COMBINING ABILITY OF COMMERCIAL WHITE PEA BEAN (*Phaseolus vulgaris* L.) VARIETIES UNDER JIMMA CONDITION

MS.c Thesis

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Jimma, Ethiopia

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**A Thesis Submitted to the School of Graduate Studies
Jimma University College of Agriculture and Veterinary Medicine**

**In Partial Fulfillment of the Requirements for the Degree of
MASTER OF SCIENCE IN AGRICULTURE (PLANT BREEDING)**

BY

TSEGAU SENBETAY HADGU

**November, 2012
Jimma, Ethiopia**

DEDICATION

This piece of work is dedicated to my father priest Senbetay Hadgu and my mother W/ro Belainesh Giday, for giving me love and their committed partnership in the success of all my life.

STATEMENT OF THE AUTHOR

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ABBREVIATIONS

ANOVA	Analysis of variance
GCA	general combining ability
SCA	Specific combining ability
REC	Reciprocal crosses
MAT	Maternal effects
NMAT	Non-maternal effects
CSA	Central statistical Authority
g	Grams
KM	Kilometer
m.a.s.l	meters above see level
JURC	Jimma Agricultural research center
mm	Millimeter
cm	Centimeter
^{0}C	Degricentigrade
CBB	common Bacterial blight
ALS	Angular leaf spot
FLS	Floury leaf spot
p	is the number of parents
Mse	is the mean square of error,
g_i	is the GCA effect for the ith parent
sij	is the SCA effect for ij cross
Sg	Sum of square of general combining ability
Ss	Sum of square of specific combining ability
Xi.	the sum of the ith array X.. = Grand sum
xii	The value for the ith parent
xij	The value of the cross between the ith male andjth female
Mg	Mean square of general combining ability
Ms	Mean square of specific combining ability
Me	Mean square of error
SE	is standard error of the estimates
r	is the number of replications
Ind.bush	Indeterminate bush

BIOGRAPHICAL SKETCH

The author was born on August 12, 1985, in Kebele Ambahasty, Southern Tigray, and Maichew. He attended his elementary school at Ashara Elementary School in from 1994 to 1997 and his junior Secondary school at Kindihaw welday from 1998 to 1999. He started his high school study in 2000 at Tilahun Yigzaw Senior Secondary School and completed it in 2003.

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ABSTRACT

Combiningability study provides very useful genetic information about the ineheritance of quantitative traits that helps to determine the type of breeding procedure to be employed to improve the crop of interest. The objective of the study was to determine the type of gene actions involved in the inheritance of the most important quantitative traits in commercial white pea bean cultivars. Forty nine entries (7 parents and 42 F_2 diallel crosses) were grown in a simple lattice design with two replications at Jimma Agricultural Research Center, South Western Ethiopia. The results revealed significant mean squares in all of the characters, except for days to 50 % flowering, days to maturity, number of nodes on the main axis, and internode length. There were significant mean squares due to general combining ability, specific combining ability, reciprocal effects, maternal effects, and non-maternal effects in almost all of the characters. The relative contribution of specific combining ability was higher than general combining ability for all of the studied traits, except for days to 50% flowering, pod length, and seed thickness. This indicating that the non-additive gene actions are influential in the expression of these traits which poses some difficulty as the non-additive gene actions are non-fixable. Thus, selfing should continue for more generation to fix the non-additive gene actions before undertaking selection. Significant general combining ability and specifi combining ability effects were found for leaf rust and angular leaf spot, respectively. This indicates that additive geneaction is important in the inheritance of rust and the segregating generation can be improved by selection. Starlight is good general combiner for 100-seed weight and grain yield. The other genotypes may also be good general combiner for other traits because they displayed positive and significant traits.

Key words: Specific combining ability, general combining ability, reciprocal effects, maternal effects, Non-maternal effects.

1. INTRODUCTION

White pea bean (*Phaseolus vulgaris* L.; 2n = 2x = 22) belongs to order Rosales, family Leguminosae, subfamily Papilionideae, tribe Phaseolea, subtribe Phaseolinae, genus Phaseolus (CIAT, 1986a). It is an erect or twinning, annual, herbaceous plant with various growth habits, morphological traits, and seed and pod characteristics. The bean flower is perfect, possessing both male and female organs on the same flower, and is self-fertilized. Pollination coincides with the time when the flower opens (Purseglove, 1968).

It is generally accepted that all species of the genus *Phaseolus* originated in tropical America (Mexico, Guatemala, and Peru). The main evidence of their origin is the genetic diversity of the materials that exists in this region; in addition, archaeological findings prove the antiquity of their cultivation in Mexico and Peru (CIAT, 1986a). Beans were introduced into Africa probably by the Portuguese and spread into the interior faster than European exploration (Sauer, 1993).

The crop is adapted to an altitude ranging from sea level to nearly 3000 m.a.s.l (CIAT, 1986a), but doesn't grow well below 600 m.a.s.l due to poor pod set caused by high temperature (Acland, 1971; Cobley, 1976). Suitable production areas of bean in Ethiopia have been indicated as areas with an altitude between 1200 – 2200 m.a.s.l, mean maximum and mean minimum temperature of less than 32^0 C and greater than 12^0 C, respectively, and a rainfall of 350-500 mm well distributed over 70-100 days (Imru, 1985; Amare and Haile, 1989). Almost all types of soil with good drainage and reasonably high nutrient content are suitable for haricot bean production (Purseglove, 1968; Acland, 1971).

The white pea bean (*Phaseolus vulgaris* L.) is the most important food legume crop grown worldwide (Wortmann and Allen, 1994; Wortmann *et al*., 1998; Buruchara, 2006). Beans are considered by many to be the perfect food as they are nutrient dense with high contents of protein, micronutrients, vitamins, dietary fibre, and also have a low glycemic index (Wortmann and Allen, 1994; Bennink, 2005; Widers, 2006).

The crop is currently the second most important source of human dietary protein and the third most important source of calories next to soybean for over 100 million people in rural and poor urban communities in Africa (Buruchara, 2006). It is one of the most important pulse crops grown in many lowland areas of Ethiopia as a main crop and protein

source. Green leaves, green pods, and immature and/or dry seeds may all be eaten, and they are very rich in iron and zinc (Kimani *et al*., 2006). Dry leaves, threshed pods, stalks and bean seeds that do not meet human food quality standards are fed to animals, or used as fuel for cooking, especially in Africa and Asia (Sperling *et al*., 1996; Buruchara, 2006).

In addition to contributing to protein requirement, haricot beans, particularly the white colored ones are very important to fetch additional income for farmers (Imru, 1985; Getahun and Yeshi, 1989; IAR, 1990). At present different types of beans are grown in Ethiopia both as a sole crop and intercropped with cereals (IAR, 1990; Kidane *et al*., 1990). These include, white pea beans as cash crop, different colored beans for local consumption, and climbing types to be used as green beans locally and other purposes.

Beans contribute a great deal to improving and sustaining soil fertility due to their ability, as legumes, to fix nitrogen in the soil. They are, hence, used in crop rotations, and mixtures with grass in leys and pastures, and as cover crops and green manures (Purseglove, 1968). Thus beans fit well in the farming systems in Ethiopia and sub-Saharan Africa.

Annual global production of white pea bean is estimated at 19.5 million t from 28 million hectares; Brazil is the highest producer, with an estimated annual production of 4 million t (FAOSTAT, 2007). Production in Africa is estimated at 2.8 million t on 4.8 million ha (FAOSTAT, 2007). East Africa accounts for over 75% of the total production in Africa.

According to CSA (2004), white pea bean has land area coverage of 209,534.89 hectares (2.38% of crop area) and a production of 1,521,66.062 tones (1.45% of total grain production) and a productivity of 7.26 quintal per hectare in Ethiopia,, which is very low. This low yield is attributed to several production constraints which include low number of improved varieties for the different agro-ecological zones, poor and untimely cultural practices, moisture stress and low soil fertility. A great loss of yield is also attributed to diseases such as rust, angular leaf spot, floury leaf spot, anthracnose, common bacterial blight and insects such as bean fly, aphids, stem maggots and bean bruchids (CIAT, 1986b; Amare, 1989; Habtu, 1990).

A coordinated pulse research program on varietal improvement and crop management was initiated in 1972 at Melkassa Agricultural Research Center (MARC) with the main emphasis given to haricot beans. The program so far depends up on evaluation of

materials from introductions and some local collection. It has released several varieties (Imru, 1985; Amare and Haile, 1989; IAR, 1990).

There is wide genetic variability in white pea beans in growth habit (determinate vs. indeterminate), in days to maturity, in seed size, color and quality (cookability and palatability), in vegetative and reproductive growth, pigmentation, and leaf size, shape and orientation and resistance to pests (Leakey, 1970). The choice of promising genotypes from diverse genetic base, and their subsequent utilization for hybridization is one of the strategies for improving the productivity of any crop including beans. A systematic study of the hybrids (F_1s) and their behavior in subsequent generations of selfing (F_2, F_3, etc.) can generate basic genetic information about the type of gene action governing the inheritance of quantitative traits such as yield. The effort made to develop recombinant inbred lines inorder to identify superior recombinant inbred lines has been very limited on commercial white pea bean cultivars in the country. The Ethiopian bean improvement program has focused on screening of introductions and could not generate basic genetic information. Effective selection for seed yield and its components requires information on the magnitude of useful genetic variance present in the population, combining ability, heterosis, and correlation of component traits. Hence, it is necessary to systematically test the performance of parental lines in order to identify superior and complementary genotypes for hybridization. A suitable means to achieve this goal is the use of diallel mating system, a method where the progeny performance can be statistically separated in to components relating to general combining ability (GCA) and specific combining ability (SCA). General and specific combining abilities are a measure of the additive and non-additive genetic variation of parents, respectively (Sprague and Tatum, 1942). Combining ability analysis is one of the powerful tools in identifying the best combiners, which may be hybridized to exploit trasngressive segregants that help in identifying superior recombinant inbred lines. It is also useful to elucidate the nature of gene action involved.

It is recommended that high yielding heterotic crosses with low inbreeding depression and showing transgressive segregation (development of a character in excess of either parent) in the F_2 generation should be considered for further breeding work. Replicated yield trials can be undertaken in the F_2 and F_3 and selection be done only in large populations and among families of high yielding crosses (Singh, 1989). Thus it is desirable to study combiningability of the released varieties of white pea beans and elite genotypes.

Although studies on combining ability and the expression of heterosis have been made in various crops, including the white pea bean in various parts of the world, little effort has been made on beans in Ethiopia.

Therefore, this study was conducted with the objective of determining general combining ability (GCA) and specific combining ability (SCA) of eight lines of export quality white pea bean genotypes and their diallel crosses.

2. LITERATURE REVIEW

2.1 Taxonomy of the white pea bean

The white pea bean (*Phaseolus vulgaris* L.) belongs to the Angiosperms phylum (flowering plants with the orubs enclosed in a carpel or in several carpels united into an ovary). Over 30 species of *Phaseolus* have been reported from the Americas (Debouck, 1991; 1999). Of these, only five, namely, common bean (*Phaseolus vulgaris* L.), year bean (*Phaseolus polyanthus* Greenman), SCArlet runner bean (*Phaseolus coccineus* L.), tepary bean (*Phaseolus acutifolius* A, Gray) and lima bean (*P. lunatus* L.) are known to be domesticated (Gepts and Debouck, 1991; Debouck, 1999; 2000). The common bean (*P. vulgaris*) possesses by far the widest adaptation of all *Phaseolus* spp. with over 85% of the cultivated species falling under this species worldwide (Singh, 2001).

White pea beans are classified in the sub-phylum Dicotyledons (embryo with two cotyledons, parallel veined leaves and the stem with the vascular bundles arranged irregularly and cambium usually present), division Magnoliophyta, class Magnoliopsida, family Leguminosae, sub-family Papilionoideae/Fabaceae/Lotoideae (pulse family characterized by edible seeds and pods) and order Leguminales. White pea beans are a diploid (2n = 2x = 22) and self-pollinated crop (Rutger and Beckham, 1970; Stoetzer, 1984) possessing complete, papilionaceous flowers with 10 stamens, and an ovary with a long, coiled style and a hairy introrse stigma; the stigma is situated laterally along the inner arc of the curved style, where it intercepts pollen dehiscing from its own anthers. The crop is highly polymorphic, showing considerable variation in growth habit, vegetative characters, flower colour and size, shape and colour of pods and seeds (Purseglove, 1968). There are two major commercial classes of common bean, snap and dry beans (Singh, 2001). Snap beans are also known as string or green beans and are mainly grown for their pods, while dry beans are mainly grown for their seed.

2.2. Origin and genetic diversity of the common bean

It is believed that white pea beans, along with maize, squash, and amaranth, probably began as weeds in fields planted to cassava and sweet potatoes in Latin America (Purseglove, 1968). Over the millennia, farmers grew complex mixtures of bean types as a hedge against drought, disease, and pest attacks, a process which has produced an almost limitless genetic array of beans with a wide bean variety of colours, textures, and sizes to

meet the growing conditions and taste preferences of many different regions (Purseglove, 1968). The crop was introduced to Africa by Portuguese traders in the 16th century where it was met with great success in the Great Lakes region. Africa is now regarded as a secondary centre of diversity for the crop (Trutmann, 1996). The common bean was domesticated more than 7,000 years ago in two centres of origin, Mesoamerica (Mexico and Central America) and the Andean region (Purseglove, 1968; Harlan, 1975; Evans, 1980; Vargas et al., 1990; Gepts and Debouck, 1991; CIAT, 1995). Hence, it is divided into two major genepools, the Middle American and Andean genepools.

According to Evans (1973; 1980), genetic diversity in white pea beans may be organised into three general classes according to seed size namely, the large-seeded (>40g 100-seed weight), Andean genepool and the medium (25-40g100-seed weight) and small (<25g 100-seed weight) seeded Middle American genepool. The presence of two genepools is evidenced by differences in seed size (small versus large),"Dl" genes and F_1 incompatibility (Gepts and Bliss, 1985; Vieira et al., 1989), phaseolin seed proteins (Gepts et al., 1986), allozymes (Koenig and Gepts, 1989; Singh et al., 1991c) and DNA markers (Becerra Velasquez and Gepts, 1994; Haley et al., 1994). Within these genepools, landraces sharing certain distinctive morphological, agronomic and adaptive traits, and differing from other groups in allelic frequencies of the genes controlling differences in those traits were defined as races by Singh et al. (1991a). Singh et al. (1991a; 1991b) further divided the Andean and Middle American cultivated genepools into six races: Andean (Chile, Nueva Granada and Peru; large-seeded) and Middle American (Durango and Jalisco; all medium-seeded and Mesoamerican; all small-seeded), based on ecological adaptation and agronomic traits. Beebe et al. (2000) further reported the existence of additional diversity within Middle American races, especially a group of Guatemalan climbing bean accessions that did not group with any of the previously defined races.

Nine major commercial seed types/market classes are grown in Africa. These include the Calima (Rosecoco or red mottled) and the reds (large and small), which together account for about 50% of the production, primarily because of their high market demand. Others are the navy beans, cream-coloured, brown tan, yellow types, purples, white and black beans (Buruchara, 2006).

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2.3. Combining ability and relative contribution of GCA and SCA

2.3.1 Combining Ability

Griffing (1956) defined diallel crosses, which has been extensively used in plant breeding. However, general and specific combining ability effects are commonly based on the average effect of the parent when it is used as a female or a male in its hybrid combinations assuming that they are likely to be similar as proposed by Yates (1947). Griffing's methods 1, where crosses and their reciprocals are included, the fixed models, only one GCA effect value for each parent and one SCA effect value for each cross combination are estimated. These estimated effects do not, separately, show the contribution of each parent to the cross combination when this particular parent is used as a male or, alternatively, female.

The diallel mating design, that produces all possible single crosses among a set of inbred lines, developed by Sprague and Tatum (1942), has been widely utilized to provide information on the potential of parents involved in hybrid combinations as well as inferences on genetic control of the traits under investigation. It is an important tool, which aids in statistically separating progeny performance in to components relating to general combining ability (GCA), and specific combining ability (SCA).

Several methods for analyzing the data from a diallel cross have been developed and utilized in a variety of crops. Of these, the most widely used are the methods of Hayman (1954), Griffing (1956), Morley-Jones (1965), Gardner and Eberhart (1966), and Walters and Morton (1978). Nevertheless, some issues are still perplexing with respect to the choice of design (including or excluding parents and/or reciprocal F_1 crosses), type of analysis to be applied, and the nature of the population studied (random or fixed model) (Wright, 1985). Various authors have provided thorough examinations of some critical issues in diallel analysis. The assumptions (homozygous parents, diploid segregation, absence of epistasis or non-allelic interactions and no multiple alleles) required for the genetic interpretation of diallel experiments were evaluated in relation to self-pollinating crops. Sokol and Baker (1977) assessed the consequences of absence of these assumptions. Baker (1978), Singh and Paroda (1984), Pooni *et al.* (1984), and Wright

(1985) have compared the various methods of diallel analysis proposed by earlier workers with respect to interrelation and advantage and disadvantage of each method.

Despite the weakness noted in its validity (applicable to only inbred parents i.e. inadequate when parents are heterozygous as in cross pollinated crops, inability to illustrate heterosis and other allied genetic parameters), the method of Griffing (1956) seems to be preferred and continues to be popular. It has been utilized in a wide range of crops as it lends itself to considerable flexibility regarding the choice of model (fixed or random), inclusion and omission of self's or reciprocals (methods I-IV). The four methods of Griffing (1956) have usually been used to obtain genetic information on the basis of data of only one year at one location, although multiple environment data were suggested to provide more reliable genetic information about the material tested (Zhang and Kang, 1997). In addition, the diallel cross technique was reported to provide early information on genetic components in the first (F_1) generation (Chowdhry *et al.*, 1992).

Combining ability refers to the capacity or ability of a genotype to transmit superior performance to its crosses. Combining ability, which is the ability to give high yield in hybrid combination, has been shown by various workers to be an inherited character. Sprague and Tatum (1942) using diallel crosses of maize inbred lines categorized gene actions into two based on the types of combing ability i.e., General combining ability, (GCA) and specific combining ability, (SCA). General combining ability is the average performance of a line or genotype in a series of cross combinations. The performance of parents in a specific cross in relation to the average performance of all combinations is known as specific combining ability. General combining ability corresponds to additive genetic variance, while specific combining ability indicates non-additive gene actions, which includes dominance and epistasis.

The term additive gene action is used to denote those gene effects in heterozygotes, where every dominant gene (allel) contributes a unit increment without affecting the other dominant allel at another locus. In such cases, the heterozygotes, perform exactly intermediate between the two homozygotes, with respect to a particular character. Dominance refers to a type of gene action, where the heterozygote deviates from the mid-parent value. Epistasis refers to a condition where two or more gene loci (non allelic genes) interact to determine the performance of a genotype.

Before embarking on any improvement program, genetic information regarding the inheritance of quantitative characters, particularly the nature and magnitude of gene action governing the inheritance of the character should be determined. Results of several investigators of combining ability analyses for seed yield, yield components and architectural traits in common beans demonstrated that both additive and non-additive types of gene actions are important in the inheritance of these traits (Foolad and Bassiri, 1983; Vaid *et al.*, 1985; CIAT, 1987). However, the additive gene action was more important than the non-additive components for most traits (Vaid *et al.*, 1985; Wassimi *et al.*, 1986; Nienhuis and Singh, 1986; 1988). On the contrary, the importance of non-additive gene action (Foolad and Bassiri, 1983; Singh and Saini, 1983) was reported for some traits including seed yield.

A study on the combining ability in common beans utilizing F_1 hybrids of eight varieties showed significant GCA (P≤0.01) for days to flowering and days to maturity, plant height, number of pods per plant, number of seeds per plant, number of seeds per pod, pod diameter, pod length and 100-seed weight, but non-significant for seed yield per plant. In addition to GCA, specific combining ability was also significant (P≤0.05) for days to flowering and maturity, pod length, pod diameter and number of seeds per pod, implying that both additive and non additive types of gene actions are important for these traits, although the magnitude of additive gene action was higher than non-additive type of gene action (Melaku, 1993).

In a combining ability analyses involving bean lines with different growth habit Nienhuis and Singh (1986) found that GCA were significant for seed yield per plant, number of pods per m^2, number of seeds per pod, seed weight, and architectural traits, whereas SCA was significant for all traits studied except seeds per pod. Although the magnitude of GCA was greater than SCA, both additive and non-additive types of gene actions were important in the inheritance of most of the traits studied. Similarly, the result presented by Vaid *et al.* (1985) indicated that both GCA and SCA mean squares were significant for days to flowering and maturity, plant height, number of branches and pods per plant, pod length, number of seeds per pod, 100-seed weight and yield per plant in F_1 crosses of *Phaseolus vulgaris* L.

In a 7 x 7 diallel cross of French bean, Singh and Saini (1982) reported that both additive

and non-additive gene actions were important in the inheritance of the traits studied i.e., plant height, pod length, pod diameter, number of pods per plant, number of seeds per pod, 100-seed weight and seed yield per plant. However, in general, GCA was more important than SCA for all the characters as its magnitude was greater. In an experiment involving a 9 x 9 complete diallel cross that was conducted at CIAT at two locations (CIAT, 1984) also, GCA was more important than SCA for yield, yield components (pods per m^2, seeds per pod, seed weight) and architectural traits.

In a 5 X 5 diallel analysis of Snap bean (*Phaseolus vulgaris* l.) varieties for some important traits i.e., days to flowering, plant height, number of pods per plant, pod weight per plant, pod length, and pod diameter Arunga, Van Rheenen and Owuoche, (2010) reported that both additive and non additive gene effects were involved in the genetic control of the traits investigated which implies that both gene effects should be considered when developing breeding schemes for the selection of superior lines. Consequently, both parents need not necessarily have high GCA during breeding because the dominance gene effects could also be exploited to enhance these traits.

A report by Navale and Patil (1982) indicated that inheritance of yield and other traits such as days to flowering and maturity, number of seeds per pod, number of pods per plant and 100-seed weight was governed mainly by non-additive gene action in *Phaseolus vulgaris* L., as indicated by high heritability values, but low predicted genetic advance.

2.3.2. Relative contribution of GCA, SCA, Reciprocal cross, maternal effects, and non maternal effects.

Partitioning of the general and specific combining ability effects would provide additional information about each parent, when it is used as a female or a male in its hybrid combinations (Mahgoub, 2004). It should, also provide precise information about the nature of the interaction between the best combinations among parents. The relative contribution of GCA, SCA, reciprocals, maternal and non-maternal cross effects is defined as the proportion of sum squares of GCA, SCA reciprocals, maternal and nonmaternal cross effects to sum squares of GCA, SCA, reciprocals (REC), maternal (MAT), and nonmaternal (NMAT) cross effects (Ekiz and Konzak, 1991).

