}$

F; $\frac{16n^5 + 80n^4 - 64n^3 + 6n^2}{n^5}$

h^2; $\frac{256n^4 + 256n^2 - 512n + 256}{n^5}$

and E_2; $\frac{n^4}{n^5}$

Thus, the components of variation with their standard errors are as :

$D \pm SE(D)$

$H_1 \pm SE(H_1)$

$H_2 \pm SE(H_2)$

$F \pm SE(F)$

$h^2 \pm SE(h^2)$

and $E_2 \pm SE(E_2)$

The significance of the variance statistics is tested by 't' test at (n-2) degrees of freedom as:

$$t = \frac{\text{Parameter}}{\text{SE of parameter}}$$

3.15 Proportion of Genetic Components

The different proportions of the genetic components are worked out according to the procedure given below:

a) Degree of dominance

The mean degree of dominance in F_2 is $[1/4\ (H_1/D)]^{1/2}$ following Verhalen and Murray (1969).

if $[1/4\ (H_1/D)]^{1/2}$ = 1 (complete dominance)
> 1 (overdominance)
< 1 (Partial dominance)

b) Proportion of genes with positive and negative effects in the parents

It is calculated as the ratio $H_2/4H_1$. It denotes the mean product of u_i and v_i averaged over all the parents of a diallel set of crosses. When u and v symmetrically distributed, i.e. u = v = 0.5, the ratio will give the value of $H_2/4H_1 = 0.25$.

c) Proportion of dominant and recessive genes in the parents

It is calculated as :

$$\frac{\frac{1}{4}(4DH_1)^{\frac{1}{2}} + F/2}{\frac{1}{4}(4DH_1)^{\frac{1}{2}} - F/2}$$

If the dominant and recessive genes are symmetrically distributed among the parental lines, this ratio equals unity within the limits of sampling variance.

a) Number of groups of genes which control the character and exhibit dominance

It is calculated as h^2/H_2. It is an approximate measure of sets of genes exhibiting dominance.

b) Estimation of heritability

In F_2 heritability in narrow sense is calculated following Verhalen and Murray (1969) as:

$$\text{Heritability} = \frac{\frac{1}{4}D}{\frac{1}{4}D + \frac{1}{16}H_1 - \frac{1}{8}F + E}$$

CHAPTER 4

RESULTS AND DISCUSSION

RESULTS AND DISCUSSION

The mean values of edible pod yield and related characters of parental genotypes and their F_2 progenies are presented in Table 2, and the corresponding analysis of variance (anova) in Table 3.

Highly significant ($p<0.001$) differences due to genotypes were observed (Table 3) for all the characters under study such as days to 1st flowering (DFF), days to 1st pod setting (DFPS), no.of inflorescences per plant (IPP), no. of flowers per inflorescence (FPI), no. of pods per inflorescence (PPI), inflorescence length (IL), pod length (PL), pod width (PW), 10-pod weight (TPW), 20-seed weight (SW) and pod yield per plant (PYP).

4.1 Performance Analysis

Mean values (Table 2) shows that flowering were earliest in KBS-2 followed by KBS-3. Among the F_2 genotypes DS-52 × DS-161 and DS-30 × DSN-26 showed earliness in flowering and KBS-3 × DS-161 and DSN-26 × KBS-2 had most late flowering habit. First pod setting was observed in KBS-3 followed by KBS-2 and in crosses DS-52 × DS-161 and DS-52 × KBS-3 (Table 2). No. of inflorescences per plant is one of the main factors influencing pod yield. Highest no. of inflorescences per plant was observed in DSN-26 and KBS-3 and in crosses DSN-26 × DS-161 and DSN-26 × KBS-2. Maximum no. of flowers was in parent DS-161 and in cross DS-52 × KBS-2 (Table 2).

Pods per inflorescence is the most decisive indicator for pod yield. Among the parental genotypes, KBS-3, KBS-2 and DS-161 produced highest no. of pods per inflorescence. The crosses DS-161 × KBS-2 and DSN-30 × KBS-2 gave maximum no. of pods among the F_2s.

Table 2. Mean values of pod yield and other characters of 6 parents and 15 F_2 population of a 6 × 6 diallel of Lablab bean

Genotype	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
DS-30	112.50	119.00	57.25	20.75	3.25	27.25	15.75	2.025	131.50	6.098	2.415
DS-52	111.25	117.50	60.75	30.25	4.5	30.75	12.75	2.525	137.25	8.798	3.68
DSN-26	106.25	112.00	92.50	22.75	4.25	18.50	21.25	3.175	165.50	7.248	6.313
KBS-3	92.75	99.25	70.00	31.00	5.75	27.25	11.25	2.40	137.75	7.868	5.465
DS-161	105.50	112.50	64.75	39.75	5.00	24.00	12.00	1.975	91.75	5.26	2.933
KBS-2	90.25	100.5	69.25	30.25	5.25	44.75	12.50	1.90	119.75	7.34	4.362
DS-30 × DS-52	120.22	130.83	72.41	20.37	3.56	29.25	17.25	2.735	143.52	7.025	3.600
DS-30 × DSN-26	101.29	108.70	61.32	17.73	3.33	33.43	20.50	2.813	140.13	7.70	2.80
DS-30 × KBS-3	135.51	142.25	68.75	33.65	4.03	32.68	13.70	2.64	135.00	5.147	3.69
DS-30 × DS-161	100.75	108.5	67.61	32.50	4.29	30.59	13.78	2.195	116.25	5.313	3.310
DS-30 × KBS-2	126.17	131.67	72.75	23.17	4.97	32.75	14.25	2.212	128.15	5.18	4.625
DS-52 × DSN-26	122.23	129.66	67.23	25.97	4.77	33.25	19.95	3.213	143.37	8.14	4.400
DS-52 × KBS-3	91.50	100.41	63.15	33.56	4.56	42.19	12.05	2.493	133.54	9.51	3.725
DS-52 × DS-161	86.30	94.07	52.277	27.38	4.82	39.93	12.34	2.25	113.9	7.932	2.80
DS-52 × KBS-2	105.52	116.42	65.45	39.29	4.09	41.93	12.50	2.188	126.98	8.855	3.35
DSN-26 × KBS-3	120.13	132.49	72.35	19.75	4.97	29.13	18.25	2.250	163.94	6.150	5.825
DSN-26 × DS-161	122.185	130.50	88.90	27.63	3.63	29.82	17.08	2.733	128.275	6.105	4.00
DSN-26 × KBS-2	126.53	134.40	81.21	25.45	4.08	33.9	16.19	2.977	143.00	8.150	4.65
KBS-3 × DS-161	128.92	135.25	64.97	26.33	4.6	42.96	12.95	2.075	120.52	7.80	3.525
KBS-3 × KBS-2	117.52	126.5	61.13	29.96	4.67	40.06	11.90	2.130	130.30	8.433	3.55
DS-161 × KBS-2	108.5	118.775	61.30	27.56	5.08	46. 37	12.27	1.932	110.25	6.53	3.40
SE (±)	2.773	2.754	2.66	1.557	0.318	2.9	0.7607	0.1867	1.174	0.4872	0.3345
Mean	111.037	119.104	68.348	27.85	4.45	33.845	14.784	2.421	131.458	7.170	3.925

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

Table 3. Analysis of variance for eleven plant characters in a 6 × 6 F_2 diallel of Lablab bean

Item	df	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
Replication	3	21.829	40.162	22.505	11.183	0.299	9.950	0.977	0.223	3.42	0.597	0.127
Genotype	20	779.991***	768.421***	375.725***	144.100***	1.712***	214.345***	39.235***	0.639***	1133.00***	7.029***	4.092***
Error	60	30.73	30.58	26.50	9.16	0.405	30.572	2.315	0.139	5.28	0.940	0.448

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

* P< 0.05 ; ** P<0.01 ; *** <0.001

In respect of inflorescence length the parental genotypes KBS-2 and DS-52 showed the highest performance and among the F_2s, the crosses DS-161 × KBS-2 and KBS-3 × DS-161 had the maximum inflorescence length.

In respect of pod length, pod width and 10-pod weight the genotype DSN-26 showed the highest performance among the parental genotypes. However, among the F_2 progenies, DS-30 × DSN-26 showed the best performance for pod length and DS-52 × DSN-26 exhibited the best performance for pod width. In case of 10-pod weight the F_2 progenies of DSN-26 × KBS-3 and DS-30 × DS-52 showed the highest performances (Table 2).

The parental genotype DS-52 and progenies of DS-52 × KBS-3 showed maximum performance for 20-seed weight. In respect of pod yield per plant the parental genotype DSN-26 by far showed the best performance and among the F_2 progenies of crosses, DSN-26 × KBS-3 showed the best performance.

The study clearly showed that DSN-26 had the best performances for pod yield, 10-pod weight, pod width, pod length and no. of inflorescences per plant.

4.2 Combining Ability Analysis

The analysis of variances for combining ability computed for 6 × 6 F_2 diallel population for edible pod yield and other plant characters are presented in Table 4. The estimates of general combining ability (gca) effect of the parents and specific combining ability (sca) effect of their F_2s are presented in Table 5 and Table 6, respectively.

In combining ability analysis, parents were categorized into i) good combiners for highest value of gca effects; ii) poor combiners for lowest value of gca effects and iii) average combiners for those having moderate gca effects between highest and lowest values. Similarly, on the basis of sca effects, specific combiners (crosses) were also defined into same grouped for different plant characters.

Table 4. Analysis of variance (MS) of combining ability for eleven plant characters in a 6 × 6 F_2 diallel of Lablab bean

Item	df	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
gca	5	78.93**	66.82**	203.5***	70.03***	1.0**	115.11**	35.76***	0.48**	1077.8***	4.49**	2.72**
sca	15	233.87***	236.9***	60.72***	24.00***	0.23*	33.646**	1.157*	0.054	27.7***	0.87**	0.457**
error	60	7.68	7.65	6.62	2.29	0.101	7.643	0.58	0.034	1.32	0.24	0.112
gca : sca		0.33:1	0.28:1	3.35:1	2.79:1	4.34:1	3.58:1	30.9:1	8.88:1	41.64:1	5.16:1	5.95:1

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

* P < 0.05 ; ** P < 0.01 ; *** P < 0.001

Table 5. Estimates of general combining ability (gca) effects for eleven plant characters in a 6 × 6 F_2 diallel of Lablab bean

Parent	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
DS-30	3.954***	3.53***	-2.49**	-3.12***	-0.56***	-3.07***	0.94***	-0.038	0.79*	-0.945***	-0.577***
DS-52	-3.63***	-3.47***	-4.4***	1.22*	-0.043	0.97	-0.49*	0.122*	2.01***	1.097***	-0.28**
DSN-26	3.46***	3.07***	9.84***	-3.98***	-0.233*	-5.15***	3.87***	0.423***	16.06**	0.076	0.85***
KBS-3	0.234	0.02	-1.31	0.99*	0.40***	0.78	-1.51***	0.069	4.698***	0.325**	0.47***
DS-161	-2.45**	-2.77**	-1.71*	3.37***	0.16	0.30	-1.38***	-0.226***	-18.38***	-0.746***	-0.57***
KBS-2	-1.57	-0.37	0.07	1.51**	0.28**	6.16***	-1.42***	-0.212***	-5.19***	0.193	0.103
SE (g_i)	0.894	0.89	0.83	0.49	0.10	0.9	0.25	0.06	0.37	0.156	0.107

