BIOMETRICAL ANALYSIS FOR GENE ACTION, HETEROSIS AND COMBINING ABILITY OF YIELD AND OTHER AGRONOMIC TRAITS IN COMMON BEAN

(*Phaseolus vulgaris* L.)

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By

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ABSTRACT

Two separate sets of experiments, 4 x 4 complete diallel involving four varieties (Roba-1, Atendaba, Gobe Rasha and Dimitu) and 6 x 6 half diallel excluding reciprocal crosses using six varieties/genotypes (Roba-1, Atendaba, Gobe Rasha, EMP - 236, FEB-147, EAP – 4) hybridized in all possible combinations, were conducted at Bako Agricultural Research Center in 2005/06 main cropping season. The former experiment was carried out to examine the maternal effects while the latter experiment was conducted to identify the major gene action, combining ability (general and specific) and the extent of heterosis (average heterosis and heterobeltosis) in common bean (Phaseolus vugaris L.). In the present study, heterosis occurred in varying degrees for different traits studied. This may be due to the joint action of favourable combinations of genes at different loci. Percent heterosis over the mid-parent and the better parent for grain yield ranged from -17.75 to 39.01 % and from -7.97 to 27.16 %, respectively. ♀Gobe Rasha x ♂EAP-4 and ♀FEB-147 x ♂EAP-4 manifested significant and positive heterosis. These crosses gave 39.01 % and 27.16 % for ♀Gobe Rasha x ♂EAP-4 and 24.98 % and 17.80 % for FEB-147 x EAP-4 for heterosis over the mid parent and the better parent, respectively. The heterosis in the former hybrid seemed to be due to genetic diversity observed between the two parents for most of their traits. On the other hand, ♀FEB-147 x♂ EAP-4 was the only hybrid that showed significant and positive heterosis over the mid parent for seed crude protein. Combining ability analysis of 6 x 6 diallel for common bean revealed that general combining ability (GCA) variances were significantly different among parental lines for all the traits studied except number of nodes per main stem, crude protein and grain seed yield. The highest grain yield was 30.95 g per plant in ♀Gobe Rasha x ♂EAP-4, while the least was 20.19 g per plant obtained from ♀EAP-4. On the other hand, the highest crude protein content per seed (22.84 %) was recorded by ♀Atendaba x ♂Gobe Rasha while the lowest was obtained by Atendaba x EAP-4 (18.20 %). Hybrid, ♀Atendaba x ♂EAP-4, also had the lowest organic matter content (95.15 %). Among twenty-one characters studied, eleven (days to flowering, days to physiological maturity, plant height, number of seeds per plant, pod length, hundred seed weight, crude protein, anthracnose per leaf, anthracnose per pod, angular leaf spot and floury leaf spot) showed significant SCA variances. The significance of both GCA and SCA indicates the importance of both additive and non-additive type of gene actions. However, the ratio of estimate of variance component due to GCA to that of SCA indicates the preponderance of non-additive type of gene action in the inheritance of the above traits. The result, therefore, suggested the breeding methods such as recurrent selection that exploits additive and dominant genetic effects. For the traits showed non-additive gene action, the suggested strategy would also be an interpopulational breeding procedure, to exploite the heterosis related to the non-additive gene effects. The F_1 crosses obtained by the combination of either FEB-147 or EMP-236 produced unique seed color as compared to their parents. This may be due to the action of modified gene. The reciprocal effects for all the traits weren't significant except for seed size, indicating the non-significance of selection for male and female parents since maternal effects weren't evident in these traits and selection based on nuclear genes inheritance would be effective. However, for seed size, ♀Roba x ♂Gobe Rasha and ♀Gobe Rasha x ♂Dimitu showed significant and negative reciprocal effects. This effect, therefore, is important as it directs the plants breeder in the choice of which parent will be the male or female.

Key Words/ Phrases: Combining ability, General combining ability, Gene action, Heterosis, *Phaseolus vulgaris*, Specific combining ability

1. INTRODUCTION

The common or haricot bean (*Phaseolus vulgaris* L.) is probably native to tropical South America (Onwueme and Sinha, 1999). Mexico has been recognized as the most probable center of origin, or at least, as the center of primary diversification (Purseglove, 1987). Africa is considered to be a secondary center for bean genetic diversity (CGIAR, 2005).

It is a self-pollinated diploid (2n = 22) and a member of the leguminosae tribe phaseoleae, sub family papilionideae (Adams *et al.,* 1985). These authors further indicated that cultivated forms are herbaceous annuals, determinate or indeterminate in growth, and bearing papilionaceous flowers in axillary and terminal racemes. Common bean is the best known and most widely cultivated species of *Phaseolus* (Purseglove, 1987). Among food legumes, common bean is the third most important after soybean [*Glycine max* (L.) Merr.] and pea nut (*Arachis hypogaea* L.) (Sharee *et al.,* 1999).

Common bean plays a great role in human nutrition and market economy in rural and urban areas of Eastern Africa (Soniia *et al.*, 2000). It is nutritionally rich, especially in protein and iron, as well as a good source of dietary fiber and complex carbohydrates (CGIAR, 2005). Beans are considered as a low status food, “the meat of the poor". It is an important and cheap source of protein in the diets of many people in tropical countries and is used as a supplement for foods rich in carbohydrates such as rice, maize, and other cereals (CIAT, 1968). The percentage of protein in the seeds of wheat, rice, and maize ranges from 8 to 12 %, whereas it exceeds 20 % in the legume seeds such as common bean. Per capital consumption of the common bean and its contribution to nutrition is highest in Africa where beans provide one-third of total protein intake and one-eighth of total calories (CIAT, 1989). In addition to high quality protein, a single serving (1 cup) of beans provides at least half the USDA-recommended daily allowance of folic acid (a B vitamin that is especially important for pregnant women) and 25-30 percent of the daily-recommended iron levels. Similarly, the same serving of beans provides 25 percent of the daily requirements of magnesium and copper, and 15 percent of potassium and zinc (CGIAR, 2005).

The largest producing countries are Kenya, Uganda, D.R Congo, Burundi, Tanzania, Rwanda and Ethiopia (Soniia *et al.,* 2000). Bean is an important cash crop of farmers in many parts of Ethiopia (Belay Samane *et al*., 1998). It is also an important export commodity of the country.

Bean is an attractive crop for farmers, because of its adaptability to different cropping systems and short growing cycle (CGIAR, 2005). The suitable areas for common bean production using present technology can be an altitude range of 1400 – 2000 m for rain fed conditions and ≥ 700 m for irrigation production where as well distributed rainfall of 350 – 550 mm for over 70 to 90 days is required depending on altitude (Amare Abebe, 1987). It is also indicated that relative humidity should not be very high, not above 75 %; however, the effect of relative humidity is also correlated to temperature. Maximum and minimum mean temperature of < 30 - 32 ^{o}C and > 10 -12 ^{o}C are required, respectively. Belay Samane *et al. (*1998) studied haricot bean agro ecology in Ethiopia. Their results suggested that the agro ecology of bean growing in Ethiopia is diverse. Altitude ranges from 1200 to 2212 m, while annual rainfall varies from 580 to 1950 mm. The length of the growing period is from as short as 80 to 220 days, accordingly the seasonal rainfall during the growing period ranges from 120 to 1636 mm.

Recent report estimates global production of dry beans at 18 million metric tons annually, with a market value of US $10.7 billion (CGIAR, 2005). The same source further indicated that dry beans account for 57 percent of the world's food legume production, having twice the production and market value of chickpeas, the next leading food pulse. Another 3 million metric tons of snap beans are also produced annually. Nearly 80 percent of dry bean production occurs in the developing countries on small-scale farms.

In production and acreage haricot bean is the fifth most important pulse in Ethiopia. In the 2004/05 cropping seasons a total of 55,700 ha of land of private peasant holding was in haricot bean production (CSA, 2005). However, MOARD (2005) reported the national area of haricot bean production is currently estimated at 245,597 ha of land and about 2.1 million quintals are produced currently.

The contribution of this crop in terms of area under pulses and production of crops to the country's total is about 13 % and 9 %, respectively (CSA, 2002). The average yields of beans obtained by the farmers are extremely low. The current national average yield of haricot bean is about 6.15 quintals per hectare (MOARD, 2005). These low yields may be attributed to a combination of several yield constraints among which low yield potential, diseases (anthracnose, angular leaf spot, rust, common bacterial blight, floury leaf spot, bean common mosaic virus, bean golden mosaic virus) and insect pests (bean stem maggot) play major roles. Moreover, about 60 percent of bean production in developing countries suffers from low soil phosphorus availability (CGIAR, 2005).

Strategies employed by common bean breeders to improve yield include early generation testing, ideotype breeding, selection for physiological efficiency, and selection based on genotypic performance and combining ability across gene pools of *Phaseolus vulgaris* (Kelly *et al*., 1998). Genotypic performance and combining ability are also critical for yield improvement. The present study, therefore, geared toward selection of promising genotypes from a diverse genetic base and utilized for hybridization with released varieties as one of the strategies for improving the productivity and quality of common bean with the following objectives.

2. LITERATURE REVIEW

2.1. HETEROSIS

The term heterosis was first coined by Shull in 1914. It was proposed to denote the stimulation in size and vigor in a hybrid as an expression of hybrid vigor. The increased vigor that is frequently observed in F_1 progeny following a cross of inbred lines, cultivar, or clonal lines is known as hybrid vigor or heterosis (Stoskopf *et al*., 1993).

According to Singh (1993), hybrid vigour has been used as a synonym of heterosis. It is generally agreed that hybrid vigour describes only the superiority of hybrids over their parents, although heterosis describes other situations as well. But a vast majority of the cases of heterosis are cases of superiority of hybrids over their parents. This superiority may be yield, quality, disease and insect resistance, general size or the size of specific parts, growth rate, enzyme activity, adaptability or plant uniformity etc (Singh, 1993; Stoskpf *et al*., 1993).

The few cases where hybrids are inferior to their parents may also be regarded as cases of hybrid vigour in the negative direction. Singh (1993) also discussed that earliness in many crops is agronomically desirable. It may be argued that the earliness of F_1 hybrids may be due to a faster development in them so that their negative phase is replaced by the reproductive phase more quickly than in their parents.

The heterosis is expressed in relation to average of two parents (relative heterosis), the better parent (heterobeltiosis) and a standard variety/check (standard heterosis or economic or useful heterosis) (Singh, 1993).

Exploitation of heterosis is considered as one of the outstanding achievements of plant breeding. In self-pollinated crops, the utilization of heterosis depends mainly upon the direction and magnitude of heterosis (Singh *et al*., 2004). In some self-pollinated crops, heterosis is large enough to be used for production of hybrid varieties. The chief drawback in the use of hybrid varieties in self pollinated crops like beans is not the absence of sufficient heterosis, but the greater difficulty encountered in the production of large quantities of hybrid seed (Singh, 1993).

Manipulation of plant breeding systems such as apomixis and male sterility (genetic and cytoplasmic) can be suggested to alleviate such kind of problems.

Studies of heterosis also provide useful information about combining ability of the parents and their usefulness in breeding programmes. Estimation of heterosis over the better parent may be useful in identifying true heterotic cross combinations (Singh *et al*., 2004).

The study carried out so far in common bean regarding heterosis is not satisfactory; however, many have been reporting in related beans. From the thirty-six F_1 hybrids of bush bean tested, significant yield heterosis above mid parent and above better parent were reported (Nienhuis and Singh, 1983) in 29 and 17 hybrids, respectively. Positive heterosis (26.4 % – 123.8 %) over the mid-parent in 31 crosses, and F_1s yielding higher (23.7 % – 91.8 %) than the better parent in 20 crosses was reported (Sharee and Carlos, 1995) in common bean. Heterosis was also estimated in F_1, F_2, F_3 and backcross generations of diallel cross in *Phaseolus aureus*. The result indicated that hybrid vigour for yield compared with the mid-parent and better parent was noted (Singh and Singh, 1974).

In contrast to the above studies, Melaku Ayale (1993) reported non-significant heterosis in common bean for seed yield. Nevertheless, his report clearly indicated that most crosses yielded in excess of the best parent for other characters. For number of seeds per plant, only one cross gave significant heterosis over the best parent. Although not significant, 10 crosses exhibited positive heterosis over the better parent for the same character. Days to flowering, days to maturity, plant height, pod length, number of seeds per pod and 100 seed weight showed significant heterosis over the mid parent and better parent.

Investigation of heterosis in 29 different hybrids of mung bean resulting from 8 x 8 diallel, excluding reciprocals indicated pronounced hybrid vigour for yield and most of the yield components (days to 50 % flowering, days to maturity, plant height, clusters per plant, pods per plant, pods per cluster, pod length, seeds per pod, 100-seed weight and grain yield per plant) (Reddy *et al.,* 2003). Heterosis values of 110.77 and 77.54 % over the mid parent and better parent, respectively, were recorded for grain yield per plant. The authors further reported that heterosis for yield was generally accompanied by heterosis for yield components. Similarly, Krishnan *et al*. (2003) reported that the highest heterosis over the mid parent and the better parent of 185.74 and 153.94 %, respectively, for seed yield per plant in the F_1 hybrid. High heterosis for seed yield was manifested through components heterosis, i.e. pods per plant and clusters per plant.

Study of heterosis in 42 different hybrids of mung bean (*Vigna radiate*) resulting from 7 x 7 complete diallel, including reciprocals indicated hybrid vigour for yield and most of the yield components (Loganathan *et al.*, 2001). The result showed that heterosis to the extent of 58.74 % and 52.65 % over the mid-parent and better parent, respectively, was recorded for grain yield per plant. Jabagirdar (2001) also studied heterosis in mung bean. His result showed that the average mid-parent and better parent heterosis were maximum for seed yield per plant, pods per plant, branches per plant and clusters per plant. However, the average heterosis for days to 50% flowering and maturity over mid and better parent was negative, respectively.

In contrast to the above studies, Rainey and Griffiths (2004) reported non-significant heterosis for yield components including pod number, seed number, and seeds per pod in snap bean whereas, Melaku Ayale (1993) reported for grain yield in common bean.

2.2. DIALLEL CROSS ANALYSIS

The diallel cross has proved to be of considerable value to plant breeders in making decisions concerning the type of breeding system to use and in selecting breeding materials that showed the greater promise for success. It has also been used successfully by quantitative geneticists attempting to gain a better understanding of the nature of gene action involved in determining quantitative traits, which are of the utmost importance in agriculture as well as in evolution (Gardner and Eberhart, 1966).

Diallel cross is used to describe a procedure in which sets of inbred lines are inter-crossed in a diallel fashion (Julia, 1989). Diallel analysis has been extensively used in both self and cross-pollinated species to understand the nature of gene action involved in the expression of quantitative traits (Singh, 1993). There are two approaches for diallel analysis: Hayman's graphical approach (Hayman, 1954) and Griffing's numerical approach (Griffing, 1956).

In the present study, the latter one is used for analysis. Griffing's numerical approach is based on the estimation of general combining ability and specific combining ability variances and effects. Griffing (1956) has given four different methods for diallel analysis, depending on material included in the experimentation (Parent, F_1's and reciprocals; parents and F_1's (without reciprocals); F_1's and reciprocals (without parent); F_1's (without parents and reciprocals).

Diallel analysis provides a sensitive approach to large-scale studies of quantitative characters (Singh, 1993). He also noticed that the analysis yields reliable information on the components of variance, and general combining ability and specific combining ability variances and effects. Thus the diallel analysis gives considerable information about the fixed set of parents used in the study information that can be useful for the selection of parents that have general combining ability in a series of crosses and good specific combining ability for specific pairs of parents. However, the disadvantage of the diallel mating design is that it is difficult to evaluate a large number of parental lines due to the number of crosses required, and that no direct estimate of gene effects can be made.

In bean breeding, we are usually interested in studying a specific set of parents, and therefore, the genetic interpretations we can make are limited to the estimate of general combining ability effects and specific combining ability effects (Julia, 1989).

2.2.1. COMBINING ABILITY

The ability of the inbred line to transmit desirable performance to the hybrid progeny is referred to as combining ability (Johan and David, 1995). A combining ability test is employed to specify the ability of an individual parent, or in some cases two specific parents, to produce high-yielding progeny. A parent that has high combining ability is inferred to be a parent whose progeny have good performance (Stoskopf *et al*., 1993). In other words, general combing ability (GCA) of an inbred line is the average contribution that the inbred makes to hybrid performance in a series of hybrid combinations in comparison to contribution of other inbred lines to hybrid performance in the same series of hybrid combinations (Johan and David, 1995). The authors also specified that the inbred lines identified as having superior GCA are crossed in all possible pairs (diallel crossing) to create single crosses, which are then evaluated in yield trials for specific combining ability (SCA).

GCA values indicate the importance of genes with predominantly additive effects. Parents with the greatest GCA are potentially superior and may be included in breeding programs to select new inbred lines in advanced generations (Rodrigues *et al*., 1999). Estimates of significantly positive or negative GCA values indicate superior or inferior parents compared with the other parents in the diallel.

Specific combining ability is the contribution of an inbred line to hybrid performance in a cross with a specific inbred line, in relation to its contributions in crosses with an array of specified inbred lines (John and David, 1995). For example, two specific parents may have very high-yielding progeny, whereas one of the parents when crossed with a third parent results in lower-yielding progeny (Stoskopf *et al*., 1993). Specific combining ability evaluates non-additive gene action whereas general combining ability evaluates additive portion of the genetics effects. As for SCA, which depends predominantly on non-additive effects of the genes, it allows to identify populations, which are potentially more useful to liberate variability in the segregating generations (Machado *et al*., 2002).

Several studies were undertaken on general and specific combining ability for yield and other characters on common bean and related crops. Mak and Yap (1980) found both GCA and SCA to be significant in long bean for crude protein, number of pods per plant, number of seeds per pod, seed weight and pod length.

In choice of common bean parents based on combining ability estimates, Machado *et al.* (2002) obtained significant GCA and SCA for grain yield while Singh and Singh (1974) reported significant GCA and SCA for grain yield, seed size, pod number, cluster number and pods per cluster in common bean.

Mean squares in common bean for general combining ability were significant at $p \leq 0.01$ for all the traits (days to flowering, days to maturity, plant height, pod length, pod per plant, seeds per pod seeds per plant and 100 seed weight) measured except for seed yield per plant (Melaku Ayale, 1993). Specific combining ability was also significant at $p \leq 0.1$ for days to flowering and pod length and significant at $p \leq 0.05$ for days to maturity and number seeds per pod. The mean squares due to SCA were not significant for seed yield, plant height, number of pods per plant, number of seeds per plant and 100 seed weight.

Similar findings were reported by Tadesse Mebrahtu and Ali Mohamed (2003) in that significant variation was observed for protein in common bean; Ali and Bhadra (1985) for grain yield per plant, pods per plant, pod length and 100 seed weight in mung bean; Jabagirdar (2001) for days to flowering, days to maturity, plant height, 100 seed weigh and grain yield in mung bean.

2.2.2. GENE ACTION

There are three basic groups of gene action. These are additive gene effects, dominance deviations and interaction or epistatic deviations.

Additive gene effects are those due to gene action whereby the effects on a genetic trait are enhanced by each additional gene, either an allele at the same locus or genes at different loci. Each additional allele adds an equal increment to genotypic value and the result forms a linear relationship. Therefore, at a given locus, genes that showed no dominance are said to act additively.

Dominance deviation is the gene action, which deviates from additive effects such that the heterozygote is more like one parent than other. It is a property of dominance alleles at a locus, and in statistical terms represents interactions between alleles, or within-locus interactions.

Dominance gene effects in self pollinating crops like beans are of little use. Only those crops where hybrids are readily made and showed significant heterosis can dominance gene effects be exploited. In beans, the only genetic effects we can use are additive and additive x additive gene effects because the genetic state of an inbred line is homozygosity at all loci (Julia, 1989). Therefore, in breeding we look for the best combination of genes that combine additively to improve quantitatively inherited traits.

Interaction or epistatic deviation occurs when the genotypic value may contain an additional deviation due to non-additive combination when the alleles at one locus influence the expression of alleles at one or more other loci. Three kinds of interaction are known:

Additive x additive
Additive x dominance
Dominance x dominance

Plant breeding and selection of a self-pollinating crop can capitalize only on additive x additive types of gene action.

In diallel analysis approach, gene action is deduced through the estimates of GCA and SCA variances and effects (Singh and Chaudhary, 1985). The GCA component is primarily a function of the additive genetic variance. But if epistasis is present, GCA will include the additive x additive interaction component as well. On the other hand, SCA variance is mainly a function of dominance variance, but it would include all the three types of epistatic interaction components, if epistasis were present (Singh, 1993).