Foolad and Bassiri (1983) reported significant GCA and SCA effects in a daillel analysis of four bean cultivars belonging to two commercial groups for yield and yield related traits, except for number of seeds per pod. However, the SCA effect was predominant for seed yield, number of pods per plant and seeds per plant; while GCA was more important thean SCA for 100-seed weight and number of days to flowering.

3. MATERIALS AND METHODS

3.1. Description of the Study Area

The experiment was conducted in the experimental field of Jimma Agricultural Research Center. Jimma is located in the South West of Ethiopia at about 355 km from Addis Ababa, and Jimma Agricultural Research Center is 14km away from Jimma town. The area is characterized by one long rainy season (May to October) with mean annual rainfall of 900-1754 mm, and an altitude of 1750 m.a.s.l. The minimum and maximum air temperature for the area is $11^{o}C$ and $26^{o}C$, respectively.

3.2. Experimental Materials

The experiment consisted of 49 materials, i.e., seven parents which were introduced commercial white pea bean varieties, 21 F_2 forward crosses and 21 F_2 reciprocals crosses between the parents produced in a diallel cross fashion. The varieties have been selected based on their performance in yield trials.

Seven white pea bean inbred lines were used as parents in crossing. The selection of parental lines was mainly based on their observed yield potential, some qualitative traits including quality of seed and distinct morphological characteristics. Crossing was made among the seven parents in all possible combinations in a full diallel fashion at Jimma agricultural research center.

Full diallel (including reciprocals) were produced at Jimma Agricultural Research Centre during August to September 2011/12 during the rainy period, and furrow irrigation was provided when the rain stopped, October to November 2011/12. Artificial polination was conducted in the morning (7:00 AM to 10:00 AM). Plants were hybridized using emasculation with protected rubbing or hook methods where the fertilized stigma of the male parent that carried ample pollen was hooked onto the stigma of the female parent. Sepals were kept intact to protect the bud, and pollination quickly followed (CIAT, 1977).

Table 1. Description of the parental lines for the 7x7 diallel crosses of white pea bean

Parents	Status/Origin	Seed color	Seed shape	Seed size	Growth habit
Avanti	Introduced variety	White	Elround	Small	Ind. bush
OR-04-DH	Introduced variety	White	Round	Medium	Ind. bush
ARGENE	Introduced variety	White	Round	Medium	Ind. bush
ER-04-AJ	Introduced variety	White	Round	Medium	Ind. bush
TA-04-JI	Introduced variety	White	Round	Medium	Ind. bush
Crest wood	Introduced variety	White	Elongated	Medium	Ind. bush
Starlight	Introduced variety	White	Elongated	Medium	Ind. bush

Ind. bush = Indeterminate bush, Ind. prost = Indeterminate prostrate.

3.3. Experimental Design and Field operations

Seeds of the seven parental genotypes and their 42F$_2$s that were obtained from controlled crossing were sown in seedbed during mid August. The experiment was laidout in simple lattice design (SLD) with two replications. A spacing of 40 cm between rows was used to facilitate supplemental irrigation, and plants were spaced 20 cm apart within the row. To ascertain full stand in a plot, two seeds per hill were planted and thinned to appropriate stand 10 days after emergence. A plot of four rows each 4 m long (1.6X4m) were used, and 100 kg/ha DAP fertilizer was applied at the time of planting. All necessary agronomic practices were done uniformly as per the recommendations.The correct stand count (80 plants per plot) was maintained after thinning. Stand count at harvest was also done.

3.4. Data collected

Data was recorded on plot and single plant basis for the following parameters to represent their respective characters.

3.4.1 Data collected on plot bases

1. **Days to 50% flowering (DFPF):** The number of days from emergence to the stage when 50% of the plants in a plot had one or more flowers.

2. **Days to maturity(DM)**: The number of days from emergence to the stage when 75% of the plants in a plot reached physiological maturity, i.e., the stage

at which pods loose their pigmentation and began to dry.

5. **Grain yield per plot (g):** The seed yield in grams harvested from the plot.

6. **100 Seed weight (g):** Sample of 1000 seeds were taken from the plot and weighed.

    This figure was multiply by 10 to obtain 1000-seed weight.

3.4.2. Data collected on individual plant basis

1. Plant height (PH)(cm): The average height of five randomly selected plants in centimeters measured from the soil surface to the top of the canopy of the plant.

2. **Pod length (PDL) (cm):** The length of 5 randomly taken pods from each of the 5 randomly selected plants

3. **Pod diameter (PDD) (cm):** The diameters of the 5 randomly selected pods from each of 5 randomly selected plants were measured using caliper.

4. Number of nodes on the main axis (NNMA): The number of nodes on the main axis of 5 randomly selected plants was counted.

5. **Internodes length (INL):** The distances between any two successive nodes on the main axis of five randomly selected plants were measured.

6. **Number of branches on the main axis (NBMA):** The numbers of branches on the main axis of 5 randomly selected plants were counted.

7. Number of pods per plant (NPPT): The numbers of pods on 5 randomly selected plants were counted.

8. **Number of seeds per pod (NSPPD):** The seeds of five randomly selected pods from each of 5 randomly taken plants were counted.

9. **Number of seeds per plant (NSPPT):** The number of seeds on 5 randomly selected plants will be counted.

11. Tap Root Length (TRL) (cm):- Tap Root length of ten randomly selected plants was measured from the crown of the plant to the final tip of root at the harvestable stage pods from each plot and the values were averaged.

12. Root Volume (RV) (ml):- Root volume of ten randomly selected plants was measured at final harvest by water displacement method.

13. Leaf Area per Plant (LA) (cm^2/plant):- Leaf area of five randomly selected plants were measured using square paper measurement to measure the leaf length and leaf breadth and then measured actual area by counting the number of squares and multiplying by 0.5 cm and measured estimated area by multiplying leaf breadth and leaf length in cm then dividing the actual to estimated area to get the constant k. Thus the constant number is multiplied with individual estimated area to get the recommended areas at final harvesting stage.

14. Fresh Root Weight (FRWT) (g): - The root weights of five randomly selected plants were measured using a sensitive balance**.**

15. Root dry weight (RDWT) (g) :-five sample plants were taken for determination of root dry weight and dried in an oven at 70°C to a constant weight.

16. Biomass fresh weight (BFWT) (g):-The shoot weight of five randomly selected plants was measured using sensitive balance**.**

17. Biomass dry weight (BDWT) (g): - five sample plants were taken for determination of shoot dry weight. After taking the fresh weight of shoots, the samples were dried in an oven at 70°C to a constant weight.

17. Pod fresh weight (PFWT) (g):-The pod fresh weight of five pods per plant was measured using sensitive balance.

18. Pod dry weight (PDWT) (g):-five sample pods per plant were selected randomly for determination of fresh and dry weight. After taking fresh weight of pods, the samples were dried in an oven at 70°C to a constant weight.

19. Seed length (mm):-The average length in millimeter of 10 seeds from five plants each measured parallel to the hillium using vernier caliper.

20. Seed thickness (mm):- Average thickness in millimeter of 10 seeds measured parallel to the seed diameter using vernier caliper.

21. Nodule count (NUCNT):- At 50% flowering stage nodule count was made from randomly selected five plants from each plot.

22. Effective nodule weight (ENUWT) (g):- When the fields was sufficiently dried for field operation, crop roots were carefully recovered, total nodule weight and effective nodule weight (pink-red in color) were weighed with a sensitive balance.

23. Total nodule weight (TNUWT) (g):- The number of nodules per plant was weighed in sensitive balance

24. Disease severity was assessed for common bacterial blight, angular leaf spot, rust, and floury leaf spot by making observations of the stem and leaf tissue using rating SCAle based on the 1-9 SCAle developed at CIAT (Abawi and Pastor Corrales, 1990), where:

- 1-4 = resistant

- 5-6= tolerant

- 7-9= susceptible

3.5. Data Analysis

3.5.1. Analysis of variance (ANOVA)

The data was subjected to ANOVA following the standard procedures provided by Steel and Torrie (1980). Analysis of variance (ANOVA) of each character was carried-out using mean values of the 42 F_2 progenies and their seven parents to know the variation among the 49 entries using SAS computer software.

3.5.2. Combining ability analysis of parents and crosses

3.5.2.1. Griffing's method one, model one

Diallel analysis was carried out according to Griffing (1956) Method one, Model one

(Random Model), which involved parents and one-way F2 hybrids (including reciprocals). Griffing portioned the total sum of squares due to the genotypes with $p(p-1)/2 - 1$ degree of freedom into sum of squares due to GCA with $p-1$ degree of freedom and sum of squares due to SCA with $p(p-1)/2$ degree of freedom. Here the experimental material itself was the population about which inferences were drawn and hence the estimates obtained from the analysis were applied to those genotypes only. Combining ability analyses was carried out using SAS computer software.

Relative importance of GCA, SCA, and the reciprocal cross effects were computed as a proportion of cross effects sum squares. Similarily relative importance of maternal and nonmaternal effects was computed as a proportion of reciprocal cross effects sum of squares.

3.5.2.1.1. Estimation of combining ability variances

Table 2. Analysis of variance for Griffing's method I, model I

Source	D.F.	Sum of Squares	Mean squares	Expectation of Mean Squares Model I
General combining ability (GCA)	p-1	S_g	M_g	$\sigma^2 + \dfrac{2(n-1)\sigma_s^2}{n} + 2n\sigma_g^2 + 2r$
Specific combining ability (SCA)	p(p-1)/2	Ss	Ms	$\sigma^2 + \dfrac{2(n^2 - n + 1)\sigma_s^2}{n^2}$
reciprocal		S_r	M_r	$\sigma^2 + 2\sigma_r^2$
Error	(r-1) ((p(p+1)/2)-1)	Se	Me'	σ^2

Mg = Mean square of GCA, represents additive gene action

Ms = Mean square of SCA, represents non-additive gene action

Me = Mean square of error

$$S_g = \frac{1}{p+2}\left(\sum_{i=1}^{p}(x_i + x_{ii})^2 - \frac{4}{p}x^2_{..} \right)$$

$$S_s = \sum_{i}^{p}\sum_{j}^{p}x_{ij}^2 - \frac{1}{p+2}\sum_{i=1}^{p}(x_i + x_{ii})^2 + \frac{2}{(p+1)(p+2)}x^2_{..}$$

Where:

Sg = Sum of square of general combining ability

Ss = Sum of square of specific combining ability

p = Number of parents

Xi. = the sum of the ith array X.. = Grand sum

xii = The value for the ith parent

xij = The value of the cross between the ith male and jth female

Combining ability was computed using the mathematical model:

$$x_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\sum_k\sum_l e_{ijkl} \begin{cases} i.j = 1,...,p, \\ k = 1,...,b, \\ l = 1,...,c. \end{cases}$$

Where μ is the population mean, gi (gj) is the g.c.a. effect, sij the s.c.a. effect, such that sij = sji, and eijkl is the effect peculiar to the ijklth observation, p,b and c are number of parents, blocks and sampled plants. The restrictions

$$\sum_i g_i = 0, and \sum_j s_{ij} + s_{ii} = 0 \text{ for each i are imposed}$$

Where Sij is specific combining ability of a cross between the ith and jth parent and Sii is the specific combining ability of a parent selfed.

Such linear model for analysis of variance helps to determine whether there is a significant difference among the genotypes tested using the F – ratio as:

$$F = \frac{MSv}{MSe}$$

If the effect of genotypes is significant, the sum of squares due to genotypes will be partitioned in to GCA, SCA and reciprocal effects. Then the additive leaner model for diallel analysis can be written as:

$$\times_{ij} = \mu + g_i + S_{ij} + r_{ij} + \sum\sum e_{ijkl} / bc$$

g = GCA

S = SCA

r = reciprocal effects

b = no. of blocks

c = no. of individuals

e = effects of environmental factors

μ = overall means

Diallel analysis is limited to the following conditions:

$S_{ij} = S_{ji}$ $\sum g_i = 0$

$r_{ij} = -r_{ij}$ $\sum S_{ij} = 0_i$

With such assumptions, the analysis was conducted as shown in Table 6.2.

Tests for significance of mean squares were made using F-test as:

$F_g = M_g/M_e$ for (p-1) and (r-1) ((p(p+1)/2)-1) degree of freedom

$F_S = M_S/M_e$ for $p(p-1)/2$ and $(r-1)$ $((p(p+1)/2)-1)$ degree of freedom

3.6.2.1.2. Estimation of general (gi) and specific (sij) combining ability effects

Estimation of general combining ability effects (g_i) was done as follows:

$$g_i = \frac{1}{(P+2)}\left(\sum(x_i + x_{ii}) - \frac{2}{p}x_{..}\right)$$

Where,

g_i = GCA effect for the ith parent

Estimation of specific combining ability effects (s_{ij}) was computed as:

$$S_{ij} = x_{ij} - \frac{1}{(p+2)}\left(x_i + x_{ii} + x_j + x_{jj}\right) + \frac{2}{(p+1)(p+2)}x_{..}$$

Where,

S_{ij} = SCA effect for ij cross

Tests of significance of the combining ability effects and their differences was made using t-test

3.6.3.1.3 Standard error of the estimates

Standard error of the estimates of GCA effects (SE(g_i)) and SCA effects (SE(s_{ij})), their differences and their respective 't' values were calculated as:

$$SE(g_i) = \frac{p-1}{p(p-2)}Mse$$

$$SE(g_i - g_j) = \frac{2}{p+2}Mse \quad i \neq j$$

$$SE(S_{ii}) = \frac{p(p-1)}{(p+1)(p-2)}Mse$$

$$SE(S_{ij}) = \frac{p^2 + p + 2}{(p+1)(p+2)}Mse \quad i \neq j$$

$$SE(s_{ii} - s_{jj}) = \frac{2(p-2)}{p+2}Mse$$

$$SE(S_{ij} - S_{ik}) = \frac{2(p+1)}{p+2}Mse \quad (i \neq j, k, j \neq k)$$

$$SE(S_{ij} - s_{kl}) = \frac{2p}{p+2}Mse \quad (i \neq j, k, l; j \neq k, l; k \neq l)$$

3.6.2.1.4. Test of significance of GCA and SCA effects

Each GCA and SCA effect was tested against zero for its significance by t-test.The t-value was calculated as follows.

$$t(g_i) = \frac{g_i}{SE(g_i)} \qquad \text{(at error degree of freedom)}$$

$$t(g_i - g_j) = \frac{g_i - g_j}{SE(g_i - g_j)} \qquad \text{(at error degree of freedom)}$$

$$t(s_{ii}) = \frac{s_{ii}}{SE(s_{ii})} \qquad \text{(at error degree of freedom)}$$

$$t(s_{ij}) = \frac{s_{ij}}{SE(s_{ij})} \qquad \text{(at error degree of freedom)}$$

$$t(s_{ii} - s_{jj}) = \frac{s_{ii} - s_{jj}}{SE(s_{ii} - s_{jj})} \qquad \text{(at error degree of freedom)}$$

$$t(s_{ij} - s_{ik}) = \frac{s_{ij} - s_{ik}}{SE(s_{ij} - s_{ik})} \qquad \text{(at error degree of freedom)}$$

$$t(s_{ij} - s_{kl}) = \frac{s_{ij} - s_{kl}}{SE(s_{ij} - s_{kl})}$$

Where p is the number of parents, Mse is the mean square of error, g_i is the GCA effect and s_{ij} is the SCA effect and the calculated t-values was tested against the tabular t-value at error degree of freedom. Genetic components: Considering the expectation of mean squares for method one model one, the estimates of the components were computed as:

Component due to GCA

$$\frac{1}{P-1}\sum g\overset{2}{i} = \frac{Mg-Me}{P+2}$$

Component due to SCA

$$\frac{2}{p(p-1)}\underset{i<}{\sum\sum}S_{ij}{}^{2}$$

The predominance of additive versus non-additive gene action were compared from the ratio of components of GCA variance to SCA variance as:

$$\frac{\dfrac{1}{p-1}\sum g_i{}^2}{\dfrac{2}{p(p-1)\displaystyle\sum_{i<}\sum_{j} Sij^2}} = \frac{\dfrac{Mg-Me}{p+2}}{Ms-Me}$$

4. RESULT AND DESCUSSION

The evaluation of 7 X 7 full diallel cross including reciprocals among seven released genotypes of white pea bean conducted at Jimma zone (Jimma Agricultural Research Center) are presented in the following sections.

4.1. Analysis of variance (ANOVA)

Analysis of variance (ANOVA) for 28 traits studied in the experiment is presented in Table 3. Highly significant (P<0.01) differences were found among the entries for number of branches on the main axis, plant height, tap root length, root fresh weight, root dry weight, biomass freshweight, biomass dry weight, root volume, 100-seed weight, grain yeild, number of pods per plant, number of seeds per plant, pod length, pod diameter, seed length, seed diameter, seed thickness, pod fresh weight, pod dry weight, total nodule weight, effective nodule weight, nodule count, and leaf area. While significan (P<0.05) mean squares were exhibited for internode length. This finding is similar with the finding of Arunga *et al*. (2010) who reported highly significant (P<0.001) mean squares among 25 genotypes for days to flowering, plant height at flowering, number of pods per plant, pod weight per plant, pod length, and pod diameter in snap bean. Machoda *et al* (2002) also reported similar result that highly significant mean squares for grain yield in F2 segregating population in a 9 X 9 diallel cross in common bean.

Crosses Avanti X OR-04-DH, Argane X OR-04-DH, and ER-04-AJ X OR-04-DH exhibited the longest days to flowering, while Avanti X Starlight and OR-04-DH X Starlight had the shortest days to flowering of 34 days (Table 5). The crosses ER-04-AJ X TA-04-AJ had the longest maturity date; while TA-04-AJ X Crest wood had the shortest days to maturity. This implies that crosses which displayed early maturity can be further evaluated for their performance in areas of short rainy season and moisture stress areas, where early maturity is an advantage. In areas such as Jimma, where relatively long growing period prevails, long maturing materials may still perform well and selected for better adaptability.

Parents Avanti, Argane, ER-04-AJ, and Crestwood had the longest internode length; while several crosses were among the highest internode length producing entries. However, crosses TA-04-AJ X Starlight, Avanti X ER-04-AJ, TA-04-AJ XArgane, Argane X ER-

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04-AJ, and ER-04-AJ X Argane were the top five crosses for internode length. These crosses had also the largest number of branches on the main axis. The widest leaf area was observed in crosses TA-04-AJ X Starlight and Crest wood X Avanti; while the largest number of nodes on the main axis was observed in the crosses ER-04-AJ X Crestwood and TA-04-AJ X OR-04-DH.

Crosses OR-04-DH X ER-04-AJ, Avanti X TA-04-AJ, OR-04-DH X TA-04-AJ, and Argane X Avanti had the longest plant height, while parents Crestwood and Starlight produced the highest mean values for 100-seed weight. The cross TA-04-AJ X Starlight had the highest grain yield (3621 gm/plot). The next high yielding crosses were OR-04-DH X ER-04-AJ, OR-04-DH X Crest wood, OR-04-DH X Starlight, Argane X Starlight, ER-04-AJ X Avanti, ER-04-AJ X TA-04-AJ, Crestwood X Avanti, and Starlight X Argane. Crosses TA-04-AJ X Crestwood and ER-04-AJ X TA-04-AJ had the highest number of pods/plant of 89.06 and 76.33 respectively; while parents with the highest number of pods per plant were Avanti and ER-04-AJ. The cross ER-04-DH X TA-04-AJ had the largest number of seeds per plant. The cross Avanti X Starlight had the highest number of seeds per pod. Crosses Avanti X Starlight and Argane X Starlight had the longest pod length. In addition, these crosses had also the highest pod diameter, seed length, seed diameter, and seed thickness.

Several crosses produced very high mean performance for biomass fresh weight, of which crosses OR-04-DH X Avanti, ER-04-AJ X Crestwood, Avanti X TA-04-AJ, and Argane X Avanti were the top four. Crosses Argane X Avanti, ER-04-AJ X Avanti, and Starlight X ER-04-AJ produced the highest biomass dry weight. The cross Avanti X Starlight had the largest pod fresh weight and root fresh weight. However, the Avanti X TA-04-AJ had the largest pod dry weight eventhough it had the smallest pod fresh weight.

The cross Crestwood X OR-04-DH had the highest nodule weight. While the highest effective nodule weight was observed in cross Avanti X OR-04-DH. The largest nodule count were observed in the cross Argane X Starlight. This implies that these crosses with the highest nodule count and effective nodule weight were important for soil fertility. Crosses Avanti X Argane and Starlight X Argane had the highest root volume. While the longest tap root length (35cm) was observed in the cross Avanti X OR-04-DH. Entries with such root traits have advantages in the uptake of moisture and soil nutrients from

deep soil surface, thereby, enabling them to adapt better to soil and misture stress. Similar findings were also reported by Araujo et al. (2005) that the erect common bean cultivar ICA Pijao had a strong root growth, with higher taproot mass and total root mass than prostrate cultivars. The author also reported that cultivar ICA Pijao had also a higher root area and root length, mainly due to its larger basal plus lateral root mass.

The analysis of variance for major foliar diseases (Table 4) obtained for common bacterial blight, angular leaf spot, leaf rust, and floury spot severity using the two rating SCAles used in this study, that is , the 1-9 scales (non transformed data) and the transformed data. Both the rating scales might be used to deffereniate between the bean lines according to resistance to common bacterial blight, angular leaf spot, leaf rust, and floury spot severity. However, discussion is based on the 1-9 scales data which is not transformed, as it was used in selecting resistance lines; however the transformed data is also presented, because it had lower CVs.

All the crosses had mean values ranging from the minimum 0.816 non transformed to the maximum 4.843 non transformed for common bacterial blight. The crosses Starlight X Crestwood is the most resistant cross for this disease as it had the minimum mean value that is 0.816 non-transformed. This implies that all those crosses and genotypes are resistant to common bacterial blight severity. There fore, all these crosses and genotypes are grouped in resistant to common bacterial blight severity. All these crosses and genotypes are also resistant to Angular leaf spot severity as they had the mean values ranging from -0.264 non-transformed to 3.67 non-transformed. The cross OR-04-DH X Argane had the minimum mean value -0.264 non-transformed and is the most resistant to angular leaf spot severity. Thus, all these crosses and genotypes are also grouped in resistant to Angular leaf spot severity.