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

* P< 0.05 ; ** P<0.01 ; *** <0.001

Table 6. Estimates of specific combining ability (sca) effects for eleven plant characters in a 6 × 6 F_2 diallel of Lablab bean

Cross	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
DS-30 × DS-52	8.85***	11.59***	11.12***	-5.43***	-0.29	-4.76	2.01**	0.23	9.33***	-0.31	0.532
DS-30 × DSN-26	-17.17***	-17.08***	-14.2***	-2.86*	-0.33	8.04**	0.91	0.006	-8.11***	1.54***	-1.4***
DS- 30 × KBS-3	20.28***	19.53***	4.36	8.07***	-0.26	1.35	-0.50	0.325*	-1.9	-1.41**	-0.13
DS-30 × DS-161	-11.79***	-11.43***	3.64	4.54***	0.24	-0.25	-0.55	0.038	2.45*	-0.18	0.53
DS-30 × KBS-2	12.74***	11.85***	6.9**	-2.9**	0.80**	-3.94	-0.04	0.04	1.16	-1.25**	1.17***
DS-52 × DSN-26	11.35***	10.97***	-6.39**	1.03	0.60*	1.32	1.78**	0.25	-6.1***	-0.22	-0.098
DS-52 × KBS-3	-16.15***	-15.32***	0.68	0.25	-0.24	6.82**	-0.729	0.01	-4.55***	0.904*	-0.39
DS-52 × DS-161	-18.66***	18.86***	-9.8***	-4.9***	0.25	5.04*	-0.57	-0.06	-1.12	0.398	-0.27
DS-52 × KBS-2	-0.323	1.08	1.6	8.9***	-0.60*	1.19	-0.37	-0.14	-1.22	0.382	-0.40
DSN-26 × KBS-3	5.49*	9.219***	-4.37	-4.96***	0.35	-0.108	1.11	-0.53**	10.29***	-1.44***	0.58*
DSN-26 × DS-161	10.17***	11.02***	12.59***	0.54***	-0.74**	1.06	-0.19	0.12	-0.79	-0.41	-0.21
DSN-26 × KBS-2	13.59***	12.52***	3.11	0.23	-0.41	-0.71	-1.04	0.35*	0.74	-0.70	-0.23
KBS-3 × DS-161	20.09***	18.82***	-1.19	-5.74***	-0.41	8.26***	1.06	-0.05	2.81**	1.15**	-0.30
KBS-3 × KBS-2	7.82**	7.67**	-8.31***	-0.24	-0.45	-0.49	0.05	-0.002	-0.59	0.73	-0.95**
DS-161 × KBS-2	1.477	2.71	-5.24*	-5.02**	0.20	6.30*	-0.29	-0.05	2.43*	-0.10	-0.06
SE (S_{ij})	2.46	2.45	2.28	1.34	0.28	2.45	0.68	0.165	1.02	0.43	0.296

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

* P<0.05 ; ** P<0.01 ; *** P<0.001

The detailed results of combining ability are presented and discussed character wise as follows:

a) Days to 1st flowering (DFF)

The gca and sca mean squares were highly significant, indicating that both additive and non additive genetic components were responsible for the expression of the trait (Table 4). Similar results were also observed by Singh and Singh (1981), Singh *et al.*(1980), Kabir and Sen (1990), Hossain (1993), Khondker (1995), Khanam (1997), Sarker (2000) and Alam (2002). The ratio of gca : sca effect (<1) indicated however the predominance of non-additive components for this trait.

The estimates of gca effect ranged from –1.57 in KBS-2 to 3.954 in DS-30 (Table 5). Negative gca effect is preferable for flowering character, because it indicates the general capacity of early parent to transmit its behaviour to progenies in cross combination with other parents. The parental genotypes KBS-2, DS-161 and DS-52 were desirable for negative gca effect. Among them DS-52 considered the best general combiner for early flowering. The genotype DSN-26 and DS-30 were the latest flowering parent, so, DSN-26 and DS-30 could be termed as poor general combiners. KBS-2, DS-161 and KBS-3 parents belonged to the average group.

Result from the study (Table 6) revealed that the estimates of sca effects ranged from –18.66 in DS-52 × DS-161 to 20.28 in DS-30 × KBS-3. For early flowering DS-52 × DS-161, DS-30 × DSN-26, DS-52 × KBS-3 and DS-30 × DS-161 were considered good specific combiners. On the other hand DS-30 × KBS-3 and KBS-3 × DS-161 were the poor specific combiners.

b) Days to 1st pod setting (DFPS)

Significant variations were observed due to gca and sca for days to 1st pod setting which suggested that both additive and non-additive genetic components

were responsible for controlling the trait. Similar result was observed by Sarker (2000) for this trait in Lablab bean.

As in days to flowering, negative gca and sca effects are desirable for days to 1st pod setting. The highest and lowest gca effects were 3.53 in DS-30 and –3.47 in DS-52. DS-52 was the best general combiner and DS-30 was the poor general combiner. DS-161 and KBS-2 were good general combiners.

The sca values (Table 6) for most of the crosses were highly significant ($P<0.001$). According to classification of crosses, DS-30 × DSN-26, DS-30 × DS-161 and DS-52 × KBS-3 were good specific combiners whereas DS-52 × DS-161 and KBS-3 × DS-161 were poor specific combiners. The rest of the crosses were average specific combiner. Among the good specific combiners, DS-30 × DSN-26 was the best specific combiners while among the poor specific combiners DS-52 × DS-161 was the latest pod setting cross.

c) No. of inflorescences per plant (IPP)

No. of inflorescences per plant is a major component of measuring pod yield. Variances due to gca and sca for no. of inflorescences per plant were highly significant which indicated that both additive and non additive gene effect played role in the expression of the character. The gca : sca ratio indicated the predominant role of additive part of the genetic component controlling this trait (Table 4). This result agrees with the reports of Patil and Patil (1986) in cowpea, Kapila *et al.* (1994) in soybean, Ali *et al.* (1995) in peanut, Sharma and Pandey (1996) in urd beans, Sarker (2000) and Alam (2002) in Lablab bean, but differs with Singh and Singh (1981) and Singh *et al.* (1986b) in *Lablab purpureus*.

For the no.of inflorescences per plant, positive gca and sca effects are preferred. The estimates of gca effects were in the range of -4.4 in DS-52 to 9.84 in DSN-26 (Table 5). Thus, the parent DSN-26 was the best general combiner for this

trait while DS-52 was the poor general combiner. The rest of the parents were average specific combiners.

The sca effects for most of the F_2 genotypes were significant except DS-30 × KBS-3, DS-30 × DS-161, DS-52 × KBS-3, DS-52 × KBS-2, DSN-26 × KBS-3, DSN-26 × KBS-2 and KBS-3 × DS-161. The highest sca effect was recorded in the cross DSN-26 × DS-161 (Table 6) which was thus the best specific combiner. Besides this DS-30 × DS-52 was also good specific combiner. The poor specific combiner was DS-30 × DSN-26, followed by DS-52 × DS-161. The rest of crosses were average specific combiners.

d) No. of flowers per inflorescence (FPI)

Highly significant mean square (Table 4) due to gca and sca effects suggest that both additive and non-additive genetic actions were involved in the inheritance of this trait. The gca : sca ratio indicated that additive part played greater role (Table 4). Singh *et al.* (1986 b) and Hossain (1993) in lablab bean, Harer and Deshmukh (1993) and Kapila *et al.* (1994) in soybean, Sarker (2000) and Alam (2002) in lablab bean reported additive and non-additive components to be important for this trait.

Positive gca and sca effects are usually preferable for flowers per inflorescence. The gca effects for all parents were significant. The gca estimates of the character (Table 5) showed that the lowest and highest gca effects were –3.98 in DSN-26 and 3.37 in DS-161 respectively. Among the parents, DS-161 and KBS-2 were good general combiners while DSN-26 and DS-30 were the poor general combiners.

The F_2 progenies of the crosses DS-52 × KBS-2 and DS-30 × KBS-3 proved to be of good specific combiners, followed by the cross DS-30 × DS-161 for this trait. The crosses KBS-3 × DS-161, DS-30 × DS-52 and DS-161 × KBS-2 were the poor specific combiners.

e) No. of pods per inflorescence (PPI)

Significant mean square (Table 4) due to gca and sca for no. of pods per inflorescence indicated that both additive and non-additive gene effects were involved in the genetic system governing the trait. The gca : sca ratio revealed the predominant role of additive gene action for the character. The similar result was also reported by Singh *et al.* (1986), Hossain (1993), Khondkar (1995), Sarker (2000) and Alam (2002) in Lablab bean, and Harer and Deshmukh (1993) and Kapila *et al.* (1994) in soybean.

Of the parents, which differed significantly from zero with regard to gca effects, KBS-3 and KBS-2 had positive effects. These two genotypes were therefore good general combiners. The parent DS-30 and DSN-26 were poor general combiners as their gca effects were negatively significantly different from zero. The other two parents were average general combiners.

Among the crosses, DS-30 × KBS-2 and DS-52 × DSN-26 showed significant positive sca effects. The sca effects of DS-52 × KBS-2 and DSN-26 × DS-161 were negative though significantly different from zero. DS-30 × KBS-2 and DSN-26 × DS-161 made the best and worst specific combiners, respectively (Table 6).

f) Inflorescence length (IL)

The variances due to gca (Table 4) showed both additive and non-additive gene actions were important for the expression of inflorescence length, with additive part however, playing greater role as suggested by higher gca : sca ratio. This result agrees with Sarker (2000) in Lablab bean.

Positive gca and sca effect is preferable for inflorescence length. Genotype KBS-2 had significant positive gca and, DS-30 and DSN-26 had significant

negative gca effect. Therefore, it can be concluded that KBS-2 was the best general combiner while DSN-26 and DS-30 were the poor general combiners (Table 5).

KBS-3 × DS-161 was the best specific cross followed by DS-30 × DSN-26, DS-52 × KBS-3, DS-161 × KBS-2 and DS –52 × DS-161. Six crosses had negative sca effects but none departed from zero significantly.

g) Pod length (PL)

Combining ability anova (Table 4) showed that mean square due to gca and sca were significant which indicated that the additive and non-additive gene actions were important for the expression of this character. The magnitude of gca : sca ratio indicates the predominant role of additive part of the genetic component. Singh and Singh (1981), Singh *et al.* (1986 b), Kabir and Sen (1990) and Sarker (2000) in Lablab bean and Neupane (1986) and Mansuria (1991) in green gram also found similar results of additive and non-additive components playing part in the genetic system of this character. But Alam (2002) reported that both additive and non-additive genetic components controlled the pod length in sowing date S_2, but only additive one in sowing date S_1, in Lablab bean.