Different workers undertook several studies on gene action for yield and other characters on common bean and related crops. Melaku Ayale (1993) reported that the ratio of GCA to SCA mean square was more than unity, for all characters (days to flowering, days to maturity, plant height, pod length, pod per plant, number of seeds per plant, 100 seed weight and gain yield), indicating that the inheritance of these characters was largely governed by additive type of gene action. The type of gene action for yield and its components was also determined using progenies obtained from biparental cross of mung bean (Chand and Rao, 2002). The result exhibited that additive genetic variances were higher in magnitude than the dominance genetic variances for all the traits except days to flowering, days to maturity, and plant height. Both additive and dominance genetic variances were significant for days to flowering, days to maturity, plant height, clusters per plant, pod per plant and grain yield per plant. The dominance ratio and average degree of dominance were greater than one for all the characters except days to flowering, suggesting the presence of interallelic (over-dominance) and interallelic interactions governing the expression of these characters.

Seven varieties of long bean, which included three local and four exotic, were crossed in a complete diallel to study the inheritance of crude protein content, protein yield, flowering date, pod yield and yield components (Mak and Yap, 1980). The result revealed that both additive and non-additive gene effects were responsible for the genetic variation in the diallel population. However, dominance variance was more important than additive variance in crude protein content, number of pods per plant and number of seeds per pod. For seed weight and pod length, additive variance was more important. The crude protein content, protein yield and number of pods per plant appeared to be controlled by over- dominance effects. Partial dominance seemed to be the case for flowering date, pod length and seed weight; complete to over-dominance for pod yield. High protein appeared to be associated with recessive genes whereas there was a general trend of high yielding parents carrying more genes that are dominant.

In choice of common bean parents based on combining ability estimates, GCA and SCA were measured by means of a complete diallel without reciprocals, using twelve cultivars/lines. Parents and corresponding F_2 segregating populations were evaluated for grain yield by a 9 x 9 triple square lattice design. Machado *et al.* (2002) found the segregating populations differed in grain yield, with predominant SCA effects, but with significant GCA effects as well. According to these results, the genetic component of SCA is about four times higher than the component of GCA, and both can be approximately estimated from the mean squares. There are indications that by adopting this procedure, the genetic variance for additive effects GCA is reduced, increasing the relative importance of the non-additive genetic effects. Thus, the results of the diallel regarding grain yield suggest that this cross scheme should be efficient in choosing the more promising segregating populations, that is, those with high SCA values, coming from parents with the highest magnitudes of GCA. Similar finding suggested that the diallel analysis of the parents and F_1 hybrids (Viana *et al*., 1999) showed that grain yield depended largely on dominance effects.

Combining ability analysis revealed that both GCA and SCA variances were important for yield, while GCA variance was more important for seed size, pod number, cluster number and Pods per cluster. The GCA variance for yield appeared to be influenced by GCA variances for yield components (Singh and Singh, 1974). In general, the crosses having high SCA had one of the parents as high combiner for yield and other traits. The diallel study of different generations, therefore, gave a comprehensive picture of combining ability.

A seven-parental diallel analysis of nutritional composition of common beans by Tadesse Mebrahtu and Ali Mohamed (2003) showed that estimates of the combining ability (general and specific) variances were significant for both protein and tannin content. The protein and tannin ratios of the general to specific combining ability variances were 1.0 and 2.0, respectively. These values indicated that both additive and non-additive genetic variances are important in the inheritance of protein. The performance of the parents for percent protein content was highly associated with their general combining ability effects. Therefore, it is suggested that caution should be exercised when selecting male and female parents in hybrid production. Recurrent selection could be suitable breeding procedures for rapid improvement.

In the study of combining ability of *Phaseolus vulgaris* L. for resistance to common bacterial blight, combining ability was determined for disease resistance in three snap bean genotypes and two common bean genotypes. In this study, Rodrigues *et al.* (1999) investigated that GCA was significant for both leaf and pod infection, whereas SCA was significant for disease reaction in pods. Differences among the GCA effects of the genotypes suggest that additive gene effects were expressed for CBB infection. SCA mean square for CBB pod reaction was highly significant ($P < 0.01$), suggesting that non-additive gene effects were involved in the expression for CBB infection of pods. The finding of additive gene effects for these traits suggests the possibility of obtaining new cultivars from segregating populations from crosses among the tested parents. The estimates of the GCA of each parent for reaction to CBB infection of leaves and pods and the standard deviation among any two-parent GCA values suggest that the parents did not differ much from the mean of all the crosses in the diallel. The lower GCA values correspond to superior parents, as lower GCA values indicate greater CBB resistance in leaves and pods

Ten snap beans were selected for differential temperature tolerance and used as parents in a complete diallel mating design (Rainey and Griffiths, 2005). Significant ($p \leq 0.01$) GCA and significant ($P \leq 0.05$) SCA were observed for yield components including pod number, seed number, and seeds per pod. Marlon *et al.* (2004) reported that additive effects were predominant for pod weight per plant, number of seeds per pod, height of the insertion of the first pod and number of days to flowering while non-additive effects were more important for number of pods per plant in snap beans.

Studies on combining ability in pulses other than haricot bean have been reported by several workers. In mung bean, Singh and Dikshit (2003) have reported from their work of combining ability studies for yield and architectural traits that variation due to parents vs. hybrids was significant for all the traits (plant height, first fruiting internodes height, clusters per plant, pod per plant, pod length, biological yield per plant, seed yield per plant, 100 seed weight and harvest index), indicating the presence of substantial heterosis in the crosses. The estimates of SCA variance were higher than GCA variance for all the traits, indicating the importance of non-additive gene effects in the expression of the traits. Similarly, Krishanan *et al.* (2003) reported that estimation of components of variance in heterosis and combining ability studies carried out in a 8 x 8 diallel of urdbean revealed the predominance of non-additive gene action for all the characters under study.

The nature of combining ability was studied in a complete 7 x 7diallel cross of mung bean for yield per plant, pods per plant, pod length and 100-seed weight. In contrast to the above results in mung bean, GCA variance was predominant for all the characters (Ali and Bhadra, 1985). Jabagirdar (2001) also reported that the estimates of general combining ability was more than the specific combining ability variance for days to 50% flowering and days to maturity, indicating the predominance of additive gene action for these traits. However, variances due to SCA were higher than GCA for plant height, 100-seed weight and seed yield, suggesting the predominance of non-additive gene action for these traits. In the other hand, both additive and non-additive gene actions were important for branches per plant, clusters per plant and seeds per pod.

On the other hand, there are many genes that do not seem to have any effect of their own but they increase or decrease the expression of other oligogenes. These genes are known as modifying genes since they modify the expression of other genes (Singh, 1993). Adams (1985) reported that modifying genes, which regulate the expression of genes for color, i.e. genes for seed color patterns, was identified in haricot bean. Singh (1993) further reported that in maize, a gene Pr has no effect of its own. But Pr modifies the action of R, which produces red color. In the presence of R, Pr changes the red color to purple. This type of gene interaction is referred to as supplementary gene action; it produces a 9: 3: 4 ratios in F_2. The author further reported that inhibitory gene action is characterized by an inhibitory gene, which steps the action of another gene, and has no effect of its own. Red color production in maize is stopped by an inhibitory gene I; the recessive allele is not inhibitory. The F_2 ratio in this case is 13: 3.

2.2.3. RECIPROCAL EFFECT

Variation in an individual's phenotype may be not only by the genotype and environment of that individual but also by maternal effects, i.e. the contribution of the maternal parent to the phenotype of its offspring beyond the equal chromosomal contribution expected from each parent (Deborah and Renata, 1987). In reciprocal crosses, a number of A♂♂ being mated to B ♀♀ and a number of B ♂♂ to A ♀♀ (Falconer and Mackay, 1996). The crossbred progeny are then measured for the characters if there is a difference between the direct F_1 hybrid and the reciprocal one using Griffing diallel analysis method 2 model 1. Testing the reciprocal effect in plant breeding is important for selection of the parents as male or female based on the performance of their progeny. Because the mother cytoplasm is passed entirely to the embryo through the egg and it is solely responsible for the cytoplasmic phenotypes of the descendants, as the pollen grain contributes practically no cytoplasm (Melo *et al*., 1997). Thus, the female parent of a given cross should be the parent, which has the positive reciprocal effects.

The studies carried out so far, in particular in reference to haricot bean, is not adequate. Few workers reported the importance of reciprocal effect in *phaseolus vulgaris* and related beans. Rainey and Griffiths (2004) reported that there was no significant reciprocal effects for yield components including pod number per plant, seed number per plant, and seeds per pod in snap bean. However, Claire *et al*. (2000) and Tadesse Mebrahtu and Ali Mohamed (2003) reported significant reciprocal effect for protein in haricot bean. Similarly, strong maternal seed size effect was observed in different species such as *Zea mays* (Eagles and Hardacre, 1979), *Raphanus raphanistrum* (Mazer *et al*., 1986) and *Brassica campestris* (Singh and Murty, 1990).

3. OBJECTIVES

General objective:

- To develop genetic combinations superior in one or more respects to the existing variety, thereby leading to better yields of quality seed

Specific Objectives:

- To estimate the magnitudes of heterosis over parents;
- To investigate the type of gene actions involved in controlling the important traits;
- To estimate the general and specific combining abilities of the varieties;
- To investigate cytoplasm/maternal effects

4. MATERIAL AND METHODS

4.1. PLANT MATERIAL

Experimental materials raised through hybridization of haricot bean (*Phaseolus vulgaris* L.) genotypes of different genetic background were used. A total of seven genotypes were involved in the hybridization (Table-1), three of which were genotypes (*EMP - 236, FEB-147, EAP - 4*) that are known to possess multiple disease resistance (MDR) for Common Bacteria Blight (caused by *Xanthomonas campestris*), Anthracnose (caused by *Colletotrichum lindemuthianum),* Rust (caused by *Uromyes phaseoli*), Angular Leaf Spot (caused by *Phaeoisariopsis griseola*) and Web Blight (caused by *Rhizoctonia solani*) and the remaining four are improved varieties (*Roba-1, Atendaba*, *Gobe Rasha and Dimitu*) released for wide adaptations. These materials were obtained from Melkassa Agricultural Research Center (MARC).

4.2. DESCRIPTION OF THE STUDY SITES

Hybridization of the genotypes was done at Melkessa and Bako Agricultural Research Center. The evaluation of the F_1 materials was done with their parents at the experimental site of Bako Agricultural Research Centre (BARC). BARC is located between 9^o 6' N 37^o 09' E in East Wollega Zone of Oromiya at an altitude of 1650 m.a.s.l. 250 km west of Addis Ababa. The area lies in a mid altitude sub humid zone with an average rainfall of 1237 mm per year. Maximum and minimum mean temperature of 27.9 ^{o}C & 13.2 ^{o}C were recorded. Previous experiences indicate that its relative humidity does not exceed 70 %.

Table 1. DESCRIPTIONS OF MATERIAL USED IN THE EXPERIMENT

Name of the varieties	Agronomic and morphological characteristics										Year of release	Breeder/maintainer	Remark
	Adaptation area		Days to flowering	Days to maturity	Plant height (cm)	Growth habit	100seed wt (g)	Seed color	Flower color	Grain yield (qt/ha)			
	Altitude (m.a.s.l)	Rainfall (mm)											
Gobe Rasha	1400 - 1900	350 - 700	42	78	40	Det. bush	40	Red	White	22.49	1998	EARO/NZARC	
Dimitu	1200 - 1800	350 - 1000	41-64	45-47	46	Bush	19	Red	White	21.40	2003	EARO/NZARC	
Roba	1400 - 1800	350 - 750	50	75 - 95	62	Int. bush	22	Cream	Cream	24.00	1999	EARO/NZARC	
Atendaba	1400 - 1900	380 - 700	46	91	89	Int. bush	34	Zebra	White	23.00	1997	EARO/NZARC	
FEB - 149	-	-	-	-	-	Int. bush	-	Cream	Purple	-	-	-	Not released
EAP – 4	-	-	-	-	-	Int. bush	-	Red	White	-	-	-	Not released
EMP - 236	-	-	-	-	-	Bush	-	Cream	Purple	-	-	-	Not released

‘-‘ it was no characterized for the traits

Source: National Seed Industry Agency, Crop Variety Register, Issue No. 1, 1998 (for the released varieties).

4.3. EXPERIMENTAL PROCEDURES

4.3.1. CROSSING TECHNIQUES

Planting had been done three times, in staggered fashion at an interval of ten days to synchronize flowering time at Bako Agricultural Research Center in 2004/05 main cropping season. It was only planted once following the flowering date of the parents using irrigation during off-season at Melkassa Agricultural Research Center to get sufficient seeds.

Two rows of female parents were alternated with one row of the respective male parents so that the male parents will be close to the female parent for easy transfer of pollen from the male parent to the female during hand pollination. Crossing was carried out on the first raceme and a maximum of five flower buds were crossed per plant. Emasculation (stripped of anthers or male parts) and pollination (transferring pollen from one flower to the stigma of another) were done by hand and the buds of the pollinated flower were covered to isolate it from being pollinated by different flower. This was done before the male parts begin to release pollen (typically just before the flower opens), when the buds in which the corolla has increased in size and has lost the green coloration of the immature bud, but has not yet started to split. Flower and hypocotyls color and growth habit were used as a marker gene to identify and remove self-fertilized hybrids during the F_1 hybrid evaluation.

4.3.2. EXPERIMENTAL DESIGN

The experiment was initially planned for 8 x 8 complete diallel. Although a number of crosses were made in 2004/05 in both main cropping and off seasons at MARC and at BARC, respectively, the seeds obtained were insufficient due to the nature of the crop at hybridization. For that reason, the number of materials was finally reduced. Six genotypes (*EMP - 236, FEB-147, EAP-4, Roba-1, Atendaba*, *and Gobe Rasha*) were used for a half diallel excluding reciprocals and four genotypes (*Roba-1, Atendaba*, *and Gobe Rasha and Dimitu*) were used for complete diallel including reciprocals. These materials were laidout in two separate sets of experiments in which twenty-one i.e. $\frac{p(p+1)}{2}$ and sixteen i.e. p^2 genotypes, including their parents in half and complete diallel, respectively, were planted in 2005/06 cropping season for evaluation at BARC experimental site. These trials were laid in Completely Randomized Block Design with three replications. Each plot had three rows with 2 m long and the distance between rows was 0.4 m. The spacing between plants within the row was 10 cm.

4.4. CHARACTERS STUDIED

Data was recorded on single plant basis for most of the traits except for days to flowering and days to physiological maturity (colleted on plot basis). Ten plants were randomly selected for the data collection following to descriptors of common bean (Fischer, 1993) were used for characterization and preliminary evaluation of bean germplasm (appendix 1):

- Number of days to flowering (DEF): number of days from date of emergence to the stage when 50 % of the plants in a plot had one or more flowers.
- Days to physiological maturity (DPM): number of days from date of emergence to the stage when 95 % of the plants in a plot have reached physiological maturity.
- Plant height (PLH): the distance from the soil surface to the tip of the main stem in cm.
- Pod length (PL): the distance between the two ends of the pod in cm.
- Number of pods per plant (PPP): the total number of pods recorded on a plant.
- Number of seeds per pod (SPO): the total number of seeds recorded on a pod.
- Number of seeds per plant (SPP): the total number of seeds recorded on a plant.
- Number of branches per plant (BPP): the total number of primary branches on main stem.
- Number of nodes per plant (NPP): the total number of nodes per plant.

- 100 seed weight (HSW): the weight of 100 seeds counted by seed counter.
- Seed yield (YIE): the total grain yield obtained from the plant in gram
- Disease reaction (DR): disease severity data were colleted at maturity. The CIAT scale of 1-9 disease severity (Makini and Makelo, 1995) was used by plant pathologist of Bako Agricultural Research Center as a measure of the degree of infection for Common Bacteria Blight (*Xanthomonas campestris*), Anthracnose *(Colletotrichum lindemuthianum),* Floury leaf spot, and Angular Leaf Spot (*Phaeoisariopsis griseola*): 1- 3 = was resistant, 4 - 6 moderately resistant and 7 - 9 susceptible.
- Leaf area (LA): the middle part of the leaf was measured using leaf area meter in cm^2.
- Crude protein: Nitrogen value multiplied by 6.25.

LABORATORY ANALYSIS

The laboratory analysis was done at International Livestock Research Institute (ILRI). Crude extracts of protein fractions were obtained by solubilisation in water and NaCl 4 % (Baudolin, and Maquet, 1999). Crude protein content (N x 6.25) was determined by semi micro-Kjeldhahl method applied to dried flour.

4.5. STATISTICAL ANALYSIS

The inheritance of quantitative differences often depends on gene differences at many loci, the effects of which are not individually distinguishable (Falconer and Mackay, 1996). The traits are usually expressed in terms of metric units such as length, weight, time, or proportions, and because of this it requires a great use of statistics in the data analysis. Analysis of variance (ANOV) and combining ability analysis were performed in MSTAT-C (Freed, 1987) and AgroBase software programs (Agrobase, 2000), respectively. Data for combining ability was analyzed according to Griffing's Model I, Method 1 for 4 x 4 reciprocal and Model I, Method 2 for 6 x 6 non-reciprocal diallel crosses (Griffing, 1956). Mean separation was done using Duncan's multiple range test (Freed, 1987). Disease data was transformed through square root transformation before executing analysis of variance.

The percentage of heterosis over the mid parent (average heterosis %) and over the better parent (heterobeltosis %) were estimated as deviation of F_1 value from the mid-parent values and better parent as suggested by Matzinger *et al.* (1962) and Fonsecca and Patterson (1968), respectively. The differences in the magnitude of heterosis were tested following the procedure given by Panse and Sukhatme (1961).

4.5.1. ANALYSIS OF HETEROSIS

4.5.1.1. RELATIVE HETEROSIS

The heterosis expressed in relation to average of two parents involved in the cross is termed relative heterosis,

$$(H\%) = \left(\frac{F_1 - MP}{MP}\right) \times 100$$

Where,

$$MP = \frac{(\ P_1 + P_2\ )}{2}$$

$$SE(F_1 - MP) = \sqrt{\frac{3MSe}{2r}}$$

4.5.1.2. HETEROBELTIOSIS

The heterosis expressed in relation to the better parent of the cross is termed heterobeltiosis*:*

$$(H\%) = \left(\frac{F_1 - BP}{BP} \right) \times 100$$

$$SE(F_1 - BP) = \sqrt{\frac{2MSe}{r}}$$

Where,

MSe = error mean squares for parents;
F_1 = the average performance of a cross;
P_1, P_2 is the average performance of parents;
BP = mean of better parents value;
MP=mean of parents
r = number of replications.
P = parents

Significant of average heterosis and heterobeltosis were tested by multiplying their corresponding SE value with table'‘t’ value at error degrees of freedom and 1 and 5 per cent probability level, i.e. Critical Difference = S.E. x ‘t’ value (at DFe) and compare this values with F_1 – MP and F_1 – BP for significant test.

4.5.2. COMBINING ABILITY ANALYSIS AND GENE ACTIONS FOR COMPLETE DIALLEL

The mathematical model for the combining ability (Griffing, 1956) is:

$$x_{ij} = \mu + g_i + g_j + s_{ij} + r_{ij} + \frac{1}{bc}\left(\sum_k \sum_l e_{ijkl}\right)$$

$S_{ij} = S_{ji}$

i, j, = 1, …, p,

k = 1, … ,b

l = 1, …, c,

Where

x_{ij} is the mean of i x jth genotype over k and l

μ is the population mean,

g_i is the general combining ability of effect of ith parent

g_j is the general combining ability effect of jth parent

s_{ij} is the interaction, i.e., specific combining ability effect

r_{ij} is the reciprocal effect and

$\frac{1}{bc}\sum_k \sum_l e_{ijkl}$ is the mean error

p, b and c = number of parents, block and sampled plants, respectively

Table 2. Analysis of variances for combining ability for method 1 giving expectations of mean squares for the assumptions of model I

Source of variation	DF	Sum of squares	Mean squares	Expected mean square
GCA	$p-1$	S_g	M_g	$\sigma^2 + 2p\left(\frac{1}{p-1}\right)\sum g_i^{\ 2}$
SCA	$p\left(\frac{p-1}{2}\right)$	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)}\sum_i \sum_j s_{ij}^{\ 2}$
Reciprocal	$p\left(\frac{p-1}{2}\right)$	S_r	M_r	$\sigma^2 + 2\left(\frac{2}{p(p-1)}\right)\sum_i \ \sum_{\langle\ j} r_{ij}^{\ 2}$
Error	m	S_e	M_e	σ^2

Source: Griffing (1956).