Crosses Avanti X Crestwood, OR-04-DH X ER-04-AJ, ER-04-AJ X Crestwood, TA-04-AJ X ER-04-AJ, Crestwood X Avanti, and Starlight X Argane had mean values ranging from 5.177 to 6.243 (mean values having 5 to 6 are tolerant) for leaf rust severity. Thus, these crosses are grouped under tolerant varieties for resistance to leaf rust severity. Crosses such as Argane X ER-04-AJ had mean values 7.599 for resistance to leaf rust severity. This implies that these crosses are grouped under susceptible to leaf rust severity. This suggests that varieties having mean values ranging from 7 to 9 are susceptible

varieties. And varieties having mean values ranging from 5 to 6 are grouped under tolerant varieties and varieties having mean values ranging from 1 to 4 are resistant varieties for these disease severities. The crosses Crestwood X Starlight is the most resistant cross for leaf rust severity as it had the minimum mean values, which is,1.861 for resistance to leaf rust severity. Crosses having mean values ranging from -1.0787 to 2.5270 are resistant to floury leaf spot severity. This implies that all these crosses are resistant for this disease severity. However, the cross Starlight X Crestwood is the most resistant cross for floury leaf spot as it had the minimum and negative mean vaues, i.e , -1.0787, for resistance to floury leaf spot severity.

Table 3. Mean squares due to genotypes and error for yield and yield related traits of 7*7 full diallel crosses of white pea bean (ANOVA)

Parameters	Replication	Genotype	Error
MD	39.22ns	101.77ns	88.73
DFPF	13.96*	4.39ns	2.51
NBMA	2.91	1.13***	0.43
NNMA	53.11	1.371ns	1.46
INL	25.68***	1.13ns	0.76
PH	81.00	323.60***	119.6
TRL	324.37	16.25**	7.45
RFWT	25.190	57.96***	8.35
RDWT	0.11	1.19**	0.61
BFWT	960	20701***	3982
BDWT	122.90	1460.60***	164.10
RV	210.69	62.79***	13.10
HSWT	45.53ns	56.87***	15.41
FOPWT	338590	396711***	104399
NPPT	21.14	316.91***	49.13
NSPPT	3516	3969***	1303
NSPD	5.70	0.71*	0.42
PDL	8.45	0.71***	0.23
PDD	0.09	0.02**	0.01
SL	0.00	2.22***	0.58
SD	0.02	0.47***	0.04
ST	0.02ns	0.10***	0.02
PFWT	0.40	1.31***	0.21
PDWT	0.05	0.32***	0.04
NUWT	4.28	2.80***	0.01
ENUWT	0.92ns	2.13***	0.08
NUCNT	489.31	772.91***	84.46
LA	2536.40	355.50**	124.60
Degree of freedom	1	48	48

Table 4: Analysis of variance (ANOVA) for angular leaf spot, common bacterial blight, rust, and floury leaf spot severity

Sources of variation	DF	Mean squares (1-9 scale)			
		ALS	CBB	Rust	FLS
Rep stratum	1	0.03(0.03)	0.03ns(0.03)	40.07***(1.94)	0.02ns(0.00ns)
Entries	48	1.04(0.11)	1.52ns(0.15)	2.98*(0.15)	0.83ns(0.12)
Residual	36	0.81(0.08)	1.25(0.13)	1.59(0.08)	0.87(0.13)
Total	97	1.14(0.12)	1.31(0.13)	2.86(0.15)	0.85(0.13)

Where; *=Significant at 0.05, **=highly significant at 0.01, ***= highly significant at 0.001, ALS=Angularleafspot, CBB=common bacterial blight, FLS=Floury leaf spot

Table 5: Mean values of yield and yield related traits:

Crosses	HSWT (gm)	GY (gm)	NPPT	NSPPT	NSPD	MD	DFPF	INL	LA (cm^2)	NBMA	NNMA	PH (cm)
	19.89	1000	45.30	152.9	3.402	94.20	39.21	6.223	63.6	5.000	10.50	79.7
1 × 2	20.87	1299	25.40	157.8	4.512	97.03	41.94	4.242	73.2	8.828	11.10	83.6
1 × 3	22.41	1580.	36.00	167.3	4.652	105.05	40.12	7.243	65.6	5.400	10.60	78.9
1 × 4	18.29	1781.	47.86	145.4	4.092	92.83	37.52	8.089	68.8	4.200	10.60	86.3
1 × 5	15.19	1700.	39.00	196.4	5.006	96.21	39.21	7.619	82.3	5.200	11.50	118.3
1 × 6	18.35	1335	37.40	138.8	3.752	110.02	36.91	7.093	68.3	4.600	11.70	81.3
1 × 7	37.85	1405	19.10	78.0	5.728	106.35	33.69	7.021	73.3	4.000	9.70	102.3
2 × 1	18.39	1686	45.90	241.5	5.215	94.44	37.73	6.679	76.2	5.600	11.30	89.2
2 × 2	19.29	1285.	29.80	126.3	4.290	104.20	39.76	5.917	60.6	4.600	9.50	93.6
2 × 3	15.48	1341	41.10	289.6	6.199	83.30	39.44	6.262	84.7	4.300	11.10	96.6
2 × 4	20.08	2110.	34.30	145.8	4.335	96.39	36.25	7.287	73.4	5.200	11.30	120.7
2 × 5	18.63	1445.	36.80	127.3	3.517	97.65	40.37	5.982	65.0	5.600	10.50	114.7
2 × 6	20.71	1886.	51.33	197.7	5.221	99.17	40.08	5.741	86.5	6.000	10.10	103.1
2 × 7	27.56	2044	34.20	133.2	3.880	95.68	33.87	6.537	59.9	4.100	9.86	90.5
3 × 1	23.99	1320	52.73	147.2	4.013	98.38	38.65	6.747	44.9	5.400	10.90	113.3
3 × 2	21.76	1300	31.10	107.0	3.442	102.70	41.52	7.373	61.1	4.900	11.50	71.3
3 × 3	20.47	1748.	34.60	158.5	4.624	105.44	37.02	6.514	66.1	4.300	10.60	73.1
3 × 4	15.91	1250	34.70	129.4	3.736	92.54	37.90	7.904	58.3	4.400	9.00	82.4
3 × 5	14.33	875	24.70	136.2	4.344	92.02	39.79	7.231	55.1	4.400	11.10	89.3
3 × 6	15.55	1371	34.10	158.6	4.684	100.91	36.22	6.094	80.2	4.000	10.70	83.5
3 × 7	26.01	2441	30.60	139.1	4.542	106.14	39.21	6.926	60.2	5.500	11.20	93.4
4 × 1	17.48	1800	34.50	240.2	4.814	93.10	36.73	6.623	62.3	5.300	10.40	89.5
4 × 2	15.12	1375	34.70	155.3	4.487	95.44	41.16	6.408	64.9	4.900	11.10	105.1
4 × 3	16.30	1200.	37.20	148.1	4.872	96.66	38.80	7.881	67.3	5.800	9.90	78.0
4 × 4	16.67	1078	39.70	163.4	4.116	108.09	39.95	7.388	75.9	5.200	11.20	91.3
4 × 5	25.93	1809.	76.33	314.2	4.326	112.54	39.02	6.206	76.0	5.400	10.60	69.2
4 × 6	13.65	1200	29.30	125.8	4.416	94.90	38.26	5.056	79.2	5.300	13.26	109.1

Table 5 (continued)

4 × 7	36.24	1520	21.80	96.4	4.389	83.94	35.20	7.274	72.3	4.100	9.70	93.9
5 × 1	18.07	1441	34.40	130.9	3.992	82.51	34.39	6.722	53.3	4.400	8.80	70.3
5 × 2	16.56	1257.	25.00	105.4	4.233	96.24	38.55	5.840	62.3	5.300	12.00	100.7
5 × 3	24.84	1300	49.66	136.5	4.859	95.92	35.76	8.030	78.7	4.400	11.50	97.6
5 × 4	16.20	1505.	38.20	172.3	4.592	103.41	37.89	6.980	69.9	4.600	10.20	82.0
5 × 5	14.34	1511	28.70	115.0	4.008	89.37	39.32	5.819	82.5	4.800	10.80	80.2
5 × 6	18.34	1175	89.06	163.0	3.101	55.5	38.13	6.535	87.1	5.100	11.40	87.7
5 × 7	29.43	3621	38.00	170.3	4.527	107.12	34.40	8.189	112.6	4.800	11.20	93.2
6 ×1	18.49	1789	44.00	199.7	4.510	101.79	38.62	6.293	104.2	5.700	11.60	81.7
6 × 2	18.74	1365	41.30	140.4	3.428	95.06	37.17	5.896	78.3	4.700	10.90	80.0
6 ×3	15.62	1759	47.93	186.4	3.827	91.02	38.82	5.035	40.6	4.800	9.30	67.1
6 ×4	20.38	1168.	34.70	158.6	4.533	99.47	37.83	6.766	57.3	5.200	10.20	78.2
6 × 5	20.82	1421	39.10	170.9	4.360	95.51	35.37	6.585	82.6	4.700	10.60	81.8
6 × 6	42.36	1425.	24.60	124.0	4.242	94.06	37.83	8.579	65.4	5.628	11.40	87.6
6 ×7	16.21	1714	35.80	150.0	4.181	94.99	36.58	7.518	68.6	5.500	9.90	77.7
7 × 1	23.02	1158	32.30	144.4	3.828	105.39	37.65	7.701	56.4	5.000	10.20	76.5
7 × 2	27.16	1512	20.00	88.8	5.265	109.25	37.02	7.446	66.1	5.100	10.50	83.0
7 × 3	30.60	2045	27.80	127.4	4.646	103.60	36.43	7.303	80.9	5.300	10.80	90.5
7 × 4	31.32	1600	25.90	125.3	4.835	92.31	37.59	7.589	67.9	5.000	9.80	77.5
7 × 5	23.31	1659.	44.60	175.3	3.850	97.36	37.10	7.522	77.0	5.000	11.30	96.3
7 × 6	24.63	705	31.20	165.6	3.847	98.11	38.38	6.076	93.7	4.400	10.10	93.6
7 × 7	36.18	1601	23.40	141.4	4.309	101.24	40.11	5.283	72.2	5.000	9.70	83.5
C.V	18.16	21.1	18.9	23.2	14.9	9.69	4.17	12.91	15.7	13.1	11.3	12.3
S.E	5.218	323.1	7.009	36.10	0.6511	12.52	2.106	1.160	11.16	0.659	1.209	10.94
L.S.D	10.77	658.2	14.155	73.14	1.3149	25.84	4.347	2.395	22.51	1.326	2.434	22.20

1=Avanti,2=OR-04-DH, 3=Argane, 4=ER-04-AJ,5=TA-04-AJ, 6=Crestwood, 7=Starlight, HSWT=handred seed weight, GY=grain yield, NPPT=number of pod per plant,NSPPT=number of seed per plant, NSPD=number of seed per pod, DM=days to maturity, DFPF=days to 50% flowering, INL=internode length, lA=leaf area

Table 5: Mean values of yield and yield related traits (continued):

treatments	PDL	PDD	SL	Sd	ST
1 × 1	8.03	1.00	8.67	6.27	4.98
1 × 2	8.13	0.91	8.29	6.30	5.22
1 × 3	7.77	0.86	7.75	6.12	5.17
1 × 4	8.34	1.00	7.76	6.14	5.35
1 × 5	7.07	0.91	7.34	6.22	5.14
1 × 6	8.56	0.87	8.06	5.83	5.25
1 × 7	9.55	1.21	11.69	7.84	5.99
2 × 1	8.21	0.90	9.01	6.24	4.98
2 × 2	8.70	0.98	9.52	6.31	5.21
2 × 3	8.48	0.95	7.53	5.92	4.69
2 × 4	8.67	0.92	11.89	6.12	5.11
2 × 5	8.20	0.94	8.41	6.32	4.96
2 × 6	8.48	0.87	8.33	6.40	5.29
2 × 7	8.96	1.10	9.22	6.66	5.44
3 × 1	7.39	0.78	8.06	6.45	5.32
3 × 2	8.63	1.01	9.10	5.84	4.89
3 × 3	8.37	0.83	9.00	6.08	4.77
3 × 4	8.44	0.96	7.39	5.81	4.97
3 × 5	7.96	0.96	8.52	5.79	4.83
3 × 6	8.43	0.96	8.02	6.28	5.39
3 × 7	9.09	1.06	10.52	7.36	5.16
4 × 1	7.22	0.87	8.12	6.05	4.95
4 × 2	8.20	0.89	8.84	6.27	5.18
4 × 3	8.07	0.96	7.95	6.14	4.82
4 × 4	8.31	1.01	8.72	6.35	5.39
4 × 5	8.10	0.94	8.09	6.13	5.27
4 × 6	8.05	0.90	7.47	6.42	5.33
4 × 7	9.78	1.12	12.00	7.86	5.85
5 × 1	7.35	0.87	8.76	6.37	5.18
5 × 2	8.64	0.94	9.32	6.12	5.20
5 × 3	8.89	0.95	9.81	6.71	5.43
5 × 4	8.23	0.98	8.52	6.08	5.17
5 × 5	8.07	0.88	8.12	6.01	5.09
5 × 6	8.06	0.93	8.94	6.14	5.26
5 × 7	9.17	1.00	10.87	7.24	5.55
6 ×1	8.36	0.99	7.38	6.19	5.17
6 × 2	8.64	0.96	7.95	6.31	5.27
6 ×3	7.53	0.73	7.24	5.16	4.68
6 ×4	8.05	0.92	8.51	5.98	5.06
6 × 5	8.33	0.96	8.84	6.46	5.55
6 × 6	9.45	1.16	11.79	7.86	5.78
6 ×7	8.28	0.82	8.64	6.15	5.16
7 × 1	8.08	0.89	8.49	6.31	5.32
7 × 2	9.64	0.95	10.13	6.28	5.16
7 × 3	8.95	1.05	10.25	6.95	5.25
7 × 4	9.15	1.11	7.76	7.53	5.32
7 × 5	7.93	0.93	9.84	6.05	5.32
7 × 6	8.200	0.99	9.04	6.42	5.53
7 × 7	8.880	1.10	10.91	7.19	5.63
S.E	0.4824	0.09	0.76	0.20	0.16
L.S.D	0.9698	0.19	2.10	0.55	0.43
C.V	5.7	9.90	8.54	3.16	3.01

Where, PDL=pod length, PDD=pod diameter, SL=Seed length, SD=Seed diameter, ST=Seed thickness

Table 6: Mean values of Biomass accumulation

treatments	BDWT	BFWT	PFWT	PDWT	RFWT	RDWT
1 × 1	82.1	305.8	3.600	1.170	29.43	3.550
1 × 2	54.2	227.8	3.670	1.280	16.14	2.750
1 × 3	105.8	365.4	3.800	1.410	13.11	2.740
1 × 4	50.4	291.3	4.170	1.260	15.34	3.057
1 × 5	110.8	450.6	3.710	3.102	25.74	4.120
1 × 6	82.0	235.4	3.970	1.820	11.43	2.730
1 × 7	31.7	147.0	5.730	2.170	10.96	1.990
2 × 1	98.9	494.0	4.240	1.390	13.77	3.335
2 × 2	37.4	129.4	4.160	1.100	10.27	2.310
2 × 3	49.9	243.0	3.450	1.290	23.89	4.066
2 × 4	54.9	323.8	4.010	1.450	23.55	4.966
2 × 5	70.0	367.8	3.760	1.250	21.47	3.830
2 × 6	80.0	325.2	4.180	1.540	16.92	3.751
2 × 7	68.6	201.4	5.590	1.650	12.89	3.545
3 × 1	137.3	439.7	3.780	1.290	17.09	3.977
3 × 2	48.3	188.5	3.330	1.300	15.47	2.750
3 × 3	48.0	173.4	3.730	1.360	13.49	2.876
3 × 4	89.1	298.9	3.810	1.240	10.52	1.971
3 × 5	35.0	146.0	3.750	1.360	15.47	3.131
3 × 6	41.8	218.9	4.620	1.320	17.32	2.520
3 × 7	71.5	275.7	5.440	2.260	16.42	2.739
4 × 1	133.8	413.9	3.950	1.310	16.59	3.070
4 × 2	45.1	216.2	3.640	1.260	16.77	3.186
4 × 3	34.3	166.5	3.890	1.400	15.17	2.547
4 × 4	51.4	199.7	3.770	1.160	16.71	2.650
4 × 5	66.8	432.5	4.050	1.310	18.15	3.366
4 × 6	52.3	471.1	3.590	1.662	19.98	3.750
4 × 7	35.1	149.1	6.350	2.110	12.28	3.046
5 × 1	28.4	105.6	3.400	1.350	5.79	2.826
5 × 2	46.5	191.6	4.090	1.270	13.56	3.072
5 × 3	43.1	216.6	5.020	1.470	23.73	2.690
5 × 4	101.1	432.1	4.230	2.382	20.41	2.550
5 × 5	66.8	144.3	4.050	1.440	11.13	2.111
5 × 6	41.1	172.7	3.590	1.270	14.61	3.007
5 × 7	56.5	314.7	4.610	2.020	28.15	4.126
6 ×1	83.5	295.3	4.600	1.390	13.22	3.486
6 × 2	61.5	239.5	4.090	1.110	13.64	2.810
6 ×3	44.7	208.8	3.080	1.662	9.04	1.852
6 ×4	52.2	193.6	3.700	1.220	7.81	2.460
6 × 5	35.3	193.0	3.910	1.320	16.91	3.007
6 × 6	59.9	210.9	6.970	2.310	11.75	1.730
6 ×7	47.7	196.7	4.330	1.720	8.77	2.007
7 × 1	33.9	135.3	3.450	1.440	13.65	2.355
7 × 2	40.6	189.8	4.680	1.880	13.62	2.900
7 × 3	41.6	195.3	4.310	1.720	25.97	5.468
7 × 4	118.4	303.5	5.320	1.880	7.37	2.230
7 × 5	81.4	377.5	3.870	1.360	12.65	3.100
7 × 6	60.1	186.5	4.643	1.578	12.62	2.180
7 × 7	43.5	223.2	5.410	1.840	10.84	2.332
C.V	20.6	24.5	10.7	13.1	18.6	26.1
S.E	12.81	63.10	0.4580	0.2023	2.890	0.7818
L.S.D	26.03	128.53	0.9215	0.4079	5.874	1.58

1=Avanti,2=OR-04-DH,   3=Argane,   4=ER-04-AJ,5=TA-04-AJ,   6=Crestwood,   7=Starlight,
BDWT=bimass dry weight, BFWT=biomass fresh weight, PFWT=pod fresh weight, PDWT=pod dry
weight, RDWT=root dry weight,RFWT= Root fresh weight

Table 7: Mean values of root and root nodulation

Crosses	TNUW (gm)	ENUWT (gm)	NUCNT	RV	TRL (cm)
1 × 1	3.670	2.762	36.10	28.53	29.10
1 × 2	4.331	4.303	85.76	17.00	35.38
1 × 3	2.825	2.630	28.80	28.53	25.10
1 × 4	2.376	1.735	38.60	18.00	25.50
1 × 5	0.640	0.480	56.36	21.00	24.90
1 × 6	4.309	3.957	40.70	19.00	30.80
1 × 7	3.490	2.970	29.10	10.00	27.63
2 × 1	1.260	1.070	65.56	18.00	25.70
2 × 2	0.800	0.760	21.00	12.00	24.10
2 × 3	3.400	2.547	69.36	28.53	23.80
2 × 4	4.365	3.230	32.30	18.00	27.78
2 × 5	1.700	1.285	41.80	21.00	31.18
2 × 6	4.011	1.530	49.60	19.00	23.60
2 × 7	1.900	1.700	63.16	16.70	26.30
3 × 1	1.641	1.253	43.90	22.00	30.50
3 × 2	1.347	1.153	19.56	14.53	30.50
3 × 3	0.871	0.480	35.96	14.53	26.18
3 × 4	2.650	1.900	31.50	11.00	25.30
3 × 5	1.235	0.925	23.60	17.50	23.40
3 × 6	3.591	3.503	81.96	15.60	29.60
3 × 7	3.950	3.335	88.76	18.00	25.70
4 × 1	2.270	2.125	39.04	18.00	29.20
4 × 2	3.615	3.020	50.76	20.53	27.80
4 × 3	1.285	1.130	70.16	18.53	26.78
4 × 4	3.295	2.555	53.60	19.00	24.80
4 × 5	2.265	2.015	57.44	19.50	32.20
4 × 6	1.311	0.730	55.76	22.00	28.60
4 × 7	3.460	3.325	80.60	11.00	26.60
5 × 1	1.080	0.883	35.96	8.50	26.63
5 × 2	1.491	1.187	45.24	17.00	30.90
5 × 3	2.671	1.143	39.10	24.53	26.80
5 × 4	1.570	1.370	43.80	22.53	22.80
5 × 5	1.790	1.150	36.00	30.53	26.90
5 × 6	1.390	1.100	27.30	17.00	30.80
5 × 7	3.430	3.040	81.16	28.53	29.60
6 ×1	1.680	1.500	75.96	16.50	29.40
6 × 2	5.271	3.863	52.76	13.00	27.90
6 ×3	2.259	2.097	40.60	21.47	23.80
6 ×4	1.020	0.865	58.64	9.00	24.18
6 × 5	1.610	1.125	32.80	18.00	26.70
6 × 6	3.650	3.250	82.44	12.53	31.18
6 ×7	1.170	0.840	47.44	9.00	24.30
7 × 1	1.441	1.203	23.20	14.00	27.20
7 × 2	0.690	0.763	19.40	14.00	27.90
7 × 3	2.270	1.836	30.10	28.53	27.58
7 × 4	2.310	2.297	26.30	12.00	26.60
7 × 5	0.965	0.890	75.0	17.00	23.90
7 × 6	1.650	0.940	38.36	12.53	25.40
7 × 7	1.859	1.337	33.70	13.00	21.20
S.E	0.261	0.285	9.190	3.619	2.729
L.S.D	0.531	0.580	18.968	7.364	5.516
C.V	11.3	15.3	19.3	20.4	10.1

Table 8.Mean values of the severity of common bacterial blight (CBB), Angular leaf spot, Floury leaf spot, and Rust in white pea bean (1-9 disease score)

Crosses	Mean values							
	CBB		ALS		Rust		Floury	
	NT	TF	NT	TF	NT	TF	NT	TF
1 × 1	3.19	1.96	1.45	1.38	6.10	2.55	0.15	0.78
1 × 2	3.25	1.95	1.69	1.45	3.00	1.91	1.45	1.32
1 × 3	3.01	1.81	2.64	1.75	5.20	2.41	0.04	0.72
1 × 4	4.07	2.12	2.71	1.81	5.28	2.42	0.30	0.82
1 × 5	3.40	2.01	2.51	1.65	3.07	1.86	1.79	1.40
1 × 6	2.32	1.47	1.28	1.29	6.09	2.58	0.09	0.74
1 × 7	3.20	1.89	1.83	1.44	3.89	2.07	-1.07	0.30
2 × 1	2.65	1.75	1.08	1.24	5.35	2.45	0.07	0.73
2 × 2	2.74	1.81	1.44	1.36	2.37	1.72	-0.25	0.610
2 × 3	1.68	1.37	-0.26	0.74	4.23	2.10	0.67	0.96
2 × 4	3.17	1.92	1.23	1.28	5.20	2.35	-0.08	0.67
2 × 5	3.05	1.80	1.11	1.22	2.24	1.66	0.80	1.02
2 × 6	1.98	1.55	1.29	1.29	3.23	1.95	0.79	1.01
2 × 7	4.68	2.31	2.74	1.74	3.73	1.96	0.67	0.96
3 × 1	3.31	2.01	2.01	1.56	3.50	1.98	0.46	0.89
3 × 2	4.11	2.15	1.45	1.37	5.23	2.32	-0.54	0.50
3 × 3	1.98	1.54	0.49	1.07	6.24	2.62	-0.27	0.60
3 × 4	4.84	2.32	1.73	1.47	7.60	2.86	-0.16	0.65
3 × 5	3.58	2.06	2.23	1.64	3.13	1.92	0.08	0.75
3 × 6	3.05	1.88	1.22	1.34	4.72	2.27	-0.07	0.68
3 × 7	3.84	2.06	1.17	1.75	6.75	2.71	-0.22	0.63
4 × 1	2.51	1.69	2.14	1.57	4.20	2.17	0.04	0.72
4 × 2	4.46	2.25	3.67	2.02	4.23	2.08	1.27	1.21
4 × 3	4.10	2.20	1.74	1.50	4.16	2.14	0.84	1.03

Table 8 (Continued).