From the results of gca effects, DSN-26 and DS-30 appeared to be good general combiners whereas DS-52, KBS-3, DS-161 and KBS-2 poor combiners of this trait (Table 5). DSN-26 could be treated as the best general combiner for its highest and positive significant gca value.

Among the F_2 progenies, the cross DS-30 × DS-52 was the best specific combiner followed by DS-52 × DSN-26. Whilst DSN-26 × KBS-2 was the poor combiner.

h) Pod width (PW)

Results on gca and sca mean squares and their ratio (Table 4) revealed that additive genetic effect was exclusively in the control of pod width, and non-additive component was unimportant. Alam (2002) also found that only additive

genetic effect was in the control of pod width in lablab bean which is similar to the present study but Singh and Singh (1981) and Khondker (1995) reported that both additive and non-additive genetic system were involved in the expression of pod width in lablab bean.

Positive gca and sca effects are desirable for broad pods and negative effects for narrow pods. Significant positive gca effects were exhibited in DSN-26 and DS-52 and significant but negative gca effects were exhibited by DS-161 and KBS-2. Thus, DS-26 was good general combiner for broad pods and KBS-2 and DS-161 for narrow pods.

From the estimates of sca effects (Table 7), significant variations were observed in the F_2 progenies of DS-30 × KBS-3, DSN-26 × KBS-3 and DSN-26 × KBS-2. Results also revealed that the cross combination DSN-26 × KBS-2 showed highest positive effect followed by DS-30 × KBS-3. F_2 progeny of DSN-26 × KBS-2 showed good specific combining ability.

i) 10-Pod weight (TPW)

Anova for combining ability (Table 4) showed significant gca and sca mean squares for 10-pod weight. Results thus clearly demonstrated that both additive and non-additive components played part in the expression of the trait. The gca : sca ratio also revealed the predominant role of additive part in the genetic system. Jacob (1983), Singh *et al.* (1986 b), Khondker (1995), Khanam (1997), Sarker (2000) and Alam (2002) reported similar result in Lablab bean.

The gca effects of all the genotypes were significant. The genotypes DS-30, DS-52, DSN-26 and KBS-3 had positive gca effect indicating that they were good general combiners. DSN-26 was by far the best general combiner. On the other hand genotypes DS-161 and KBS-2 had negative gca effects suggesting them to be poor general combiners.

DS-30 × DS-52, DS-30 × DS-161, DSN-26 × KBS-3, KBS-3 × DS-161 and DS-161 × KBS-2 had positive and significant sca effect. They were thus good specific combiners, and DSN-26 × KBS-3 was the best. The crosses DS-30 × DSN-26, DS-52 × DSN-26 and DS-52 × KBS-3 were poor specific combiners.

j) 20-seed weight (SW)

Analysis of variance for combining ability suggested influence of additive and non-additive genetic components on the control of the trait. The gca: sca ratio revealed the predominant role of additive part in the genetic system (Table 4). Alam (2002) reported that only additive genetic component played role on the control of the 20-seed weight in Lablab bean in two growing seasons, which partially supports the present investigation.

Genotypes DS-52 and KBS-3 had significant and positive gca effects, they were thus good general combiners. On the other hand genotypes DS-30 and DS-161 had significant but negative gca effects which made them poor general combiners. The other two genotypes DSN-26 and KBS-2 were average general combiners. The parental genotype DS-52 was the best general combiner for 20-seed weight (Table 5).

The estimates of sca effects showed that the F_2 progeny of DS-30 × DSN-26, DS-52 × KBS-3, and KBS-3 × DS-161 had positive and significant sca effects indicating their potential as good general combiners. Among them DS-30 × DSN-26 was the best general combiner. On the other hand, the F_2 progenies of DS-30 × KBS-3, DS-30 × KBS-2 and DSN-26 × KBS-3 had negative and significant sca effects, which indicated them to be poor general combiners. The remaining nine crosses were of average specific combining abilities.

k) Pod yield per plant (PYP)

The anova for combining ability for pod yield per plant demonstrated that both additive and non-additive genetic components played role in the expression of

the character. However, additive component seemed to be more influential as shown by relatively larger gca mean square. The importance of additive component in pod yield was also supported by Jacob (1983), Khanam (1997), Sharker (2000) and Alam (2002) in Lablab bean. But Singh and Singh (1981) and Khondker (1995) observed non-additive effect to be more important.

The estimates of gca effect showed significant (<0.001) effect in all genotypes except genotype KBS-2 (Table 5). The parental genotypes DSN-26 and KBS-3 had positive gca effect, indicating them to be good general combiners. The genotype DSN-26 had the highest positive gca effect. The genotypes DS-30, DS-52 and DS-161 had negative gca effects, they were thus poor general combiners.

The highest value of sca effect was obtained in the F_2 progeny of DS-30 × KBS-2, followed by DSN-26 × KBS-3. The lowest value of sca effect was found in DS-30 × DSN-26 followed by KBS-3 × KBS-2. The other crosses were considered as being average specific combiners.

4.3 Diallel Analysis Following Hayman and Jinks' Approach

Results on Hayman analysis of variance following Morley Jones' modification and Vr-Wr analysis including graphical presentation for pod yield and other plant characters are provided as follows:

a) Days to 1st flowering (DFF)

Hayman anova (Table 7) shows that both additive (a) and dominance (b) genetic components were significant, which indicated that they were important in the regulation of flowering date. The results were similar to Griffing's combining ability analysis (Table 4). Mean dominance (b_1) and dominance due to array (b_2) and residual dominance effect (b_3) were highly significant for the character.

Table7. Hayman analysis of variance following Morley Jones' modification for eleven plant characters in a 6×6 F_2 diallel of Lablab bean (Mean square)

Item	df	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
a	5	78.76**	65.19**	202.00***	70.03***	1.00**	115.11**	35.76***	0.48**	1077.86***	4.5**	2.72**
b	15	233.74***	235.16***	59.34***	24.00***	0.23*	33.08**	1.157*	0.054	27.71***	0.84**	0.457**
b_1	1	531.37**	677.85**	4.64	13.54*	0.39	218.03**	2.39*	0.06	3.41	0.039	0.612*
b_2	5	207.15***	194.19***	28.03**	12.35**	0.07	27.40**	0.98	0.04	12.16**	0.45	0.273*
b_3	9	213.45***	207.00***	81.13***	32.78***	0.306**	15.68*	1.12	0.05	39.04***	1.09**	0.543**
Error	60	7.68	7.65	6.62	2.29	0.101	7.643	0.58	0.034	1.32	0.24	0.112

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g); PYP = pod yield per plant (kg).

*P<0.05;**P<0.01;***P<0.001

The Vr-Wr analysis suggested that on an average there was overdominance since the regression line cut Wr axis below the origin (Fig. 1). The regression of Wr on Vr gives the slope b = 0.3938± 0.457 which is close to unity. The results, therefore, suggested an additive-dominance situation without any complication of non-allelic interaction. The distribution of array points in the graph showed the parental genotype DSN-26 to have contained the larger number of dominant alleles, whereas the genotype KBS-3 had the largest number of recessive alleles. Genotype DS-30 and KBS-2 appeared to have nearly equal proportion of dominant and recessive alleles.

Singh *et al.* (1986a), Sarker (2000) and Alam (2002) observed overdominance in Lablab bean. Patil and Patil (1986) reported completed dominance in cowpea for flowering date.

b) Days to 1st pod setting (DFPS)

Hayman analysis of variance with Morely Jones' modification shows both additive (a) and dominance (b) genetic components were significant for the regulation of pod setting (Table 7). Griffing's combining ability analysis suggests the same results. Other dominance fractions viz. mean dominance (b_1), dominance due to arrays (b_2) and residual (b_3) dominance effect were significant for this trait.

The Vr-Wr graph (Fig. 2) shows the regression line cutting below the origin, thereby indicating the presence of overdominance. From the regression of Wr on Vr, which yielded b value (0.3723 ± 0.417) statistically equal to one, it seems likely that additive-dominance nature of gene action was involved in the genetic background of the character. Regarding the proportion of dominant to recessive alleles, parent DSN-26 by far contained the most dominant genes and parent KBS-3 contained the most recessive genes (Fig. 2)

Sarker (2000) observed overdominance in Lablab bean for days to pod setting.