Where,

$$S_g = \frac{1}{2p}\sum_i \left(X_i. + X_{.i}\right)^2 - \frac{2}{p^2}X..^2,$$

$$S_s = \frac{1}{2}\sum_i \sum_j x_{ij}\left(x_{ij} + x_{ji}\right) - \frac{1}{2p}\sum_i \left(X_{.i} + X_{i.}\right)^2 + \frac{1}{p^2}X..^2,$$

$$S_r = \frac{1}{2}\sum_{i\langle} \sum_j \left(x_{ij} - x_{ji}\right)^2$$

$$M_e' = \frac{M_e}{bc}$$

Where,

$X_{i.}$ = array total of the crosses involving the i^{th} parent;
$X_{..}$ = grand total for all the observations in the diallel table;
x_{ii}, x_{ij} = parent and hybrid mean value in the diallel table, respectively
M_e' = error mean square for combining ability analysis
S_e= error sum of square for combining ability analysis

The following F ratios were used to test for GCA and SCA effects. Testing for overall differences among the various classes of effects can be accomplished as follows:

To test GCA effects

$$F[(p-1),m] = \frac{M_g}{M_e'}$$

To test SCA effects

$$F\left[\left(\frac{p(p-1}{2}\right),m\right] = \frac{M_s}{M_e'}$$

To test for reciprocal effects

$$F\left[\left(\frac{p(p-1}{2}\right),m\right] = \frac{M_r}{M_e'}$$

Estimation of combining ability effects

General combining ability effects

$$g_i = \frac{1}{2p}\left(x_{i.} + x_{.i}\right) - \frac{1}{p^2}x..,$$

Specific combining ability effects

$$s_{ij} = \frac{1}{2}\left(x_{ij} + x_{ii}\right) - \frac{1}{2}\left(x_{i.} + x_{.i} + x_{j.} + x_{.j}\right) + \frac{1}{2}x$$

Reciprocal effects

$$r_{ij} = \frac{1}{2}\left(x_{ij} - x_{ji}\right)$$

Estimate for mean effects

$$\mu = \frac{1}{p^2}x..,$$

Standard errors of effects and different between effects are estimated as follows:

$$SE(\mu) = \sqrt{\frac{1}{p^2}\sigma^2},$$

$$SE(g_i) = \sqrt{\frac{p-1}{2p^2}\sigma^2},$$

$$SE(s_{ii}) = \sqrt{\frac{(p-1)^2}{p^2}\sigma^2},$$

$$SE(s_{ij}) = \sqrt{\frac{1}{2p^2}\left(p^2 - 2p + 2\right)\sigma^2} \qquad (i \neq j),$$

$$SE\left(r_{ij}\right)=\sqrt{\frac{1}{2}\sigma^{2}} \qquad (i\neq j),$$

$$SE\left(g_{i}-g_{j}\right)=\sqrt{\frac{1}{p}\sigma^{2}}$$

$$SE\left(s_{ii}-s_{jj}\right)=\sqrt{\frac{2(p-2)}{2}\sigma^{2}} \qquad (i\neq j),$$

$$SE\left(s_{ii}-s_{ij}\right)=\sqrt{\frac{1}{2p}(3p-2)\sigma^{2}} \qquad (i\neq j),$$

$$SE\left(s_{ii}-s_{jk}\right)=\sqrt{\frac{3}{2p}(p-2)\sigma^{2}} \qquad (i\neq j,k;\, j\neq k),$$

$$SE\left(s_{ij}-s_{ik}\right)=\sqrt{\frac{p-1}{p}\sigma^{2}} \qquad (i\neq j,k;\, j\neq k),$$

$$SE\left(s_{ij}-s_{kl}\right)=\sqrt{\frac{p-2}{p}\sigma^{2}} \qquad (i\neq j,k,l;\, j\neq k,l;\, k\neq l),$$

$$SE\left(r_{ij}-s_{kl}\right)=\sigma^{2} \qquad (i\neq j;\, k\neq l),$$

Significant test was done comparing the GCA, SCA and recipocal effects with tabular 't' values (at DFe) multiplied by standard errors in which they were associated at 1 % and 5% probability levels. If the estimated values of g_i, s_{ij} and r_{ij} were greater than the SE x 't' values, the effects are significant at given probability level. On the other hand, positive or negative estimates indicate that the respective parent is better or worse than the other hybrids/ lines included in the diallel, as compared to the mean yield of the crosses (Griffing, 1956).

ESTIMATE OF VARIANCE COMPONENTS AND GENE ACTIONS

In order to obtain information on the type of gene action involved in the inheritance of the studied quantitative characters, the data for each trait measured were subjected to diallel cross analysis of genetic components and the ratio of GCA variance to SCA variance gave the importance of additive and non-additive gene effect. If the ratio of GCA to SCA variance is greater than unity, additive type of gene action will govern the inheritance of the trait. Otherwise, non-additive type of gene action will rule the inheritance of the character under investigation.

Keeping in view the expectation of the mean squares for model I, estimate of variance components are obtained as under:

Variance component due to GCA

$$\frac{1}{p-1}\sum_{i} g_i^{\,2} = \frac{M_g - M'_e}{2p}$$

Variance component due to SCA:

$$\frac{2}{p(p-1)}\sum_{i\langle}\sum_{j} s^2{}_{ij} = M_s - M'_e$$

Variance component due to reciprocal:

$$\frac{2}{p(p-1)}\sum_{i\langle}\sum_{j} r^2{}_{ij} = \left(\frac{M_r - M'_e}{2}\right)$$

The ratio of GCA to SCA variance

$$\frac{\sigma^2 GCA}{\sigma^2 SCA} = \frac{\frac{1}{p-1}\sum_{i} g_i^{\,2}}{\frac{2}{p(p-1)}\sum_{i<}\sum_{j} s^2_{\,ij}} = \frac{\frac{M_g - M'_e}{2p}}{M_s - M'_e}$$

Where,

M_g =mean sum of squares due to general combining ability

M_s = mean sum of squares due to specific combining ability

M_r = mean sum of squares due to reciprocal

M_e = error mean sum of square in the combining ability ANOVA

p = number of parents

4.5.3. COMBINING ABILITY ANALYSIS AND GENE ACTIONS FOR HALF DIALLEL

The mathematical model for the combining ability (Griffing, 1956) is:

$$x_{ij} = \mu + g_i + g_j + s_{ij} + \frac{1}{bc}\left(\sum_{k}\sum_{l} e_{ijkl}\right)$$

$S_{ij} = S_{ji}$; i, j, = 1, …, p ; k = 1, … ,b ; l = 1, …, c,

Where

x_{ij} is the mean of i x jth genotype over k and l

μ is the population mean,

g_i is the general combining ability of effect of ith parent

g_j is the general combining ability effect of jth parent

s_{ij} is the interaction, i.e., specific combining ability effect

$\frac{1}{bc}\sum_{k}\sum_{l} e_{ijkl}$ is the mean error

p, b and c = number of parents, block and sampled plants, respectively

Table 3. Analysis of variances for combining ability for method 2 giving expectations of mean squares for the assumptions of model I

Source of variation	DF	Sum of squares	Mean squares	Expected mean square
GCA	p-1	S_g	M_g	$\sigma_2 + (p+2)\left(\frac{1}{p-1}\right)\sum g_i^{\ 2}$
SCA	$\frac{p(p-1)}{2}$	S_s	M_s	$\sigma^2 + \frac{2}{p(p-1)}\sum_i\sum_j s_{ij}^{\ 2}$
Error	m	S_e	M_e	σ^2

Source: Griffing, B. (1956).

Where,

$$S_g = \frac{1}{(p+2)}[\ \sum_i (x_i. + x_{ii})^2 - \frac{4}{p^2} x..^2\ ],$$

$$S_s = \sum_{i\langle}\sum_j x_{i\,j}^{\ 2} - \frac{1}{p+2}\sum_i (x_{i.} + x_{ii})^2 + \frac{2}{(p+1)(p+2)} x..^2$$

$$M_e' = \frac{Me}{bc}$$

Where,

$x_{i.}$ = array total of the crosses involving the i^{th} parent;

x.. = grand total for all the observations in the half diallel table;

x_{ii}, x_{ij} = parent and hybrid mean value in the diallel table, respectively

M_e’ = error mean square for combining ability analysis

S_e= error sum of square for combining ability analysis

The following F ratios were used to test for GCA and SCA effects. Testing for overall differences among the various classes of effects can be accomplished as follows:

To test GCA effects

$$F[(p-1),m] = \frac{M_g}{M_e'}$$

To test SCA effects

$$F\left[\left(\frac{p(p-1}{2}\right),m\right] = \frac{M_s}{M_e'}$$

Where,

$x_{i.}$ = array total of the crosses involving the i^{th} parent;
x.. = grand total for all the observations in the half diallel table;
x_{ii}, x_{ij} = parent and hybrid mean value in the diallel table, respectively
M_e' = error mean square for combining ability analysis
S_e= error sum of square for combining ability analysis

Estimation of mean effects

$$\mu = \frac{2}{p(p+1)} x..$$

General combining ability effects

$$g_i = \frac{1}{p+2}\left[\ (x_{i.} + x_{ii}) - \frac{1}{p} x..\ \right],$$

Specific combining ability effects

$$s_{ij} = x_{ij} - \frac{1}{p+2}\left(x_{i.} + x_{ii} + x_{j.} + x_{jj}\right) + \frac{2}{(p+1)(p+2)} x..$$

Standard errors of effects and different between effects are estimated as follows:

$$SE(\mu) = \sqrt{\frac{2}{p(p+1)}\sigma^2},$$

$$SE(g_i) = \sqrt{\frac{p-1}{p(p+2)}\sigma^2},$$

$$SE(s_{ii}) = \sqrt{\frac{p(p-1)}{(p+1)(p+2)}\sigma^2},$$

$$SE(s_{ij}) = \sqrt{\frac{p2+p+2}{(p+1)(p+2)}\sigma^2} \qquad (i \neq j),$$

$$SE(g_i - g_j) = \sqrt{\frac{2}{p+2}\sigma^2} \qquad (i \neq j),$$

$$SE(s_{ii} - s_{jj}) = \sqrt{\frac{2(p-2)}{p+2}\sigma^2} \qquad (i \neq j),$$

$$SE(s_{ij} - s_{ik}) = \sqrt{\frac{2(p+1)}{p+2}\sigma^2} \qquad (i \neq j,k;\ j \neq k),$$

$$SE(s_{ij} - s_{kl}) = \sqrt{\frac{2p}{p+2}\sigma^2} \qquad (i \neq j,k,l;\ j \neq k,l; k \neq l),$$

Significant test was done comparing the GCA and SCA effects with tabular‘t’ values (at DFe) multiplied by standard errors in which they were associated at 1 % and 5% probability levels. If the estimated values of g_i and s_{ij} were greater than the SE x‘t’ values, the effects are significant at given probability level.

ESTIMATE OF VARIANCE COMPONENTS AND GENE ACTIONS

As in complete diallel, the data for each trait measured were subjected to diallel cross analysis of genetic components and the ratio of GCA variance to SCA variance gave the importance of additive and non-additive gene effect. If the ratio of GCA to SCA variance is greater than unity, additive type of gene action will govern the inheritance of the trait otherwise, non-additive type of gene action will rule the inheritance of the character under investigation.

Keeping in view the expectation of the mean squares for model I, estimate of variance components are obtained as under:

Variance component due to GCA

$$\frac{1}{p-1}\sum_{i} g_i^{2} = \frac{M_g - M'_e}{p+2}$$

Variance component due to SCA:

$$\frac{2}{p(p-1)}\sum_{i\langle}\sum_{j} s^{2}{}_{ij} = M_s - M'_e$$

The ratio of GCA to SCA variance

$$\frac{\sigma^2 GCA}{\sigma^2 SCA} = \frac{\frac{1}{p-1}\sum_i g_i^{\,2}}{\frac{2}{p(p-1)}\sum_{i\langle}\sum_j s^2{}_{ij}} = \frac{\frac{M_g - M'_e}{p+2}}{M_s - M'_e}$$

Where,

M_g =mean sum of squares due to general combining ability

M_s = mean sum of squares due to specific combining ability

M_r = mean sum of squares due to reciprocal

M_e = error mean sum of square in the combining ability ANOVA

p = number of parents

5. RESULTS

5.1. ANALYSIS OF VARIANCE

The analysis of variance was done for twenty one characters from the 6 x 6 half diallel crosses of haricot bean varieties as presented by the mean square due to genotypes in Table 4 and 5. Significant variations were observed for number of days to flowering, days to physiological maturity, plant height, pod length, number of seeds per pod, number of seeds per plant, number of branches per main stem, hundred seed weight, leaf area, organic matter, crude protein, common bacterial blight (CBB) per leaf, anthracnose per leaf, anthracnose per pod, angular leaf spot (ALS) and floury leaf spot (FLS) at $p \leq 0.01$ and for number of pods per plant at $p \leq 0.05$. There was no significant difference among the entries for genotypes were recorded for grain yield per plant, number of nodes per main stem, dry matter and CBB per pod.

Table 4. Genotype and error mean squares for yield and other traits in 6 x 6 half diallel crosses of haricot bean

Character	Mean Square of		CV (%)
	Genotype (DF = 20)	Error (DF=40)	
Days to flowering	6.33**	1.35	3.14
Days to physiological maturity	16.51**	5.56	2.89
Plant height	533.63**	97.05	13.14
Pod length	1.29**	0.37	6.52
Pods per plant	27.87*	13.19	18.41
Seeds per pod	1.07**	0.09	6.01
Seeds per plant	939.14**	342.19	20.93
Number of branches per plant	0.41**	0.16	14.66
Number of nodes per plant	8.69	6.36	24.53
Hundred seed weight	156.75**	3.85	7.28
Leaf area	90.75**	32.88	13.03
Dry matter	0.36	0.212	0.51
Organic matter	0.15**	0.045	0.22
Crude protein	4.45**	1.886	6.79
Seed Yield	17.39	14.954	15.97

*, ** = Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively.

Table 5. Genotype and error mean squares for resistance to common diseases of haricot bean in the F_1 diallel crosses

Character	Mean Square of		CV (%)
	Genotype (DF=20)	Error (DF=40)	
CBB/LEAF	0.11 (1.63)**	0.04 (0.53)	10.37 (20.34)
CBB/POD	0.11 (0.85) ^{ns}	0.08 (0.59)	21.39 (41.08)
ANTH/LEAF	0.33 (3.08)**	0.05 (0.43)	17.49 (40.32)
ANTH/POD	0.26 (2.22)**	0.03 (0.22)	13.90 (32.17)
ALS	0.34 (2.85)**	0.07 (0.55)	19.78 (40.81)
FLS	0.22 (1.56)**	0.03 (0.24)	14.65 (30.84)

*, **, ns significant differences from zero at P ≤ 0.01 and P≤ 0.05 and non-significant, respectively. Data analysis was made based on square root transformed values (without brackets) of the original data (means in brackets). CBB=common bacterial blight; ANTH=anthracnose, ALS=angular leaf spot; FLS=floury leaf spot

5.2. MEAN PERFORMANCE

The mean performance of parents and their F_1 hybrids are presented in Table 6. Seed yield per plant ranged from 20.19 g to 30.95 g. The highest value was recorded for an F_1 cross of G. Rasha x EAP-4 and it was about 1.5 times the lowest value recorded for the cross Roba x G. Rasha. Among parental lines, the maximum yield per plant was 24.76 g (Roba) while the minimum was 20.19 g (EAP-4). The top yielders were found to be hybrids. The F_1 hybrids of the crosses gave better seed yield as compared to their parental lines and the result of which can be found in Table 6. The hybrids which gave better yields than their parents include G. Rasha x EAP-4 (30.95 g), FEB-147 x EAP-4 (26.87 g), Atendaba x EMP-236 (25.72 g), EMP-236 x EAP-4 (25.63 g), Atendaba x G. Rasha (25.58 g), Roba x Atendaba (25.45 g), Roba x FEB-147 (25.38 g) and Gobe Rasha x FEB-147 (25.29 g) in a decreasing order.

Laboratory analysis of the seed revealed that Atendaba x Gobe Rasha had the highest amount of crude protein content per seed (22.84 %) while the lowest was obtained in Atendaba x EAP-4

(18.20 %) hybrid. Similarly, it was found that the hybrid, Atendaba x EAP-4, had the lowest organic matter content (95.15 %). It can also be observed that the F_1 hybrids have a relatively higher amounts of the crude protein than their parental sources as the range was from 18.27 % (FEB-147) to 20.70 % (Roba) for parents while it ranged from 18.20 % (Atendaba x EAP -4) to 22.84 (Atendaba x Gobe Rasha) for the F_1 hybrids.

The organic matter content of the seed among entries ranged from 96.13 % (FEB-147 x EAP-4) to 95.15 % (Atendaba x EAP-4). This range was very narrow and it looks insignificant between parental lines, the highest score being 95.91 % for FEB-147 and the lowest score was 95.50 % for EAP-4. The dry matter content of the seed of the parental lines and F_1 hybrids, on the other hand, ranged from 90.82 % (EAP-4) to 91.50 % (Atendaba) and from 90.12 % (FEB-147 x EAP-4) to 91.56% (Atendaba x EMP-236), respectively.

The maximum number of seeds per plant for the entries was 127.4 in EMP-236 x FEB-147 while the minimum was 51.93 in G. Rasha. Among parental lines and F_1 hybrids, number of seeds per plant ranged from 51.93 (G. Rasha) to 109.3 (Roba) and 64.50 (Roba x G. Rasha) to 127.4 (EMP-236 x FEB-147), respectively. Significant variations were obtained between EMP-236 x FEB-147 (127.4), Atendaba x EMP-236 (112.4), Roba (109.3), FEB-147 x EAP-4 (107.7) and Atendaba x G. Rasha (67.53), Roba x G. Rasha (64.50), G. Rasha (51.93).

The number of pods per plant ranged from 14.30 (G. Rasha) to 26.80 (EMP-236 x FEB-147). The highest number of pods per plant from parental lines 22.10 (EMP-236) whereas the least was from hybrids 14.30 (Gobe Rasha). There was no significant difference among the entries for number of pods per plant except between EMP-236 x FEB-147 (26.80) and Roba x G. Rasha (14.30), G. Rasha (14.30). The greatest seeds per pod was 5.92 for Roba followed by Roba x EMP-236 (5.77) while the least was 3.89 in G. Rasha. Statistically significant variations were observed among some entries for the character (Table 6). The longest and shortest pod was obtained from the hybrids with the pod length of 10.24 cm (G. Rasha x FEB-147) and 7.81 cm (EMP-236 x EAP-4), respectively. The hybrids were statistically different from each other for the character.

Significant differences were observed among entries for plant height. The plant height ranged from 35.53 to 99.10 and 63.03 to 77.70 for parental lines and hybrids, respectively. The tallest genotype was found to be Atendaba while the shortest was Gobe Rasha.

Significant variation was observed among the entries for leaf area. The largest leaf area size was attained by G. Rasha (57.13 cm^2) while the smallest was obtained in EMP-236 x EAP-4 (33.07 cm^2). Number of primary branches per main stem per plant and number of nodes per main stem ranged from 2.17 (Atendaba x FEB-147) to 3.63 (EAP-4) and 6.33 (G. Rasha) to 14.80 (Roba x FEB-147). Statistically, there were significant differences observed among the entries for hundred seed weight. This ranged from 18.12 (Roba) to 47.52 (G. Rasha) for parental lines and from 25.59 (EMP-236 x EAP-4) to 41.11 (Atendaba x G. Rasha) for hybrids.

Significant difference was obtained among the entries for days to flowering and days to maturity. Days to flowering and days to maturity ranged from 34.67 to 41.00 and 76.67 to 86.00, respectively. The earliest hybrid to flower was Atendaba x G. Rasha, followed by parental line, G. Rasha. These entries were significantly different from the latest entries (EAP-4, Roba, EMP-236, Atendaba x FEB-147, FEB-147 x EAP-4, Roba x EAP-4) to flower (Table 6). The latest hybrid, G. Rasha x EAP-4, took 86.00 days to maturing, whereas the earliest hybrid, EMP-236 x EAP-4 required 76.67 days to mature. Days to maturity ranged from 79.67 (Roba) to 85.67 (EAP) for parental lines.

The highest disease score values for common bacterial blight (CBB) per leaf and CBB per pod were 5.00 and 3.33 while the least were 2.33 and 1.67, respectively. Among parental lines and F_1 hybrids, the CBB per leaf ranged from 3.00 (Gobe Rasha and EMP-236) to 5.00 (Atendaba) and from 2.33 (FEB-147 x EAP-4) to 5.00 (Atendaba x FEB-147), respectively, while the CBB per pod ranged from 1.68 (Gobe Rasha x Atendaba) to 3.33 (Atendaba) and from 1.00 (EMP-236) to 2.67 (Roba x Atendaba), respectively. Atendaba was found to be with highest score for CBB per leaf and pod.