4 × 4	0.92	1.09	0.77	1.06	3.13	1.93	0.27	0.81
4 × 5	2.03	1.53	1.09	1.25	4.70	2.26	1.29	1.20
4 × 6	400	2.14	1.51	1.41	5.61	2.46	0.47	0.89
4 × 7	4.49	2.23	2.50	1.75	4.65	2.20	0.06	0.73
5 × 1	1.75	1.52	0.44	1.08	1.90	1.59	0.50	0.89
5 × 2	3.31	2.01	1.51	1.38	3.00	1.87	0.32	0.89
5 × 3	3.79	2.09	2.45	1.73	3.14	1.89	0.32	0.84
5 × 4	3.47	2.02	2.18	1.62	5.26	2.36	0.50	1.62
5 × 5	3.15	1.90	0.61	0.99	5.27	2.38	0.46	1.08
5 × 6	1.52	1.28	1.35	1.34	4.01	2.12	0.32	0.83
5 × 7	3.84	2.06	3.17	1.86	3.75	1.99	2.53	1.22
6 ×1	2.08	1.60	0.87	1.16	5.18	2.38	0.24	0.80
6 × 2	2.11	1.61	0.51	1.09	2.75	1.79	0.47	0.88
6 ×3	2.00	2.09	1.37	1.34	4.61	2.27	1.90	1.45
6 ×4	3.26	2.02	1.46	1.36	5.07	2.38	0.09	0.73
6 × 5	3.42	1.53	2.01	1.59	3.04	1.91	0.63	0.96
6 × 6	3.28	1.92	2.40	1.69	5.59	2.42	-0.17	0.63
6 ×7	4.32	2.19	1.83	1.48	1.86	1.60	-1.08	0.29
7 × 1	3.63	2.04	1.45	1.41	2.75	1.77	0.22	0.78
7 × 2	2.99	1.85	1.94	1.57	4.25	2.14	-0.52	0.51
7 × 3	3.62	2.02	1.63	1.45	5.60	2.41	0.14	0.76
7 × 4	3.73	2.02	2.47	1.63	4.84	2.31	-0.76	1.02
7 × 5	2.90	1.82	1.89	1.53	2.24	1.70	0.11	1.01
7 × 6	0.82	1.10	0.83	1.04	4.36	2.18	-1.08	0.96
7 × 7	3.22	1.90	1.73	1.46	6.79	2.67	0.07	0.72
CV	35.99	18.78	54.73	19.69	29.17	13.20	304.68	43.26
L.S.D	2.57	0.81	2.07	0.65	2.90	0.66	2.15	0.82
S.E.	1.27	0.40	1.02	0.32	1.43	0.32	1.06	43.26

Where, CBB= common bacterial blight, ALS=Angular leaf spot, NT=non transformed, TF=transformed

4.2. Diallel Analysis: Griffing's model I and method I

Estimation of combining ability (GCA, SCA, REC, MAT, and NMAT) effects and the actual values of genotypes are presented for yield and yield related traits (Table 9). Highly significant (P<0.01) GCA effects were found for days to flowering, 100-seed weight, and number of pods per plant, pod length, pod diameter, seed length, seed diameter, seed thickness and leaf area; while grain yield and internode length showed significant (P<0.05) GCA effects (Table 9). This implies that the additive gene effect was important in the inheritance of these traits. Arunga *et al.* (2010) reported similar finding for days to flowering. Earlier researchers reported that the GCA effect was significant for number of seeds per plant, number of seeds per pod, and 100-seed weight (Mulugeta, 2006).

Highly significant (P<0.01) SCA effects were found for number of branches on the main axis, 100-seed weight, grain yield, number of pods per plant, number of seed per plant, seed length, seed diameter, and seed thickness; while significant (P<0.05) SCA mean squares were exhibited for the internode length, pod length, pod diameter, seed thickness. Arunga *et al* (2010) reported similar reports that there were significant SCA effects for days to flowering, plant height at flowering, number of pods per plant, pod weight per plant, pod length, and pod diameter. This implies that the non-additive type of gene action contributed for the inheritance of these traits. Mulugeta (2006) also reported similar findings that SCA effects were significant for number of pods per plant, number of seeds per plant, and number of seeds per pod.

There were highly significant reciprocal effects for number of branches on the main axis, plant height, 100-seed weight, number of pods per plant, number of seed per plant, number of seed per pod, seed length, seed diameter, seed thickness, and leaf area; while for days to flowering, was significant (P<0.05)s. This implies that the cytoplasmmic genes of the reciprocal crosses were important for the inheritance of these traits (Arunga *et al.*, 2010). Reciprocal differences for days to flowering and silking dates have been reported in maize (Jinks, 1954; Khehra and Bhalla, 1976). It is recommended that crosses portraying reciprocal effects should not be mixed with direct crosses (Khan et al., 1991; Pavasia et al., 1999; Arunga et al, 2010).

There were highly significant maternal effects for plant height, grain yield, number of pod per plant, number of seed per plant, seed diameter, and seed thickness; while there was significant maternal effects for 100-seed weight, pod length, and seed length. This indicates that the cytoplasm of the maternal effects were important for the inheritance of these traits. There were also highly significant non-maternal effects for number of branches on the main axis, 100-seed weight, number of pods per plant, number of seed per pod, seed diameter, and leaf area; while plant height, seed length, and seed thickness displayed significant non-maternal effects. This implies that the interaction of cytoplasm and nuclear genes were important for the inheritance of these traits. This is similar with earlier reports (Arunga et al., 2010) who reported that there were significant non-maternal and maternal effects in days to flowering and plant height. Generally, the choice of female parent is critical in a breeding programme (Khan et al., 1991; Pavasia et al., 1999; Mugisha, 2008; Arunga et al, 2010).

Significant variations among the genotypes indicate considerable genetic diversity among the parents and their respective crosses. This is appropriate for further biometrical assessments of the traits under consideration (El-Bramawy and Shaban, 2007). The significant GCA mean squares for all traits indicated variability of GCA among the parents and this suggests that genetic gain is achievable through selection over the segregant population. The significant GCA and SCA mean square for all traits showed the importance of both additive and non-additive gene effects (Arunga *et al.*, 2010).

Evidence that both additive and non-additive gene effects were involved in the genetic control of the traits investigated implies that both gene effects should be considered when developing breeding schemes for the selection of superior lines. Consequently, both parents need not necessarily have high GCA during breeding because the dominance gene effects could also be exploited to enhance these traits.

In contrast, the predominance of the additive gene effects suggests that the best progeny might be derived from crosses with genotypes having the greatest positive GCA. The snap bean is a self-pollinating crop, and autogamous plants are homozygous and thus they do not make use of the dominance effects of genes at individual loci (Moreno-Gonzalel and Cubero, 1993). Usually, varieties of autogamous plants are pure-lines or multi-lines whose seed are commercially produced by self-pollination, even though a few exceptions, like

wheat, tobacco, cotton and tomato can produce commercial hybrids. Therefore, crosses involving genotypes with greater estimates of general combining ability should be potentially superior for the selection of lines in advanced generations (Francoet al., 2001).

Table 9: Mean squares of GCA, SCA, REC, MAT, and NMAT effects for yield and yield components

Parameters	GCA	SCA	REC	MAT	NMAT
			Mean squares		
MD	84.15ns	86.59ns	99.99ns	96.62ns	101.37ns
DFPF	8.60**	1.93ns	5.00*	5.57ns	4.80ns
NBMA	0.86ns	0.98**	0.93**	0.55ns	1.13**
NNMA	0.70ns	1.67ns	1.03ns	1.08ns	1.09ns
INL	2.25*	1.87*	1.33ns	1.22ns	1.36ns
PH	220.52ns	05.42ns	262.28**	363.82**	243.98*
HSWT	164.11***	54.58***	33.31**	31.21*	34.28**
FOPWT	343718.96*	318384.47**	223852.66*	436162.71**	157661.64ns
NPPT	386.20***	219.72***	227.90***	173.94**	254.40***
NSPPT	2148.86ns	2983.01**	3170.60**	6675.02***	2252.49ns
NSPD	0.43ns	0.29ns	0.94**	0.58ns	1.13**
PDL	2.10***	0.49*	0.39ns	0.63*	0.29ns
PDD	0.04**	0.02*	0.01ns	0.01ns	0.01ns
SL	6.47***	2.42***	1.43**	1.71*	1.32*
SD	1.62***	0.59***	0.27***	0.40***	0.23***
ST	0.40***	0.08**	0.07**	0.10**	0.06*
LA	445.19**	214.81ns	361.23**	238.68ns	372.62**

Where; ns=non significant,*=significant at 5%,**=highly significant at 1%,***= highly significant at 0.1%, Where; GCA=general combining ability, SCA=specific combining ability,REC= reciprocal effects, MTA=maternal effects, NMAT=non maternal effects, MD= days to maturity, DFPF=days to fifty percent flowering, NBMA= number of branches on the main axis, NNMA=number of nodes on the main axis, INL=inter node length, PH= plant height, HSWT=Hundred seed weight, GY= Grain yield, NPPT=number of pods per plant, NSPPT=number of seed per plant, NSPD=number of seed per pod, PDL=pod length, PDD=pod diameter, Seed length, SD=Seed diameter, ST= Seed thickness

The GCA and SCA effect of yield and yield relatecd components are presented in table 18. The variety OR-04-DH had positive and significant GCA effects for days to flowering, plant height, and pod length (Table 10); while parents TA-04-AJ and crestwood displayed positive and significant GCA effects for leaf area and number of pods per plant. Starlight exhibited positive and significant GCA effects for 100-seed weight, grain yield, seed length, seed diameter, seed thickness, pod length, and pod diameter. This implies that these genotypes were good general combiners for the respective traits.

The cross Crestwood X Starlight displayed significant and positive SCA effects for days to maturity. The cross Avanti X OR-04-DH displayed positive and significant SCA effects for number of branches on the main axis and number of seeds per plant. Crosses Avanti X

Arage and OR-04-DH X ER-04-AJ had positive and significant SCA effects for plant height and seed thickness. Mulugeta (2006) reported significant SCA effects for number of branches on the main axis and number of seeds per plant. Crosses Avanti X Crestwood and OR-04-DH X Avanti were exhibited positive and significant (P<0.05) SCA effects for leaf area and pod length. Crosses OR-04-DH X ER-04-AJ, Argane X TA-04-AJ, TA-04-AJ X Starlight, and Crestwood X Starlight had displayed positive and significant (P<0.05) SCA effects for internode length; while crosses TA-04-AJ X Starlight, TA-04-AJ X Crestwood, and ER-04-AJ X TA-04-AJ were displayed positive and significant SCA effects for number of pods per plant. Crosses Avanti X OR-04-DH, OR-04-DH X Argane, ER-04-AJ X TA-04-AJ, TA-04-AJ X Starlight exhibited positive and significant SCA effects for number of branches on the main axis and number of seed per plant. The cross Avanti X Starlight displayed positive and significant SCA effects for number of seeds per pod; while crosses Avanti X ER-04-AJ, TA-04-AJ X Starlight, and Crestwood X Starlight exhibited positive and significant SCA effects for grain yield.

Significant and positive SCA effects were displayed in crosses OR-04-DH X ER-04-AJ and Argane X TA-04-AJ for seed length; while the cross ER-04-AJ X Starlight exhibited positive and significant SCA effects for seed dimeter. Crosses Avanti X Argane, Avanti X Starlight, and Argane X TA-04-AJ exhibited positive and significant SCA effect for seed thickness. This implies that these crosses displayed larger mean values than expected from the performance of their respective parents. A similar findings reported that there were positive and significant SCA effects for plant height, pod length, number of pods per plant, grain yield in five crosses of common bean (Mulugeta, 2006). Arunga et al (2010) also reported similar results that there was positiove and significant SCA effects for crosses of snap bean for plant height, number of pods per plant.

Crosses OR-04-DH X Avanti, Argane X Avanti, Crestwood X OR-04-DH, TA-04-AJ X Argane displayed positive and significant reciprocal effects for number of branches on the main axis; while crosses TA-04-AJ X Avanti and Crestwood X ER-04-AJ had positive and significant reciprocal effects for plant height. Significant and positive reciprocal effects were observed in reciprocal crosses TA-04-AJ X Avanti, Crestwood X Argane, Crestwood X ER-04-AJ, and Starlight X TA-04-AJ for leaf area; while reciprocal crosses TA-04-AJ X Avanti and Crestwood X Avanti exhibited positive and significant reciprocal effects for number of nodes on the main axis. The reciprocal crosses Starlight X OR-04-

DH, TA-04-AJ X ER-04-AJ, Crestwood X TA-04-AJ displayed positive and significant reciprocal effects for number of pods per plant, while reciprocal crosses Argane X OR-04-DH and TA-04-AJ and TA-04-AJ X ER-04-AJ exhibited positive and significant reciprocal effects for number of seed per plant.

Starlight X Avanti, Argane X OR-04-DH, and Crestwood X OR-04-DH displayed positive and significant reciprocal effects for number of seeds per pod; while reciprocal crosses Starlight X TA-04-AJ, Starlight X Crestwood exhibited positive and significant reciprocal effects for grain yield. The reciprocal cross Starlight X Avanti had positive and significant reciprocal effects for seed length; while reciprocal crosses Starlight X Avanti, Starlight X OR-04-DH, Starlight X TA-05-AJ, and Crestwood X Argane exhibited positive and significant reciprocal effects for seed diameter. Significant and positive reciprocal effects were displayed in reciprocal crosses Starlight X Avanti, Crestwood X Argane, and Crestwood X ER-04-AJ for seed thickness. The reciprocal cross ER-04-AJ X Avanti, Starlight X Avanti, and Starlight X TA-04-AJ displayed positive and significant reciprocal effects for pod length. Moreever, the reciprocal cross Starlight X Avanti had positive and significant reciprocal effects for pod diameter. This indicates that the cytoplasm of the reciprocal crosses was important for the inheritance of these traits.

The variety OR-04-DH displayed positive and significant maternal effects for plant height, number of pod per plant, number of seed per plant, grain yield, seed length, and seed diameter. The cross Argane X Starlight displayed positive and significant non-maternal effects for days to flowering; while the crosses Avanti X OR-04-DH had shown positive and significant non-maternal effects for number of branches on the main axis. Crosses Avanti X TA-04-AJ and TA-04-AJ X Starlight exhibited positive and significant non-maternal effects for leaf area. Moreever, the cross Avanti X TA-04-AJ displayed positive and significant non-maternal effects for number of nodes on the main axis, number of pods per plant, plant height and number of seed per plant.

The TA-04-AJ X Starlight exhibited positive and significant non-maternal effects for leaf area and grain yield. Crosses Avanti X ER-04-AJ, ER-04-AJ X TA-04-AJ, and TA-04-AJ X Crestwood were exhibited positive and significant non-maternal effects for number of pods per plant. Moreever, the cross ER-04-AJ X TA-04-AJ displayed positive and significant non-maternal effect for number of seed per plant; while the cross OR-04-DH X

Crestwood displayed positive and significant non-maternal effects for number of seed per plant and number of seed per pod. Crosses Avanti X Starlight, OR-04-DH X Argane, OR-04-DH X Crestwood, and Argane X Crestwood exhibited positive and significant non-maternal effects for number of seed per pod. There was significant and positive non-maternal effect in crosses Avanti X Starlight and OR-04-DH X ER-04-AJ for seed length. Moreever, the non-maternal cross Avanti X Starlight also displayed positive and significant non-maternal effect for seed diameter; while crosses Avanti X Starlight and Argane X Crestwood exhibited positive and significant non-maternal effects for seed diameter, seed thickness, and pod diameter. This implies that the interaction of the cytoplasm and nuclear gene had an important influence in the inheritance of these traits. Evidence shows that both maternal and non-maternal reciprocal effects were observed in days to flowering and plant height at flowering (Arunga *et al*, 2010). Reciprocal differences for days to flowering and silking dates have been reported in maize (Jinks, 1954; Khehra and Bhalla, 1976). Generally, the choice of female parent is critical in a breeding programme. Moreover, it is recommended that crosses portraying reciprocal effects should not be mixed with direct crosses (Khan et al., 1991; Pavasia et al., 1999, Arunga *et al.*, 2010).

Table10.1a: General combiningability (GCA), (SCA),and Reciprocal (REC) effects of yield and yield related components

Days to 50% flowering

	1	2	3	4	5	6	7
1		1.16 ns	-0.41 ns	-0.59 ns	0.27 ns	0.02 ns	-1.41 ns
2	0.75 ns		0.77 ns	-0.15 ns	-0.30 ns	-0.30 ns	-0.84 ns
3	1.00 ns	-0.75 ns		-0.73 ns	-0.63 ns	0.62 ns	-1.02 ns
4	0.75 ns	-2.25*	-1.00 ns		-0.05 ns	0.45 ns	-1.61 ns
5	1.50 ns	-0.50 ns	1.00 ns	-1.00 ns		0.55 ns	0.06 ns
6	-0.50 ns	0.25 ns	0.00 ns	-0.25 ns	1.25 ns		-0.44 ns
7	-1.50 ns	-1.50 ns	1.50 ns	0.48 ns	-1.75 ns	-1.00 ns	
gi	0.02ns	0.59*	0.41ns	0.34ns	0.23ns	-0.52ns	-1.07**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, and gi=general combining ability

Table 10.1b: Estimates of maternal (MAT) and non-maternal effects of yield and yield related components

Days to flowering

	1	2	3	4	5	6	7
1	**0.29**	-0.32 ns	0.89 ns	0.71 ns	1.00 ns	-1.04 ns	-1.25 ns
2		**-0.79***	0.21 ns	-1.22 ns	0.07 ns	0.79 ns	-0.18 ns
3			**0.17 ns**	-0.93 ns	0.61 ns	-0.43 ns	1.86*
4				**0.24 ns**	-1.46 *	-0.75 ns	0.77 ns
5					**-0.21 ns**	1.21 ns	-0.99 ns
6						**-0.25 ns**	-0.21 ns
7							**0.53 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.2a. Estimation of GCA, SCA , and REC effects and the actual value of yield and yield related components

				Days to maturity			
	1	2	3	4	5	6	7
1		-1.34 ns	-0.48 ns	0.75 ns	0.09 ns	4.41 ns	1.03 ns
2	-0.75 ns		-1.09 ns	-1.85 ns	0.48 ns	2.05 ns	-2.36 ns
3	3.50 ns	-1.25 ns		-3.99 ns	3.08 ns	0.16 ns	4.21ns
4	0.00 ns	0.75 ns	-4.00 ns		2.82 ns	4.65 ns	-7.85
5	2.50 ns	2.25 ns	0.25 ns	-0.75 ns		-16.52ns	-0.7ns
6	-0.75 ns	-0.25 ns	5.75 ns	-0.50 ns	-21.00***		21.14*
7	1.75 ns	0.50 ns	1.75 ns	0.35 ns	-0.75 ns	-0.25 ns	
gi	1.98ns	0.84ns	-0.27ns	1.99ns	1.84ns	-2.41ns	-0.30ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%

Table 10.2b. Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Days to maturity			
	1	2	3	4	5	6	7
1	**0.89**	-1.25	2.82	-0.56	-2.10	0.71	-1.43
2		**0.39ns**	-1.42 ns	0.69 ns	-1.85 ns	1.71 ns	-0.37 ns
3			**0.21ns**	-3.88 ns	-3.68 ns	7.89 ns	1.05 ns
4				**0.34ns**	-4.80 ns	1.52 ns	-0.47 ns
5					**-3.71***	-14.92**	2.49 ns
6						**2.36ns**	-3.09 ns
7							**-0.48ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.3a. Estimation of GCA, SCA , and REC effects and the actual value of yield and yield related components

				Number of branches on the main axis (NBMA)			
	1	**2**	**3**	**4**	**5**	**6**	**7**
1		1.72***	0.37ns	-0.48	-0.32ns	-0.17ns	- 0.13ns
2	1.62***		-0.44ns	-0.19ns	0.32ns	0.02ns	0.37 ns
3	0.00***	-0.30ns		0.33ns	0.266ns	-0.46ns	1.01 ns
4	*-0.55ns*	*0.15ns*	*-0.70**		*0.13ns*	*0.18ns*	-0.43 ns
5	*0.40ns*	*0.15ns*	*0.00****	*0.40ns*		*-0.05ns*	0.10 ns
6	*-0.55ns*	*0.65**	*-0.40ns*	*0.05ns*	*0.20ns*		0.20 ns
7	*-0.50ns*	*-0.50ns*	*0.10ns*	*-0.34ns*	*-0.10ns*	*0.55ns*	
gi	0.23ns	0.24ns	-0.23ns	-0.03ns	-0.14ns	0.06ns	-0.14ns