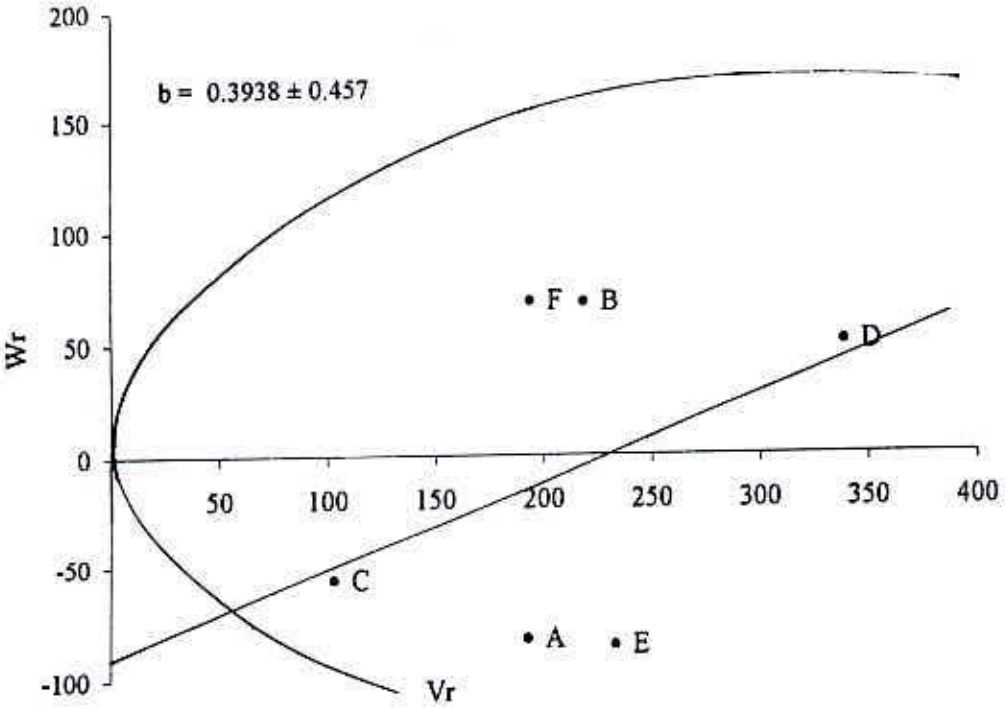


Fig. 1. Vr-Wr graph for days to 1st flowering

LEGEND

A = DS-30
B = DS-52
C = DSN-26
D = KBS-3
E = DS- 161
F = KBS-2

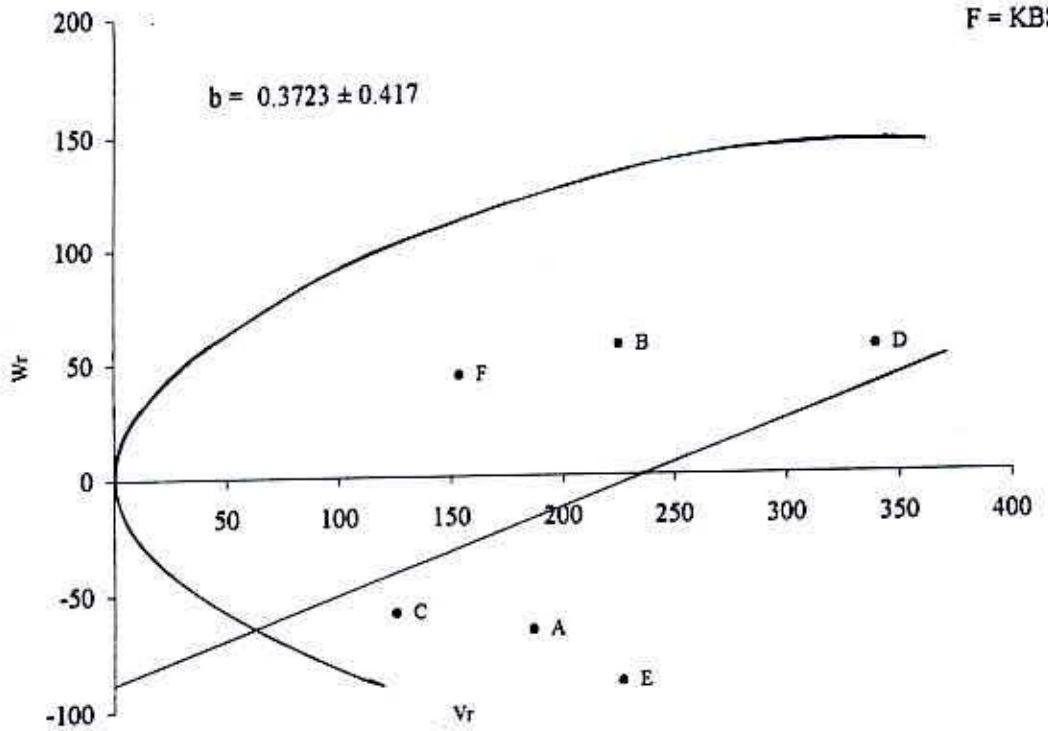


Fig.2. Vr-Wr graph for days to 1st pod setting

c) No. of inflorescences per plant (IPP)

Both additive (a) and dominance (b) effect were highly significant (P<0.001) for this character (Table 7). Similar result was obtained in Griffing's combining ability analysis (Table 4). Dominance due to arrays (b_2) and residual dominance effect (b_3) were significant. However, mean dominance (b_1) was not significant for this character.

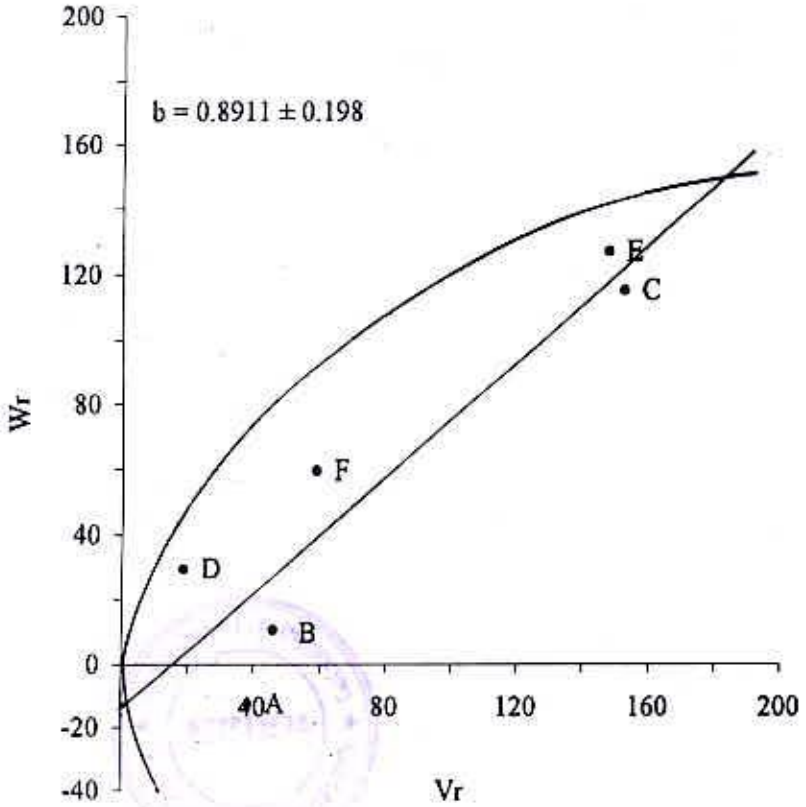
The Vr-Wr analysis yielded b value (0.8911 ± 0.198), which is not significantly different from unity. There results therefore, clearly suggested that simple additive-dominance genetic model was adequate without any complication of non-allelic interaction. On an average there was overdominance since the regression line cut Wr axis below the origin (Fig. 3). The distribution of array points along the regression line suggested that KBS-3 contained the most dominant alleles while DS-161 and DSN-26 contained the highest number of recessive genes.

Sarker (2000) and Alam (2002) reported overdominance for inflorescence per plant in Lablab bean. However, Jacob (1983) reported partial dominance for this trait in the same crop.

d) No. of flowers per inflorescence (FP1)

Hayman anova with Morely Jones' modification shows both additive (a) and dominance (b) components were involved in the inheritance of the trait (Table 7). The result is similar to Griffing's combining ability analysis. Dominance components such as mean dominance (b_1), dominance due to arrays (b_2) and residual dominance (b_3) were significant with varying significant levels (P<0.05 - 0.001).

On average partial dominance was observed for this trait since the regression line cut the Wr axis above the origin (Fig. 4). DSN-26 appeared to have contained the most dominant genes and the parent DS-30 contained the largest number of recessive alleles. From the arrays points it is clear that the gene order containing higher number of dominant alleles was DSN-26> KBS-3> DS-161> KBS-2> DS-52> DS-30.



LEGEND
A = DS-30
B = DS-52
C = DSN-26
D = KBS-3
E = DS-161
F = KBS-2

Fig. 3. Vr-Wr graph for no. of inflorescences per plant

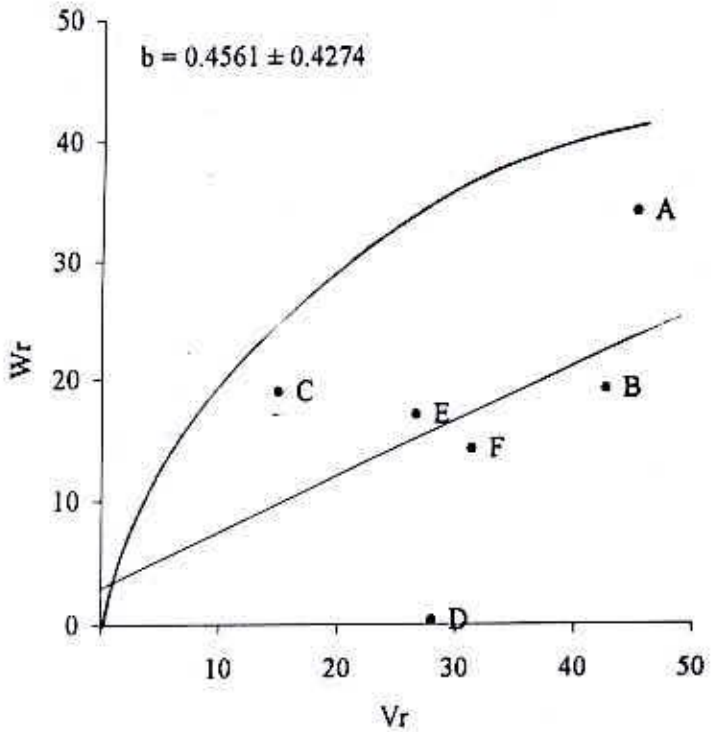


Fig. 4. Vr-Wr graph for no. of flowers per inflorescence

Sarker (2000) and Alam (2002) also observed partial dominance effect for this trait in Lablab bean.

e) No. of pods per inflorescence (PPI)

Both the additive (a) and dominant (b) components (Table 7) were significant for pods per inflorescence. This result is similar to Griffing's combining ability analysis (Table 4). It implies that both additive and dominant components played predominant role for the expression of this character in Lablab bean. Mean dominance (b_1) and dominance due to arrays (b_2) were non- significant but only the residual dominance (b_3) was significant.

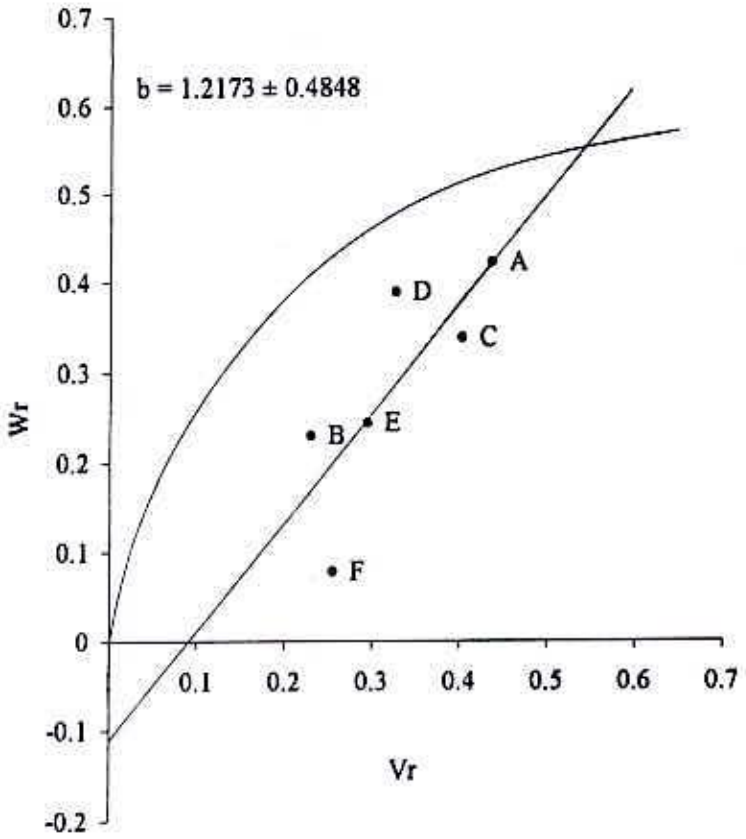
The Vr-Wr graph shows the regression line passing below the origin, which means on an average there was overdominance condition for this trait. The regression of Wr or Vr gives the slope b = 1.2173 ± 0.4848 which is not significantly different from one. It seems likely that non-allelic interaction was not involved and the genetic system governing the character was of simple additive-dominance model. The distribution of arrays points in the graph (Fig. 5) suggests that parent KBS-2 had the largest number of dominance alleles while DS-30 contained the highest number of recessive alleles.