Disease score for anthracnose per leaf and per pod was ranged from 1.00 (Atendaba and Gobe Rasha) to 2.67 (EMP-236 and FEB-147) and from 1.00 (Atendaba and Gobe Rasha) to 2.67

(FEB-147), respectively for parental lines. It also ranged from 1.00 (Table 6) to 5.00 (Roba x FEB-147) and from 1.00 (Table 6) to 4.33 (Roba x FEB-147), respectively for F_1 hybrids. Parents, FEB-147 and EAP-4, followed by Roba were found to be with high score for anthracnose per leaf except EAP- for anthracnose per pod.

The highest score for angular leaf spot (ALS) among entries was 4.00 (Atendaba x EAP-4) while the least was 1.00 (Table 6). The range for parental lines and F_1 hybrids was from 1.00 (EMP-236) to 2.67 (EAP-4) and from 1.00 (Table 6) to 4.00 (Atendaba x EAP-4), respectively. Among parental lines and F_1 hybrids, the Floury leaf spot (FLS) ranged from 1.00 (Table 6) to 2.00 (Gobe Rasha) and from 1.00 to 3.00 (Atendaba x Gobe Rasha), respectively.

In general, the above results reveled that the hybrids/genotypes were in the range of resistant to moderately resistant for all the disease evaluated.

Table 6. Mean values for yield and other characters of 6 parents and 15 F$_1$ hybrids of haricot bean in 6 x 6 half diallel cross

Genotype	DEF	DEM	PLH	PL	PPP	SPO
Parents						
P1	39.33^{AB}	79.67^{BCD}	74.20^{CDE}	9.71^{ABC}	20.27^{ABC}	5.92^{A}
P2	37.00^{CDEF}	80.00^{BCD}	99.10^{A}	8.47^{DEF}	17.77^{BC}	4.24^{HI}
P3	35.33^{FG}	83.33^{AB}	35.53^{F}	10.24^{A}	14.30^{C}	3.89^{I}
P4	37.67^{BCDE}	84.33^{AB}	67.43^{CDE}	8.55^{CDEF}	22.10^{AB}	4.89^{DEF}
P5	38.67^{BC}	81.00^{BCD}	77.70^{BCDE}	9.32^{ABCD}	19.40^{BC}	5.31^{BCD}
P6	41.00^{A}	85.67^{A}	66.13^{DE}	9.27^{ABCD}	17.63^{BC}	5.03^{CDE}
Crosses						
P1 x P2	36.33^{DEFG}	80.00^{BCD}	86.40^{ABC}	9.607^{ABCD}	18.23^{BC}	5.507^{ABC}
P1 x P3	37.33^{BCDEF}	80.67^{BCD}	85.30^{ABCD}	9.820^{AB}	14.30^{C}	5.073^{CDE}
P1 x P4	36.00^{EFG}	80.33^{BCD}	82.30^{ABCDE}	9.500^{ABCD}	18.33^{BC}	5.773^{AB}
P1 x P5	36.67^{CDEFG}	80.67^{BCD}	83.40^{ABCD}	9.507^{ABCD}	21.57^{AB}	5.28^{BCD}
P1 x P6	37.67^{BCDE}	82.67^{AB}	63.03^{E}	9.800^{AB}	18.47^{BC}	5.56^{ABC}
P2 x P3	34.67^{G}	81.00^{BCD}	83.43^{ABCD}	9.05^{ABCDE}	18.70^{BC}	3.91^{I}
P2 x P4	35.67^{EFG}	78.00^{CD}	96.07^{AB}	9.293^{ABCD}	23.93^{AB}	5.03^{CDE}
P2 x P5	36.33^{DEFG}	79.67^{BCD}	79.33^{BCDE}	9.013^{BCDE}	19.60^{BC}	4.30^{GHI}
P2 x P6	38.33^{BCD}	82.00^{ABC}	75.97^{CDE}	9.893^{AB}	17.80^{BC}	4.82^{DEFG}
P3 x P4	37.33^{BCDEF}	83.33^{AB}	69.39^{CDE}	9.407^{ABCD}	18.41^{BC}	4.37^{FGHI}
P3 x P5	36.00^{EFG}	83.67^{AB}	66.07^{DE}	10.24^{A}	18.97^{BC}	4.64^{EFGH}
P3 x P6	36.00^{EFG}	86.00^{A}	73.80^{CDE}	9.67^{ABC}	23.33^{AB}	4.26^{HI}
P4 x P5	36.67^{CDEFG}	80.67^{BCD}	66.56^{DE}	7.99^{EF}	26.80^{A}	5.31^{BCD}
P4 x P6	36.67^{CDEFG}	76.67^{D}	67.53^{CDE}	7.81^{F}	23.52^{AB}	5.078^{CDE}
P5 x P6	36.33^{DEFG}	80.67^{BCD}	76.13^{CDE}	9.59^{ABCD}	20.80^{ABC}	5.57^{ABC}
MEAN	37.00	81.43	74.99	9.31	19.73	4.94
LSD (5%)	1.917	3.89	16.27	1.01	5.99	0.49
CV (%)	3.14	2.89	13.14	6.53	18.41	6.01

Means with the same letter are not significantly different. DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 6. Continued

Genotype	SPP	BPP	NPP	SW	LA	YIE
Parents						
P1	109.30^{AB}	2.50^{DE}	11.60	18.12^{K}	45.67^{BCDE}	24.76
P2	71.50^{CDE}	2.53^{CDE}	11.17	27.54^{EF}	35.12^{FG}	20.79
P3	51.93^{E}	2.33^{DE}	6.33	47.52^{A}	57.13^{A}	24.34
P4	82.83^{BCDE}	3.07^{ABCD}	8.87	20.21J^{K}	40.33^{BCDEFG}	24.21
P5	90.89^{BCD}	2.73^{CDE}	9.67	21.50J^{K}	45.40^{BCDE}	22.79
P6	83.13^{BCDE}	3.63^{A}	11.13	22.40^{HIJ}	42.99^{BCDEF}	20.19
Crosses						
P1 x P2	95.40^{ABCD}	2.67^{CDE}	10.73	25.21^{FGHI}	40.07^{CDEFG}	25.45
P1 x P3	64.50^{DE}	2.60^{CDE}	9.80	28.67^{DEF}	43.80^{BCDEF}	20.33
P1 x P4	98.03^{ABCD}	2.70^{CDE}	10.77	22.30^{HIJ}	44.73^{BCDE}	23.64
P1 x P5	98.23^{ABCD}	2.87^{BCDE}	14.80	21.98^{IJ}	49.67^{AB}	25.38
P1 x P6	85.33^{BCDE}	2.53^{CDE}	10.10	22.56^{GHIJ}	46.20^{BCDE}	23.35
P2 x P3	67.53^{DE}	2.60^{CDE}	13.00	41.11^{B}	42.20^{BCDEFG}	25.58
P2 x P4	112.40^{AB}	2.40^{DE}	11.17	25.67^{FGH}	42.47^{BCDEFG}	25.72
P2 x P5	78.93^{BCDE}	2.17^{E}	10.17	26.86^{EF}	47.80^{ABC}	22.48
P2 x P6	81.64^{BCDE}	2.87^{BCDE}	10.37	29.79^{DE}	38.20^{DEFG}	24.01
P3 x P4	76.66^{BCDE}	2.87^{BCDE}	8.39^{B}	31.86^{CD}	49.40^{ABC}	23.99
P3 x P5	82.05^{BCDE}	2.43^{DE}	8.90	31.23^{CD}	48.60^{ABC}	25.29
P3 x P6	93.17^{ABCD}	2.83^{BCDE}	9.30	33.62^{C}	47.27^{BCD}	30.95
P4 x P5	127.40^{A}	3.51^{AB}	9.90	20.59^{JK}	37.67^{EFG}	22.28
P4 x P6	97.09^{ABCD}	3.31^{ABC}	10.31	20.85^{JK}	33.07^{G}	25.63
P5 x P6	107.70^{ABC}	2.73^{CDE}	9.40	26.07^{FG}	46.73^{BCDE}	26.87
MEAN	88.37	2.76	10.28	26.94	44.03	24.19
LSD (5%)	30.57	0.67	4.16	3.23	9.47	6.38
CV (%)	20.93	14.66	24.53	7.28	13.03	15.98

Means with the same letter are not significantly different, DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 6. Continued

Genotype	CBB/LEAF	CBB/POD	ANTH/LEAF	ANTH/POD	ALS
Parents					
P1	2.08 (4.33) ^{ABC}	1.49 (2.33)	1.53 (2.33) ^{BC}	1.53 (2.33) ^{BC}	1.29 (1.67) ^{DE}
P2	2.24 (5.00) ^{A}	1.82 (3.33)	1.00 (1.00) ^{D}	1.00 (1.00) ^{D}	1.41 (2.00) ^{CDE}
P3	1.73 (3.00) ^{CDE}	1.29 (1.67)	1.00 (1.00) ^{D}	1.00 (1.00) ^{D}	1.29 (1.67) ^{DE}
P4	1.73 (3.00) ^{CDE}	1.29 (1.67)	1.29 (1.67) ^{D}	1.15 (1.33) ^{D}	1.00 (1.00) ^{E}
P5	1.82 (3.33) ^{BCDE}	1.29 (1.67)	1.61 (2.67) ^{BC}	1.61 (2.67) ^{B}	1.15 (1.33) ^{E}
P6	2.00 (4.00) ^{ABCD}	1.53 (2.33)	1.61 (2.67) ^{BC}	1.29 (1.67) ^{CD}	1.61 (2.67) ^{BCD}
Crosses					
P1 x P2	2.16 (4.67) ^{AB}	1.61 (2.67)	1.15 (1.33) ^{DE}	1.00 (1.00) ^{D}	1.82 (3.33) ^{AB}
P1 x P3	1.82 (3.33) ^{BCDE}	1.69 (1.67)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P1 x P4	2.08 (4.33) ^{ABC}	1.53 (2.33)	1.15 (1.33) ^{DE}	1.15 (1.33) ^{D}	1.00 (1.00) ^{E}
P1 x P5	1.88 (3.37) ^{ABCDE}	1.53 (2.33)	2.24 (5.00) ^{A}	2.08 (4.33) ^{A}	1.00 (1.00) ^{E}
P1 x P6	1.91 (3.67) ^{ABCDE}	1.29 (1.67)	1.73 (3.00) ^{B}	1.63 (2.67) ^{B}	1.41 (2.00) ^{CDE}
P2 x P3	1.91 (3.67) ^{ABCDE}	1.41 (2.00)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.29 (1.67) ^{DE}
P2 x P4	2.91 (3.67) ^{ABCDE}	1.29 (1.67)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P2 x P5	2.24 (5.00) ^{A}	1.41 (2.00)	1.29 (1.67) ^{CDE}	1.15 (1.33) ^{D}	1.92 (3.67) ^{AB}
P2 x P6	1.63 (2.67) ^{DE}	1.15 (1.33)	1.15 (1.33) ^{DE}	1.00 (1.00) ^{D}	2.00(4.00) ^{A}
P3 x P4	1.73 (3.00) ^{CDE}	1.29 (1.67)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P3 x P5	1.73 (3.00) ^{CDE}	1.29 (1.67)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P3 x P6	1.73 (3.00) ^{CDE}	1.29 (1.67)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P4 x P5	1.82 (3.33) ^{BCDE}	1.00 (1.00)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.73 (3.00) ^{ABC}
P4 x P6	1.82 (3.33) ^{BCDE}	1.15 (1.33)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.00 (1.00) ^{E}
P5 x P6	1.52 (2.33) ^{E}	1.15 (1.33)	1.00 (1.00) ^{E}	1.00 (1.00) ^{D}	1.41 (2.00) ^{CDE}
MEAN	1.88 (3.59)	1.34 (1.87)	1.22 (1.62)	1.17 (1.46)	1.29 (1.81)
LSD (5%)	0.32 (1.20)	0.47 (1.27)	0.35 (1.08)	0.27 (0.78)	0.42 (1.22)
CV (%)	0.37 (20.34)	21.39 (41.08)	17.49 (40.32)	13.90 (32.17)	19.78 (40.81)

Data analysis was made based on square root transformed values (without brackets) of the original data (means in brackets) for disease. Means with the same letter are not significantly different, DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 6. Continued

		Laboratory analysis		
Genotype	FLS	Dry matter	Organic matter	Crude protein
Parents				
P1	1.29(1.67) ^{CDE}	90.84	95.82 ^{ABCD}	20.70^{ABC}
P2	1.00(1.00) ^{E}	91.50	95.74 ^{ABCD}	20.08^{BC}
P3	1.41(2.00) ^{BCD}	91.03	95.90 ^{ABC}	20.18^{BC}
P4	1.00(1.00) ^{E}	90.91	95.82 ^{ABCD}	19.71^{BC}
P5	1.00(1.00) ^{E}	90.82	95.91 ^{ABC}	18.27^{C}
P6	1.15(1.33) ^{DE}	91.09	95.50 ^{CDE}	19.11^{BC}
Crosses				
P1 x P2	1.28 (2.67) ^{AB}	90.57	95.76 ^{ABCD}	21.63^{AB}
P1 x P3	1.63 (2.67) ^{AB}	90.24	95.45 ^{DE}	19.39^{BC}
P1 x P4	1.15 (1.33) ^{DE}	90.77	95.98 ^{AB}	19.25^{BC}
P1 x P5	1.63 (2.67) ^{AB}	90.58	95.69 ^{BCD}	19.73^{BC}
P1 x P6	1.52 (2.33) ^{ABC}	90.80	95.80 ^{ABCD}	19.28^{BC}
P2 x P3	1.73 (3.00) ^{A}	90.18	95.47 ^{DE}	22.84^{A}
P2 x P4	1.00 (1.00) ^{E}	91.56	95.47 ^{DE}	19.34^{BC}
P2 x P5	1.00 (1.00) ^{E}	91.15	95.68 ^{BCD}	21.62^{AB}
P2 x P6	1.45 (1.33) ^{DE}	91.03	95.15 ^{E}	18.20^{C}
P3 x P4	1.53 (2.33) ^{ABC}	90.71	95.69 ^{BCD}	21.60^{AB}
P3 x P5	1.00 (1.00) ^{E}	90.48	95.63 ^{BCD}	19.24^{BC}
P3 x P6	1.00 (1.00) ^{E}	90.80	95.57 ^{BCD}	21.32^{AB}
P4 x P5	1.00 (1.00) ^{E}	90.61	95.74 ^{ABCD}	20.01^{BC}
P4 x P6	1.00 (1.00) ^{E}	90.79	95.95 ^{AB}	20.39^{ABC}
P5 x P6	1.00 (1.00) ^{E}	90.12	96.13 ^{A}	21.48^{AB}
MEAN	1.22 (1.59)	90.836	95.710	20.161
LSD (5%)	0.29 (0.81)	0.760	0.351	2.266
CV (%)	14.65 (30.84)	0.510	0.220	6.810

Data analysis was made based on square root transformed values (without brackets) of the original data (means in brackets) for disease. Means with the same letter are not significantly different, DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

5.3. HETEROSIS

The estimates of heterosis percentage over mid parent and better parent for grain yield and other characters in 6 x 6 half diallel set are presented in Table 7.

Eight crosses (Roba x Atendaba, Roba x EMP-236, Roba x FEB-147, Roba x EAP-4, Atendaba x EMP-236, Gobe Rasha x EAP-4, EMP-236 x EAP-4 and FEB-147 x EAP-4) showed significant and negative heterosis over the mid parent for days to flowering. The highest heterosis over the mid parent was manifested by Gobe Rasha x EMP-236 (2.28 %) while the least was observed by FEB-147 x EAP-4 (-8.79 %). All of the fourteen crosses showed significant and negative heterosis over the better parent for days to flowering. The range of heterosis over the better parent was from –12.2 % (Gobe Rasha x EAP-4) to –0.88 % (Gobe Rasha x EMP-236).

Only two crosses, Atendaba x EMP-236 (-5.07 %) and EMP-236 x EAP-4 (-9.8 %) manifested significant heterosis over the mid parent for days to physiological maturity. The range for this trait was from –9.8 % (EMP-236 x EAP-4 to 1.83 % (Gobe Rasha x FEB-147). Heterosis over the better parent for days to physiological maturity ranged from –10.51 % (EMP-236 x EAP-4) to 0.40 % (Gobe Rasha x FEB-147). The same crosses exhibited the maximum and minimum values for both heterosis over the mid parent and over the better parent.

Four crosses expressed significant heterosis over the mid-parent and all of which had positive value for plant height. The highest heterosis over the mid parent was exhibited by Roba x Gobe Rasha (55.47 %) while the lowest value was obtained from Atendaba x EAP-4 (8.05 %). Only hybrid of Atendaba x FEB-147 had significant and negative heterosis over the better parent for the same character. The range of heterosis over the better parent for plant height was from –19.95 % to 14.96 %.

Atendaba x EAP-4, EMP-236 x FEB-147 and EMP-236 x EAP-4 showed significant heterosis over the mid-parent for pod length. All, except Atendaba x EAP-4, had negative values for average heterosis. Three crosses also showed significant and negative heterobeltosis for pod length. The range of heterosis over the mid parent and over the better parent were from –12.31 to 11.54 % and –15.72% to 8.74 %, respectively.

The highest value for pod per plant was recorded by Gobe Rasha x EAP-4 (46.14 %) which was positive and significant for heterosis over mid-parent and followed by hybrid EMP-236 x FEB-147 with the value of 29.16 %. Only Roba x Gobe Rasha (-29.44 %) showed significant heterosis over the better parent for pod per plant. Heterosis over the mid parent ranged from –17.26 to 46.14 % while heterosis over the better parent ranged from –29.44 to 32.33 %.

For number of seeds per pod, percent heterosis over mid-parent and better parent ranged from –9.92 % (Atendaba x FEB-147) to 10.3 % (Atendaba x EMP-236) and from –18.97 (Atendaba x FEB-147) to 4.91 % (FEB-147 x EAP-4), respectively. All crosses, which exhibited significant heterosis over the better parent, had negative values while only one hybrid had negative value for heterosis over mid-parent.

Significant and positive heterosis over the mid-parent were exhibited for number of seeds per plant by hybrids Roba x EMP-236 (45.66 %) and EMP-236 x FEB-147 (46.71 %). Hybrid Roba x EAP-4 had positive and significant value of average heterosis for the same trait.

Only two crosses, Roba x Gobe Rasha (-40.97 %) and EMP-236 x FEB-147 (40.20 %) showed significant heterosis over the better parent. The range for heterosis over the mid-parent and better parent was from –19.98 % to 46.71 % and from –40.97 % to 40.02 %, respectively.

None of the crosses showed significant heterosis over the mid-parent for the number of branches per main stem. However, five crosses showed significant and negative heterosis over the better parent. The value for heterobeltosis varied from –30.28 % (Roba x EAP-4) to 14.31 % (EMP-236 x FEB-147).

Hybrid Roba x FEB-147 and Atendaba x Gobe Rasha were the only crosses that showed significant and positive heterosis over the mid-parent while none of the crosses exhibited significant heterobeltosis for number of nods per plant. Average heterosis and heterobeltosis ranged from –11.14 % (Roba x EAP-4) to 48.57 % (Atendaba x Gobe Rasha), respectively.

Out of the six significant heterosis over mid-parent, four of which had positive values for hundred seed weight as expected since most of the hybrids involved atleast one large seeded bean in the combinations (Figure 8, 11). Similarly, six crosses showed significant heterosis over the better parent for the same character. Out of which all but one had negative values. The cross that had minimum value for heterosis over mid-parent had also minimum value for heterobeltosis.

Six out of fifteen crosses expressed significant heterosis over the mid-parent for leaf area. The highest score for leaf area was 18.72 % which was obtained by hybrid Atendaba x FEB-147 followed by Atendaba x EMP-236 (12.56 %) while the least score was obtained in EMP-236 x EAP-4 (23.08 %). Four crosses exhibited significant heterosis over the better parent for leaf area and all of them had negative values. Heterosis over the better parent for leaf area varied from –26.14 % (Atendaba x Gobe Rasha) to 8.76 (Roba x FEB-147).