Table 10.3 b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Number of branches on the main axis			
	1	2	3	4	5	6	7
1	**0.06** ns	1.35***	-0.16 ns	-0.44 ns	0.22 ns	-0.52***	-0.45ns
2		**-0.21** ns	-0.19 ns	0.53 ns	0.24 ns	0.95 ns	-0.18ns
3			**-0.10** ns	-0.43 ns	-0.02 ns	-0.21 ns	0.31ns
4				**0.17** ns	0.11 ns	-0.04 ns	-0.40ns
5					**-0.12** ns	0.40 ns	0.13ns
6						**0.08ns**	0.58*
7							**0.11ns**

Table 10.4a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Plant height(PH)			
1		-7.46 ns	12.06*	-0.88 ns	5.03 ns	-3.38 ns	9.35 ns
2	-2.80 ns		-6.87 ns	17.34**	11.63 ns	-0.13 ns	-0.40 ns
3	-17.19 ns	12.64 ns		-5.54 ns	7.21 ns	-6.55 ns	15.47 ns
4	-1.59 ns	7.80 ns	2.20 ns		15.38**	7.07 ns	-4.23 ns
5	24.01***	7.01 ns	-4.15 ns	-6.40 ns		-2.34 ns	16.42 ns
6	-0.20 ns	11.54 ns	8.21 ns	15.46*	2.95 ns		7.47 ns
7	12.89 ns	3.75 ns	1.45 ns	8.20 ns	-1.55 ns	-7.95 ns	
gi	-0.83ns	5.96**	-3.87ns	0.87ns	1.38ns	-3.02ns	-0.49ns

Table 10.4b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Plant height (PH)			
1	**2.16** ns	1.55 ns	-17.60**	-2.49 ns	19.12**	-8.92 ns	8.34 ns
2		**6.51**	7.89 ns	2.56 ns	-2.22 ns	-1.52 ns	-5.16 ns
3			**1.75** ns	1.71 ns	-8.62 ns	-0.10 ns	-2.70 ns
4				**1.26** ns	-10.39*	7.63 ns	4.53 ns
5					**-2.72** ns	-0.88 ns	-1.22 ns
6						**-6.56**	-3.79 ns
7							**-2.40** ns

Table 10.5a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Leaf Area (LA)			
	1	2	3	4	5	6	7
1		8.00ns ns	-6.94 ns	-0.86 ns	-5.59 ns	13.52*	-4.35 ns
2	-1.53 ns		9.51*	1.51 ns	-10.96*	8.46 ns	-2.00 ns
3	10.36 ns	11.79*		-0.31 ns	-3.22 ns	-9.02 ns	-4.50 ns
4	3.23 ns	4.23 ns	-4.47 ns		-1.43 ns	-5.42 ns	-10.57 ns
5	14.51**	1.33 ns	-11.81*	3.06 ns		4.22 ns	14.62 ns
6	-17.93**	4.09 ns	19.84***	10.97*	2.28 ns		11.58 ns
7	8.45 ns	-3.08 ns	-10.36 ns	2.05 ns	17.76*	-12.58 ns	
gi	-2.81ns	-1.60ns	-6.10**	-1.85ns	5.11**	4.45*	0.80ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi= general combining ability of the genotypes

Table 10.5b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Leaf Area (LA)			
	1	2	3	4	5	6	7
1	**2.44** ns	-1.13 ns	3.78 ns	2.66 ns	13.92**	-24.92***	-4.35 ns
2		**2.84** ns	4.82 ns	3.26 ns	0.33 ns	-3.29 ns	-2.00 ns
3			**-4.13***	1.53 ns	-5.82 ns	19.42***	-4.50 ns
4				**1.87** ns	3.04 ns	4.55 ns	-10.56 ns
5					**1.85** ns	-4.12 ns	14.62 **
6						**-4.55***	11.58 ns
7							**-0.32** ns

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Table 10.6a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	Number of nodes on the main axis (NNMA)						
	1	2	3	4	5	6	7
1		0.48 ns	0.14 ns	-0.05 ns	-0.71 ns	0.77 ns	-0.31 ns
2	-0.10 ns		0.63 ns	0.59 ns	0.33 ns	-0.44 ns	0.96 ns
3	-0.15 ns	-0.20 ns		-1.06*	0.48 ns	-0.83 ns	0.59 ns
4	0.10 ns	0.10 ns	-0.45 ns		-0.36 ns	0.94 ns	-1.56 ns
5	1.35*	-0.75 ns	-0.20 ns	0.20 ns		-0.09 ns	0.89 ns
6	0.05 ns	-0.40 ns	0.70 ns	1.52*	0.40 ns		0.71 ns
7	-0.25 ns	-0.33 ns	0.20 ns	-0.29 ns	-0.05 ns	-0.10 ns	
gi	-0.015ns	0.04ns	-0.06ns	-0.12ns	0.19ns	0.21ns	-0.25ns

Table 10.6b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	Number of nodes on the main axis (NNMA)						
	1	2	3	4	5	6	7
1	**0.14** ns	-0.45 ns	-0.21ns	0.20 ns	1.17*	-0.43 ns	-0.27ns
2		**-0.21** ns	0.09 ns	0.55 ns	-0.57 ns	-0.53 ns	0.00 ns
3			**0.09** ns	-0.30 ns	-0.32 ns	0.28 ns	0.23 ns
4				**0.24** ns	-0.07 ns	0.94 ns	-0.41 ns
5					**-0.04** ns	0.10 ns	0.10 ns
6						**-0.34** ns	0.36 ns
7							**0.12** ns

Table 10.7a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

Internod length

	1	2	3	4	5	6	7
1		-0.32	-0.32 ns	0.38 ns	0.44 ns	0.028 ns	-0.36 ns
2	-0.99 ns		0.08 ns	0.99*	-0.53 ns	-0.10 ns	-0.15 ns
3	0.33 ns	-0.47 ns		0.19 ns	1.14**	-1.04*	1.41 ns
4	0.84 ns	0.18 ns	-0.53 ns		-0.96*	-0.32 ns	-0.30 ns
5	0.60 ns	0.07 ns	-0.69 ns	-0.88 ns		-0.15 ns	2.38*
6	-0.02 ns	-0.09 ns	0.78 ns	-0.82 ns	-0.23 ns		1.37*
7	0.26 ns	-0.25 ns	-0.34 ns	-0.62 ns	0.58 ns	0.79 ns	
gi	-0.10ns	-0.48**	0.25ns	0.29ns	0.06ns	-0.22ns	0.20ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=general combining ability

Table 10.7b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

Interned length

	1	2	3	4	5	6	7
1	**0.14 ns**	-1.08*	0.09 ns	0.30 ns	0.64 ns	0.00 ns	-0.06 ns
2		**0.06 ns**	-0.63 ns	-0.29 ns	0.19 ns	0.02 ns	0.06 ns
3			**-0.09 ns**	-0.84 ns	-0.42 ns	1.03 ns	-0.37 ns
4				**-0.40***	-0.30 ns	-0.25 ns	-0.31 ns
5					**0.18 ns**	-0.24 ns	-0.28 ns
6						**0.17 ns**	0.34 **ns**
7							**0.56 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.8a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Number of pod per plant			
1		-0.10 ns	6.08 ns	2.02 ns	-7.00*	-1.02 ns	-10.75 ns
2	-10.25*		1.95 ns	-0.45 ns	-8.63**	8.80**	1.978 ns
3	-8.41*	5.00 ns		-1.58 ns	-4.96 ns	0.92 ns	1.86 ns
4	6.64ns	-0.20 ns	-1.25 ns		14.40***	-8.93*	-8.20 ns
5	2.30 ns	5.90 ns	-12.44*	19.11***		18.54***	25.23***
6	-3.30 ns	5.06 ns	-6.96 ns	-2.70ns	24.90***		-12.09*
7	-6.60 ns	7.10 *	1.40 ns	-2.45ns	-3.30 ns	2.30 ns	
gi	1.40ns	-2.77*	-0.19ns	0.60ns	5.19***	3.21*	-7.45***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%

Table 10.8b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Number of pod per plant			
1	**-2.80***	-2.72 ns	-7.87*	10.70 *	6.07*	-2.60 ns	-3.58 ns
2		**4.73***	-1.99 ns	-3.68 ns	2.14 ns	-1.79 ns	2.59 ns
3			**-2.26 ns**	2.26 ns	-9.21*	-6.80 ns	3.89 ns
4				**1.25 ns**	18.82***	-6.06*	-3.48 ns
5					**0.97 ns**	21.871***	-4.05 ns
6						**-2.11 ns**	4.63 ns
7							**0.22 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.9a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Number of seed per plant(NSPPT)			
	1	2	3	4	5	6	7
1		38.10 *	-7.70 ns	21.16 ns	-4.07 ns	3.32 ns	-11.92 ns
2	-41.84 ns		44.14*	-10.31 ns	-40.58*	13.91 ns	3.68 ns
3	10.05 ns	91.29***		-25.49 ns	-23.96 ns	13.98 ns	-2.88 ns
4	-47.41*	-4.75 ns	-9.35 ns		76.24***	-23.02 ns	-23.48 ns
5	32.75 ns	10.95 ns	-0.14 ns	70.96*		5.64 ns	82.95 *
6	-30.45 ns	28.65 ns	-13.91 ns	-16.40 ns	-3.96 ns		29.21 ns
7	-33.21 ns	22.20 ns	5.85 ns	-14.45 ns	-2.50 ns	-7.81 ns	
gi	8.53 ns	-2.26ns	1.13ns	7.83ns	3.91ns	2.11ns	-21.24*

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),gi=general combining ability of individual genotypes*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%,gi=general combining ability of the genotypes

Table 10.9b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Number of seed per plant			
	1	2	3	4	5	6	7
1	**-15.73***	1.06 **ns**	8.80 **ns**	-17.16 **ns**	31.20*	-10.68 **ns**	-13.20 **ns**
2		**27.17***	47.14 **ns**	-17.40*	-33.50 **ns**	5.52*	-0.70 **ns**
3			**-16.98***	22.15 **ns**	-0.44 **ns**	7.11 **ns**	27.11 **ns**
4				**14.52***	39.20 *	-26.88 **ns**	-24.69 **ns**
5					**-17.28***	17.36 **ns**	19.056 **ns**
6						**4.04 ns**	-7.57 **ns**
7							**4.27 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.10a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Number of seed per pod			
	1	2	3	4	5	6	7
1		0.43ns	-0.15 ns	0.09 ns	0.32 ns	-0.02 ns	1.19*
2	-0.35 ns		0.23 ns	-0.06 ns	-0.40 ns	0.07 ns	0.21 ns
3	0.32 ns	1.38 ***		-0.21 ns	0.28 ns	-0.05 ns	-0.05 ns
4	-0.36 ns	-0.08 ns	-0.57 ns		0.25 ns	0.29 ns	0.22 ns
5	0.51 ns	-0.36 ns	-0.26 ns	-0.13 ns		-0.26 ns	-0.15 ns
6	-0.38*	0.90 **	0.43 ns	-0.06 ns	-0.62 ns		0.10 ns
7	0.95***	-0.70 ns	-0.05 ns	-0.36 ns	0.34 ns	0.17 ns	
gi	-0.02ns	0.08ns	0.14ns	0.02ns	-0.17ns	-0.20ns	0.16ns

Table 10.10b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Number of seed per pod			
	1	2	3	4	5	6	7
1	**0.10** ns	-0.24 ns	-0.08 ns	-0.39 ns	0.40 ns	-0.49 ns	0.80**
2		**0.21** ns	0.85**	-0.22 ns	-0.58*	0.67**	-0.96**
3			**-0.30****	-0.20 ns	0.04 ns	0.72**	0.21 ns
4				**0.07** ns	-0.20 ns	-0.13 ns	-0.48 ns
5					**-0.01** ns	-0.63*	0.29 ns
6						**-0.01** ns	0.13 ns
7							**-0.05** ns

Table 10.11a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	Hundred seed weight						
	1	2	3	4	5	6	7
1		-0.55	0.97	-2.22	-0.73	-2.05	1.29
2	2.17		0.43	0.76	0.87	-0.67	0.56
3	-0.88	-0.05		-3.77*	2.29	-4.09*	0.26
4	0.18	2.63	-0.93		0.83	-2.29	7.57*
5	-0.13	2.20	-6.35**	2.93		0.20	0.87
6	0.43	-0.83	1.38	-0.83	-1.48		-1.49
7	7.95***	1.35	-0.63	1.24	5.28**	-2.68	
gi	-0.82ns	-1.45*	-0.92ns	-0.73ns	-1.87**	-0.15ns	5.94***

Table 10.11b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	Hundred seed weight						
	1	2	3	4	5	6	7
1	**1.39***	1.23	-3.06	-1.01	-0.78	-1.16	4.77**
2		**0.45**	-1.30	2.39	2.49	-1.46	-0.88
3			**-0.80**	0.08	-4.81*	1.98	-1.61
4				**0.20**	3.45*	-1.23	-0.76
5					**0.74**	-2.40	2.75
6						**-0.19**	-4.26**
7							**-1.79**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.12a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Grain yield			
1		71.07 ns	18.74 ns	418.80*	65.72 ns	238.80 ns	-88.48 ns
2	-188.64 ns		-179.58 ns	306.84 ns	-212.88 ns	238.09 ns	186.99 ns
3	130.00 ns	15.64 ns		-210.52 ns	-481.35*	172.87 ns	203.67 ns
4	-14.36 ns	362.64 ns	24.75 ns		157.43 ns	-143.96 ns	59.11 ns
5	134.36 ns	94.00 ns	-212.50 ns	156.86 ns		-167.65 ns	911.19**
6	-227.00 ns	260.25 ns	-203.72 ns	16.25 ns	-118.14 ns		942.61**
7	128.36 ns	270.86 ns	193.14 ns	-102.79 ns	971.28***	504.25*	
gi	-85.86 ns	-21.89 ns	-16.92 ns	-81.35 ns	51.74 ns	-124.98 ns	279.26 ***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.12b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
				Grain yield			
1	**-5.33 ns**	-13.03 ns	86.19 ns	-52.28 ns	236.89 ns	-110.73 ns	-147.04 ns
2		**170.29***	-203.79 ns	149.11 ns	20.91 ns	200.90 ns	-180.16 ns
3			**-49.14 ns**	30.64 ns	-66.16 ns	-43.63 ns	-38.45ns
4				**-43.24 ns**	297.31 ns	170.44 ns	-340.27**
5					**97.20 ns**	-104.40 ns	593.35**
6						**110.94 ns**	112.58 ns
7							**-280.73***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.13a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	Seed length (SL)						
	1	2	3	4	5	6	7
1		0.09 ns	-0.10 ns	-0.41 ns	0.13 ns	-0.29 ns	0.13 ns
2	0.19 ns		-0.33 ns	1.05**	0.01 ns	-0.55 ns	0.41 ns
3	-0.11 ns	0.21 ns		-0.65 ns	0.74 *	-0.39 ns	0.23 ns
4	-0.09 ns	1.77***	-0.38 ns		-0.71*	-0.46 ns	0.99 ns
5	-0.16 ns	0.08 ns	-0.72 ns	0.09 ns		0.06ns	0.30 ns
6	0.07 ns	0.29 ns	0.31 ns	0.13 ns	0.19 ns		-0.01 ns
7	1.68***	-0.13 ns	0.31 ns	0.10 ns	0.62 ns	-0.01 ns	
gi	-0.41**	0.07ns	-0.35**	0.02ns	-0.28*	-0.17ns	1.12***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.13b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	seed length (SL)						
	1	2	3	4	5	6	7
1	**0.23** ns	0.25 ns	-0.41 ns	-0.45 ns	-0.17 ns	-0.30 ns	1.08**
2		**0.29 ***	-0.17 ns	1.34***	0.01 ns	-0.14 ns	-0.78*
3			**-0.08** ns	-0.44 ns	-0.42 ns	0.25 ns	0.03 ns
4				**-0.14** ns	0.45 ns	0.13 ns	-0.13 ns
5					**0.22** ns	-0.17 ns	0.04 ns
6						**-0.14** ns	-0.23 ns
7							**-0.37**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.14a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
		Seed diameter (SD)					
1		0.058 ns	0.15 ns	-0.17 ns	0.10 ns	-0.24**	0.28 ns
2	-0.00 ns		-0.10 ns	-0.16 ns	0.08 ns	0.05 ns	-0.39*
3	-0.10 ns	0.12 ns		-0.18 ns	0.14 ns	-0.45***	0.23 ns
4	-0.03 ns	0.00 ns	-0.16 ns		-0.09 ns	-0.13 ns	0.57**
5	-0.04 ns	0.12 ns	-0.40***	0.06 ns		-0.01 ns	-0.038 ns
6	-0.06 ns	0.17 ns	0.53***	0.14 ns	-0.02 ns		-0.11 ns
7	0.78***	0.23*	0.10 ns	0.03 ns	0.41***	-0.18 ns	
gi	-0.03ns	-0.16***	-0.23***	-0.03ns	-0.14***	0.03ns	0.56***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.14b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

	1	2	3	4	5	6	7
		Seed diameter (SD)					
1	**0.08***	0.01 ns	-0.17 ns	-0.05 ns	-0.02 ns	-0.28**	0.51***
2		**0.09***	0.04 ns	-0.03 ns	0.12 ns	-0.05 ns	-0.06 ns
3			**0.01** ns	-0.11 ns	-0.31***	0.39***	-0.11 ns
4				**0.06** ns	0.09 ns	-0.05 ns	-0.22**
5					**0.09 ****	-0.24**	0.12ns
6						**-0.13***	-0.24**
7							**-0.20***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.15a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Seed thickness (ST)			
	1	2	3	4	5	6	7
1		-0.05 ns	0.21**	-0.05 ns	-0.03 ns	-0.08 ns	0.36**
2	0.01 ns		-0.14 ns	-0.03 ns	-0.02 ns	0.12 ns	-0.33*
3	-0.01 ns	0.01 ns		-0.10 ns	0.22**	-0.12 ns	0.07 ns
4	0.04 ns	-0.03 ns	-0.01ns		-0.15 ns	-0.09*	0.07 ns
5	0.06 ns	0.00 ns	-0.24**	0.15ns		0.06 ns	-0.04 ns
6	0.01 ns	0.08 ns	0.30***	0.20*	-0.04ns		-0.19 ns
7	0.33***	0.07 ns	-0.02ns	0.06ns	0.10ns	-0.11ns	
gi	0.01ns	-0.09**	-0.21***	-0.01ns	0.02ns	0.09**	0.19***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.15b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Seed thickness			
	1	2	3	4	5	6	7
1	**0.06***	-0.04 ns	-0.07 ns	0.04 ns	0.01 ns	-0.14 ns	0.20**
2		**0.02** ns	-0.00 ns	0.01 ns	-0.00 ns	-0.03 ns	-0.01 ns
3			**0.01** ns	0.05ns	-0.23**	0.20**	-0.08 ns
4				**0.06** ns	0.10 ns	0.05 ns	-0.06 ns
5					**0.01** ns	-0.16*	0.03 ns
6						**-0.09***	-0.08 ns
7							**-0.06***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.16a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Pod length (PDL)			
	1	2	3	4	5	6	7
1		-0.04 ns	-0.35 ns	-0.17 ns	-0.56**	0.42*	-0.20 ns
2	-0.04ns		0.04 ns	-0.20 ns	0.07 ns	-0.07 ns	0.30 ns
3	0.19ns	-0.08 ns		0.00 ns	0.35 ns	-0.37 ns	0.07 ns
4	0.56*	0.24 ns	0.16 ns		0.07 ns	-0.31 ns	0.42 ns
5	-0.14ns	-0.22 ns	-0.47 ns	-0.07 ns		0.01 ns	-0.26 ns
6	0.10ns	-0.08 ns	0.45 ns	0.00 ns	-0.14 ns		-0.11 ns
7	0.74**	-0.34 ns	0.07 ns	0.14 ns	0.62 **	0.04 ns	
gi	-0.38***	0.21*	-0.07ns	-0.06ns	-0.24**	0.03ns	0.50***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.16b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Pod length (PDL)			
	1	2	3	4	5	6	7
1	**0.20***	-0.30 ns	0.01 ns	0.23 ns	-0.14 ns	-0.14 ns	0.35 ns
2		**-0.06** ns	0.01 ns	0.12 ns	0.04 ns	-0.06 ns	-0.46*
3			**0.02** ns	0.04 ns	-0.29 ns	0.39 ns	-0.13 ns
4				**-0.13** ns	0.26 ns	0.09 ns	0.10 ns
5					**0.20***	-0.37 ns	0.24 ns
6						**-0.04** ns	-0.10 ns
7							**-0.18***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 10.17a: Estimation of GCA, SCA, and REC effects and the actual value of yield and yield related components

				Pod diameter (PDD)			
	1	2	3	4	5	6	7
1		-.022 ns	-.078 ns	-.011 ns	-.021 ns	0.008 ns	-0.056 ns
2	0.005 ns		0.065 ns	-.058 ns	0.012 ns	-.024 ns	-0.044 ns
3	0.040 ns	-.030 ns		0.026 ns	0.056 ns	-.064 ns	0.107 ns
4	0.065 ns	0.015 ns	0.000 ns		0.013 ns	-.047 ns	0.020 ns
5	0.020 ns	-.000 ns	0.005 ns	-.020 ns		0.022 ns	-0.020 ns
6	-.060 ns	-.045 ns	0.115 ns	-.010 ns	-.015 ns		-0.074 ns
7	0.160**	0.075 ns	0.005 ns	-.010 ns	0.035 ns	-.085 ns	
gi	-.023 ns	-.006 ns	-.035*	0.013 ns	-.022 ns	-.011 ns	0.083***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 10.17b: Estimation of MAT and NMAT effects and the actual value of yield and yield related components

				Pod diameter (PDD)			
	1	2	3	4	5	6	7
1	**0.033** ns	-.026 ns	0.024 ns	0.015 ns	-.011 ns	-.103*	0.101*
2		**0.00** ns	-.015 ns	-.003 ns	0.000 ns	-.056 ns	0.048 ns
3			**0.016** ns	-.034 ns	-.009 ns	0.089*	-0.037 ns
4				**-.017** ns	-.000 ns	-.003 ns	-0.019 ns
5					**0.002** ns	-.027 ns	0.007 ns
6						**-.010** ns	-0.101*
7							**-0.026** ns

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M), 1= Avanti, 2= OR-04-Du, 3=Argane, 4=ER-04-AJ, 5= TA-04-AJ, 6= Crestwood, 7= Starlight

The GCA SCA, REC, Mat, and NMAt effects of above ground and root biomass accumulation traits are presented in Table 11. There were highly significant GCA, SCA, reciprocal, maternal, and non-maternal effects for root fresh weight, biomass fresh weight, biomass dry weight, pod fresh weight, and pod dry weight. This implies that both the additive and non-additive type of gene action were important for the inheritance of these traits. Moreever, the cytoplasmic genes of the reciprocal crosses and the maternal effects had an importatnt influence in the inheritance of theser traits. In addition to this, the interaction of the cytoplasm and nuclear gene had important contribution in the expression of these traits. Earlier researchers reported that significant and positive GCA and SCA effects for plant fresh weight in common bean (Franco *et al.*, 2010). Kimani *et al* (2003) also reported significant GCA and SCA effects for root dry weight in common beans.