Sarker (2000) found overdominance, Khondker (1995) partial dominance and Khanam (1997) complete dominance for pod per inflorescence in Lablab bean.

f) Inflorescence length (IL)

Mean square for the items (a) and (b) are significant for inflorescence length (Table 7) suggesting that both additive and dominance gene actions were important in the control of inflorescence length. The result is similar to the Griffing's combining ability analysis (Table 4).

On average there was overdominance for this character since the regression line cut the Wr axis below the origin (Fig. 6). The model was over whelmingly of



LEGEND
A = DS-30
B = DS-52
C = DSN-26
D = KBS-3
E = DS-161
F = KBS-2

Fig.5. Vr-Wr graph for no. of pods per inflorescence

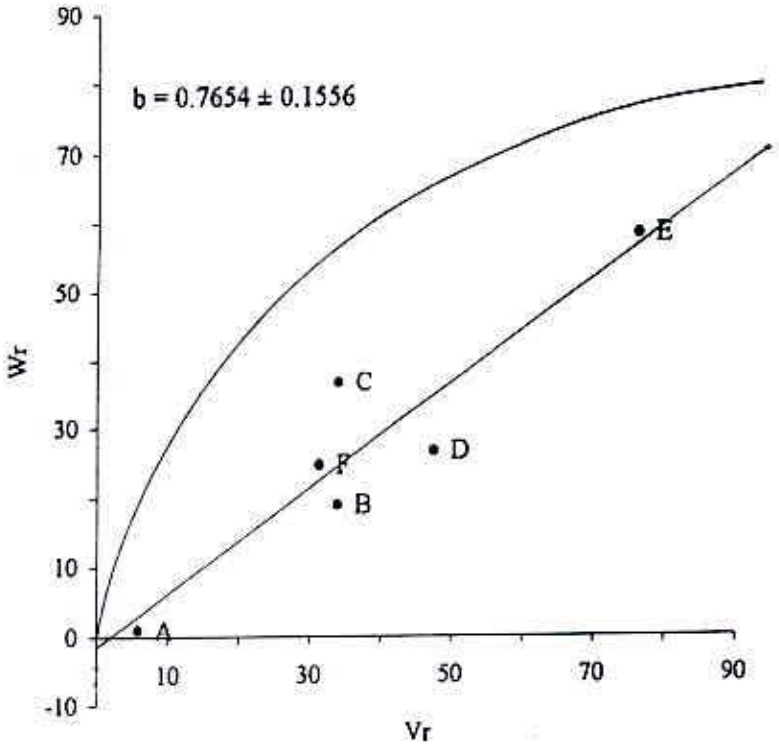


Fig. 6. Vr-Wr graph for inflorescence length

additive-dominance nature of genetic system because the slope b (0.7654±0.1556) was very close to unity. Khondker (1995) also obtained similar result in Lablab bean. The parent DS-30 is close to the origin indicating that it contained the highest number of dominant genes; whereas the genotype DS-161 is farthest from the origin which indicating it had the highest number of recessive genes.

g) Pod length (PL)

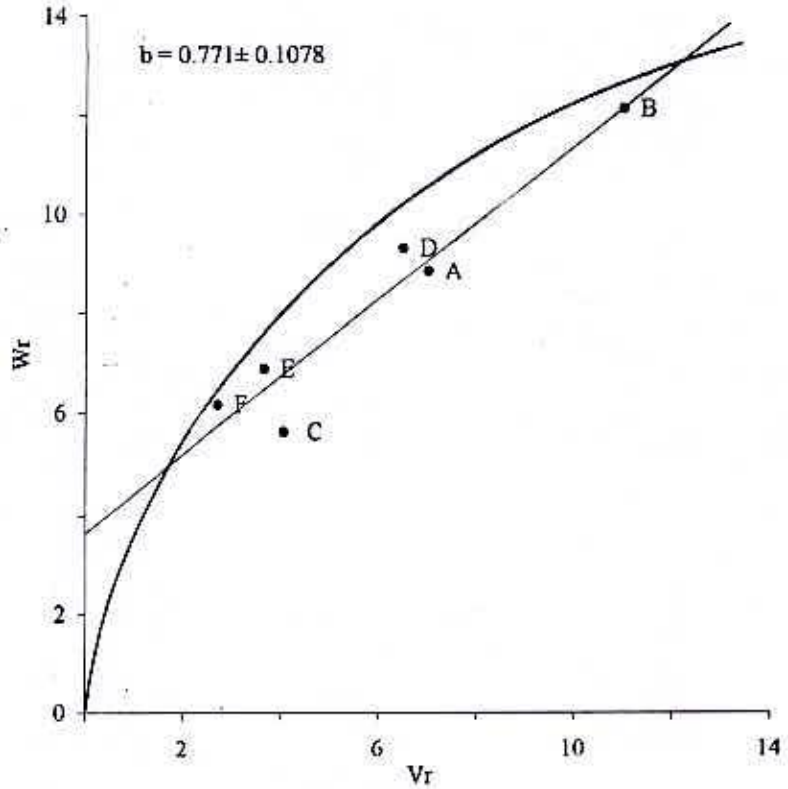
Modified Hayman anova shows the variance due to additive (a) and dominance (b) genetic components were significant (Table 7). Anova further shows only the mean dominance (b_1) was significant, dominance deviation due to array (b_2) and residual dominance (b_3) were not significant.

The Vr-Wr graph shows the regression line passing above the origin, thereby indicating the presence of partial dominance. The regression of Wr on Vr gave the slope b (0.771 ± 0.1078) which may be accepted for being statistically equal to unity; so there is no evidence of any non-allelic gene interaction in the expression of this trait. The distribution of array points on the graph (Fig. 7) suggests that the parent DSN-26 contained the largest number of dominant alleles and the parent DS-52 the most recessive genes. The order of the parents with decreasing no. of dominant alleles may be shown as follows: DSN-26> KBS-2> DS-161> DS-30> KBS-3> DS-52.

Sarker (2000) and Alam (2002) found partial dominance for Pods/ inflorescence in Lablab bean.

h) Pod width (PW)

Hayman anova (Table 7) shows only the additive (a) genetic component was significant for pod width, which is similar to the Griffing's combining ability analysis (Table 4). The overall dominance component (b) and the fractions (b_1, b_2, and b_3) were not significant. Such result could be obtained with the preponderance of additive part in the genetic system.



LEGEND
A = DS-30
B = DS-52
C = DSN-26
D = KBS-3
E = DS-161
F = KBS-2

Fig. 7. Vr-Wr graph for pod length

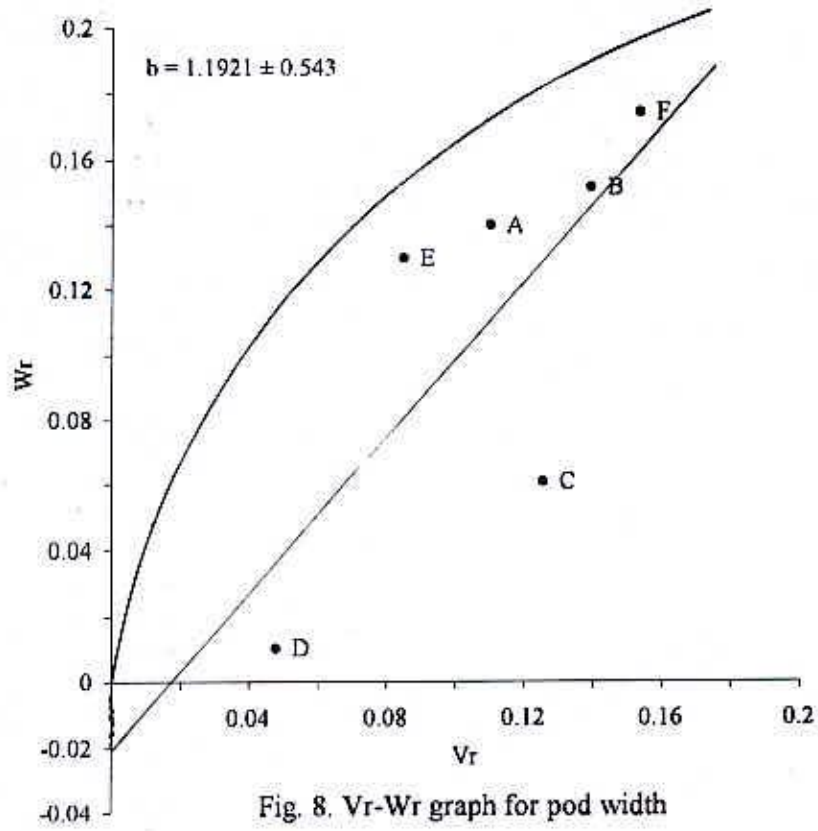


Fig. 8. Vr-Wr graph for pod width

The regression of Wr on Vr yielded b value (1.1921 ± 0.543) which is statistically equal to unity, the additive-dominance genetic model is thus adequate. Contrary to the both Hayman and Griffing anova graphical presentation of Wr-Vr analysis clearly demonstrate that on average there was nearly complete dominance (Fig. 8). From the Vr-Wr graph, it is obvious that the genotype KBS-3 contained the largest number of dominant alleles, while KBS-2 had the highest number of recessive genes.

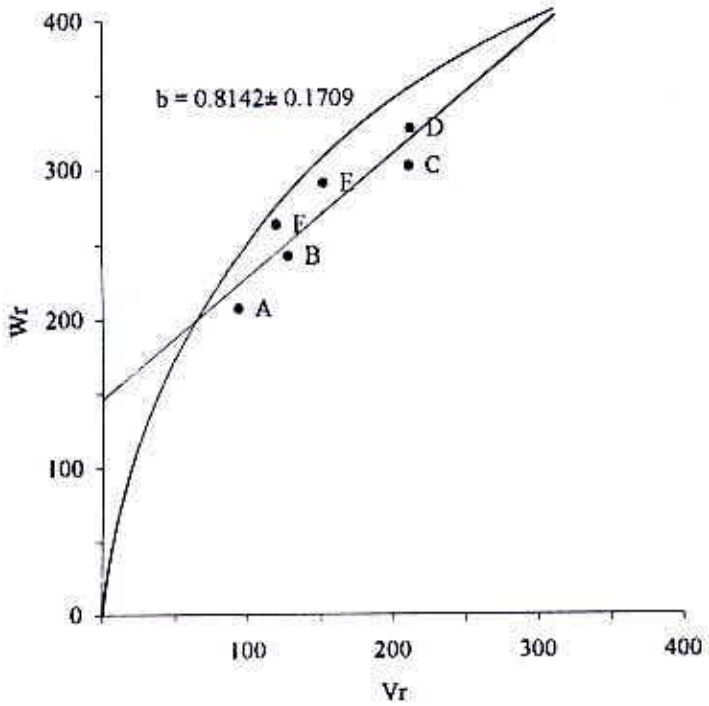
Khondker (1995) reported partial and Khanam (1997) reported over-dominance for this character.

i) 10-pod weight (TPW)

Result demonstrated (Table 7) that both additive (a) and dominance (b) genetic effects were important for the expression of this trait, as the components were highly significant. The result is similar to the Griffing's combing ability analysis (Table 4).