Three hybrids (Roba x Gobe Rasha, Atendaba x Gobe Rasha and FEB-147 x EAP-4) showed significant and negative heterosis over the mid-parent while four hybrids (Roba x Atendaba, Roba x Gobe Rasha, Atendaba x Gobe Rasha and FEB-147 x EAP-4) exhibited significant and negative heterosis over the better parent for dry matter. Four hybrids (Roba x Gobe Rasha, Atendaba x Gobe Rasha, Atendaba x EMP-236 and Atendaba x EAP-4) for seed crude protein showed significant and negative heterosis over mid-parent and better parent while FEB-147 x EAP-4 was the only cross that manifested significant and positive heterosis over the mid parent for the same character. This hybrid also showed significant and positive heterosis over the mid parent and the better parent next to Gobe Rasha x EAP-4 for seed yield. Moreover, it had greater mean crude protein and seed yield compared to the parental lines (Figure 1 and 2).

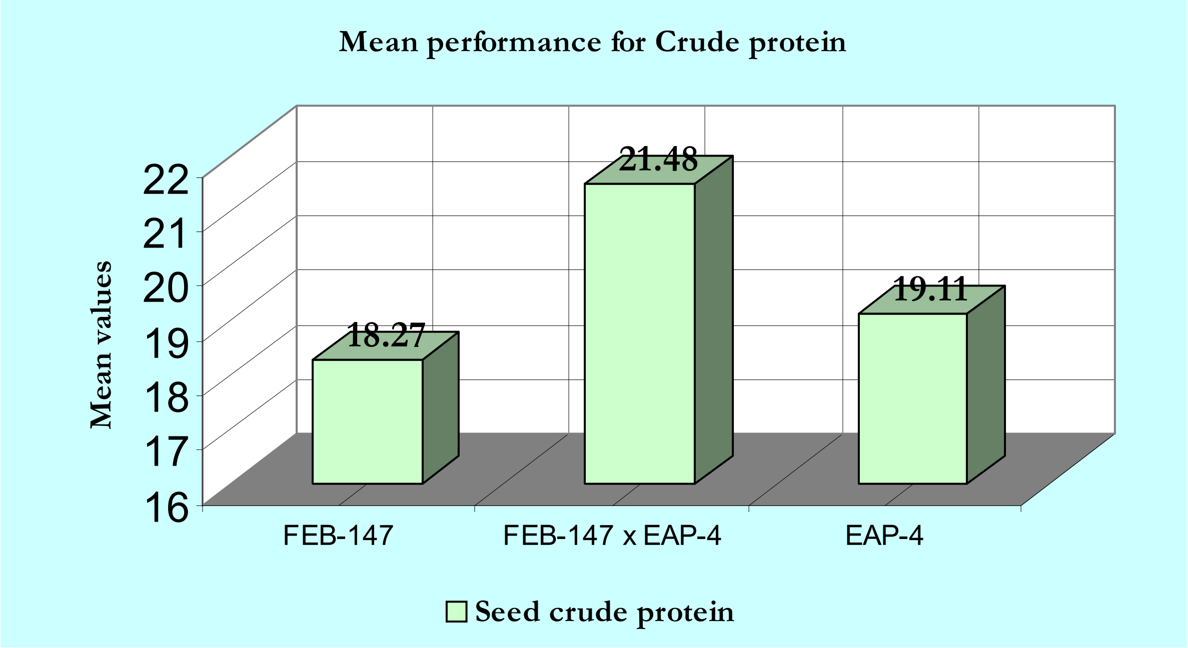

Figure 1. Seed crude protein of parent vs. crosses

For grain yield, heterosis over the mid parent ranged from -17.19 to 39.01 % while over the better parent for seed yield varied from -7.97 to 27.16 %. None of the crosses showed significant and negative heterosis for heterosis over the mid and the better parent. Only two hybrids (Gobe Rasha x EAP-4 and FEB-147 x EAP-4) manifested significant and positive heterosis over the mid-parent and the better parent. Gobe Rasha x EAP-4 gave 39.01 % and 27.16 % for heterosis over the mid-parent and over the better parent, respectively. While FEB-147 x EAP-4 exhibited 24.98 % and 17.80 % of heterosis more than mid-parent values and better parent, respectively. It was observed that these crosses had high mean performance as compared to the remaining crosses (Table 6). The hybrids were also higher mean performance than their parents (Figure 2).

For organic matter, three hybrids exhibited significant and positive heterosis over the mid-parent while two crosses showed significant and positive heterosis over the better parent. Atendaba x Gobe Rasha, Atendaba x FEB-147 and FEB-147 EAP-4 gave heterosis over the better parent of 13.46 %, 12.75 % and 14.93 %, respectively, while Atendaba x Gobe Rasha and FEB-147 x EAP-4 gave 13.18 % and 12.40 %, respectively, for heterosis over the better parent.

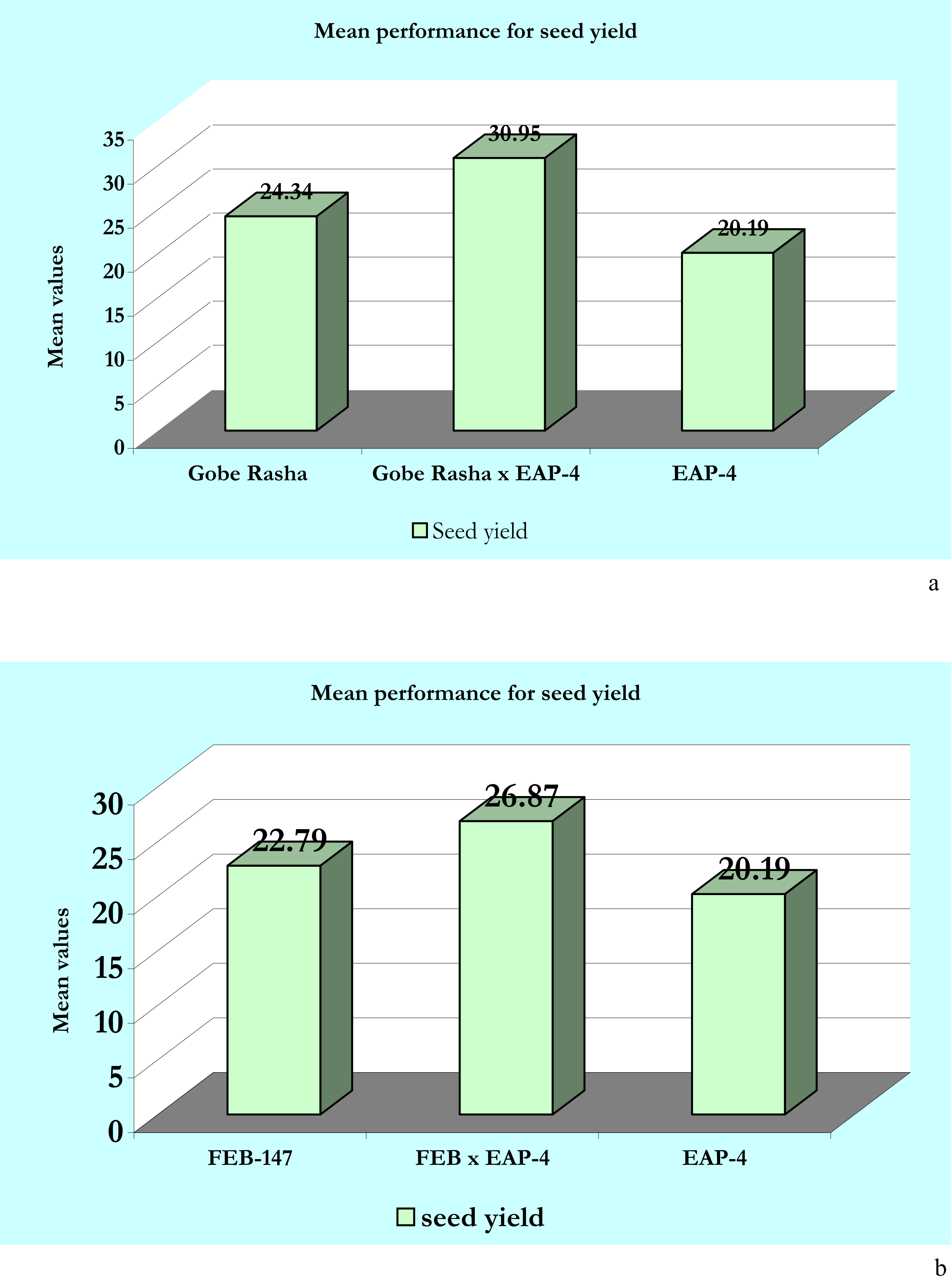

Figure 2. Seed grain yield of parent vs. crosses.

Only one out of the fifteen crosses combinations showed significant ($p \leq 0.01$) and negative heterosis over the mid-parent for common bacterial blight (CBB). The hybrid, Atendaba x EAP-4, gave -40.67 % and -53.00 % heterosis over the mid-parent for CBB per leaf and CBB per pod, respectively. None of the crosses showed significant heterosis over the better parent for CBB.

For anthracnose per leaf, only one hybrid (Roba x FEB-147) showed significant and positive heterosis over the mid-parent. But three out of fifteen crosses showed significant heterosis over the better parent for the same character. Except Atendaba X FEB-149, they had positive values. The highest heterosis over the better parent was recorded for the cross Roba x FEB-147 (114.59 %) while the lowest was for Atendaba x FEB-147 (-100 %).

Four out of fifteen crosses manifested significant heterosis over the mid-parent for anthracnose per pod. Of which, two had positive values. Two crosses exhibited significant and positive heterosis over the better parent. Heterosis over mid-parent and better parent for anthracnose per pod was ranged from -53.92 % (FEB-147 x EAP-4) to 73.20 % (Roba x FEB-147) and from –100.00 % (Atendaba x FEB-147) to 85.84 % (Roba x FEB-147), respectively.

For angular leaf spot, significant and positive heterotic effect over the mid-parent was found in four crosses and negative while significant heterosis was observed in one cross. Only two hybrids showed significant heterosis over the better parent. Six hybrids for floury leaf spot (FLS) showed significant and positive average heterosis while three hybrids showed significant and positive heterosis over the better parent for the same traits.

Table 7. Percent F_1 heterosis above mid-parent (MPH) and above better parent (BPH) for seed yield and other characters in 6 x 6 half diallel cross of haricot bean

Cross	DEM		DPM		PLH (cm)		PL		PPP		SPO		SPP	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MHP	BPH	MPH	BPH
P1 x P2	-4.80*	-7.63**	0.21	0.00	-0.29	-12.82	5.68	-1.03	-4.12	-10.03	8.40*	-6.98	5.55	-12.69
P1 x P3	0.00	-5.08*	-1.02	-3.20	55.47**	14.96	-1.54	-4.10	-17.26	-29.44*	3.40	-14.30**	-19.98	-40.97**
P1 x P4	-6.49**	-8.47**	-2.03	-4.74*	16.22	10.92	4.09	-2.13	-13.45	-17.04	6.85	-2.48	2.06	-10.28
P1 x P5	-5.98**	-6.78**	0.41	-0.41	9.81	7.34	-0.07	-2.06	8.74	6.41	-5.94	-10.81*	-1.84	-10.10
P1 x P6	-6.22**	-8.13**	0.00	-3.50	-10.17	-15.05	3.30	0.96	-2.55	-8.88	1.58	-6.08	-11.30*	-21.90
P2 x P3	-4.15	-6.31*	-0.82	-2.80	23.94*	-15.81	-3.24	-11.59*	16.63	5.25	-3.92	-7.85	9.41	-5.56
P2 x P4	-4.46*	-5.31*	-5.07*	-7.51**	15.37	-3.06	9.20	8.74	20.07	8.30	10.30*	3.00	45.66*	35.69
P2 x P5	-3.96	-6.03*	-1.04	-1.65	-10.26	-19.95*	1.31	-3.29	5.47	1.03	-9.92*	-18.97**	-2.79	-13.16
P2 x P6	-1.71	-6.50**	-1.01	-4.28	-8.05	-23.34	11.54*	6.76	0.56	0.19	3.97	-4.17	5.60	-1.79
P3 x P4	2.28	-0.88	-0.60	-1.19	34.79*	2.91	0.14	-8.14	1.18	-16.68	-0.53	-10.64*	13.76	-7.46
P3 x P5	-2.70	-6.90**	1.83	0.40	16.69	-14.97	4.70	0.00	12.56	-2.23	0.87	-12.56**	14.89	-9.73
P3 x P6	-5.68*	-12.20**	1.78	0.39	45.18**	11.59	-0.82	-5.53	46.14**	32.33	-4.48	-15.25**	37.96	12.07
P4 x P5	-3.93	-5.17*	-2.42	-4.35	-8.28	-14.34	-10.55*	-14.26*	29.16*	21.27	4.25	0.13	46.71**	40.20*
P4 x P6	-6.78**	-10.57**	-9.80**	-10.51**	1.12	0.15	-12.31*	-15.72**	18.40	6.44	2.44	1.02	17.00	16.79
P5 x P6	-8.79**	-11.38**	-3.20	-5.84*	5.86	-2.02	3.14	2.85	12.33	7.22	7.75	4.91	23.81	18.53
SE (d)	0.821	0.948	1.667	1.925	6.966	8.043	0.430	0.496	2.568	2.965	0.209	0.242	13.080	15.103

*, ** Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=Pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=Leaf area; YIE=seed yield, MPH= heterosis above mid parents, BPH=heterosis above better parent, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 7. Continued

Cross	BPS		NPP (cm)		SW		LA		Yield		Crude protein	
	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MPH	BPH	MHP	BPH
P1 x P2	5.96	5.26	-5.71	-7.47	10.44	-8.44	-0.81	-12.26	11.75	2.78	-0.02	-0.02
P1 x P3	7.59	4.00	9.29	-15.52	-12.65**	-39.67**	-14.79	-23.34**	-17.19	2.79	-0.43**	-0.06*
P1 x P4	-2.99	-11.96	5.21	-7.18	16.31*	10.30	4.03	-2.04	-3.45	-4.52	0.17	0.17
P1 x P5	9.55	4.88	39.18*	27.59	10.93	2.21	9.08	8.76	6.71	2.50	-0.18	-0.23
P1 x P6	-17.39	-30.28**	-11.14	-12.93	11.32	0.69	4.23	1.17	3.89	-5.69	0.15	-0.02
P2 x P3	2.63	2.63	48.57*	16.42	9.54*	-13.49**	-8.52	-26.14**	13.36	5.09	-0.37*	-0.45*
P2 x P4	-14.29	-21.74*	11.48	0.00	7.51	-6.79	12.56	5.29	14.31	6.24	-0.32*	-0.37*
P2 x P5	-17.72	-20.73	-2.40	-8.96	9.55	-2.45	18.72	5.29	3.12	-1.45	-0.15	-0.24
P2 x P6	-7.03	-21.10*	-7.03	-7.16	19.31**	8.18**	-2.19	-11.14	17.18	15.49	-0.49**	-0.62**
P3 x P4	6.17	-6.52	10.33	-5.43	-5.94	-32.97**	1.37	-13.54	-1.17	-1.44	-0.18	-0.22
P3 x P5	-3.95	-10.98	11.25	-7.93	-9.51*	-34.28**	-5.20	-14.94*	7.27	3.90	0.03	0.02
P3 x P6	-5.03	-22.02*	6.49	-16.47	-3.83	-29.25**	-5.58	-17.27*	39.01**	27.16*	-0.14	-0.34
P4 x P5	20.88	14.31	6.83	2.41	-1.26	-4.23	-12.13	-17.03*	-5.23	-7.97	-0.13	-0.18
P4 x P6	-1.16	-8.87	3.11	-7.39	-2.12	-6.91	-23.08*	-23.08**	15.45	5.87	0.30	0.14
P5 x P6	-14.14	-24.77**	-9.62	-15.57	18.78**	16.40	5.75	2.94	24.98*	17.80*	0.44**	0.23
SE (d)	0.285	0.329	1.783	2.058	1.386	1.601	4.055	4.681	2.73	3.16	0.15	0.17

*, ** Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=Pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=Leaf area; YIE=seed yield, MPH= heterosis above mid parents, BPH=heterosis above better parent, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 7. Continued

Cross	Dry matter		Organic matter		CBB/LEAF		CBB/POD		ANTH/LEAF		ANTH/POD		ALS		FLS	
	MPH	BPH	MPH	MPH	BPH	MPH	BPH	MPH	BPH	BPH	MHP	BPH	MPH	BPH	MPH	MPH
P1 x P2	-0.66	-0.66*	6.08	6.08	0.11	7.85	-5.65	14.59	-20.12	33.00	-39.94	0.00	81.47**	99.40**	100.00**	167.00**
P1 x P3	-0.76*	-1.02*	-5.14	4.49	-9.14	11.00	-16.50	0.00	-39.94	0.00	-39.94	0.00	-40.12	-40.12	45.50*	59.88
P1 x P4	-0.12	-0.15	-4.73	-2.33	18.14	44.33	16.50	39.52	-33.50	-20.36	-27.32	0.00	-25.09	0.00	-0.37	33.00
P1 x P5	-0.28	-0.29	1.26	-4.69	-12.01	1.20	16.50	39.52	100.00**	114.59**	73.20**	85.84**	-33.33	-24.81	100.00**	167.00**
P1 x P6	-0.18	-0.32	-3.14	-6.86	-11.88	-8.25	-28.33	-28.33	20.00	28.76	33.50*	59.88**	-7.83	19.76	55.33*	75.19*
P2 x P3	-1.19**	-1.44**	13.46**	13.18*	-8.25	22.33	-20.00	19.76	0.00	0.00	0.00	0.00	-8.99	0.00	100.00**	200.00**
P2 x P4	0.39	0.07	-2.79	-3.69	-8.25	22.33	-33.20	0.00	-25.09	0.00	-14.16	0.00	-33.33	0.00	0.00	0.00
P2 x P5	-0.01	-0.38	12.75*	7.67	20.05	-370.71	-20.00	-100.00	-8.99	-100.00	-27.52	-100.00	120.42**	-100.00**	0.00	-100.00
P2 x P6	-0.29	-0.51	-7.12	-9.36	-40.67**	-33.25	-53.00**	-42.92	-27.52	33.00**	-25.09	0.00	71.31**	100.00	14.16	33.00
P3 x P4	-0.29	-0.35	8.30	7.04	0.00	0.00	0.00	0.00	-25.09	0.00	-14.16	0.00	-25.09	0.00	55.33*	133.00
P3 x P5	-0.49	-0.60	0.08	-4.66	-5.21	0.00	0.00	0.00	-45.50	0.00	-45.50*	0.00	-33.33	0.00	-33.33	0.00
P3 x P6	-0.29	-0.32	8.53	5.65	-14.29	0.00	-16.50	0.00	-45.50	0.00	-25.09	0.00	-53.92*	-40.12	-39.94	-24.81
P4 x P5	-0.28	-0.33	5.37	1.52	5.21	11.00	-40.12	-40.12	-53.92	-40.12	-50.00**	-24.81	157.51**	200.00	0.00	0.00
P4 x P6	-0.23	-0.33	5.05	3.45	-4.86	11.00	-33.50	-20.36	-53.92	-40.12	-33.33	-24.81	-45.50	0.00	-14.16	0.00
P5 x P6	-0.92*	-1.06*	14.93**	12.40*	-36.43	-30.03	-33.50	-20.36	-62.55	-62.55**	-53.92**	-40.12	0.00	50.38	-14.16	0.00
SE (d)	0.33	0.38	0.97	1.12	0.51	1.73	0.54	063	0.46	0.54	0.33	0.38	0.52	0.61	0.35	0.40

*, ** Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=Pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=Leaf area; YIE=seed yield, MPH= heterosis above mid parents, BPH=heterosis above better parent, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

5.4. COMBINING ABILITY

5.4.1. ANALYSIS OF VARIANCE FOR COMBINING ABILITY

The variances due to general combining ability and specific combining ability effects were presented in Table 8. Almost all of the traits studied showed significant GCA and SCA variances.

Table 8. General combining ability (GCA) and specific combining ability (SCA) for different characters in 6 x 6 half diallel cross of haricot bean at Bako in 2005

Characters	Mean squares		
	GCA (DF=5)	SCA (DF=15)	Error (DF=40)
DEF	3.54**	1.60**	1.35
DPM	8.88**	4.37*	3.89
PLH	415.18**	98.77**	6.27
PL	0.93**	0.26*	1.01
PPP	16.93**	6.74	5.99
SPO	1.23**	0.07*	0.49
SPP	685.43**	188.92^{ns}	30.57
BPS	0.31**	0.08^{ns}	0.67
NPP	5.03^{ns}	2.18^{ns}	4.16
SW	193.78**	5.07**	3.23
LA	72.13**	16.29^{ns}	9.47
DM	0.17^{ns}	0.10^{ns}	0.07
OM	0.05**	0.05**	0.02
CP	0.79^{ns}	1.70**	0.63
YIE	1.48^{ns}	7.22^{ns}	4.98

*, ** Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield; DM=dry matter; OM=organic matter; CP=crude protein.