Table 11. Diallel analysis for above ground and underground biomass accumulation (Griffing's Method I model I)

	Mean squares				
parameters	GCA	SCA	REC	MAT	NMAT
RFWT	44.04***	37.49***	52.62***	34.38**	56.74***
RDWT	1.01ns	1.07 ns	0.84 ns	0.84 ns	0.72 ns
BFWT	16984.40**	15499.71***	15162.50***	16621.91**	14509.18***
BDWT	1548.33***	944.55***	1148.03***	1042.00***	1260.14***
PFWT	3.30***	1.02***	0.75***	1.36***	0.47**
PDWT	0.52***	0.20***	0.23***	0.30***	0.22***

Where; ns=non significant,*=significant at 5%**=highly significant at 1%, ***= highly significant at 0.1%, RFWT= root fresh weight, RDWT=root dry weight, BFWT=biomass fresh eight, BDWT= biomass dry weight, PFWT= pod fresh weight, PDWT= pod dry weight

There was significant and positive GCA effect for pod dry weight and pod fresh weight in the genotype Starlight; while Crestwood displayed positive and significant GCA effect for pod fresh weight. Only genotype TA-04-AJ exhibited positive and significant GCA effect for root fresh weight. Parents Avanti and ER-04-AJ exhibited positive and significant GCA effects for biomass fresh weight. Moreover, the variety avanti displayed positive and significant GCA effects for biomass dry weight. This implies that this variety is good general combiner for this trait.

Crosses Avanti X TA-04-AJ, Avanti X Starlight, ER-04-AJ X TA-04-AJ, and ER-04-AJ X Starlight displayed positive and significant SCA effect for pod dry weight; while crosses OR-04-DH X ER-04-AJ and ER-04-AJ X Starlight exhibited positive and significant SCA effects for root fresh weight. There were significant and positive SCA

effects in crosses Avanti X OR-04-DH, Avanti X Argane, ER-04-AJ X TA-04-AJ, ER-04-AJ X Starlight, TA-04-AJ X Starlight, and Crestwood X Starlight for biomass fresh weight; while crosses Avanti X Argane, OR-04-DH X Crestwood, ER-04-AJ X TA-04-AJ, ER-04-AJ X Starlight, and Crestwood X Starlight displayed positive and significant SCA effect for biomass dry weight. This indicates that these crosses have better performance than it would be expected from the performance of their parents.

The reciprocal crosses TA-04-AJ X Avanti, Crestwood X Avanti, Starlight X Avanti, Starlight X Argane, and starlight X TA-04-AJ displayed positive and significant reciprocal effects for pod dry weight; while reciprocal crosses Starlight X Avanti, Starlight X Argane, and starlight X TA-04-AJ, and Crest wood X Argane displayed positive and significant reciprocal effects for pod fresh weigh. Crosses Starlght X Avanti, Starlight X Argane, Crestwood X Argane, and Starlight X TA-04-AJ displayed significant and positive reciprocal effects for root fresh weight; while reciprocal crosses TA-04-AJ X Avanti, TA-04-AJ X OR-04-DH, and Crestwood X ER-04-AJ displayed positive and significant reciprocal effects for biomass fresh weight. Reciprocal crosses TA-04-AJ X Avanti, ER-04-AJ X Argane, Starlight X OR-04-DH, and Starlight X Argane exhibited positive and significant reciprocal effects for biomass dry weight. This implies that the cytoplasm of the reciprocal crosses was important in the inheritance of this trait.

The variety Avanti displayed significant and positive maternal effects for pod dry weight; while TA-04-AJ had shown positive and significant maternal effects for pod fresh weight. The variety OR-04-DH displayed positive and significant maternal effects for root fresh weight, biomass fresh weight, and biomass dry weight. This implies that the cytoplasm gene of these varieties was important inthe inheritance of these traits.

Crosses Avanti X TA-04-AJ and ER-04-AJ X Crestwood displayed positive and significant non-maternal effects for pod dry weight; while crosses Avanti X Starlight and Argane X Crestwood displayed significant and positive non-maternal effect for pod fresh weight. The non-maternal effects of crosses Avanti X TA-04-AJ, Argane X Crestwood, ER-04-AJ X Crestwood, and TA-04-AJ X Starlight were positive and significant for root fresh weght. Crosses Avanti X TA-04-AJ and ER-04-AJ X Crestwood exhibited positive and significant non-maternal effects for biomass fresh weight; while Avanti X TA-04-AJ and Argane X Starlight displayed positive and significant non-maternal effects for these

traits. This indicates that the interaction of cytoplasmic and nuclear genes had an important influence in the inheritance of these traits.

Evidence that both additive and non-additive gene effects are involved in the genetic control of the traits investigated implies that both gene effects should be considered when developing breeding schemes for the selection of superior lines. Consequently, both parents need not necessarily have high GCA during breeding because the dominance gene effects could also be exploited to enhance these traits. In contrast, the predominance of the additive gene effects suggests that the best progeny might be derived from crosses with genotypes having the greatest positive GCA. The white pea bean is a self-pollinating crop, and autogamous plants are homozygous and thus they do not make use of the dominance effects of genes at individual loci (Moreno- Gonzalel and Cubero, 1993). Usually, varieties of autogamous plants are pure lines or multi-lines whose seed are commercially produced by self-pollination, even though a few exceptions, like wheat, tobacco, cotton and tomato can produce commercial hybrids. There fore,crosses involving genotypes with greater estimates of general combining ability should be potentially superior for the selection of lines in advanced generations (Franco et al., 2001; Arunga *et al.*,2010).

The predominance of SCA variance on pod weight per plant denotes that selection for pod yield may not be made in early breeding generations (Wu et al., 2000). If dominance effects are important for a trait, the most appropriate selection methods are those that take advantage of heterosis and the general and specific combining abilities (Moreno-Gonzalel and Cubero, 1993; Arunga *et al.*, 2010).

Crestwood and Starlight had the largest pod weight per plant. Consequently, incorporating Crestwood and Starlight in white pea bean could improve yield and resistance to Common bacterial blight, angular leaf spot, floury leaf spot, bean rust, and an additional series of desirable traits. However, to improve its pod quality, other parents have to be incorporated in the programme. The quality of white pea bean pods depends on pod length and diameter, seed length, seed diameter, and seed thickness, leaf area. Long slender pods are preferred to short bobby beans and, as a result, alleles that increase pod length are of great new variety and had the largest GCA value for pod length. Hence these varieties can be valuable when breeding for increased pod length. SCA values provide important information about the performance of the hybrid relative to its parents. The SCA effect

alone has limited value in the choice of parents in breeding programmes for self-pollinated crops like bean (Cruz and Regazzi, 1994; Arunga *et al.*,2010). The SCA effect should be used in combination with other parameters, such as the hybrid mean value of a trait and the GCA of the respective parents. Thus, hybrid combinations with high means, favourable SCA estimates and involving at least one of the parents with high GCA, would tend to increase the concentration of favourable alleles. Moreover, it was observed that parents having low GCA might show good potential in varietal combinations. For example, avanti had low GCA value for pod weight while its cross with TA-04-AJ had the highest and significant SCA. Similar phenomenon of some parents has been noted in studies of upland cotton (*Gossypium hirsutum*) (Azhar and Rana,1993; Ilyas et al., 2007) and (Arunga *et al.*,2010) in white pea bean.

Table 12.1a: Estimation of GCA, SCA, and REC effects of Underground and above ground biomass accumulation

			Pod dry weight (PDDWT)				
	1	2	3	4	5	6	7
1		-0.07ns	-0.10ns	-0.18*	0.64***	0.03ns	0.35*
2	-0.06 ns		0.03 ns	0.08 ns	-0.14 ns	-0.06 ns	0.17 ns
3	0.06 ns	-0.01 ns		-0.07 ns	-0.09 ns	-0.01 ns	0.26 ns
4	-0.03 ns	0.10 ns	-0.08 ns		0.32**	-0.08 ns	0.42**
5	0.88***	-0.01 ns	-0.06 ns	-0.54***		-0.34***	0.02 ns
6	0.22*	0.22*	-0.17 ns	0.22 ns	-0.03 ns		0.16 ns
7	0.37***	-0.12 ns	0.27**	0.05 ns	0.33**	0.07 ns	
gi	-0.01ns	-0.20***	-0.09*	-0.07ns	0.05ns	0.04ns	0.28***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.1b: Estimation of MAT and NMAT effects of Underground and Above ground biomass accumulation

	Pod dry weight (PDDWT)						
	1	2	3	4	5	6	7
1	**0.21*****	-0.23**	-0.16 ns	-0.27**	0.68***	-0.05 ns	0.02 ns
2		**0.03** ns	-0.05 ns	0.02 ns	-0.04 ns	0.13 ns	-0.29**
3			**-0.01** ns	-0.10 ns	-0.04 ns	-0.21*	0.14 ns
4				**-0.07** ns	-0.50***	0.2*	-0.05 ns
5					**0.00** ns	-0.08 ns	0.19 *
6						**-0.05** ns	-0.01 ns
7							**-0.14** ***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table12.2a: Estimation of GCA, SCA, and REC effects of Underground and above ground biomass accumulation

Pod fresh weight (PDFWT)

	1	2	3	4	5	6	7
1		0.17 ns	0.10 ns	0.23 ns	-0.34 ns	0.10 ns	-0.09 ns
2	-0.29 ns		-0.40 ns	-0.11 ns	-0.07 ns	-0.15 ns	-0.00 ns
3	0.01 ns	0.06 ns		0.01 ns	0.49*	-0.34 ns	0.07 ns
4	0.11 ns	0.19 ns	-0.04 ns		0.10 ns	-0.69***	0.88*
5	0.16 ns	-0.17 ns	-0.64**	-0.09 ns		-0.49*	-0.76 ns
6	-0.32 ns	0.05 ns	0.77**	-0.06 ns	0.03 ns		0.20 ns
7	1.14 ***	0.46 ns	0.57*	0.26 ns	0.85***	-0.16 ns	
gi	-0.29***	-0.19**	-0.29***	-0.14ns	-0.08ns	0.21**	0.79***

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.2b: Estimation of MAT and NMAT effects of Underground and above ground biomass accumulation

Pod fresh weight (PDFWT)

	1	2	3	4	5	6	7
1	**0.12** ns	-0.28 ns	-0.02 ns	-0.02 ns	0.27 ns	-0.52 **	0.58**
2		**0.12** ns	0.02 ns	0.04 ns	-0.06 ns	-0.17 ns	-0.11 ns
3			**0.08** ns	-0.14 ns	-0.49**	0.60**	0.04 ns
4				**-0.02** ns ns	0.16 ns	-0.13 ns	-0.16 ns
5					**0.23** **	-0.29 ns	0.17 ns
6						**-0.09** ns	-0.51*
7							**-0.44***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 12.3 a Estimation of GCA, SCA, and REC effects of Underground and Above ground biomass accumulation

				Root fresh weight (RFWT)			
	1	2	3	4	5	6	7
1		-1.97 ns	-2.40 ns	-0.62 ns	-2.34 ns	-2.01 ns	-14.45***
2	1.19 ns		2.89 ns	4.29**	0.07 ns	1.63 ns	5.08ns
3	-1.99 ns	4.21*		-3.63*	1.60 ns	-1.04 ns	10.32**
4	-0.63 ns	3.39 ns	-2.35 ns		2.20 ns	0.59 ns	-5.09*
5	9.98***	3.96**	-4.16*	-1.16 ns		0.93 ns	12.54***
6	-0.92 ns	1.64 ns	4.14**	6.09***	-1.15 ns		4.11 ns
7	-1.35 ns	-0.34 ns	-4.80**	2.53 ns	7.78***	-1.93 ns	
gi	1.03ns	**0.37ns**	**0.95ns**	**0.03ns**	**1.56****	**-2.25*****	**-1.69****

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.3b: Estimation of MAT and NMAT effects of Underground and above ground biomass accumulation

				Root fresh weight (RFWT)			
	1	2	3	4	5	6	7
1	**0.90** ns	1.96 ns	-4.23***	-0.52 ns	8.79***	-3.49**	-2.51*
2		**1.67****	1.20 ns	2.73 ns	2.00 ns	-1.70 ns	-2.28 ns
3			**-1.34***	-0.00 ns	-3.10*	3.81**	-3.73**
4				**1.01** ns	-2.45 ns	3.41**	1.25 ns
5					**-0.28** ns	-2.54*	7.79***
6						**-1.67****	-0.52 ns
7							**-0.27** ns

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 12.4a: Estimation of GCA, SCA, and REC effects of Underground and above ground biomass accumulation

	Root dry weight(RDWT)						
	1	2	3	4	5	6	7
1		-0.34 ns	0.21 ns	-0.01 ns	0.27 ns	0.34 ns	-1.10 ns
2	-0.29 ns		0.12 ns	0.86*	0.10 ns	0.36 ns	1.33 *
3	-0.62 ns	0.66 ns		-0.72*	-0.20 ns	-0.49 ns	1.40 ns
4	-0.01 ns	0.89 ns	-0.29 ns		-0.08 ns	0.50 ns	-0.03 ns
5	0.64 ns	0.38 ns	0.22 ns	0.41 ns		0.27 ns	1.75 **
6	-0.38 ns	0.47 ns	0.34 ns	0.65 ns	0.00 ns		0.41 ns
7	-0.18 ns	0.32 ns	-1.37**	0.28 ns	0.52 ns	-0.09 ns	
gi	**0.13 ns**	**0.27 ns**	**0.03 ns**	**0.04 ns**	**0.09 ns**	**-0.33***	**-0.15 ns**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.4b: Estimation of MAT and NMAT effects of Underground and above ground biomass accumulation

	Root dry weight(RDWT)						
	1	2	3	4	5	6	7
1	**-0.12 ns**	0.26 ns	-0.66 ns	0.21 ns	0.60 ns	-0.43 ns	0.01 ns
2		**0.43ns**	0.07 ns	0.57 ns	-0.21 ns	-0.13 ns	-0.04 ns
3			**-0.16 ns**	-0.02 ns	0.22 ns	0.33 ns	-1.13**
4				**0.11 ns**	0.14 ns	0.37 ns	0.24 ns
5					**-0.16 ns**	-0.00 ns	0.75 ns
6						**-0.16 ns**	0.15 ns
7							**0.07 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M

Table12.5a: Estimation of GCA, SCA, and REC effects of Underground and above ground biomass accumulation

			Biomass fresh weight			
	1	**2**	**3**	**4**	**5**	**6**	**7**
1		70.82*	123.98**	15.66 ns	-28.29 ns	-17.69 ns	-88.16 ns
2	-133.52**		-10.62 ns	-13.47 ns	26.32 ns	53.10 ns	89.14 ns
3	-37.12 ns	26.84 ns		-39.26 ns	-60.54*	-3.88 ns	74.81 ns
4	-62.11 ns	53.81 ns	66.60 ns		132.92***	56.29 ns	108.32*
5	172.51***	87.68*	-35.31 ns	1.00 ns		-62.31*	241.09***
6	-30.33 ns	42.84 ns	4.63 ns	138.32***	-10.12 ns		178.80***
7	5.86 ns	5.81 ns	40.19 ns	-64.94*	-31.80 ns	5.51 ns	
gi	42.88**	-10.53ns	-21.67ns	35.87**	5.38ns	-18.38ns	-33.55**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.5b: Estimation of MAT and NMAT effects of Underground and above ground biomass accumulation

			Biomass fresh weight(BFWT)			
	1	**2**	**3**	**4**	**5**	**6**	**7**
1	**-12.10 ns**	-71.35*	-12.67 ns	-47.71 ns	146.36***	-38.21 ns	23.58 ns
2		**50.07*****	-10.89 ns	6.03 ns	-0.66 ns	-27.21 ns	-38.64 ns
3			**12.34 ns**	56.55 ns	-85.91**	-27.69 ns	33.47 ns
4				**2.30 ns**	-39.55 ns	116.05 ***	-61.61*
5					**-38.26****	8.16 ns	12.09 ns
6						**-19.98 ns**	31.11 ns
7							**5.63 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 12.6a: Estimation of GCA, SCA, and REC effects of Underground and above ground biomass accumulation

		Biomass dry weight					
	1	2	3	4	5	6	7
1		2.71 ns	44.61***	8.03 ns	-7.70 ns	8.11 ns	-26.11**
2	-22.48**		-5.04 ns	-11.16*	3.97 ns	19.22*	17.45 ns
3	-15.74 ns	0.79 ns		-2.62 ns	-18.48**	-11.46*	12.24 ns
4	-41.85***	4.92 ns	27.52***		19.29**	-9.50 ns	35.98**
5	41.23***	11.76 ns	-4.06 ns	-17.06*		-16.50*	10.53 ns
6	-0.89 ns	9.25 ns	-1.44 ns	0.03 ns	3.01 ns		31.46**
7	-1.11 ns	13.99*	14.91*	-41.72***	-12.57 ns	-6.09 ns	
gi	17.26***	-5.74*	-2.52ns	4.50ns	-2.38ns	-5.18ns	-5.95*

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 12.6b: Estimation of MAT and NMAT effects of underground and above ground biomass accumulation

		Biomass dry weight					
	1	2	3	4	5	6	7
1	**-5.83***	-7.62 ns	-2.49 ns	-43.06***	41.15***	2.65 ns	9.39 ns
2		**9.03***	-0.83 ns	-11.16*	-3.19 ns	-2.07 ns	9.62 ns
3			**7.41**	13.06*	-17.39**	-11.14*	12.15*
4				**-7.049**	-15.93**	4.78 ns	-30.02***
5					**-5.92***	6.64 ns	-1.99 ns
6						**-2.29 ns**	0.86 ns
7							**4.66 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M) 1= Avanti, 2= OR-04-Du, 3=Argane, 4=ER-04-AJ, 5= TA-04-AJ, 6= Crestwood, 7= Starlight

Significant mean squares due to GCA, SCA, REC, MAT, and NMAT effects were found for total nodule weight and effective nodule weight (Table 13). Thus, both the additive and non-additive gene actions were important for the inheritance of these traits. Similarly, the cytoplasm gene of the reciprocal crosses and maternal effects were also important for the inheritance of total nodule weight and effective nodule weight. Moreover, the interaction of cytoplasmic and nuclear gene have an important influence in the inheritance of these traits as the mean squares due to non-maternal effect displayed positive and significant effects.

Mean squares due to SCA, REC, MAT, and NMAT effects were highly significant for nodule count. This indicates that the non-additive type of gene actions; the cytolplasm of the reciprocal and maternal effects; and the interaction of cytoplasmic X nuclear genes were important in the inheritance of these traits. Significant mean squares ($p<0.05$ due to GCA, $P<0.01$ due to REC, $P<0.05$ due to MAT, and $P<0.05$ due to NMAT) effects was observed for tap root length; while significant mean squares due to GCA, SCA, REC, MAT, NMAT ($P<0.001$, $P<0.01$, $P<0.001$, $P<0.01$, and $P< 0.01$ respectively) were observed for root volume.

Previuos studies also reported significant GCA effect for number of nodules per plant, nodule dry weight, mean nodule weight, and plant fresh weight (Franco *et al.*, 2001). Significant SCA mean squares for these characters, except nodule dry weight, which indicates the importance of additive gene effects for the observed genetic variation for nodule dry weight.

The significance of both GCA and SCA for nodule weight and effective nodule indicates displayed the importance of both additive and non-additive (dominance/epistasis) gene effects. Pereira et al. (1993) analyzing the combining ability of F1 plants of 10 black bean lines, found significant GCA effects only for nodule number. Moreover, the significance of REC, MAT, and NMAT effects for nodule weight, effective nodule weight, and nodule count per plant showed the importance of both the cytoplasm of maternal effects, the cytoplasm of the reciprocal crosses, and the interaction of cytoplasm and nuclear gene for these traits. The existence of significant effects due to GCA indicates the possibility of genetic gain to be obtained through selection practice over the segregant population due to interracial crosses.

According the earlier findings both additive and non additive gene effects were important in the inheritance of number of nodules per plant (Kimani *et al, 2007*). However, they reported mean squares due to GCA effects were twelve times higher than those due to SCA effects. This is a clear manifestation of the predominant role of fixable additive genetic effects in the control of these traits. It implies that heritability of these traits can be exploited by carrying out selection for the desirable traits. These findings are similar with the present findings that the additive gene effect is more important than the non additive gene effects for effective nodule weight, tap root length, and root volume as the variance component due to GCA is greater than the variance component due to SCA. However, the non additive gene action is more important than the additive gene action for total nodule weight per plant and nodule count as the variance component due to SCA is greater than the variance component due to GCA. The selection of parents for breeding programs was one of the aims of this study. Thus, the estimate of the general combining ability (gi) of a parent in the diallel is an important indicator of its potential for generating superior breeding populations. A low gi estimate, positive or negative, indicates that the mean of a parent in crossing with the other does not differ greatly from the general mean of the crosses. On the contrary, a high gi estimate indicates that the parental mean is superior or inferior to that general mean. This represents a strong evidence of favorable gene flow from parents to offspring at high frequency and gives information about the concentration of predominantly additive genes (Cruz and Regazzi, 1994). Thus, crosses involving genotypes with greater estimates of general combining ability should be potentially superior for the selection of lines in advanced generations. Franco *et al.*, (2001) also reported that the Andean genotypes WAF 15 and Mineiro Precoce showed best results for nodule number, nodule dry weight, and plant fresh weight and presented the highest positive estimates of gi and these Andean cultivars show greatest potential for breeding programs aiming to select lines with superior nodulation traits. Pereira et al. (1986, 1993) also reported that WAF 15 showed good potential for increased N2 fixation as a parent.

Table 13. Griffing's Method I model I AND and hayman's diallel analysis for Root nodulation and root characters (nodule weight, effective nodule weight, nodule count, tape root length, and root volume)

			Mean squares		
Parameters	GCA	SCA	REC	MAT	NMAT
NUWT	2.33***	2.70***	1.70***	3.00***	1.23***
ENUWT	2.00***	1.95***	1.40***	2.35***	1.05***
NUCNT	188.50ns	533.86***	492.57***	661.18***	407.81***
TRL	18.15*	8.9197ns	18.16**	20.70*	15.45*
RV	93.49***	30.62**	47.79***	54.35**	43.10**

Where; ns=non significant,*=significant at 5%,**=highly significant at 1%,***= highly significant at 0.1%, GCA= General combining ability, SCA, specific combining ability, REC= reciprocal crosses, MAT= Maternal effects, NMAT= non-maternal effects.