The results of Vr-Wr graph (Fig. 9) shows the regression line intercept the Wr axis above the origin, which indicated that on average there was partial dominance. The regression of Wr on Vr gave the slope b= 0.8142±0.1709, which is close to unity, with clear indication that additive-dominance genetic model was adequate for 10-pod weight of the present experiment. Thus the results of Vr –Wr graph can be interpreted with reasonable confidence. The parent DS-30 appeared to be have contained most dominant genes and the parent KBS-3 contained most recessive alleles.

Khondker (1995), Khanam (1997) and Sarker (2000) also obtained partial dominance for 10-pod weight, in Lablab bean.



LEGEND
A = DS-30
B = DS-52
C = DSN-26
D = KBS-3
E = DS-161
F = KBS-2

Fig. 9. Vr-Wr graph for 10-pod weight

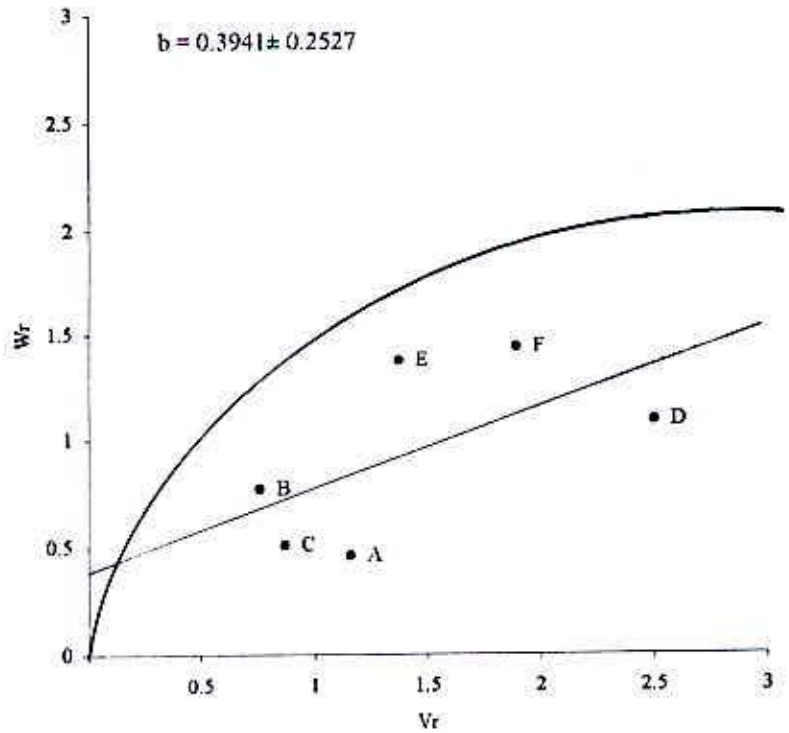


Fig. 10. Vr-Wr graph for 20-seed weight

j) 20-Seed weight (SW)

The analysis of variance following Hayman approach (Table7) demonstrated that both additive (a) and dominance (b) genetic components were highly significant ($P<0.001$) for this trait. Results of Griffing's combining ability analysis also suggested the same (Table 4).

On average dominance might be partial since regression line cut the Wr axis above the origin (Fig. 10). The examination of regression of Wr on Vr ($b= 0.3941 \pm 0.2527$) revealed that the slope was close to unity, with clear indication that additive genetic model was adequate for 20-seed weight of the present experiment. The parent DSN-26 appeared to be have contained most dominant genes and parent KBS-3 contained most recessive genes.

Alam (2002) reported partial dominance for 20-seed weight in Lablab bean under two growing seasons.

k) Pod yield per plant (PYP)

The variance due to additive (a) and dominance (b) items were significant (Table 7). That is, both the components were important for the expression of this character. The results of combining ability analysis also suggested the similar facts (Table 4). It was observed that mean dominance (b_1), dominance deviation form array to array (b_2) and residual dominance effect (b_3) were also significant.

The graphical presentation (Vr-Wr graph) of Hayman approach is shown in Fig. 11. The regression of Wr on Vr gave b value (1.1063 ± 0.3723) which was not significantly different from unity. This indicates that simple additive-dominance model was adequate without any non-allelic interaction. On an average complete dominance was observed in the inheritance of pod yield per plant since the regression line passing almost through the origin. The distribution of array points on graph shows that the genotype KBS-2 contained the largest number of dominant genes whereas DSN-26 contained the highest number of recessive alleles.

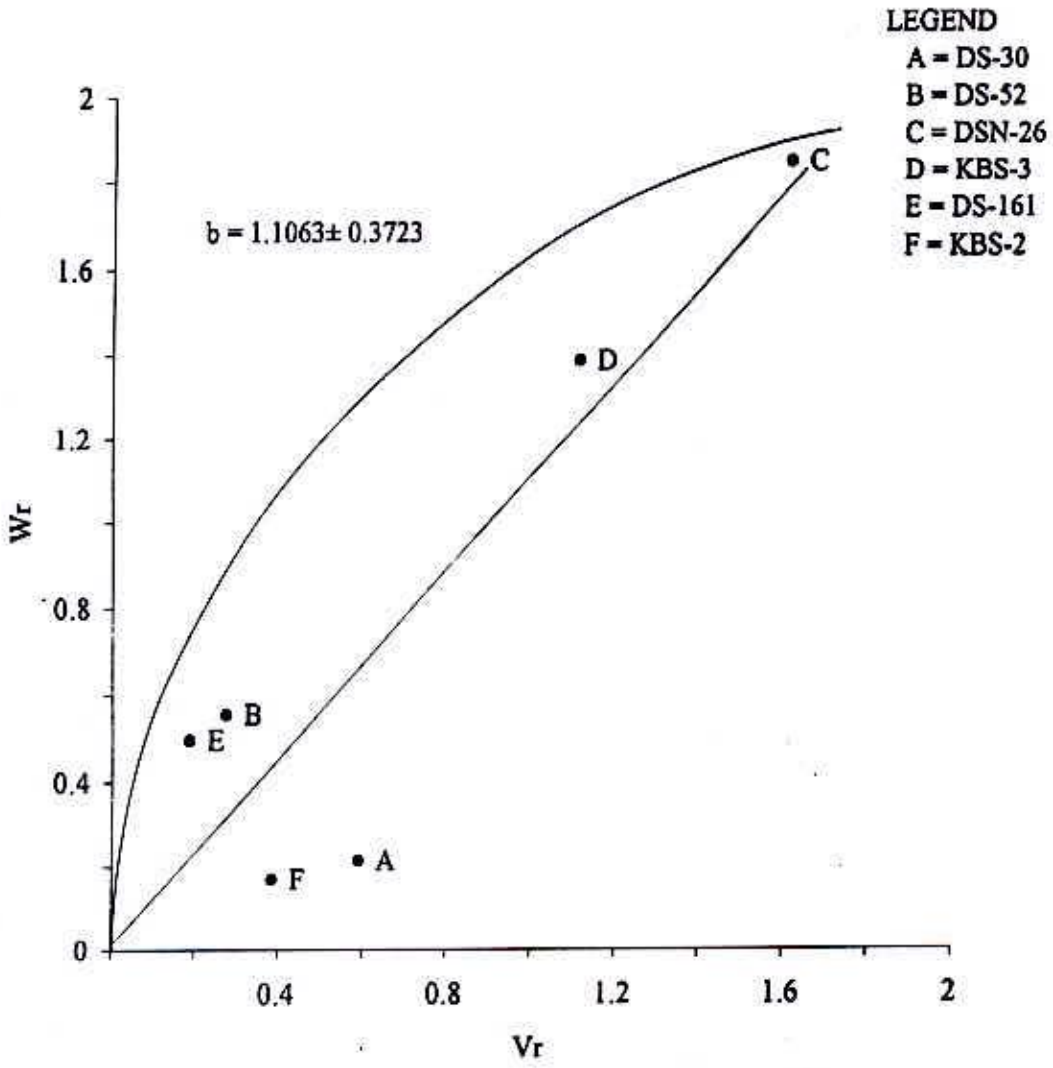


Fig. 11. Vr-Wr graph for pod yield per plant

Sarker (2000) and Alam (2002) also observed complete dominance effect for pod yield plant in Lablab bean.

4.4 Components of Variation and Genetic Parameters

Components of variation and genetic parameters such as D, H_1, H_2, F, h^2, E, $[^1/_4(H_1/D)]^{1/2}$, $H_2/4h_1$, $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$, h^2/H_2 and heritability in narrow sense (h^2_n) were estimated in pursuance of Hayman-Jinks' approach of diallel analysis and are presented in Table 8.

Among the components of variation, D, H_1, H_2, and F are the genetic components and E is the environmental component (cf. Mather and Jinks, 1977). D measures only additive effects of genes while H_1 and H_2 measure only dominance effect; and one of which, H_1 has the same coefficient as D so that $[1/4(H_1/D)]^{1/2}$ is a measure of degree of dominance. The relationship of H_1 and H_2 parameters is reflected in $H_2/4H_1$ index that estimates the frequency of positive and negative alleles showing dominance in parents. The sign and magnitude of F shows the relative frequencies of dominant to recessive alleles in the parental genotypes and variation in the dominance level over all loci. F is positive for an excess of dominant alleles, irrespective of whether or not the dominant alleles are increasing or decreasing in their effective on the character and negative for an excess of recessive alleles. The $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ ratio represents the proportion of dominant and recessive genes in the parents. The ratio of h^2 and H_2 gives information about the number of genes, which control the character and exhibit dominance.

The components of variation are described character wise as follows:

a) Days to 1st flowering (DFF)

The components H_1 and H_2 are significant but D is not significant for days to first flowering (Table 8). This indicates the importance of dominance effect of

Table 8. Components of variation and genetic parameters for eleven plant characters in a 6 × 6 F_2 diallel of Lablab bean

Item	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
D	80.956 ± 63.846	62.94 ± 59.63	148.452** ± 18.19	43.502** ± 8.656	0.667** ± 0.061	70.291** ± 6.889	13.562** ± 0.73	0.196** ± 0.032	586.88** ± 14.592	1.355* ± 0.4	2.121** ± 0.203
H_1	3740.56** ± 646.62	3662.48** ± 603.95	855.669** ± 184.25	367.688* ± 87.67	1.975* ± 0.619	339.991** ± 69.77	9.429 ± 7.39	0.291 ± 0.321	425.067* ± 147.788	10.009* ± 4.053	5.641* ± 2.056
H_2	3034.38** ± 579.07	3000.46** ± 540.86	785.301** ± 165.0	333.632* ± 78.512	2.123* ± 0.554	275.195* ± 62.482	8.205 ± 6.625	0.291 ± 0.294	395.675* ± 132.349	9.149 ± 3.629	5.093 ± 1.842
h^2	26.117 ± 389.75	40.944 ± 364.038	-105.57 ± 111.058	- 52.8 ± 52.84	- 4.853** ± 0.373	- 26.933 ± 42.05	1.037 ± 4.459	0.976** ± 0.198	-4.069 ± 89.08	-1.987 ± 2.443	- 5.787* ± 1.239
F	387.067 ± 310.66	340.728 ± 290.164	164.467 ± 88.521	38.424 ± 42.12	0.529 ± 0.297	70.457 ± 33.52	-10.217* ± 3.554	-0.056 ± 0.158	175.917 ± 71.003	- 1.797 ± 1.947	2.399 ± 0.988
E	7.586 ± 24.152	7.704 ± 22.55	7.04 ± 6.882	2.44 ± 3.275	0.1** ± 0.023	8.134** ± 2.606	0.563 ± 0.276	0.036* ± 0.012	1.354 ± 5.52	0.233 ± 0.151	0.11 ± 0.077
$[(H_1/D)/4]^{1/2}$	3.339	3.814	1.2	1.454	0.86	1.1	0.417	0.609	0.426	1.359	0.815
$H_2/4H_1$	0.203	0.205	0.229	0.227	0.269	0.202	0.218	0.25	0.233	0.229	0.226
$\frac{(4DH_1)^{1/2}/4 + F/2}{(4DH_1)^{1/2}/4 - F/2}$	5.743	5.889	2.714	1.886	0.712	2.675	0.051	0.620	2.087	0.344	5.524
h^2/H_2	0.0086	0.0136	-0.134	-0.158	-2.286	-0.097	0.126	3.351	-0.01	-0.217	-1.136
h^2_n	0.095	0.075	0.482	0.346	0.515	0.461	0.583	0.445	0.961	0.238	0.765

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g), PYP = pod yield per plant (kg).