Table 8. Continued

Characters	Mean squares		
	GCA	SCA	Error
CBB/LEAF	1.22**	0.32^{ns}	0.18
CBB/POD	0.58*	0.19^{ns}	0.19
ANTH/LEAF	1.88**	0.74**	0.14
ANTH/POD	1.52**	0.48**	0.07
ALS	1.51**	0.76**	0.18
FLS	0.97**	0.37**	0.08

*, **, ns = significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$ and non significant, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=Number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield; DM=dry matter; OM=organic matter; CP=crude protein.

5.4.2. ESTIMATES OF GENERAL COMBINING ABILITY EFFECTS

Four parents had significant GCA effects for days to flowering, out of which EAP-4 (1.00) and Roba (0.46) had positive significant GCA effects while Gobe Rasha and Atendaba (-0.46) was the lowest with negative significant GCA effect. For days to physiological maturity, three parents showed significant ($P \leq 0.01$) GCA effects. These are Atendaba (-1.17), EAP- 4 (1.17) and Gobe Rasha (1.42).

Out of six parents, Atendaba, EAP-4 and Gobe Rasha, showed significant GCA effects for plant height. Similarly, three parents found to be with significant GCA effects for pod length. EMP-236, Gobe Rasha and roba had 0.52, 0.43 and 0.29 values.

Only EMP-236 (2.14) and Gobe rasha (-1.97) exhibited significant ($P \leq 0.05$) positive GCA effects for pods per plant. Similarly, Gobe Rasha (-16.36) showed significant GCA effects for seeds per plant while four parents showed significant GCA effects for seeds per pod.

EAP-4 and EMP-236 showed significant ($P \leq 0.01$) and positive GCA effects while Atendaba x Gobe Rasha exhibited significant ($P \leq 0.01$) and negative GCA effects for number of branches per main stem. The highest was recorded by EAP-4 (0.28) while the lowest was by EMP-236 (0.20).

All the six parents had significant ($P \leq 0.01$) GCA effects for hundred seed weight. Out of which only two had positive GCA effects. The highest GCA effect was obtained in Atendaba (1.89) while the lowest was obtained in Roba (-3.96). For Leaf area, only Atendaba exhibited significant GCA effect.

Significant ($P \leq 0.01$) and positive GCA effect was exhibited for common bacterial blight. For CBB per leaf, Roba (0.40), Atendaba (0.57) and Gobe Rasha (-0.39) had significant GCA effects whereas only Roba and Atendaba exhibited significant and positive GCA effects for CBB per pod.

All except EAP-4 showed significant ($P \leq 0.01$) GCA effects for anthracnose. Parents that showed significant GCA effect for anthracnose per leaf also had significant GCA effect for anthracnose per pod. Four parents (Atendaba, Gobe Rasha EMP-236 and EAP-4) for angular leaf spot and five parents for floury leaf spot had significant GCA effects.

Atendaba was found to be with significant GCA effect for CBB per leaf, CBB per pod, anthracnose per leaf, anthracnose per pod and angular leaf spot whereas Gobe Rasha, exhibited significant GCA effects for CBB per leaf, anthracnose per pod and angular leaf spot and floury leaf spot. EAP-4 showed no significant GCA effects for all the disease evaluated in this experiment except for ALS and FLS. Only one parent (Atendaba) showed significant GCA effect for organic matter. This parent had -0.119 estimate of GCA value. None of the parents showed significant and positive GCA effects for all the diseases.

Table 9. Estimates of general combining ability effects for yield and other traits in six varieties of haricot bean in 6 x 6 half diallel cross at Bako, 2005

Genotypes	DEF		DPM		PLH		PL	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
Atendaba	37.00	-0.46*	80.00	-1.17**	99.10	11.79**	8.47	-0.18
EAP-4	41.00	1.00**	85.67	1.17**	66.13	-4.52*	9.27	0.01
EMP-236	37.67	-0.17	84.30	-0.29	67.43	-1.02	8.55	-0.52**
FEB-147	38.67	0.04	81.00	-0.33	77.70	0.25	9.32	-0.03
Gobe Rasha	35.33	-0.88**	83.33	1.42*	35.53	-9.48**	10.24	0.43**
Roba	39.33	0.46*	79.69	-0.79	74.20	2.99	9.71	0.29*
S.E (g_i)		0.217		0.439		1.836		0.113
S.E. (g_i-g_j)		0.335		0.681		2.844		0.176

*, ** = significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield; DM=dry matter; OM=organic matter; CP=crude protein.

Table 9. Continued

Genotypes	PPP		SPO		SPP	
	Mean	GCA	Mean	GCA	Mean	GCA
Atendaba	17.77	-0.53	4.24	-0.31**	71.50	-4.98
EAP-4	17.63	0.14	5.03	0.09	83.13	1.54
EMP-236	22.10	2.14**	4.89	0.09	82.83	7.36*
FEB-147	19.40	1.06	5.31	0.14*	90.89	7.20*
Gobe Rasha	14.30	-1.97**	3.89	-0.57**	51.93	-16.36**
Roba	20.27	-0.83	5.92	0.56**	109.27	5.23
S.E (g_i)		0.677		0.055		3.447
S.E. (g_i-g_j)		1.049		0.857		5.340

*, ** = Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield; DM=dry matter; OM=organic matter; CP=crude protein.

Table 9. Continued

Genotypes	BPS		HSW		LA		OM	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
Atendaba	2.53	-0.19*	27.54	1.89**	95.82	0.05	35.12	-3.39**
EAP-4	3.63	0.28**	22.40	-1.35**	95.74	-0.12	42.99	-1.34**
EMP-236	3.07	0.20**	20.21	-3.36**	95.90	-0.04	40.33	-2.52**
FEB-147	2.73	-0.01	21.50	-2.36**	95.82	0.07	45.40	1.64**
Gobe Rasha	2.33	-0.16*	47.52	9.12**	95.91	0.09	57.13	4.67**
Roba	2.50	-0.12	18.12	-3.96**	95.50	-0.05	45.67	0.95**
S.E (g_i)		0.075		0.365		1.069		0.039
S.E. (g_i-g_j)		0.117		0.566		1.655		0.062

*, ** = Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield; DM=dry matter; OM=organic matter; CP=crude protein.

Table 9. Continued

Genotypes	CBB/LEAF		CBB/POD		ANTH/LEAF		ANTH/POD	
	Mean	GCA	Mean	GCA	Mean	GCA	Mean	GCA
Roba	4.33	0.40**	2.33	0.28*	2.33	0.63**	2.33	0.59**
Atendaba	5.00	0.57**	3.33	0.40**	1.00	-0.38**	1.00	-0.36**
Gobe Rasha	3.00	-0.39**	1.67	-0.14	1.00	-0.54**	1.00	-0.40**
EMP-236	3.00	-0.18	1.67	-0.22	1.67	-0.33*	1.33	-0.28**
FEB-147	3.33	-0.14	1.67	-0.18	2.67	0.46**	2.67	0.47**
EAP-4	4.00	-0.26	2.33	-0.14	2.67	0.17	1.67	-0.03
S.E (g_i)		0.136		0.143		0.122		0.087
S.E. (g_i-g_j)		0.211		0.222		0.188		0.136

*, ** Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. CBB/LEAF = common bacterial blight per leaf; CBB/POD= common bacterial blight per pod; ANTH/LEAF=anthracnose per leaf; ANTH/LEAF=anthracnose per.

Table 9. Continued

Genotypes	ALS		FLS	
	Mean	GCA	Mean	GCA
Roba	1.67	-0.13	1.67	0.49**
Atendaba	2.00	0.63**	1.00	-0.01
Gobe Rasha	1.67	0.46**	2.00	0.36**
EMP-236	1.00	0.46**	1.00	-0.31**
FEB-147	1.33	0.08	1.00	-0.31**
EAP-4	2.67	0.33*	1.33	-0.22*
S.E (g_i)		0.138		0.091
S.E. (g_i-g_j)		0.213		0.141

*, ** Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. ALS=angular leaf spot; FLS=floury leaf spot

5.4.3. ESTIMATES OF SPECIFIC COMBINING ABILITY EFFECTS

Out of fifteen crosses, only four showed significant SCA effects for days to flowering. Gobe Rasha x EMP-236 had the highest value while FEB-147 x EAP- had the lowest value. Among the crosses, only EMP-236 x EAP-4 had significant SCA effects for days to physiological maturity.

Four crosses exhibited significant positive SCA effects for plant height. Roba x Gobe Rasha had the highest (16.80) SCA value while Roba x EAP-4 had the lowest (12.82) SCA value. For pod length, five crosses exhibited significant SCA effects. The highest value was observed in Atendaba x EAP-4 while the lowest was observed in EMP-236 x EAP-4.

Six crosses for hundred seed weight expressed significant SCA effects. Four of them showed positive significant SCA effects while the rest two showed negative significant SCA effects. The maximum value was 3.17, which was obtained by Atendaba x Gobe Rasha while the lowest was -3.44 in Roba x Gobe Rasha.

Roba x Gobe Rasha, Roba x FEB-147 and EMP-236 x FEB-147 showed significant SCA effect for anthracnose per leaf whereas four hybrids showed significant SCA effects for anthracnose per pod. Of which two hybrids had positive SCA values. The highest value among the significant crosses was 1.80 which was obtained from Roba x FEB-147 while the lowest was -0.69 in Roba x Atendaba.

For angular leaf spot, five crosses showed significant SCA effects. Of which only one cross had negative value. Among significant hybrids, the highest value was 1.57 (EMP-236 x FEB-147) while the lowest value was -0.98 (Atendaba x EMP-236). Four out of fifteen hybrids exhibited significant SCA effects for floury leaf spot. Of which only one hybrid (Gobe Rasha x EAP-4) had negative SCA value.

Significant SCA effect was obtained by Roba x Gobe Rasha (--0.29), Atendaba x EAP-4 (-0.39), EMP-236 x EAP-4 (0.23) and FEB-147 x EAP-4 (0.38) for organic matter content of the seed. For crude protein content of the seed Atendaba x Gobe Rasha (1.89), Gobe Rasha x FEB-147 (1.46), Atendaba x EAP-4 (-2.02) and FEB-147 x EAP-4 (1.89) exhibited significant SCA effect.

Table 10. Estimates of specific combining ability effects for yield and other traits in 6 x 6 half diallel cross of haricot bean at Bako, 2005

Genotypes	DEF		DPM		PLH		SPO		PL		SW	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
P1 x P2	36.33	-0.67	80.00	0.53	86.40	-3.37	5.51	0.33*	9.61	0.18	25.21	0.35
P1 x P3	37.33	0.75	80.67	-1.39	85.30	16.80**	5.07	0.15	9.82	-0.25	28.67	-3.44**
P1 x P4	36.00	-1.29*	80.33	-0.01	82.30	5.35	5.77	0.18	9.50	0.39	24.29	2.67**
P1 x P5	36.67	-0.83	80.67	0.36	83.40	5.18	5.28	-0.36*	9.51	-0.67*	21.98	1.34
P1 x P6	37.67	-0.79	82.67	0.86	63.03	-10.42*	5.56	-0.03	9.80	0.17	22.56	0.93
P2 x P3	34.67	-1.00	81.00	-0.68	83.43	6.13	3.91	-0.15	9.05	-0.52	41.11	3.17**
P2 x P4	35.67	-0.71	78.00	-1.97	96.07	10.31*	5.03	0.32*	9.29	0.67*	25.67	0.19
P2 x P5	36.33	-0.25	79.67	-0.26	79.33	-7.70	4.30	-0.46**	9.01	-0.09	26.86	0.39
P2 x P6	38.33	0.79	82.00	0.57	75.97	-6.29	4.82	0.09	9.89	0.75*	29.79	2.31*
P3 x P4	37.33	1.38*	83.33	0.78	69.39	4.92	4.37	-0.09	9.41	0.17	31.86	-0.87
P3 x P5	36.00	-0.17*	83.67	1.16	66.07	0.32	4.64	0.13	10.24	0.54	31.23	-2.47*
P3 x P6	36.00	-1.13	86.00	1.99	73.80	12.82*	4.26	-0.21	9.67	-0.09	33.62	-1.08
P4 x P5	36.67	-0.21	80.67	-0.14	66.56	-7.65	5.31	0.14	7.99	-0.78*	20.59	-0.63
P4 x P6	36.67	-1.17*	76.67	-5.64**	67.53	-1.91	5.08	-0.05	7.81	-0.99**	20.85	-1.37
P5 x P6	36.33	-1.71**	80.67	-1.59	76.13	5.42	5.57	0.39*	9.59	0.28	26.07	2.83**
SE (s_{ij}) 5%		0.590		1.210		5.040		0.151		0.310		1.000
SE (s_{ij} –s_{ik})		0.890		1.800		7.524		0.227		0.460		1.490
SE (s_{ij}-s_{kl})		0.820		1.670		6.966		0.209		0.430		1.390

*, ** Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 10. Continued

Genotypes	ANTH/LEAF		ANTH/POD		ALS		FLS	
	Mean	SCA	Mean	SCA	Mean	SCA	Mean	SCA
P1 x P2	1.33	-0.54	1.00	-0.69**	3.33	1.02*	2.67	0.61*
P1 x P3	1.00	-0.70*	1.00	-0.65**	1.00	-0.23	2.67	0.23
P1 x P4	1.33	-0.58	1.33	-0.45	1.00	-0.23	1.33	-0.43
P1 x P5	5.00	2.29**	4.33	1.80**	1.00	-0.77	2.67	0.89**
P1 x P6	3.00	0.59	2.67	0.64**	2.00	-0.02	2.33	0.48
P2 x P3	1.00	0.29	1.00	0.30	1.67	-0.31	3.00	1.07**
P2 x P4	1.00	0.09	1.00	0.18	1.00	-0.98**	1.00	-0.27
P2 x P5	1.67	-0.04	1.33	-0.24	3.67	1.15**	1.00	-0.27
P2 x P6	1.33	-0.08	1.00	-0.07	4.00	1.23**	1.33	-0.02
P3 x P4	1.00	0.26	1.00	0.22	1.00	0.11	2.33	0.69**
P3 x P5	1.00	-0.54	1.00	-0.53	1.00	-0.43	1.00	-0.64*
P3 x P6	1.00	-0.24	1.00	-0.03	1.00	-0.68	1.00	-0.73**
P4 x P5	1.00	-0.74*	1.00	-0.65	3.00	1.57**	1.00	0.02
P4 x P6	1.00	-0.45	1.00	-0.15	1.00	-0.68	1.00	-0.26
P5 x P6	1.00	-0.12	1.00	-0.15	2.00	-0.23	1.00	-0.06
SE (s_{ij}) 5%		0.334		0.240		0.378		0.251
SE (s_{ij} –s_{ik})		0.499		0.359		0.564		0.374
SE (s_{ij}-s_{kl})		0.462		0.332		0.522		0.346

*, ** Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

Table 10. Continued

Genotypes	Organic matter		Crude protein	
	Mean	SCA	Mean	SCA
P1 x P2	95.76	0.13	21.63	1.19
P1 x P3	95.45	-0.29**	19.39	-0.16
P1 x P4	95.98	0.17	19.25	-0.72
P1 x P5	95.69	-0.15	19.73	-0.07
P1 x P6	95.8	0.09	19.28	-0.54
P2 x P3	95.47	-0.09	22.84	1.89**
P2 x P4	95.47	-0.17	19.34	-1.03
P2 x P5	95.68	-0.02	21.62	1.46*
P2 x P6	95.15	-0.39**	18.20	-2.02**
P3 x P4	95.69	-0.05	21.60	1.15
P3 x P5	95.93	-0.16	19.24	-1.07
P3 x P6	95.57	-0.02	21.32	0.99
P4 x P5	95.74	-0.14	20.01	0.28
P4 x P6	95.95	0.23*	20.39	0.67
P5 x P6	96.13	0.38**	21.48	1.89**
SE (s_{ij}) 5%		0.109		0.702
SE ($s_{ij} - s_{ik}$)		0.163		1.047
SE (s_{ij}-s_{kl})		0.151		0.969

*, ** Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively. DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=leaf area; YIE=seed yield, Roba = P1, Atendaba = P2, G. Rasha = P3, EMP-236 = P4, FEB-147 = P5, EAP-4 = P6, Roba x Atendaba = P1 x P2, Roba x G. Rasha = P1 x P3, Roba x EMP-236 = P1 x P4, Roba x FEB-147 = P1 x P5, Roba x EAP-4 = P1 x P6, Atendaba x G. Rasha = P2 x P3, Atendaba x EMP-236 = P2 x P4, Atendaba xFEB-147 = P2 x P5, Atendaba x EAP-4 = P2 x P6, G. Rasha x EMP-236 = P3 x P4, G. Rasha x FEB-147 = P3 x P5, G. Rasha x EAP-4 = P3 x P6, EMP-236 x FEB-147 = P4 x P5, EMP-236 x EAP-4 = P4 x P6, FEB-147 x EAP-4 = P5 x P6.

5.5. GENE ACTION AND ESTIMATES OF COMPONENTS OF GENERAL AND SPECIFIC COMBINING ABILITIES

In the present study, the SCA variance component was found to be greater than that of GCA for most traits (Table 10), implying that non-additive gene effects were predominant. The ratio of GCA to that of SCA was less than unity for days to flowering, days to physiological maturity, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, number of nodes per plant, leaf area, common bacterial blight (CBB) per leaf, CBB per pod, anthracnose per leaf, anthracnose per pod, angular leaf spot (ALS), floury leaf spot (FLS), dry matter, organic matter, crude protein and grain yield per plant.

The variance component due to GCA was greater than that of SCA for hundred seed weight, indicating that additive type of gene actions was important in governing the inheritance of this trait. On the other hand, the ratio of variance component due to GCA to SCA indicated that pod length and number of seeds per pod were more or less influenced by both additive and non-additive gene actions.

Moreover, some of the hybrids expressed intermediate seed colour between their parents; however, the F_1 crosses obtained by the combination of either FEB-147 or EMP-236 produced unique seed colour as compared to their parents (Figures 3- 17).