Only the variety TA-04-AJ exhibited positive and highly significant (P<0.001) GCA effects for root volume; while Varieties Avanti, OR-04-DH, ER-04-AJ and Starlight had positive and highly significant GCA effects for total nodule weight. Varieties Avanti, ER-04-AJ, and Crestwood had positive and significant GCA effects for effective nodule weight. Only Crestwood had positive and significant (P<0.05) GCA effects for total nodule count per plant. Similarly, only Avanti had positive and significant (P<0.05) GCA effects for tap root length. This implies that the additive type of gene action of these varieties was important in the inheritance of these traits.

Crosses Argane X Starlight had highly significant (P<0.01) and positive SCA effects for root volume, while Crosses OR-04-DH X ER-04-AJ, OR-04-DH X Crestwood, OR-04-DH X Starlight, Argane X TA-04-AJ, Argane X Crestwood, Argane X Starlight, and Crestwood X Starlight had positive and significant SCA effects for total nodule weight. This implies that these crosses had more total nodule weight than the weight of their parental lines. This also implies that the non- additive type of gene action had important role in the inheritance of these traits.

Crosses Avanti X OR-04-DH, Avanti X Crestwood, OR-04-DH X ER-04-AJ, OR-04-DH X Crestwood, OR-04-DH X Starlight, Argane X Crestwood, Argane X Starlight, and Crestwood X Starlight had significant and positive SCA effects for effective nodule weight; while Crosses Avanti X OR-04-DH, TA-04-AJ X Starlight, and Crestwood X Starlight had positive and highly significant SCA effects for nodule count. Crosses OR-04-DH X TA-04-AJ, OR-04-DH X Starlight had positive and significant (P<0.05) SCA

effects for tap root length. This indicates that the non-additive type of gene action had important contribution for the inheritance of this trait.

The reciprocal crosses Argane X OR-04-DH, TA-04-AJ X Avanti, Crestwood X ER-04-AJ, and Starlight X TA-04-AJ had positive and highly significant reciprocal effects for root volume; while the reciprocal crosses OR-04-DH X avanti, Argane X Avanti, Argane X OR-04-DH, ER-04-AJ X OR-04-DH, Er-04-AJ X Argane, TA-04-AJ X ER-04-AJ, Crestwood X Avanti, Crestwood X Argane, Starlight X Avanti, Starlight X OR-04-AJ, Starlight X Argane, Starlight X ER-04-AJ, and Starlight X TA-04-AJ had positive and highly significant reciprocal effects for total nodule weight. The reciprocal crosses OR-04-DH X Avanti, Argane X Avanti, Argane X OR-04-DH, ER-04-AJ X Argane, TA-04-AJ X ER-04-AJ, Crestwood X Avanti, Crestwood X Argane, Starlight X Avanti, Starlight X OR-04-DH, Starlight X Argane, Starlight X ER-04-AJ, and Starlight X TA-04-AJ had positive and significant reciprocal effects for active nodule weight; while reciprocal crosses Argane X OR-04-DH, Starlight X Argane, Starlight X OR-04-DH, Starlight X Argane, and Starlight X ER-04-AJ had positive and highly significant reciprocal effects for nodule count. Thus, the cytoplasm of these reciprocal crosses had the important contribution for the inheritance of these traits. Positive and significant reciprocal effects were found in crosses OR-04-DH X Avanti, TA-04-AJ X ER-04-AJ, Crestwood X Argane, and Starlight X TA-04-AJ for tap root length. This implies that the cytoplasm of the reciprocal crosses for these traits had important role in the inheritance of these traits.

Varieties OR-04-DH and ER-04-AJ had positive and significant maternal effects for root volumewhile Varieties Avanti and TA-04-AJ had positive and highly significant (P<0.001) maternal effects for total nodule weight. Varieties Avanti and TA-04-AJ had positive and highly significant maternal effects for effective nodule weight. However, only the variety ER-04-AJ had positive and significant (P<0.01) Maternal effects for this nodule count. This implies that the cytoplasm gene had an impact on governing the inheritance of this trait. However, the variety ER-04-AJ had positive and significant (P<0.05) maternal effects for tap root length. This shows that the cytoplasm gene of these varieties exhibited the important contribution for the inheritance of these traits.

Crosses Avanti X TA-04-AJ, ER-04-AJ X Crestwood, and TA-04-AJ X Starlight had positive and significant non maternal effects for root volume while Crosses Avanti X OR-04-DH, Avanti X Crestwood, OR-04-DH X Argane, OR-04-DH X ER-04-AJ, OR-04-DH X TA-04-AJ, Argane X ER-04-AJ, Argane X Crestwood, Argane X Starlight, ER-04-AJ X TA-04-AJ, and TA-04-AJ X Starlight had positive and highly significant non maternal effects for total nodule weight. This implies that the interaction of cytoplasm and nuclear gene had important contribution for the inheritance of these traits.

Positive and highly significant non-maternal effects were displayed in crosses Avanti X OR-04-DH, Avanti X Crestwood, OR-04-DH X Argane, OR-04-DH X ER-04-AJ, OR-04-DH X TA-04-AJ, Argane X ER-04-AJ, Argane X Crestwood, ER-04-AJ X TA-04-AJ, ER-04-AJ X Starlight for effective nodule weight. Crosses OR-04-DH X Argane, Argane X Crestwood, and Argane X Starlight had positive and significant ($P<0.01$) non maternal effects for nodule count; while crosses Avanti X OR-04-DH, OR-04-DH X ER-04-AJ, ER-04-AJ X TA-04-AJ, and TA-04-AJ X Starlight displayed positive and significant non-maternal effects for tap root length. This implies that the interaction of cytoplasmic and nuclear gene had important contribution for the inheritance of these traits. These findings are similar reports of previous studies (Kimani et al., 2007) as they reported both GCA and SCA were highly significant for basal root length, root dry weight, number of nodules, leaf area, and grain yield in common bean.

Table 14.1a: Estimation of GCA, SCA, MAT, NMAT, and REC effects and actual values of nodule and nodule characters

	Root volume						
	1	2	3	4	5	6	7
1		-0.54 ns	0.72 ns	-1.18 ns	-3.99*	-0.06 ns	-13.43***
2	-0.50 ns		2.81 ns	2.86 ns	-1.98 ns	1.20 ns	5.20ns
3	-1.27 ns	7.00**		-3.61 ns	-1.92 ns	1.76 ns	12.54**
4	-1.50 ns	-1.27 ns	-3.77 ns		0.40 ns	1.06 ns	-5.42 ns
5	9.75 ***	2.00 ns	-3.52 ns	-1.52 ns		-1.56 ns	-1.72 ns
6	-0.50 ns	3.00 ns	-2.93 ns	6.50***	-0.50 ns		5.15 ns
7	-2.00 ns	1.35 ns	-5.27*	0.09 ns	5.77**	-1.77 ns	
gi	0.80ns	-0.46ns	1.50ns	-0.82ns	3.74***	-2.43**	-2.32**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 14.1b: Estimation of MAT and NMAT effects and actual values of nodule and nodule characters

	Root volume						
	1	2	3	4	5	6	7
1	**0.57** ns	0.73 ns	-4.87**	-0.41 ns	8.98***	-2.12 ns	-2.31 ns
2		**1.80****	2.17 ns	-1.41 ns	-0.00 ns	0.15 ns	-0.19 ns
3			**-3.03*****	0.92 ns	-0.70 ns	-0.94 ns	-1.98 ns
4				**1.66***	-3.39 ns	3.79*	-1.31 ns
5					**-0.20** ns	-1.35 ns	6.24***
6						**-1.05** ns	-0.46 ns
7							**0.26** ns

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 14.2a: Estimation of GCA, SCA, MAT, NMAT, and REC effects and actual values of nodule and nodule characters

	total nodule weight (TNUWT)						
	1	2	3	4	5	6	7
1		0.13 ns	-0.14 ns	-0.35**	-0.99***	0.21ns	-0.90***
2	1.5***		-0.02 ns	1.29***	-0.28*	1.84***	0.81***
3	0.59***	1.02***		-0.43***	0.37**	0.42**	2.27***
4	0.05ns	0.38**	0.68***		0.03ns	-1.64***	-0.08ns
5	-0.22ns	0.10ns	-0.72***	0.35**		-0.49***	-0.08ns
6	1.31***	-0.63***	0.67***	0.15ns	-0.11 ns		1.14***
7	1.02***	0.61***	0.84***	0.58***	1.23***	-0.24 ns	
gi	0.17**	0.19***	-0.10ns	0.20***	-0.62***	0.30***	-0.13**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 14.2b: Estimation of MAT and NMAT effects and actual values of nodule and nodule characters

	Total nodule weight (NUDWT)						
	1	2	3	4	5	6	7
1	**0.61*****	0.91***	-0.04 ns	-0.57***	-0.60***	0.47***	-0.17 ns
2		**-0.01** ns	1.01***	0.38**	0.34**	-0.85***	0.04 ns
3			**-0.02** ns	0.70***	-0.47***	0.45**	0.28**
4				**-0.01** ns	0.58***	-0.08ns	0.00ns
5					**0.23*****	-0.57***	0.43***
6						**-0.23*****	-0.58***
7							**-0.58*****

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 14.3a: Estimation of GCA, SCA, MAT, NMAT, and REC effects and actual values of nodule and   nodule characters

	Effective nodule weight (EFNudWT)						
	1	2	3	4	5	6	7
1		0.49**	-0.06ns	-0.39**	-0.84***	0.43**	-0.40 ns
2	1.62***		0.02ns	0.98***	-0.11ns	0.56***	0.57*
3	0.69***	0.70***		-0.43***	-0.12ns	0.88***	2.00***
4	-0.20ns	0.11ns	0.39**		0.22 ns	-1.44**	0.47 ns
5	-0.20ns	0.05ns	-0.11ns	0.32*		-0.34**	0.24 ns
6	1.23***	-1.17***	0.70***	-0.08ns	-0.01ns		1.05***
7	0.88***	0.47**	0.75***	0.51**	1.08***	-0.05ns	
gi	0.26***	0.08ns	-0.12*	0.20***	-0.59***	0.18**	-0.02ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 14.3b: Estimation of MAT and NMAT effects and actual values of nodule and nodule characters

	Effective nodule weight (EFNudWT)						
	1	2	3	4	5	6	7
1	**0.57***	0.83***	0.16ns	-0.70***	-0.63***	0.55***	-0.21ns
2		**-0.21**	0.95***	0.38**	0.40**	-1.06***	0.16ns
3			**0.05ns**	0.40**	-0.02ns	0.55**	0.18ns
4				**0.07ns**	0.40**	-0.24ns	-0.07ns
5					**0.14**	-0.26*	0.41**
6						**-0.11ns**	-0.47***
7							**-0.52***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table14.4.a: Estimation of GCA, SCA, MAT, NMAT, and REC effects and actual values of nodule and nodule characters

			Nodule count (NUCUNT)				
	1	2	3	4	5	6	7
1		32.45***	-7.41 ns	-7.36 ns	3.51 ns	5.81 ns	-12.43 ns
2	10.10 ns		0.88 ns	-4.48 ns	0.10 ns	-1.54 ns	18.19 ns
3	-7.55 ns	24.90**		4.64ns	-12.05*	8.39 ns	21.18 ns
4	-0.03 ns	-9.42 ns	-19.52*		4.80 ns	1.88 ns	-9.47 ns
5	10.20 ns	-1.53 ns	-7.75 ns	6.63 ns		-22.29***	39.26**
6	-17.82*	-1.77 ns	20.87**	-1.06 ns	-2.75 ns		54.89***
7	2.95 ns	22.07**	29.52***	17.71**	3.44 ns	4.16 ns	
gi	-2.09ns	-1.89ns	-1.71ns	0.52ns	-2.45ns	7.22*	0.39ns

Table

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 14.4b: Estimation of MAT and NMAT effects and actual values of nodule and nodule characters

			Nodule count (NUCUNT)				
	1	2	3	4	5	6	7
1	**-0.31** ns	13.86 ns	-6.42 ns	7.74 ns	9.53 ns	-16.55*	-8.15 ns
2		**3.45** ns	22.27**	-5.41 ns	-5.96 ns	-4.26 ns	7.21 ns
3			**0.82** ns	-12.88 ns	-9.55 ns	21.00**	17.29**
4				**7.46 ****	-1.81 ns	-7.57 ns	-1.16 ns
5					**-0.98** ns	-0.81 ns	-6.99 ns
6						**0.96** ns	-8.20 ns
7							**-11.41***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 14.5a Estimation of GCA, SCA, MAT, NMAT, and REC effects and actual values of nodule and nodule characters

	Tape root length						
	1	2	3	4	5	6	7
1		1.72 ns	0.08 ns	-0.36 ns	-2.83*	1.22 ns	0.95 ns
2	4.86**		0.08 ns	0.75 ns	3.12*	-2.48*	4.98*
3	-2.70 ns	-3.35 *		0.12 ns	-1.73 ns	-0.41 ns	1.30 ns
4	-1.85 ns	0.01 ns	-0.76 ns		0.68 ns	-0.68 ns	1.76 ns
5	-0.87 ns	0.16 ns	-1.70 ns	4.70***		0.77 ns	1.59 ns
6	0.70 ns	-2.15 ns	2.90*	2.19 ns	2.05 ns		0.02 ns
7	0.22 ns	-0.80 ns	-0.96 ns	-0.90 ns	2.85*	-0.55 ns	
gi	1.19*	0.54ns	-0.58ns	-0.59ns	0.29ns	0.58ns	-1.44**

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 14.5b: Estimation of MAT and NMAT effects and actual values of nodule and nodule characters

	Tape root length						
	1	2	3	4	5	6	7
1	**0.05** ns	3.24*	-1.96 ns	-0.67 ns	-0.55 ns	-0.24 ns	0.18 ns
2		**-1.57****	-0.99 ns	2.81*	2.10 ns	-1.47 ns	0.79 ns
3			**0.79** ns	-0.32 ns	-2.12 ns	1.22 ns	-1.73 ns
4				**1.23***	3.84 **	0.07 ns	-2.10 ns
5					**0.37** ns	0.79 ns	2.50*
6						**-0.89** ns	0.36 ns
7							**0.02** ns

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M), 1= Avanti, 2= OR-04-Du, 3=Argane, 4=ER-04-AJ, 5= TA-04-AJ, 6= Crestwood, 7= Starlight

The GCA mean square was significant for rust disease (Table 15). This implies that the additive type of gene action had an impact on the inheritance of rust resistance. Significant SCA effect was found for angular leaf spot. This suggests that the non-additive gene action had important influence in the inheritance of this disease.

Table 15: Mean squares for angular leaf spot, common bacterial blight, rust, and resistance to floury spot severity (Griffing's Method I model I)

Parameters	Mean squares				
	GCA	SCA	REC	MAT	NMAT
ALS	0.13ns	0.16*	0.12ns	0.15ns	0.12ns
CBB	0.16ns	0.13ns	0.15ns	0.21ns	0.12ns
Rust	0.31*	0.18ns	0.07ns	0.16ns	0.04ns
FLS	0.22ns	0.09ns	0.11 ns	0.05ns	0.13 ns

Where; GCA=general combining ability, SCA=specific combining ability,REC= reciprocal effects, MTA=maternal effects, NMAt=non maternal effects, ALS=Angular leaf spot, CBB=common bacterial blight, FLS=Floury leaf spot

Generally, negative and lower GCA effects were important in the combining ability studies of diseases, because negative and low GCA effects indicate the contriution of disease reducing additive genes to the progeny populations. Variety starlight showed negative and significant maternal effect was for Angular leaf spot. This implies that the cytoplasm of this variety with negative and significant maternal effects displayed the maximum contribution for resistanc to Angular leaf spot severity. Only the cross OR-04-DH X ER-04-AJ had negative and significant (P<0.05) maternal effects for Angular leaf spot. This indicates that the interaction of cytoplasmic and nuclear gene exhibited important contribution for the inheritance of resistance to Angular leaf spot. The reciprocal crosss Argane X OR-04-DH had negative and significant (P<0.05) reciprocal effect for common bacterial bligh. This indicates that the cytoplasmic gene of this cross displayed important contribution for resistance to common bacterial blight. t everity. Only variety Starlight had negative and significant (P<0.05) maternal effect for resistance to common bacterial blight.

The variety TA-04-AJ displayed negative and highly significant GCA effect for Rust. Only crosses Avanti X Starlight and TA-04-AJ X Crestwood exhibited negative and significant SCA effects for rust disease. This implies that the non additive type of gene action was important in the inheritance of resistance to rust. The variety ER-04-AJ had

negative and significant (P<0.05) maternal effects for rust disease. Earlier findings reported that the mean square of GCA and SCA effects were significant and positive for rust disease severity. Implies that both the additive and non additive genes were important for resistance to rust severity in soybean (M.KIYOWA *et al.*, 2008).GCA was twelve times as large as SCA, suggesting the dominant role of additive gene effects (Osiru*et al.,* 2001). Negative and lower GCA effects was diserable in this study because it indicated a larger contribution towards resistance; while positive values suggested towards susceptibility (Lokko *et al., 2004,* M.KIYOWA *et al.*, 2008*).* Mugisha (2008*)* was also reported significant and negative GCA, SCA, reciprocals, maternal and non-maternal effects in common bean for fusarium root rot severity. This implies implies that the predominance of additive, non-additive, cytoplasm, and the interaction of cytoplasm and nuclear gene for resistance to fusarium root rot in in some of his crosses and genotypes.

Table 16.1a: Estimation of GCA, SCA, and REC effects for disease score for CBB, ALS, Rust, and Floury disease severity (1-9 scale)

	Resistance to Angular leaf spot						
	1	2	3	4	5	6	7
1		-0.15 ns	0.14 ns	0.16 ns	0.01 ns	-0.13 ns	0.11 ns
2	0.00 ns		-0.24 ns	0.21 ns	-0.12 ns	0.03 ns	0.43 ns
3	0.16 ns	-0.13 ns		0.03 ns	0.17 ns	0.09 ns	0.13 ns
4	0.09 ns	-0.37 ns	-0.07 ns		0.09 ns	-0.05 ns	0.62*
5	0.23 ns	0.00 ns	-0.16 ns	-0.32 ns		0.07 ns	0.66**
6	0.00 ns	0.00 ns	0.18 ns	0.09 ns	-0.01 ns		0.15 ns
7	0.06 ns	0.12 ns	0.09 ns	0.00 ns	0.36 ns	0.22 ns	
gi	0.02ns	-0.07ns	-0.02ns	0.04ns	-0.01ns	-0.09ns	0.12*

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 16.1b: Estimation of MAT and NAMT effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity

	Resistance to Angular leaf spot						
	1	2	3	4	5	6	7
1	**0.08ns**	-0.13 ns	0.09 ns	0.03 ns	0.23 ns	-0.08 ns	-0.14 ns
2		**-0.05ns**	-0.07 ns	*-0.30 *	0.14 ns	0.05 ns	0.05 ns
3			**0.00ns**	-0.05 ns	-0.08 ns	0.17 ns	-0.03 ns
4				**0.02ns**	-0.25 ns	0.06 ns	-0.14 ns
5					**0.07ns**	-0.10 ns	0.15 ns
6						**-0.01ns**	0.10 ns
7							**-0.12***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 16.2a: Estimation of GCA, SCA, and REC effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity

	Resistance to Common bacterial blight						
	1	2	3	4	5	6	7
1		0.02 ns	0.05 ns	0.11 ns	-0.09 ns	-0.15 ns	-0.00 ns
2	0.00 ns		-0.20 ns	0.14 ns	0.04 ns	-0.07 ns	0.07 ns
3	0.06 ns	-0.41*		0.23 ns	0.13 ns	0.05 ns	0.25 ns
4	0.12 ns	-0.19 ns	0.05 ns		-0.09 ns	0.24 ns	0.93 ns
5	0.15 ns	0.00 ns	0.00 ns	-0.23 ns		-0.12 ns	-0.03 ns
6	-0.02 ns	-0.07 ns	0.16 ns	0.00 ns	-0.30 ns		0.17 ns
7	0.00 ns	0.18 ns	0.06 ns	0.03 ns	0.12 ns	0.55**	
gi	-0.01ns	0.00ns	0.04ns	0.03ns	-0.03ns	-0.14ns	0.11*

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 16.2b: Estimation of MAT and NAMT effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity.

	Resistance to Common bacterial blight						
	1	2	3	4	5	6	7
1	**0.04 ns**	-0.11 ns	0.11 ns	0.05 ns	0.09 ns	0.04 ns	-0.18 ns
2		**-0.08ns**	-0.25 ns	-0.15 ns	0.06 ns	0.11 ns	0.12 ns
3			**0.09ns**	-0.07	-0.10 ns	0.19 ns	-0.16 ns
4				**-0.02ns**	-0.22 ns	0.14 ns	-0.08 ns
5					**-0.01ns**	-0.18 ns	0.00 ns
6						**0.11ns**	0.30*
7							**-0.13***

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 16.3a: Estimation of GCA, SCA, and REC effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity.

	Resistance to Rust Severity						
	1	2	3	4	5	6	7
1		0.08 ns	-0.15 ns	-0.03 ns	-0.19 ns	0.19 ns	-0.54*
2	-0.12 ns		0.16 ns	0.16 ns	-0.13 ns	-0.10 ns	0.06 ns
3	0.14 ns	-0.05 ns		0.14 ns	-0.13	-0.23	0.08 ns
4	0.23 ns	0.20 ns	0.20 ns		0.09 ns	0.15	0.32 ns
5	0.06 ns	-0.06 ns	0.12 ns	-0.23 ns		-0.01 ns	-0.98***
6	0.16 ns	0.08 ns	0.01 ns	0.05 ns	0.07 ns		-0.27 ns
7	0.07 ns	0.15 ns	0.03 ns	-0.03 ns	0.00 ns	-0.29 ns	
gi	-0.03ns	-0.10ns	0.11ns	0.12*	-0.16**	0.06ns	0.00ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 16.3b: Estimation of MAT and NAMT effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity.

	Resistance to Rust Severity						
	1	2	3	4	5	6	7
1	**0.08 ns**	-0.14 ns	0.10 ns	0.03 ns	0.01 ns	-0.01 ns	0.01 ns
2		**0.06 ns**	-0.07 ns	0.01 ns	-0.10 ns	-0.08 ns	0.10 ns
3			**0.04 ns**	0.05 ns	0.11 ns	-0.12 ns	0.00 ns
4				**-0.12***	-0.08 ns	0.08 ns	0.10 ns
5					**0.02 ns**	-0.05 ns	-0.01 ns
6						**-0.09 ns**	-0.19 ns
7							**0.01 ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M)

Table 16.4a: Estimation of GCA, SCA, and REC effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity.