* P<0.05; ** P<0.01

genes in the inheritance of flowering. The magnitude of H_1 was much higher than D, suggesting the preponderance of dominance type of gene action for this trait. Positive of F revealed that the dominant alleles were proportionately in excess in its inheritance. Dominance effect (h^2) was found positive and non-significant.

The $[(H_1/D)/4]^{1/2}$ value was greater than one indicating overdominance for the character. Positive and negative alleles were asymmetrically distributed, as indicated by $H_2/4H_1$ value (0.203) which was smaller than the expected value of 0.25. The ratio $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ was greater than unity, suggesting excess of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritabilty as 9.5% (Table 8).

b) Days to 1st pod setting (DFPS)

Dominance component was significant and H_1 was greater in magnitude than additive component, indicating greater role of dominance component in the inheritance. Positive value of F revealed that the dominant alleles were predominantly in excess in its inheritance (Table 8); but then the estimate was non-significant. H_2 value differed form H_1 suggesting that there was unequal frequency of increasing and decreasing alleles. The results of dominants effect (h^2) were positive and non-significant.

Overdominance was found for days to 1st pod setting. The value of $H_2/4H_1$ was not exactly 0.25, indicating an asymmetrical distribution of positive and negative alleles. The ratio $[1/4(4DH_1)^{1/2} + F/2]/[1/4(4DH_1)^{1/2} - F/_2]$ was greater than unity, suggesting excess of dominant alleles and lesser recessive alleles. The analysis gives narrow sense heritabilty as 7.5% (Table 8).

c) No of inflorescences per plant (IPP)

Both additive and dominant components were significant, but due to higher magnitude dominant gene effects the latter appeared to have more control of the character. Positive F value indicates there were more no. of dominant alleles

predominantly in excess in its inheritance (Table 8), the estimate was however non-significant. The dominance effect (h^2) was negative and non-significant.

By being greater than unity, $[(H_1/D)/4)]^{1/2}$ suggested the presence of over-dominance for this trait. The value of $H_2/4H_1$ was not exactly 0.25, indicating an asymmetrical distribution of positive and negative alleles. Since the $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ was on an average equal to unity, which indicates that dominant and recessive genes were not equally distributed and in excess of dominant genes. The analysis gave narrow sense habitability (h^2_n) estimate of 48.2% (Table 8).

d) No. of flowers per inflorescence (FPI)

For flowers per inflorescence most of the genetic parameters (D, H_1, H_2,) were significant (Table-8). Both additive and dominant effects of genes were important for the character expression. But H_1 was greater than D indicating greater role of dominance component in the inheritance of the trait. Positive F value revealed that the dominant alleles were predominantly in excess in its inheritance, but then the estimate was non-significant. Negative and non-significant result was found for dominance effect (h^2).

Overdominance was found for flowers per inflorescence. Positive and negative alleles were more or less asymmetrically distributed as $H_2/4H_1$ value was not exactly near the desired value of 0.25. Since the ratio $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ is greater than unity there was an unequal distribution of dominant and recessive genes. The narrow sense heritability was 34.6% (Table 8).

e) No. of pods per inflorescence (PPI)

The estimate suggested the role of additive and dominance components as both of them were significant, with however preponderance of the latter. Overall difference between parents and crosses were substantiated by significant h^2 value. Positive F value indicated the excess of dominant alleles in the parents.

Partial dominance was considered for the character expression as $[(H_1/D)/4]^{1/2}$ is less than unity. A symmetrical distribution of positive-negative genes was found since $H_2/4H_1$ value, on an average, near the expected value of 0.25. As $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ was less than unity, this indicates unequal distribution of dominant and recessive genes and also indicates an excess of recessive genes. The narrow sense heritability was 51.5% (Table 8).

f) Inflorescence length (IL)

Table 8 shows both additive and dominance components were significant for the trait. But dominance component was preponderant. Positive value of F suggested that the presence of more dominant alleles, but the estimate was non-significant. The result of dominance effect (h^2) was negative and non-significant.

On an average complete dominance was found for this trait. The $H_2/4H_1$ value (0.202) was not equal to the expected value (0.25), which indicated that there was asymmetrical distribution of positive and negative alleles in the parents. Since the ratio $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ is greater than unity, there was an unequal distribution of dominant and recessive genes. The narrow sense heritability was 46.1%.

g) Pod length (PL)

Results suggested that only additive component played role in the expression of the trait. Significant and negative F value indicated that the recessive alleles were predominantly in excess in its inheritance (Table 8).

Partial dominance was considered for the character expression since $[(H_1/D)/4]^{1/2}$ parameter is less than unity. An asymmetrical distribution of positive and negative alleles was indicated, as $H_2/4H_1$ value was not equal to 0.25. As the value of $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ was less than unity, it suggested an unequal distribution of dominant and recessive alleles; it also indicated an excess of recessive genes. The narrow sense heritability was 58.3%.

h) Pod width (PW)

The estimates of D, H_2 and E (Table 8) show that additive component was all the more important in the control of the character. Overall difference between parents and crosses were substantiated by significant h^2 value.

Since $[(H_1/D)/4]^{1/2}$ value is less than unity, there was partial dominance for the expression of this trait. The $H_2/4H_1$ value is equal to 0.25, which indicated that there was symmetrical distribution of positive and negative alleles. The dominant and recessive genes were unequally distributed in the parents since the ratio of $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ was less than unity. The narrow sense heritability was 44.5%.

i) 10-pod weight (TPW)

The estimates suggested that both additive and non-additive components played important role in the expression of individual pod weight as typified herein by 10-pod weight (Table 8). But the additive component (D) had more prominent role than the dominant component. The positive F value indicated the excess of dominant genes in their effect, but the value is non-significant.

Partial dominance was observed for the character as $[(H_1/D)/4]^{1/2}$ is less than unity. The $H_2/4H_1$ value (0.233) is on an average equal to the expected value (0.25), which indicated that there was more or less symmetrical distribution of positive and negative alleles in the parents. Also the dominant-recessive genes were unequally distributed as the ratio of $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ is more than unity.

j) 20-seed weight (SW)

For 20-seed weight, additive and dominance components were significant indicating that both components were important for the expression of the trait. But dominant component was more important than the additive as H_1>D. The non-significant value of h^2 indicated that there was no significant difference between

parents and crosses. The negative F value indicated that recessive genes were preponderant, but then the estimate was non-significant.

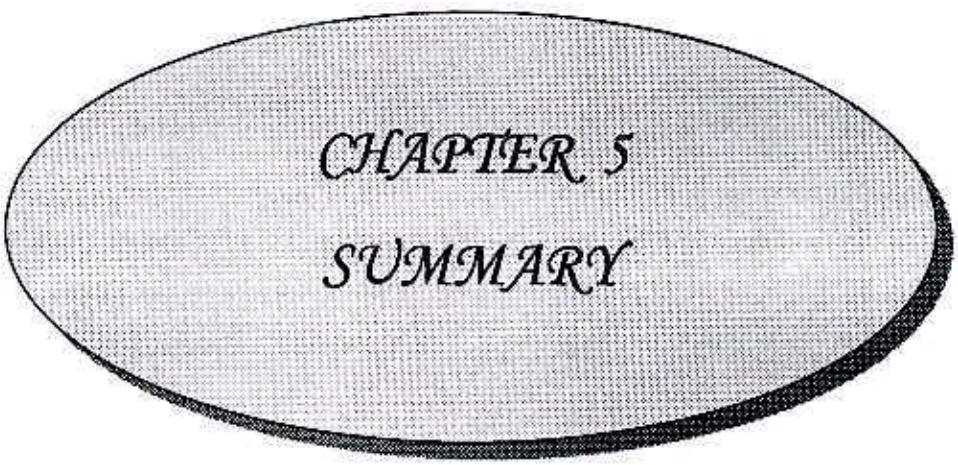
Overdominance was demonstrated by the estimate $[(H_1/D)/4]^{1/2}$ which is greater than unity. Positive and negative alleles were asymmetrically distributed because $H_2/4H_1$ value was not exactly equal to 0.25. The dominant and recessive genes were unequally distributed since the relevant parameter had a value of less than one. The narrow sense heritability was 23.8% (Table 8).

k) Pod yield per plant (PYP)

Significant D and H_1 values indicate the importance of both additive and dominance components for the expression of the trait. But the dominant component was predominant. There were significant differences between the parents and hybrids since the h^2 value was significant. The positive of F suggested that dominant genes in the parent population were in the excess, but then the parameter is non-significant.

It appears that partial dominant condition existed for pod yield per plant as $[(H_1/D)/4]^{1/2}$ value is less than unity. An asymmetrical distribution of positive and negative alleles was indicated, as $H_2/4H_1$ value is not equal to the desired value of 0.25. The dominant and recessive alleles were distributed unequally because the ratio of $[1/4(4DH_1)^{1/2} + F/2] / [1/4(4DH_1)^{1/2} - F/_2]$ is grater than unity. The narrow sense heritability was 76.5% (Table 8).

Uddin and Newaz (1997) and Sarker (2000) observed high heritability for pod yield in Lablab bean.


CHAPTER 5
SUMMARY

SUMMARY

The research work in this thesis which concerned a 6 × 6 F_2 diallel population of Lablab bean (*Lablab purpureus* L.) excluding reciprocals was carried out during July, 2001 to March, 2002 with the aim of obtaining various genetic information on edible pod yield and important quantitative traits and, also of identifying the best parents and specific crosses.

The parental genotypes used in the study are DS-30, DS-52, DS-161, DSN-26, KBS-2 and KBS-3 which were chosen for their genetic differences and diverse origin. The characters studied are days to 1st flowering, days to 1st pod setting, no. of inflorescences per plant, no. of flowers per inflorescence, no. of pods per inflorescence, inflorescence length, pod length, pod width, 10-pod weight, 20-seed weight and pod yield per plant.