HYBRIDS VS PARENTS USED IN 6 X 6 HALF DIALLEL CROSSES OF COMMON BEAN

FIGURE 3. ♀ROBA X ♂GOBE RASHA

FIGURE 4. ♀ROBA X ♂ATENDANA

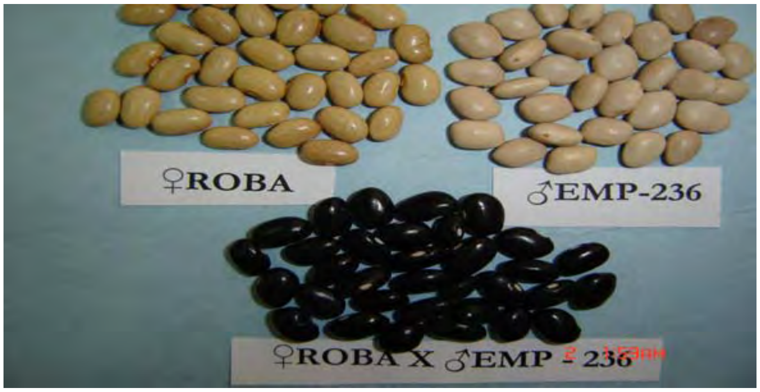

FIGURE 5. ♀ROBA X ♂EMP-236

FIGURE 6. ♀ROBA X ♂FEB-4

FIGURE 7. ♀ROBA X ♂EAP-4

FIGURE 8. ♀ATENDABA X ♂GOBE RASHA

FIGURE 9. ♀ ATENDABA X ♂EMP-236

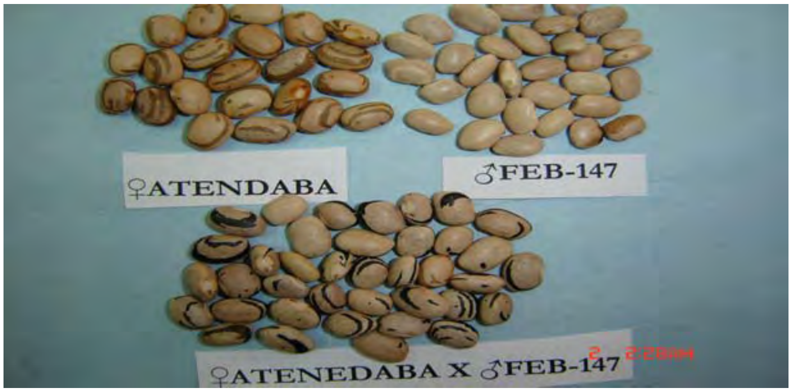

FIGURE 10. ♀ATENDABA X ♂FEB-147

FIGURE 11. ♀ATENDABA X ♂EAP-4

FIGURE 12. ♀GOBE RASHA X ♂EMP-236

FIGURE 13. ♀GOBE RASHA X ♂FEB-147

FIGURE 14. ♀GOBE RASHA X ♂EAP-4

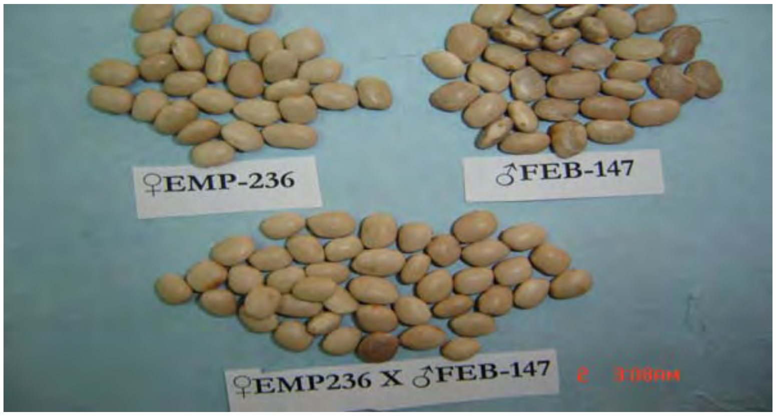

FIGURE 15. ♀EMP-236 X ♂FEB-147

FIGURE 16. ♀EMP-236 X ♂EAP-4

FIGURE 17. ♀FEB-147 X ♂EAP-4

Table 11. Estimates of general and specific combining ability variances componentsand gene actions in 6 x 6 half diallel cross of common bean

Character	Variance component due to		GCA/SCA
	GCA	SCA	
DEF	0.386	1.150	0.336
DEM	0.948	3.074	0.308
PLH	51.640	96.680	0.534
PL	0.074	0.077	0.961
PPP	1.867	4.743	0.394
SPO	0.133	0.093	1.430
SPP	84.405	178.730	0.472
BPS	0.010	0.143	0.070
NPP	0.455	0.793	0.574
SW	24.088	3.993	6.033
LA	8.622	13.133	0.657
CBB/L	0.018	0.079	0.228
CBB/P	0.006	0.044	0.136
ANTH/L	0.074	1.492	0.050
ANTH/P	0.022	5.564	0.004
ALS	0.145	0.260	0.558
FLS	0.007	0.443	0.016
DM	0.229	0.693	0.330
OM	0.187	0.457	0.409
CP	0.181	0.700	0.259
YIE	0.118	0.343	0.344

DEF =number of days to flowering; DPM=days to physiological maturity; PLH=Plant height; PL=pod length; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; BPS= number of branches per plant; NPP; HSW = 100 seed weight; LA=Leaf area; OM =organic matter; DM=dry matter; CP=crude protein; YIE=Seed yield; GCA=general combining ability; SCA=specific combining ability; GCA/SCA=the ratio of GCA to SCA variance; CBB/L=common bacterial blight/leaf; CBB/P=common bacterial blight/pod; ANTH/L=anthracnose/leaf; ANTH/P=anthracnose/pod, ALS=angular leaf spot; FLS=floury leaf spot.

5.6. RECIPROCAL EFFECT

The analysis of variance was done for thirteen important characters from the 4 x 4 complete diallel crosses of haricot bean varieties as presented by the mean square due to reciprocal cross in Table 12. Significant reciprocal effect variation was not observed among varieties for all the traits except for hundred seed weight.

Table 12. General combining ability (GCA), specific combining ability (SCA), Reciprocal effect (R), error mean for different characters in four parents of 4 x 4 complete diallel cross of haricot bean at Bako in 2005

Characters	Mean squares			
	GCA	SCA	R	Error
DEF	3.19**	1.36**	0.59	0.29
DPM	11.78**	5.14*	2.31	1.94
PLH	438.08**	255.25**	16.54	23.86
PL	1.18**	0.17	0.06	0.11
PPP	21.79**	7.33	4.41	4.16
SPO	2.62**	0.22**	0.05	0.03
SPP	1898.11**	79.37	74.78	139.70
PD	0.36**	0.08*	0.02	0.03
HSW	220.87**	7.89**	3.94**	1.09
DM	0.03	0.12	0.10	0.075
OM	0.07	0.03	0.026	0.02
CP	0.63	3.62**	0.43	0.42
YIE	14.67	6.71	4.10	9.05

*, ** = Significant differences from zero at P ≤ 0.01 and P ≤ 0.05, respectively DEF =number of days to flowering; DPM=days to physiological maturity; PLH=plant height; PPP=number of pods per plant; SPO=number of seeds per pod; SPP=number of seeds per plant; PD= pod diameter; HSW = 100 seed weight; LA=leaf area; OM =organic matter; DM=dry matter; CP=crude protein; YIE=seed yield; GCA=general combining ability; SCA=specific combining ability, R=reciprocal effect.

Reciprocal differences in seed weight were found in crosses between small and large size seeded beans. Two hybrids, Gobe Rasha x Roba and Dimitu x Gobe Rasha, showed significant and negative recipocal effects. On the other hand, Dimitu x Gobe Rasha exhibited significant and positive specific combining ability. Furthermore, all of the parents showed significant general combining ability effect. Among which Gobe Rasha was the best combiner for hundred seed weight followed by Atendaba (Table 13).

Table 13. Estimates of reciprocal effect (above diagonal) and specific combining ability (below diagonal) and general combining ability (gi) for hundred seed weight (in gram).

	Roba (1)	Atendaba (2)	Gobe Rasha (3)	Dimitu (4)
Roba (1)	-	0.84	-2.05 **	1.21
Atendaba (2)	0.46	-	1.32	1.19
Gobe Rasha (3)	-0.81	-0.09	-	-2.11**
Dimitu (4)	-0.47	0.07	2.32**	-
gi	**-4.79****	**1.01****	**6.98****	**-3.19****

*, **, Significant differences from zero at $P \leq 0.01$ and $P \leq 0.05$, respectively. ALS=angular leaf spot; FLS=floury leaf spot; $DF_e = 30$; $DF_{gca} = 3$; $DF_{sca} = 6$; $DF_r = 6$; S.E $(g_i) = 0.321$; S.E $(s_{ij}) = 0.585$, S.E $(r_{ij}) = 0.740$

6. DISCUSSION

6.1. ANALYSIS OF VARIANCE

Analysis of variance for genotype revealed that there was significant variation observed among entries for all the parameters measured except number of nodes per main stem, grain yield, dry matter and common bacterial blight per pod (Table 4 and 5). This indicated the presence of genetic variability among the genotypes and F_1 hybrids. Rodrigues *et al*. (1999) reported similar findings in different bean materials. Significant differences among the entries for yield component but lack in grain yield was in agreement with the findings of Melaku Ayale (1993). The highest grain yield was 30.95 g per plant in ♀Gobe Rasha x ♂EAP-4 while the least was 20.19 g obtained from EAP-4.

6.2 HETEROSIS

In the present study, most of the hybrids had significant and negative heterosis over the mid-parent and better parents for days to 50 % flowering. This result agrees with the works of Melaku Ayale (1993) and Jabagirdar (2001) for common bean and Reddy *et al*. (2003) for mung bean. Loganathan *et al*., 2001 also found similar result in mung bean. In most cases, crosses, which had significant and negative heterosis over the better parent, are useful when earliness is the major objective of the breeding program (Melaku Ayale, 1993). Thus, most of the crosses are important for areas receiving less rainfall. Crosses involving parent EAP-4 as one of their parents exhibited significant and negative heterosis for days to flowering and for grain yield (Table 7). This parent was also the best combiner for days to flowering and for seed crude protein. But it was the late maturing and low grain yielder as compared to the remaining parents.

The highest heterosis over the mid parent for days to physiological maturity was expressed by the hybrid Gobe Rasha x FEB-147. This hybrid also scored the highest value for heterosis over better parents even though it was not significant for this trait. Out of 15 crosses evaluated in this experiment, two crosses showed significant and negative heterosis over the mid-parent and four crosses exhibited significant and negative heterosis over the better parent for days to physiological maturity. Crosses involving EMP-236, as one of their parents were early in attaining days to physiological maturity.

Similar findings were reported that significant and negative heterosis over the mid-parent was observed in 5 out of 28 crosses (Melaku Ayale, 1993) and 3 out of 13 crosses (Gutierrez and Singh, 1985) for days to physiological maturity. Jabagirdar (2001) also reported significant and negative heterosis over mid-parent and better parent for common bean and Reddy *et al.* (2003) found pronounced hybrid vigour for days to maturity in mung bean.

Crosses, Atendaba x EMP-236 and EMP-236 x EAP-4 showed significant and negative heterosis over mid-parent and better parent in both days to flowering and days to physiological maturity. Therefore, combination of these parents seemed to be important for further manipulation in breeding program for earliness with acceptable quality.

The four hybrids (Roba x Gobe Rasha, Atendaba x Gobe Rasha, Gobe Rasha x EMP-236, Gobe Rasha x EAP-4) were significantly taller than the mid-parent and none of the hybrids was taller than their better parent. It seemed that Gobe Rasha contribute to the tallness of the hybrids though it was the shortest parent in its mean performance. The highest values for plant high were 55.47 % and 14.96 % in heterosis over the mid-parent and heterosis over the better parent, respectively. Melaku Ayale (1993) has also reported similar results in that only few of the crosses had heterosis over the mid-parent and better parent.

Significant heterosis over the mid parent and better parent was observed for pod length. Similar results were also reported in beans (Melaku Ayale, 1993 for common bean and Reddy *et al.* (2003) for mung bean). The highest and significant heterosis over the mid-parent and heterosis over the better parent were 11.54 % and -11.59 %, respectively. It was noticed that EMP-236 x FEB-147 and EMP-4 x EAP-4 showed significant and negative heterosis over the mid-parent and better parent, respectively.

Nine crosses produced more pods per plant than mid-parent and better parent. However, out of fifteen hybrids produced, only two hybrids (Gobe Rasha x EAP-4 and EMP-4 x FEB-147) significantly produced more pods than their mid-parent. It was also noticed that Gobe Rasha x EAP-4 gave higher grain yield than their mid and better parent. This may be attributed due to their complementary gene interactions. On the contrary, only Roba x Gobe Rasha produced less pods than its better parent. The remaining did not produce significant pods per plant as compared to their better and mid-parents. Similar results were reported by (Patil and Chaudhari, 1986) in that only one cross which had showed significant and positive heterosis over the better parent. But Melaku ayale (1993) reported that there was no significant heterosis in any of the crosses for number of pods per plant.

Hybrids with good number of pods per plant should be selected in order to increase yield, since number of pods per plant directly affects seed yield in common bean (Adams, 1967; Duarte and Adams, 1972).

Three crosses showed significant heterosis over the mid-parent and six crosses exhibited significant heterosis over the better parent for seeds per pod. Among the significant average heterosis, Roba x Atendaba (8.40 %) and Atendaba x EMP-236 (10.30 %) produced more seeds than their mid-parent while Atendaba x FEB-147 (-9.92 %) produced less seeds as compared to its better parent. All the six hybrids that were significant for heterosis over the better parent produced less seeds than their better parent. Similar results were reported by Melaku Ayale (1993) in common bean and Reddy *et al*. (2003) in mung bean.

Two crosses, EMP-236 x FEB-147 (46.71 %) and Atendaba x EMP-236 (45.66 %) gave significant higher number of seeds per plant than the mid-parent while only one cross, Roba x EAP-4 produced less seeds per plant as compared to the mid-parent. Two crosses showed significant heterosis over the better parent. Of which Roba x Gobe Rasha gave lower number of seeds (-40.97 %) while EMP-236 x FEB-147 gave higher number of seeds per plant (40.20 %). Roba x Gobe Rasha also gave significantly less seed crude protein as compared to mid and better parent.

Of the fifteen F_1 hybrids, four hybrids, Atendaba x EAP-4 (19.31 %), FEB-147 x EAP-4 (18.78 %), Roba x EMP-236 (16.31 %) and Atendaba x Gobe Rasha 9.54 %) exhibited significant and positive heterosis over the mid-parent while two crosses (Roba x Gobe Rasha and Gobe Rasha x FEB-147) showed significant reduction in seed size compared to their better parent.

In general, the overall heterosis above the mid-parent was positive and this results contract the findings of Gutierrez and Singh (1985) and Melaku Ayale (1993). However, Nienhuis and Singh (1986) showed positive heterosis above the mid-parent for seed size in common bean.

All the hybrids showed significant heterosis over the mid-parent and the better parent had negative values for leaf area. However, most of these hybrids with higher leaf area had better seed yield. This may be due to complementary gene actions between two traits.

Out of fifteen crosses, only two hybrids showed significant and positive heterosis above the mid-parent and better parent for seed yield. These hybrids, Gobe Rasha x EAP-4 gave 39.01 % and 27.16 % and FEB-147 x EAP-4 gave 24.98 % and 17.80 % more grain yield than the mid-parent and better parent, respectively. On the other hand, they were the best in their mean performance as compared to the remaining hybrids. FEB-147 x EAP-4 also showed significant and positive heterosis over the mid parent for seed crude protein.

The highest heterosis in Gobe Rasha x EAP-4 seemed to be due to the divergent relationship detected between the two parents for days to flowering, days to maturity, seeds size, plant height, pod per plant, seeds per plant main branch per plant, number of nods per plant, seed size, leaf area and grain yield (Table 7). The greater genetic diversity of the parents is associated with the greater heterosis in F_1 hybrids of common bean (Vasal *et al*., 1992). The limited significant heterosis in the present study is in agreement with that of Melaku Ayale (1993) in that he observed no significant heterosis above the mid-parent and better parent. In contrast to the present study for grain yield, bean yield heterosis was reported by several workers (Singh and Singh, 1974; Nienhus and Singh, 1986; Patil and Chaudhari, 1986; Sharee and Carlos, 1995; Longanathan *et al*., 2001; Jabagirdar, 2001; Krishnan *et al*., 2003; Reddy *et al*., 2003)

Three hybrids showed significant and positive heterosis above the mid-parent while two hybrids exhibited heterosis over the better parent for organic matter. These hybrids, FEB-147 x EAP-4, Atendaba x Gobe Rasha and Atendaba x FEB-147 gave 14.93 %, 13.46%, and 12.75 % more crude protein than their mid-parent whereas Atendaba x Gobe Rasha and FEB-147 x EAP-4 gave 13.18 % and 12.40 % greater organic matter than their better parent, respectively.

Three and five crosses exhibited significant heterosis over the mid-parent for dry matter and crude protein, respectively. Of which all had negative value except one hybrid (FEB-147 x EAP-4) had positive value for crude protein. On the other hand, four and three crosses showed significant and negative heterobeltosis for dry matter and organic matter, respectively. FEB-147 x EAP-4 was also showed greater grain yield heterosis over the better. The cross also selected for it's better yield performance.

Development of hybrids with resistant to disease is probably one of the cheapest and most effective management strategies. Use of chemicals is not only expensive for small-scale producers but also poses environmental hazards (Kimani *et al*., 1995). Consequently, breeding for resistance has been a major objective in most bean improvement. The disease mean performance revealed that all the hybrids/genotypes were rated as resistant to moderately resistant to all the diseases. This may be due to the absence of artificial disease inoculation during evaluation.

All of the hybrids except Atendaba x EAP-4 did not deviate significantly from their mid parent and better parent for common bacterial blight. Atendaba x EAP-4 showed significant and negative heterosis over the mid parent. Estimate of GCA effects reveled that Atendaba was poor combiner whereas EAP-4 was good combiner. On the other hand, the mean performances of the two parents indicated that both of the parents show resistant to CBB (Table 4).

Most of the crosses involved Roba or FEB-147 as one of their parents exhibited significant and positive heterosis for anthracnose (Table 7). Estimate of SCA also showed similar results for these parents. Both of the parents were also poor combiners for anthracnose. Gobe Rasha x EAP-4 and Atendaba x EMP-236 showed significant and negative heterosis for angular leaf spot. However, none of the crosses showed significant and negative heterosis for floury leaf spot.

6.3. COMBINING ABILITY

6.3.1. ANALSIS OF VARIANCE FOR COMBINING ABILITY

Analysis of variance of combining ability (general and specific) showed significant variation among entries for many of the traits measured. Mean squares for GCA were significant for number of days to flowering, days to physiological maturity, plant height, pod length, number of seeds per pod, number of seeds per plant, number of branches per main stem, hundred seed weight, leaf area, common bacterial blight per pod at $p \leq 0.01$ and for number of pods per plant, organic matter, common bacterial blight, anthracnose per leaf, anthracnose per pod, angular leaf spot and floury leaf spot at $p \leq 0.05$. Whereas, specific combining ability was significant for number of days to flowering, plant height, hundred seed weight, crude protein, organic matter, anthracnose per leaf, anthracnose per pod, angular leaf spot and floury leaf spot at $p \leq 0.01$ and for days to physiological maturity, number of seeds per pod and pod length at $p \leq 0.05$. This finding is in agreement with the work of several authors who reported more significant differences for GCA than SCA in different sets of beans (Melaku Ayale, 1993; Melllo *et al*., 1997; Rodrigues *et al*., 1999; Machado *et al*., 2002). In contrary to the present study more significant SCA to that of GCA were found (Marlon *et al*., 2004).

6.3.2. ESTIMATES OF GENERAL COMBINING ABILITY

Estimates of general combining ability effects indicated that EMP-236 showed significant positive GCA value for number of pod per plant, indicating that the parent was good for this character. Roba and FEB-147 significantly increased the number of seeds per pod. However, Gobe Rasha reduced the number of pods per plant, seeds per pod and seeds per plant. Similarly, Atendaba reduced the number of seeds per pod as it showed significant negative GCA value. On the other hand, Gobe Rasha was the best combiner for pod length whereas EMP-236 revealed poor combiner for the same character.

Although EAP-4 and EMP-236 revealed significant ($p \leq 0.01$) and positive for number of main branches per plant, they exhibited significant and negative GCA value for hundred seed weight.

All parents showed significant ($p \leq 0.01$) GCA values for hundred seed weight. Of which large seeded beans (Atendaba and Gobe Rasha) showed positive and significant GCA values while all small seeded beans (Roba, EAP-4, EMP-236, FEB-147) showed negative and significant GCA values. The results indicate that hybridization of parents with small seeded beans is important for seed size increment.

Positive and significant GCA for days to flowering and maturity was exhibited by EAP-4. On the contrary, negative and significant GCA was observed in Atendaba though days to maturity were not significant for this character. Gobe Rasha, respectively, showed positive and negative GCA values for days to maturity and days to flowering. In general, parents with significant negative GCA for days to maturity should be used in breeding for earliness. Similarly, those with positive GCA should be useful for incorporation of delayed maturity, which would serve farmers who are living in different agro ecological zones.

Though Atendaba was poor combiner for grain yield component and organic matter, it had positive and significant ($p \leq 0.01$) GCA value for plant height. Negative and significant ($p \leq 0.01$) GCA was observed in Gobe Rasha for this character. In this study, none of the parents was good combiner for all traits.

Roba is currently in production with good productivity, it had the highest general combining ability for both anthracnose per leaf and per pod, indicating the importance of improving this parent against anthracnose disease. Roba also showed significant and positive GCA effect for common baterial blight per pod and floury leaf spot.

Atendaba exhibited significant combining ability effect for common bacterial blight per leaf and per pod, anthracnose per leaf and per pod and angular leaf spot. It had positive value for all except for anthracnose, indicating that it was poor combiner for anthracnose but good for common bacterial blight and angular leaf spot. Gobe Rasha was good combiner (significant and negative GCA effects) for common bacterial blight per leaf and anthracnose. On the other hand, it had significant and positive GCA effects for angular leaf spot and floury leaf spot.

EMP-236 showed significant GCA effect for anthracnose per leaf and per pod, angular leaf spot and floury leaf spot. Of which it had only negative value for angular leaf spot. The results indicated that it was good combiner for anthracnose and floury leaf spot. FEB-147 exhibited significant and positive GCA for anthracnose per leaf and per pod and negative for floury leaf spot for GCA effects. Thus, it was only good combiner for floury leaf spot.

In contrary to the present study, the estimates of the general combining ability effect of each parent for reaction to CBB infection of leaves and pods among any two parent gi values suggest that the parents did not differ much from the mean of all the crosses in the diallel (Rodrigues *et al*., 1999).

In general, parents that showed significant and negative GCA effects could be favorably exploited in future breeding program, as their hybrids was poor combiners for the above diseases.