	Resistance to floury leaf spot						
	1	2	3	4	5	6	7
1		0.11 ns	0.00 ns	-.09 ns	0.04 ns	-.04 ns	0.03 ns
2	0.22 ns		-.08 ns	0.12 ns	-.05 ns	0.17 ns	0.11
3	0.00 ns	0.00 ns		-.06 ns	-.22 ns	0.28 ns	-0.00 ns
4	0.00 ns	-.29 ns	0.00 ns		0.33*	-.10 ns	0.09 ns
5	0.29 ns	0.29 ns	0.00 ns	-.06 ns		-.27 ns	-0.03
6	0.00 ns	0.29 ns	-.29 ns	0.00 ns	-.00 ns		0.33 ns
7	0.00 ns	0.00 ns	0.00 ns	-.00 ns	0.29 ns	0.00 ns	
gi	-.05ns	0.04ns	-.08ns	0.02 ns	0.18*	-.04ns	-0.08 ns

Where, diagonal and above diagonal are specific combining ability (SCA) and below diagonals are reciprocals (REC),*=significant at 5%,**=Significant at 1%,***=Significant at 0.1%, gi=combining ability of the genotypes

Table 16.4b: Estimation of MAT and NAMT effects for disease score (1-9 scale) for CBB, ALS, Rust, and Floury disease severity.

	Resistance to floury leaf spot Severity						
	1	2	3	4	5	6	7
1	**0.07ns**	0.16 ns	-.11 ns	.04 ns	0.18 ns	-.07 ns	-0.11 ns
2		**0.01ns**	-.05 ns	.26 ns	0.25 ns	0.28 ns	-0.05 ns
3			**-.04ns ns**	).07 ns	0.01 ns	-.25 ns	0.00 ns
4				**).03ns**	-.13 ns	-.03 ns	-0.07 ns
5					**-.03ns**	0.03 ns	0.28 ns
6						**0.00ns**	-0.04 ns
7							**-0.04ns**

Where, above the diagonals are non maternal effects (NM) and the diagonals are maternal effects (M), 1= Avanti, 2= OR-04-Du, 3=Argane, 4=ER-04-AJ, 5= TA-04-AJ, 6= Crestwood, 7= Starlight

4.3. Relative contribution

The relative contribution of GCA effects was higher than all the other components (SCA, REC, Mat, and Nmat) for pod length and seed thickness with respective relative contribution of 32.15 and 34.48 % (Table17). This implies that the additive gene action predominant in the inheritance of these traits. Mulugeta (2006) reported similar findings that the relative contribution of GCA was greater than the relative contribution of SCA for number of seeds per pod; while only the relative contribution of GCA was important for the inheritance of number of seed per plant and 1000-seed weight. Results of previous studies indicated the predominance of additive gene effects for number of days to flowering (Barelli et al., 1999; Silva *et al.,* 2004). According to Machida *et al* (2010), the relative contribution for general combining ability (GCA) effects, ranging between 73 and

87 % of the cross sum of squares, superior to SCA effects for all traits (anthesis date, kernel endosperm modification, protein content, tryptophan content, and quality index), except grain yield where SCA accounted for about 69 % of the hybrid variation in maize. The authers indicated that genes with additive effects were predominant for quality traits and anthesis date.

High relative contribution due to SCA effects were displayed in traits number of branches on the main axis, number of nodes on the main axis, internode length, root dry weight, biomass fresh weight, 100-seed weight, grain yield, pod length, pod diameter, seed length, pod fresh weight, nodule weight, effective nodule weight, and nodule count. This indicates that the inheritance of most of the studied traits predominatly influenced by non-additive gene action. Rodrigues *et al*. (1998) reported higher contribution of dominance gene effects for plant height; while Arunga *et al*. (2010) reported additive gene effect play a major role for plant heightSilva et al. (2004) reported that non-additive gene effect was important for the inheritance of number of pods per plant.

The highest relative contribution due to reciprocal effects were displayed in traits days to maturity, days to flowering, plant heght, tap root length, root fresh weight, biomass dry weight, root volume, number of pods per plant, number of seeds per plant, number of seeds per pod, pod dry weight, and leaf area. This implies that the cytoplasm of the reciprocal crosses had the maximum contribution for the inheritance of these traits. Arunga et al. (2010) reported the greater contribution of the reciprocal effects in common bean for yield and yield related traits and other nodule characters. The relative contributions of maternal and non-maternal effects in all of the twenty eight traits were low. This implies that the cytoplasm of the maternal effects and the interaction of the cytoplasm and nuclear gene had the minimum impact on the inheritance of these traits. The relative contribution of SCA was higher than GCA and other variance components ie., REC, MAT, and NMAT effects which displayed (43.09%) relative contribution for rust and (37.69%) for angular leaf spot. This implies that the non-additive type of gene action had the highest contribution for the inheritance of resistance reaction for these disease severities. The relative contribution of REC was high for common bacterial blight and floury leaf spot i.e., 30.9 and 29.3 %, respectively. This indicates that the cytoplasm of the reciprocal crosses had the highestcontribution for the resistance reaction of these diseasess.

Table 17. Relative contributions of GCA, SCA, Reciprocals, maternal, and non maternal effects for seed yield and some yield related characters for dry bean

Parameters	GCA	SCA	REC	MAT	NMAT
MD	7.74	27.88	32.19	8.89	23.31
DFPF	17.06	13.36	34.74	11.04	23.80
NBMA	7.94	31.35	29.80	5.05	25.86
NNMA	5.02	41.97	25.80	7.76	19.45
INL	12.43	36.31	25.72	6.73	18.82
PH	7.79	25.39	32.42	12.85	21.54
TRL	10.54	18.12	36.90	12.02	22.42
RFWT	8.22	24.49	34.38	6.42	26.48
RDWT	9.43	34.81	27.45	11.35	16.96
BFWT	9.59	30.62	29.95	9.38	20.47
BDWT	11.85	25.30	30.76	7.98	24.11
RV	17.64	20.22	31.56	10.25	20.33
HSWT	27.88	32.45	19.80	5.30	14.55
GY	11.19	36.28	25.52	14.20	12.83
NPPT	13.98	27.84	28.87	6.30	23.02
NSPPT	5.97	29.01	30.83	18.55	15.65
NSPD	5.31	12.51	40.32	7.14	34.72
PDL	32.15	26.15	20.86	9.60	11.23
PDD	20.47	30.73	24.39	6.17	18.25
SL	25.96	33.94	20.04	6.86	13.21
Sd	28.78	36.71	17.13	7.09	10.29
ST	34.48	24.12	20.64	8.36	12.41
PFWT	27.43	29.65	21.80	11.30	9.82
PDWT	18.23	24.41	27.67	10.36	19.33
NUWT	9.79	39.70	24.95	12.60	12.96
ENUWT	10.66	36.56	26.23	12.53	14.02
NUCNT	3.45	34.21	31.56	12.11	18.67
LA	12.26	20.70	34.81	6.57	25.65

MD= days to maturity, DFPF= days to fifty percent flowering, NBMA= number of branches on the main axis, NNMA= number of nodes on the main axis, INL= inter node length, PH= plant height, TRL=Tape root length, RFWT=root fresh weight, RDWT=root dry weight, BFWT=biomass fresh weight, BDWT= biomass dry weight, RV=root volume, HSWT= handred seed weight, GY=grain yield, NPPT= number of pods per plant, NSPPT= number of seed per plant, NSPD= number of seed per pod, PDL= pod length, PDD=pod diameter, SL= seed length, SD=Seed diameter, ST= seed thickness, PFWT= pod fresh weight, PDWT=pod dry weight, NUWT= nodule weight, ENUWT= effective nodule weight, NUCNT= nodule count, LA= leaf area.

Table 18. Relative contributions of GCA, SCA, Reciprocals, maternal, and non maternal effects for LR, CBB, ALS, and FLS severity For Dry bean varieties

Sources	GCA	SCA	REC	MAT	NMAT
Leaf Rust	21.02	43.09	17.85	11.21	6.84
CBB	9.61	28.39	30.93	12.95	18.12
ALST	8.66	37.69	26.68	9.69	17.28
FLS	17.66	23.59	29.32	4.08	25.35

5. SUMMARY AND CONCLUSIONS

Breeders cross two or more varieties or inbreedlines inorder to creat variability for a character, which they wish to improve. In the proceses, they have to take decisions regarding the choice of parents to be employed for hybridization and the choice of cross (crosses) effected to them. For qualitaitive characters the choice of parents for hybridization may not pose a serious problem. However, the task becomes difficult for quantitatively inherited characters like grain yield. As a result, information on the genetic mechanism that governs the inheritance of quantitative characters has got paramount importance in devising an effective breeding strategy. The present study was, therefore, undertaken to determine general combining ability (GCA), specific combining ability (SCA), reciprocals (REC), maternal (MAT), and non-maternal (NMAT) effects of the parents and crosses, respectively, in a 7 X 7 diallel cross of white pea bean commercial varieties for yield and yield related traits, fresh and dry matter accumulation, root and nodulation traits and disease resistance. In addition, relative contribution of GCA, SCA, REC, MAT, and NMAT effects were also determined.

In this study 28 traits and four disease score in a 1-9 scale were analysed. The analysis of varance revealed significant differences between the parents and crosses in all of the traits, except in three traits (days to maturity, days to flowering, and number of nodes on the main axis). The significant variation among the entries indicates considerable genetice variation is created by the crossing program. Significant GCA mean squares were observed in all of the characters, except eight (number of branches on the main axis, plant height, days to maturity, number of seed per plant, number of seed per pod, root dry weight, and nodule count). The significant GCA mean squares indicated variability of GCA among the parents and this suggests that genetic gain is achievable through selection over the segregating population. Significant SCA mean squares were found for all the studied traits, except eight traits (number of nodes on the main axis, plant height, maturity date, days to flowering, number of seed per pod, leaf area, root dry weight, tape root length) out of the twenty eight traits. The significant GCA and SCA mean squares exhibited the importance of both additive and dominance gene effects.

Almost all of the characters displayed significant reciprocal mean squares, except for

number of nodes on the main axis, days to maturity, pod length, and root dry weight. This implies that that the cytoplasm of the reciprocal crosses had important role in the inheritance of these traits. The positive mean squares of the maternal effects of the genotypes displayed the importance of the cytoplasm of the maternal effects of the genotypes. Significant non-maternal mean squares were observed in all of the cahrcters, except nine traits (number of nodes on the main axis, maturity date, days to fifty percent flowering, internode length, grain yield, number of seed per plant, pod length, pod diameter, and root dry weight). This indicates the importance of the interactions of the cytoplasm and nuclear gene for the inheritance of these traits.

Both the additive and non-additive gene actions were important for days to flowering, internode length, 100-seed weight, grain yield, number of pods per plant, pod length, pod diameter, seed length, seed diameter, seed thickness, root fresh weight, biomass fresh weight, biomass dry weight, pod fresh weight, pod dry weight, effective nodule weight, and root volume, as they displayed significant GCA and SCA effects. It was only for number of branches on the main axis, nodule count per plant, and number of seed per plant that the dominance gene action was important for the inheritance of these traits as it displayed significant mean squares. Both additive and non-additive types of gene action were important for number of nodes on the main axis, number of seed per plant, and nodule weight per plant. However, the non-additive type of gene action was more important than the additive type of gene action as the variance component due to SCA was greater than the variance component due to GCA effects. Predominance of additive genetice variation in the F_2 generation would indicate higher heritability and possibility of identifying transgressive segregants. This also indicates that conventional breeding methods like recurrent selection and pedigree selection can be employed to improve traits.

OR-04-DH proved to be good general combiner for seven characters (days to fifty perecent flowering, plant height, pod length, nodule weight, effective nodule weight, and nodule count). Therefore, this variety can be selected as good parent for future hybridization. Starlight is good general combiner for days to flowering and maturity. Moreever, it is good general combiner for number of seed per pod, hundred seed weight, grain yield, seed diameter, seed thickness, pod length, pod dry weight, and pod fresh weight. Thus, this parent can be selected as good combiner parent for future

hybridization, especially in improving seed size and weight.

Avanti is good general combiner for number of seed per plant, biomass fresh weight, biomass dry weight, nodule weight, effective nodule weight, and tap root length. ER-04-AJ was good general combiner for biomass fresh weight, biomass dry weight, nodule weight, and effective nodule weight. Therefore, these varieties can be used as a parent to improve these traits in breeding programs. The variety TA-04-AJ is good general combiner for leaf area, number of pod per plant, root fresh weight, and root volume. Crestwood is good general combiner for leaf area, pod fresh weight, nodule weight, effective nodule weight, and nodule count. The variety TA-04-AJ exhibited negative and significant GCA effect for rust resistance reaction. The variety starlight displayed negative and significant maternal effect for angular leaf spot and common bacterial blight. These varieties can have paramount significance for further use in hybridization program to improve the respective traits. The cross OR-04-DH X ER-04-AJ exhibited negative and significant non-maternal effect for angular leaf spot.

The cross TA-04-AJ X Crestwood is the best hybrid for earliness and the hybrid ER-04-AJ X TA-04-AJ is also best hybrid as late maturing variety for long growing season areas, such as Jimma condition. The value of SCA effect clearly suggested that there are crosses, such as Argane X Avanti that produced positive SCA effect for grain yield. There were significant and negative SCA effects in crosses Avanti X Starlight and TA-04-AJ X Starlight for leaf rust resistance. The reciprocal cross Argane X OR-04-DH displayed negative and significant reciprocal effect for common bacterial blight. This indicates that crossing of the two parents made better progress than the *per se* performance of either parents. The present study displayed that, there were many crosses manifesting significant significant SCA effects for yield and yield related traits, biomass accumulation, and root nodulation and root characters that would appear to be promising to choose transgressive segregants.

Evidence that both additive and non-additive gene effects are involved in the genetic control of the traits investigated implies that both gene effects should be considered when developing breeding schemes for the selection of superior lines. Consequently, both parents need not necessarily have high GCA during breeding because the dominance gene effects could also be exploited to enhance these traits. In contrast, the predominance

of the additive gene effects suggests that the best progeny might be derived from crosses with genotypes having the greatest positive GCA.

SCA values provide important information about the performance of the hybrid relative to its parents. The SCA effect alone has limited value in the choice of parents in breeding programmes for self-pollinated crops like bea.The SCA effect should be used in combination with other parameters, such as the hybrid mean value of a trait and the GCA of the respective parents. Thus, hybrid combinations with high means, favourable SCA estimates and involving at least one of the parents with high GCA, would tend to increase the concentration of favourable alleles. Moreover, it was observed that parents having low GCA might show good potential in varietal combinations. For example, avanti had low GCA value for pod weight while its cross with TA-04-AJ had the highest and significant SCA.

Maternal and non-maternal reciprocal effects were significant for some of the traits suggesting that the choice of parents is critical for these traits. The best general combiners were Crestwood and Starlight for pod weight, pod length, pod diameter, seed length and seed diameter, grain yield, handred seed weight,OR-04-DH For plant height, TA-04-AJ and Crestwood for lean area. These varieties can be incorporated into white pea bean bean breeding programmes. Generally, the choice of female parent is critical in a breeding programme. Moreover, it is recommended that crosses portraying reciprocal effects should not be mixed with direct crosses.

FUTURE LINE OF WORK

- ✓ As this study is a one year and one location experiment, it has to be repeated across location or year to obtain more reliable information

- ✓ Nutritional and canning quality need to be further analyzed

- ✓ Identification of superior Recombinant Inbred Lines should continue

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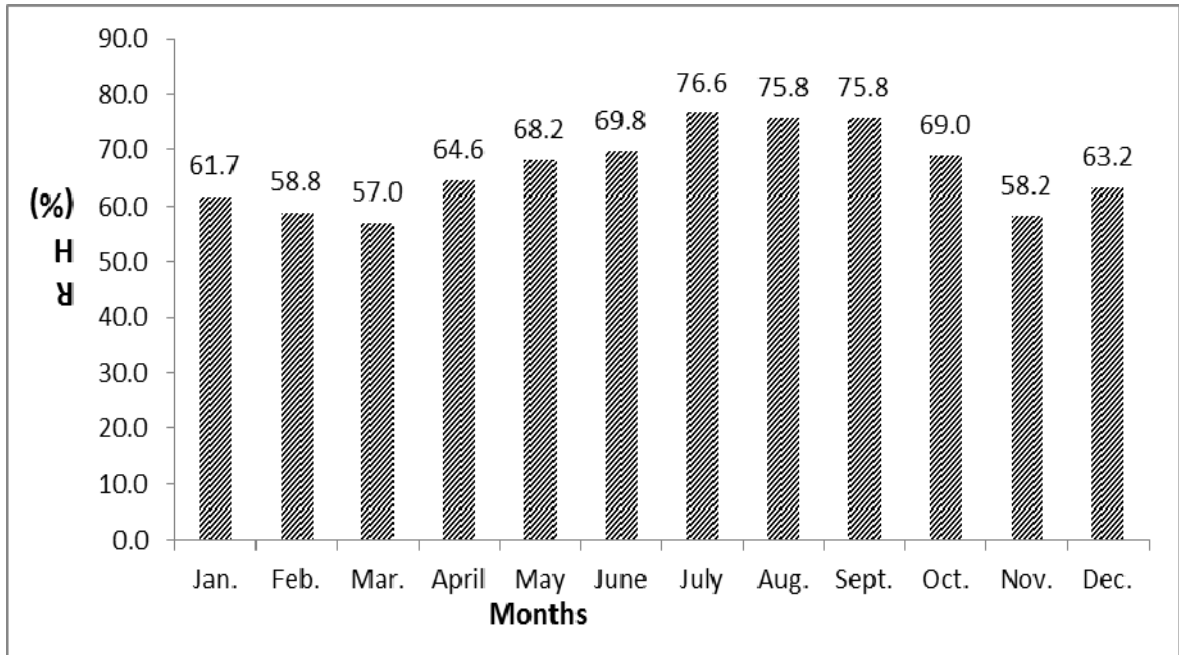
8. Appendices
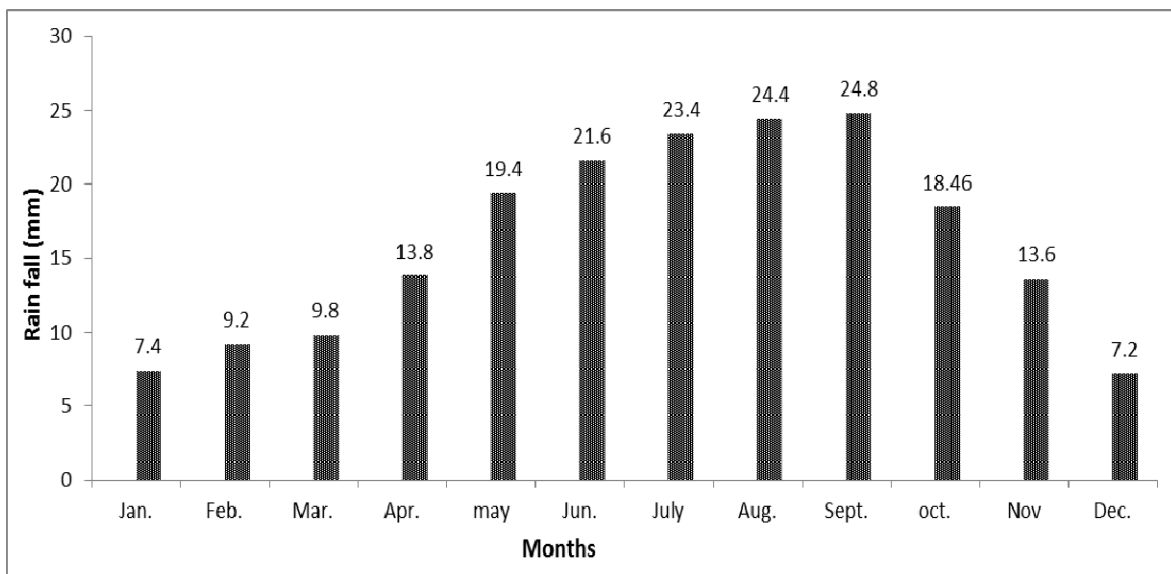
Appendix figure 1. Mean Monthly rain fall (mm) of Jimma Agricultural research center (2007-2011 Years).
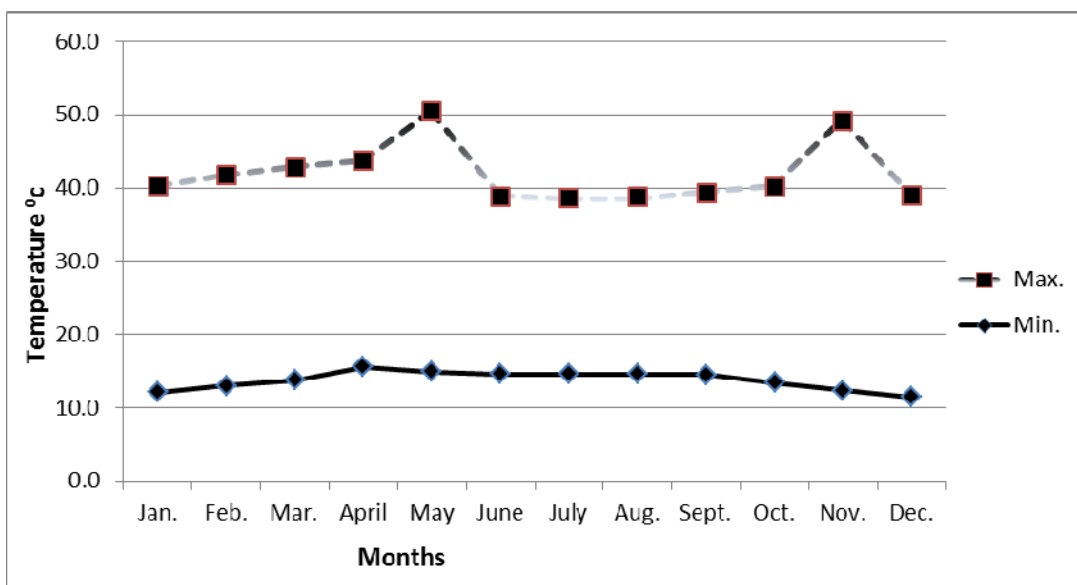
Appendix figure 2. Average Monthly maximum and minimum temperature (^{0}C) of Jimma Agricultural research center (2007-2011 Year).

Appendix figure 3. Mean monthly relative humidity (%) of Jimma Agricultural research center (2007-2011 Year).