The results of the investigation are summarized as follows:

5.1 Genotypic Performance

All the 21 genetic populations showed significant differences ($P<0.001$) for various characters under study. Among the parents KBS-2, and cross DS-52 × DS-161 were the earliest in days to flowering. For pod setting KBS-3 showed the earliest performance. Highest no. of inflorescences per plant was observed in DSN-26 and in cross DSN-26 × DS-161. The parental genotype DS-161 and cross DS-52 × KBS-2 had maximum no. of flowers per inflorescence. The parental genotype KBS-3 and cross DS-161 × KBS-2 gave maximum no. of pods per inflorescence. In respect of inflorescence length the genotype KBS-2 and cross DS-161 × KBS-2 produced the largest inflorescence stalk. For pod length, pod width and 10-pod weight the parental genotype DSN-26 showed highest performance. The F_2 progenies of cross DS-30 × DSN-26 for pod length, DS-52 × DSN-26 for pod width, and DSN-26 × KBS-3 for 10-pod weight showed highest performance. The

genotype DS-52 and cross DS-52 × KBS-3 had bold and heaviest seed as reflected in 20-seed weight. In respect of pod yield per plant the parental genotype DSN-26 and the F_2 progenies of cross DSN-26 × KBS-3 displayed the best performance.

5.2 Combining Ability Studies (Griffing's approach)

Analysis of combining ability following Griffing's approach showed significant gca and sca variances ($P<0.05$-0.001) for nearly all the characters studied, indicating the role of both additive and non-additive components in the genetic system controlling those characters. In most of the characters except days to 1st flowering and days to 1st pod setting, gca : sca ratio was greater than unity, which indicted the preponderance of additive component in their expression. Estimates of gca effects for different characters suggested that DS-52 was the best general combiner for early flowering, early pod setting and 20-seed weight. The best general combiners for other characters were DS-161 for flowers per inflorescence, KBS-3 for pods per inflorescence, KBS-2 for inflorescence length and DSN-26 for inflorescences per plant, pod length, pod width, 10-pod weight and pod yield per plant.

The sca estimates of various characters revealed that DS-52 × DS-161 was the best specific cross for days to 1st flowering followed by DS-30 × DSN-26; DS-52 × KBS-3 and DS-30 × DSN-26 for 1st pod setting. The best specific crosses for other characters were DSN-26 × DS-161 for inflorescences per plant, DS-52 × KBS-2 for flowers per inflorescence, DS-30 × KBS-2 for pods per inflorescence, KBS-3 × DS-161 for inflorescence length, DS-30 × DS-52 for pod length, DSN-26 × KBS-2 for pod width, DSN-26 × KBS-3 for 10-pod weight, DS-30 × DNS-26 for 20-seed weight and DS-30 × KBS-2 for pod yield per plant.

5.3 Diallel Analysis After Hayman's Approach

Mean square for additive and dominance components in Hayman anova following Morely Jones' modification suggested that both additive and dominance

components played role in the expression of characters studied. The additive components were generally more important in most of the characters except days to 1st flowering and 1st pod setting. Dominance was predominant in these two characters (days to 1st flowering and 1st pod setting).

Vr-Wr Graph Analysis: Results showed by and large simple additive-dominance genetic model to be adequate without presence non-allelic interaction. Complete dominance was observed only for pod yield/plant. Partial dominance was noticed for no. of flowers per inflorescence, pod length, 10-pod weight and 20-seed weight. While overdominance was recorded for days to 1st flowering, days to 1st pod setting, no. of inflorescences per plant, no. of pods per inflorescence, inflorescence length and pod width.

In Vr-Wr graphical presentation, the distribution of array points along the regression line suggested that the parent DSN-26 contained more dominant genes controlling the expression of days to 1st flowering, days to 1st pod setting, no. of flowers per inflorescence, pod length and 20-seed weight. The parent KBS-3 contained more dominant alleles for no. of inflorescences per plant and pod width. While the parent DS-30 contained more dominant genes for inflorescence length and 10-pod weight. The parental genotype KBS-2 apparently contained higher number of dominant alleles for no. of pods per inflorescence and pod yield per plant.

5.4 Components of Variation and Genetic and Parameters

The components of variation revealed that both additive and dominance genetic components were important in inflorescences per plant, flowers per inflorescence, pods per inflorescence, inflorescence length, 10-pod weight, 20-seed weight and pod yield per plant. For pod length and pod width, additive genetic components were important while for days to 1st flowering and days to 1st pod setting, the dominance components were all the more important. The components of variation due to dominance effect of the genes (H_1) was greater than H_2

component for nearly all the characters, indicating the presence of unequal proportion of positive and negative alleles in the loci governing the characters. The dominant alleles were predominantly in excess for all characters except pod length, pod width and 20-seed weight.

The degree of dominance indicated overdominance for days to 1st flowering days to 1st pod setting, inflorescences per plant, flowers per inflorescence, inflorescence length and 20-seed weight. Partial dominance was observed for pods per inflorescence, pod length, pod width, 10-pod weight and pod yield per plant. An asymmetrical distribution of positive and negative alleles was found for days to 1st flowering, days to 1st pod setting, no. of inflorescences per pant, number of flowers per inflorescence, inflorescence length, pod length, 20-seed weight and pod yield per plant. But the distribution of alleles was more or less symmetrical for other characters (eg. no. of pods per inflorescence, pod width and 10-pod weight). Dominant and recessive genes were unequally distributed in the parental genotypes for all the characters studied. High narrow sense heritability was observed for pod yield per plant, 10-pod weight, pod length and pods per inflorescence.

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APPENDICES

APPENDICES

Appendix I. Meteorological data recorded during the experimental period at BAU farm Mymensingh

Month	Year	Air Temperature* (°C)			Average* Humidity (%)	Total** Rainfall (mm)	Total** Sunshine (hrs.)
		Maximum	Minimum	Average			
July	2001	31.73	26.46	29.09	86.29	178.4	145.3
August	2001	32.66	26.80	29.73	84.16	223.5	155.1
September	2001	32.08	26.09	29.08	86.97	371.0	152.8
October	2001	31.61	24.34	27.97	86.16	205.9	185.2
November	2001	29.49	19.55	24.52	84.27	10.7	222.7
December	2001	26.52	13.19	19.85	80.84	00.0	220.2
January	2002	25.43	12.43	19.18	78.00	05.3	213.2
February	2002	27.70	15.39	21.55	72.68	Trace	247.6
March	2002	30.00	19.00	24.50	73.61	34.4	239.3
April	2002	29.90	21.69	25.79	80.90	259.8	213.3

* Monthly average   ** Monthly total

Source: Weather yard Department of Irrigation & Water Management, BAU, Mymensingh.

Appendix II. First and second degree statistics for pod yield and other characters of 6 parents and 15 F_2 population of a 6 × 6 diallel of Lablab bean

Genotype	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
Parental value (P)											
DS-30	112.50	119.00	57.25	20.75	3.25	27.25	15.75	2.025	131.50	6.098	2.415
DS-52	111.25	117.50	60.75	30.25	4.5	30.75	12.75	2.525	137.25	8.798	3.68
DSN-26	106.25	112.00	92.50	22.75	4.25	18.50	21.25	3.175	165.50	7.248	6.313
KBS-3	92.75	99.25	70.00	31.00	5.75	27.25	11.25	2.40	137.75	7.868	5.465
DS-161	105.50	112.50	64.75	39.75	5.00	24.00	12.00	1.975	91.75	5.26	2.933
KBS-2	90.25	100.5	69.25	30.25	5.25	44.75	12.50	1.90	119.75	7.34	4.362
Variance (V_p)	88.54	70.64	155.49	45.94	0.77	78.43	14.13	0.23	588.24	1.58	2.23
Array mean (r)											
DS-30	116.07	123.49	66.68	24.69	3.91	30.99	15.87	2.43	132.42	6.07	3.41
DS-52	106.17	114.81	63.54	29.47	4.38	36.21	14.47	2.56	133.09	8.37	3.59
DSN-26	116.43	124.62	77.25	23.21	4.17	29.67	18.87	2.86	147.36	7.25	4.67
KBS-3	114.38	122.69	66.72	29.04	4.76	35.71	13.55	2.33	136.84	7.48	4.29
DS-161	108.69	116.59	66..63	30.19	4.57	35.61	13.40	2.19	113.49	6.49	3.33
KBS-2	112.41	121.37	68.51	29.28	4.69	39.96	13.26	2.22	126.40	7.41	3.40
Variance (V_r)	17.24	15.82	22.13	8.55	0.11	14.17	4.72	0.07	126.75	0.66	0.28

Appendix II. (Contd.)

Genotype	DFF	DFPS	IPP	FPI	PPI	IL	PL	PW	TPW	SW	PYP
Array variance (V_r)											
DS-30	192.60	187.27	38.49	45.24	0.435	5.81	7.01	0.110	93.97	1.16	0.592
DS-52	218.31	224.89	46.14	42.63	0.229	33.86	10.99	0.139	127.51	0.754	0.272
DSN-26	103.06	126.05	152.42	14.87	0.402	33.98	4.05	0.125	211.07	0.865	1.610
KBS-3	338.43	339.34	18.72	28.00	0.326	47.50	6.49	0.047	211.72	2.498	1.109
DS-161	233.18	227.17	147.52	26.60	0.294	76.39	3.65	0.084	151.78	1.368	0.186
KBS-2	193.72	153.79	59.13	31.31	0.254	31.32	2.71	0.153	119.84	1.886	0.385
Mean variance ($\overline{V_r}$)	213.22	209.75	77.07	31.44	0.323	38.14	5.82	0.11	152.64	1.42	0.69
Parent-array covariance (W_r)											
DS-30	-82.81	-66.35	-12.55	34.11	0.422	0.929	8.84	0.139	207.01	0.461	0.213
DS-52	67.31	56.34	10.69	19.18	0.230	18.94	12.12	0.151	242.17	0.767	0.556
DSN-26	-56.27	-58.70	114.95	18.98	0.338	36.75	5.61	0.060	301.17	0.507	1.85
KBS-3	49.73	55.14	29.44	0.32	0.389	26.56	9.30	0.010	326.73	1.105	1.38
DS-161	-85.84	-89.09	127.04	17.03	0.244	58.39	6.88	0.129	290.24	1.370	0.497
KBS-2	68.03	43.65	59.46	14.18	0.078	24.58	6.15	0.173	262.44	1.437	0.169
Mean covariance ($\overline{W_r}$)	-6.64	-9.83	54.83	17.30	0.283	27.70	8.15	0.11	271.63	0.94	0.777

Note:
DFF = Days to 1st flowering ; DFPS = Days to 1st pod setting ; IPP = No. of inflorescences per plant ; FPI = No. of flowers per inflorescence ; PPI = No. of pods per inflorescence ; IL = Inflorescence length (cm) ; PL = Pod length (cm) ; PW = Pod width (cm) ; TPW = 10-pod weight (g); SW = 20-seed weight(g), PYP = pod yield per plant (kg).