6.3.3. ESTIMATES OF SPECIFIC COMBINING ABILITY

Significant and positive SCA effects between Roba x Atendaba, Atendaba x EMP-236 and FEB-147 x EAP-4 for number of seeds per pod; Gobe Rasha x EMP-236 for days to flowering; Atendaba x EAP-4 for pod length; Roba x EMP-236, Atendaba x Gobe Rasha, Atendaba x EAP-4 and FEB-147 x EAP-4 for hundred seed weight; Roba x Gobe Rasha, Gobe Rasha x EAP-4 and Atendaba x EMP-236 for plant height, EMP-236 x EAP-4 and FEB-147 x EAP-4 for organic matter, Atendaba x Gobe Rasha, Atendaba x FEB-147, FEB-147 x EAP-4 for crude protein, suggesting that these specific crosses would be useful to breeders in improvements of haricot bean with specified traits. Heterosis estimates were reliable with the SCA estimates. Hybrid combinations (FEB-147 x EAP-4) with high SCA value produced high value of heterosis in crude protein. This association suggests that heterosis can be used for the choice of potentially more segregating materials in situation where SCA cannot be estimated (Machado, 2002).

There are specific cross combinations that are selected against some important diseases of haricot bean. These hybrids are Roba x Atendaba, Roba x Gobe Rash, EMP-236 x EAP-4 for anthracnose per pod; Atendaba x EAP-4 for angular leaf spot; Gobe Rasha x FEB-147, Gobe

Rasha x EAP-4 for floury leaf spot because they exhibited significant and negative SCA effects for the indicate traits. On the other hands, there are some crosses, Roba x FEB-147 for anthracnose per leaf, anthracnose per pod, and floury leaf spot; Roba x EAP-4 for anthracnose per pod; Roba x Atendaba, Atendaba x FEB-147, Atendaba x EAP-4 and EMP-236 x FEB-147 for angular leaf spot; Atendaba x Gobe Rasha and Gobe Rasha for floury leaf spot, that showed significant and positive specific combining ability effects for some of the diseases, suggesting that improving gain yield and yield component with these hybrid combinations might lead to incorporation of deleterious traits to the hybrid. In general, low specific combining ability values for disease reaction in leaves and pods indicate greater resistance.

6.4. GENE ACTION AND ESTIMATES OF COMPONENTS OF GENERAL COMBINING ABILITY AND SPECIFIC COMBINING ABILITY

The estimates of variance components of general combining ability and specific combining ability revealed that additive type of gene action was more important in the inheritance of hundred seed weight as the ratio of GCA to SCA variance component was greater than unity for the traits. The magnitude of GCA variance component was 6.03 times greater than that of SCA. This has got breeding implication for the improvement of a given trait under investigations. In contrast to the present study, the importance of both additive and non-additive type of gene action was reported in mung bean for 100 seed weight (Ali and Bhadra, 1985; Jabagirdar, 2001).

In the present study, non-additive type of gene action was of greater importance for most of the traits (days to flowering, days to physiological maturity, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, number of nodes per plant, leaf area, common bacterial blight (CBB) per leaf, CBB per pod, anthracnose per leaf, anthracnose per pod, angular leaf spot (ALS), floury leaf spot (FLS), dry matter, organic matter, crude protein and grain yield per plant). These findings are in agreement with the work of Mak and Yap (1980) and Viana *et al*. (1999) for number of pods per plant, crude protein, Machado *et al*. (2002) for grain yield and Rodrigues *et al*. (1999) for common bacterial blight per pod.

Similarly, non-additive effects were more important for number of pods per plant in snap bean (Marlon *et al*., 2004).

This shows that non-additive gene action contributes more to the expressions of most of the traits under study than additive gene action. For these traits, therefore, the indicated strategy would be an interpopulational breeding procedure, to exploite the heterosis related to the non-additive effects.

However the importance of additive type of gene action in the inheritance of the above characters was reported by several workers, Singh and Singh (1974) for number of pods per plant; Nienhuis and Singh (1986) for grain yield and yield components; Melaku Ayale (1993) for all characters studied; Rodrigues *et al*. (1999) for common bacterial blight per leaf; Marlon *et al*. (2004) for pod weight per plant, number of seeds per pod, height of the insertion of the first pod and number of days to flowering.

In contrast to the present study, the preponderance of both additive and non-additive gene action in the inheritance of the indicated traits was reported by several authors in beans for grain yield (Singh and Singh, 1974; CIAT, 1984; Ali and Bhadra, 1985; Vaid *et al*., 1985; Ramalho *et al*., 1988; Jabagirdar, 2001; Chand and Rao; 2002 Machado *et al*., 2002; Singh and Dikshit, 2003), for days to flowering, days to maturity, plant height in mung bean (Jabagirdar, 2001), for days to flowering, days to maturity, plant height, grain yield per plant, (Chand and Rao, 2002) for plant height and pod length (Singh and Dikshit, 2003), for protein (Tadesse Mebrahtu and Ali Mohamed, 2003).

In present study, both additive and non-additive types of gene actions were more or less equally importance in the inheritance of pod length and number of seeds per pod. Similar finding was reported for pod length in mung bean (Ali and Bhadra, 1985) and for number of seeds per pod (Rainey and Griffiths, 2005). Other reports indicated the predominance of non-additive gene action in the inheritance of number of seeds per pod (Mak and Yap, 1980). In general, both additive and non-additive gene actions were important in the inheritance of the traits studies. The result, therefore, suggested the breeding methods such as recurrent selection would be useful.

The F_1 crosses obtained by the combination of either FEB-147 or EMP-236 produced unique seed color as compared to their parents. This finding may be explained in terms of modified gene action. In maize, a gene Pr modifies the action of R, which produces red seed color. In the presence of R, Pr changes the red color to purple due to supplementary gene action (Singh, 1993). Similarly, Adams (1985) reported that modifying genes regulate the expression of genes for seed color patterns in haricot bean.

6.5. RECIPROCAL EFFECT

Significant variation was not observed for reciprocal effects among the genotypes for all the traits studied except for seed size. These findings were supported by the work of Rainey and Griffiths (2005) for yield components including pod number, seed number, and seeds per pod in snap bean. To the contrary, Leleji *et al*. (1972) and Tadesse Mebrahtu and Ali Mohamed (2003) reported the importance of reciprocal effect in protein of haricot bean. In several crops, a large maternal effect on seed size has been identified through differences between reciprocal crosses. This was found in *Zay mays* (Eagles and Hardacre, 1979), *Rraphanus raphanistrum* (Mazer *et al*., 1986), *Brassica campestris* (Singh and Murty, 1990) and Pea (Claire *et al.*, 2000).

Genetic studies of cultivated plants have showed that maternal cytoplasm may directly influence seed size; however, in the case of dry beans and in most cases with soybeans, these differences did not persist into the F_2, suggesting the non-cytoplasmic maternal effects (Roach and Wulff, 1987). Fowler *et al.* (1993) commented that although reciprocal effects are not usually significant in the composition of the variation of bean plant population under normal temperature conditions, they are significant under low temperature conditions. Therefore, a multiple generation study has to be done to confirm this conjecture.

7. CONCLUSIONS AND RECOMMENDATIONS

The ultimate objective of a bean breeder is to produce hybrids that are superior in some way to those in commercial productions. To accomplish this, the breeder must devise a breeding program, which will allow him to produce and reproduce genotypes that represent, as best as possible, the optimum combination of genes. Therefore, the information generated from this study could be basically important for breeders in planning future breeding program. However, the experiment should be tested across different locations and years to obtain stable and consistent results for further use.

In general, the highest yield and yield components were attained in hybrids than in parental lines. Moreover, most of the hybrids showed resistant to most of the diseases evaluated than the parent lines though the score ranged from resistant to moderately resistant for all genotypes.

In the present study, the two F_1 hybrids, viz., Gobe Rasha x EAP-4 and FEB-147 x EAP-4 are recommendable for the selection of segregant population as they out shined their parents by 17.80 – 39.01 % in grain yield. However, in self-pollinated crops like haricot bean, hybridization is very difficult i.e. it is impossible to emasculate by hand on a large scale. Therefore, there is a need to investigate commercial hybrid seed production in haricot bean using modern breeding techniques such as apomixis, male sterility and restoration of fertility. FEB-147 x EAP-4 was also selected for its better seed crude protein content than the mid parent as it showed significant and positive heterosis. The most important hybrids recommended for early maturity are Roba x EMP-236, Atendaba x EMP-236 and EMP-236 x EAP-4.

The parents EAP-4 and Gobe Rasha were good combiners for physiological maturity. Nevertheless, Atendaba was the poor combiner for the same trait. For plant height, Atendaba was good general combiner. In contrast, Gobe Rasha was the least general combiner. EMP-236 and Roba were good combiners for number of pods per plant and number of seeds per plant, respectively. For seed size in general, the large size seeded beans, Atendaba and Gobe Rasha, were good combiners while the small size seeded (Roba, EMP236, FEB-147 and EAP-4) were poor combiners for hundred seed weight.

Roba is currently in production with good productivity, it had the highest general combining ability (significant and positive GCA effects) for anthracnose per leaf and per pod, indicating the importance of improving this parent against anthracnose disease. Gobe Rasha was good combiner for anthracnose and common bacterial blight per leaf. EMP-236 was good combiner for anthracnose and floury leaf spot. In general, parents with significant and positive GCA effects could be favorably exploited in future breeding program, as their hybrids was poor combiners for the diseases evaluated. The study, therefore, suggests a backcross breeding scheme and molecular techniques such as RFLP markers, which can be linked to specific heritable traits so as to accelerate a breeding program in improving beans for resistant to the diseases evaluated using the identified promising hybrids.

Specific cross combinations were best performed and would be useful to breeders in future breeding scheme. These hybrids were Atendaba x EAP-4 for pod length; Roba x EMP-236, Atendaba x Gobe Rasha, Atendaba x EAP-4 and FEB-147 x EAP-4 for hundred seed weight; Roba x Gobe Rasha and Gobe Rasha x EAP-4 for plant height, Atendaba x EAP-4 for dry matter, Atendaba x Gobe Rasha, FEB-147 x EAP-4 for crude protein; Roba x Atendaba, Roba x Gobe Rash, EMP-236 x EAP-4 for anthracnose per pod; Atendaba x EAP-4 for angular leaf spot; Gobe Rasha x EAP-4 for floury leaf spot. In general, crosses with significant positive or negative SCA values for desirable traits indicated that hybridization is necessary to increase and decrease the traits.

Recipocal effects, which are due to cytopasmic genes, were not observed in the genotypes used, indicating nuclear genes were responsible for the inheritance of the traits. Thus, breeders should not worry to choice of which parent will be the male or female using these materials for hybridization. However, reciprocal differences in seed weight were found in crosses between small and large size seeded beans. These finding, therefore, suggested a multiple generation study to identify the type of maternal effect involved in the seed weight. Because persistence of these differences into the F_2 and F_3 hybrids indicated that the effects were due to maternal cytoplasm.

Pod length and number of seeds per pod were more or less influenced by both additive and non-additive gene actions. Whereas, non-additive gene effects were predominant for days to flowering, days to physiological maturity, plant height, number of pods per plant, number of seeds per pod, number of branches per plant, number of nodes per plant, leaf area, common bacterial blight (CBB) per leaf, CBB per pod, anthracnose per leaf, anthracnose per pod, angular leaf spot (ALS), floury leaf spot (FLS), dry matter, organic matter, crude protein and grain yield per plant. Further more, additive type of gene actions was important in governing the inheritance of seed size.

In general, both additive and non-additive gene actions were important in the inheritance of the traits studied. The results, therefore, suggested the breeding methods such as recurrent selection that capitalize on different types of gene action, including recurrent selection for GCA and inbred per se selection (additive effects), recurrent selection for SCA (dominant effects), and recipocal recurrent selection (both additive and dominance effects). For the traits showed non-additive gene action, the suggested strategy would also be an interpopulational breeding procedure, to exploite the heterosis related to the non-additive effects.

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APPENDIX 1. DESCRIPTORS USED FOR CHARACTERIZATION AND PRELIMINARY EVALUATION OF BEAN GERMPLASM.

Abbreviation	Description and legend
PGH	Plant growth habit: 1=bush determinate, type I; 2=bush indeterminate, type II; 3=semi-climber/prostrate indeterminate, type II; 4=climber indeterminate, type IV
DEF	Number of days from emergence to stage where 50% of plants ended flowering
DPM	Days from emergence to physiological maturity
PLH	Plant height (average, in cm, at maturity from 10 plants, measured from cotyledon scar to tip of plant).
NFR	Nodes on stem to first raceme, measured at physiological maturity.
PFC	Pod fibre content in fully expanded immature pods (0=string less; 3=few strings; 5=mod. Stringy; 7=very stringy).
PCO	Pod colour at physiological maturity (1=dark purple; 2=red; 3pink; 4=yellow; 5 cream; 6=brown; 7=green).
DHA	Days to harvest (Number of days from emergence until 90% of pods are dry)
PPP	Number of pods per plant (average of 10 plants at harvest).
SPP	Number of seeds per pod (average number of seeds from one pod taken from 10 plants).
SCP	Seed coat pattern (1=plain; 2=mottled; 3=striped; 4=spotted; 5=speckled; 6=ringed).
SSH	Seed shape (1=round; 2=ovoid; 3=cuboid; 4=kidney shaped; 5=truncate fastigate)
SCL	Seed coat lustre (brilliance; 1=dull (matt); 2=medium; 3=shiny).
HSW	100 seed weight (in g to first decimal place at 12 - 14% seed moisture content).
YIE	Seed yield g/plant)
BCM	Bean common mosaic virus, BCMV (scores 1 -9 where: 0=absent, 3=low; 5= medium; 7=high susceptibility).
CBB	Common bacterial blight (scores as for BCMV).
ALS	Angular leaf spot (scores as for BCMV).
RST	Rust (scores as for BCMV).
ASC	Ascochyta (scores as for BCMV).
Anth	Anthracnose (BCMV).
BSM	Bean stem maggots (scores as for BCMV).

APPENDIX 2. LONG –TERM (1961-2005) WEATHER DATA OF BAKO AGRICULTURAL RESEARCH CENTER

Month	Year 1961-2005					Year 2005				
	RF (mm)	RH (%)	Air temperature (^{0}C)			RF (mm)	RH (%)	Air temperature (^{0}C)		
			Min.	Max.	Ave.			Min.	Max.	Ave.
January	13.1	54.1	11.1	29.8	20.5	10.4	55.6	12.2	31.0	21.6
February	17.0	50.7	12.5	30.8	21.7	0.0	42.7	14.1	32.2	23.1
March	52.1	51.8	14.2	31.1	22.7	43.0	46.3	14.5	32.7	23.6
April	65.0	53.1	14.8	30.8	22.8	99.5	47.2	15.0	32.6	23.8
May	143.8	62.5	15.0	28.7	21.9	79.0	54.4	14.7	30.3	21.5
June	215.5	71.1	14.7	26.0	20.4	221.2	64.4	14.1	29.0	21.5
July	253.8	74.2	14.6	23.9	19.3	268.8	72.5	14.8	25.2	20.0
August	232.2	78.8	14.5	24.1	19.3	230.8	74.9	15.0	26.5	20.7
September	142.4	66.4	14.0	25.2	19.6	242.2	75.6	14.6	26.6	20.6
October	69.2	65.8	12.7	27.2	20.0	26.2	69.4	14.2	28.2	20.9
November	24.3	61.9	11.1	28.5	19.8	37.1	64.7	11.5	29.5	20.3
December	13.7	57.6	10.4	29.2	19.8	0.0	58.9	7.0	32.0	19.5
Total	1242.1	748.0	159.6	335.3	247.8	1258.2	726.6	161.7	355.8	257.1
Mean	-	62.3	13.3	27.9	207	-	60.6	13.5	29.7	21.4

Source: Bako Agricultural Research Center

APPENDIX 3. DRY BEANS AREA HARVESTED PER HECTARES (HA), GRAIN YIELD IN HECTOGRAMME (100 GRAMMAS) PER HECTARE (HG/HA), AND PRODUCTION PER METRIC TONS (MT) IN ETHIOPIA, AFRICA AND WORLD FROM 1995 TO 2005)

Country	Year										
Area harv. (HA)	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005
Ethiopia	123,170	101,170	104,500	100,000	187,020	218,940	336,900	206,771	181,583	240,963	241,000
Africa	3,634,407	3,663,661	3,724,409	3,820,850	3,910,525	4,141,415	4,516,344	4,567,678	4,597,602	4,526,407	4,551,743
World	25,757,829	25,669,759	25,299,976	24,449,228	25,190,048	25,276,711	24,777,892	27,023,934	25,526,929	26,677,352	26,778,102
Yield (HG/HA)											
Ethiopia	3,499	10,784	9,249	7,759	6,696	6,724	6,262	4,900	6,471	7,281	7,303
Africa	6,249	5,713	5,503	6,073	6,227	6,117	6,282	6,256	6,083	5,997	6,089
World	6,729	6,525	6,347	6,586	6,879	6,746	6,725	7,167	7,276	6,885	7,092
Production (MT)											
Ethiopia	43,102	109,104	96,652	77,590	125,237	147,210	210,961	101,324	117,499	175,457	176,000
Africa	2,271,085	2,093,062	2,049,566	2,320,494	2,434,998	2,533,155	2,837,193	2,857,567	2,796,716	2,714,505	2,771,447
World	17,331,156	16,748,524	16,057,338	16,103,136	17,327,620	17,051,608	16,662,910	19,368,604	18,572,155	18,368,480	18,991,954

Source: FAO, 2004. Book of a year.

APPENDIX 4. MAJOR PULSES AREA HARVESTED PER HECTARES (HA), GRAIN YIELD IN HECTOGRAMME (100 GRAMMAS) PER HECTARE (HG/HA), AND PRODUCTION PER METRIC TONS (MT) IN ETHIOPIA FROM 1995 TO 2005

		Year										
Type of the crop		**1995**	**1996**	**1997**	**1998**	**1999**	**2000**	**2001**	**2002**	**2003**	**2004**	**2005**
Area harvested (HA)	Beans, Dry	123,170	101,170	104,500	100,000	187,020	218,940	336,900	206,771	181,583	240,963	241,000
	Broad Beans, Dry	342,940	339,120	338,010	420,140	297,510	362,430	433,350	371,670	389,994	381,998	380,000
	Peas, Dry	162,560	203,710	167,100	136,650	158,720	159,450	216,060	204,025	204,048	228,766	230,000
	Chick-Peas	178,890	150,400	118,890	179,880	167,650	184,790	211,910	194,981	140,244	168,089	170,000
	Lentils	61,870	83,360	50,070	66,110	66,870	75,000	95,000	75,444	65,500	57,806	58,000
	Vetches	85,330	76,680	81,970	93,000	95,050	110,580	114,060	84,986	83,500	82,713	83,000
	Pulses nes	13,900	13,020	29,510	20,530	21,430	16,260	13,520	27,226	25,543	33,735	35,000
Yield (HG/HA)	Beans, Dry	3,499	10,784	9,249	7,759	6,696	6,724	6,262	4,900	6,471	7,281	7,303
	Broad Beans, Dry	10,935	10,647	10,677	8,065	9,638	10,743	10,473	12,192	9,274	11,175	11,316
	Peas, Dry	9,132	6,527	8,527	7,124	6,496	7,375	6,784	9,796	6,853	7,447	7,478
	Chick-Peas	6,960	9,448	9,958	7,624	8,281	8,909	8,293	9,580	8,138	8,087	7,941
	Lentils	6,126	4,836	6,682	5,466	5,001	7,867	6,868	5,094	5,496	6,102	6,082
	Vetches	7,432	10,522	11,637	9,677	8,272	9,720	8,716	10,865	10,180	10,035	10,000
	Pulses nes	5,288	6,317	5,496	4,780	5,662	6,638	5,923	5,876	5,872	5,124	5,429
Production (MT)	Beans, Dry	43,102	109,104	96,652	77,590	125,237	147,210	210,961	101,324	117,499	175,457	176,000
	Broad Beans, Dry	375,002	361,051	360,895	338,844	286,743	389,343	453,841	453,125	361,675	426,892	430,000
	Peas, Dry	148,456	132,963	142,484	97,347	103,108	117,595	146,581	199,854	139,843	170,365	172,000
	Chick-Peas	124,507	142,097	118,388	137,133	138,837	164,627	175,734	186,801	114,128	135,930	135,000
	Lentils	37,904	40,311	33,456	36,137	33,440	59,000	65,250	38,430	36,000	35,275	35,275
	Vetches	63,417	80,682	95,388	90,000	78,624	107,483	99,419	92,339	85,000	83,000	83,000
	Pulses nes	7,351	8,225	16,219	9,813	12,134	10,793	8,008	15,998	15,000	17,286	19,000

Source: FAO, 2004. Book of a year.

DECLARTION

This thesis is the product of my original work, has not been presented for the degree in any other university and that all sources of material used for the thesis have been duly acknowledged.

Name: ________________________________

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Place: ________________________________

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