RESISTANCE OF COMMON BEAN GENOTYPE TO FOLIAR FUNGAL AND BACTERIAL DISEASES

BATUMIKE NSHOBOLE RUPHINE

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DECLARATION

This thesis is my original work and has not been presented for award of a degree in any other university.

Batumike Nshobole Ruphine.....Date 09/06/2018

The thesis is submitted for examination with our approval as the University supervisors:

Dr. Felister Mbute Nzuve ...fmbute.....Date...9/6/2018.....

Department of Plant science and Crop protection

University of Nairobi

Prof. James W. Muthomi .....Date.....9/6/2018

Department of Plant science and Crop protection

University of Nairobi

Dr. Reuben Otsyula (PhD) ....Date..1.6/6/2018

Kenya Agricultural and Livestock Research Organization –Kakamega

DEDICATION

To my parents Batumike Cikomola Richard and M'Nakamya Ngomora Ursule;

My husband Elois Cinyabuguma and my lovely daughters Marie Laure Mwaliw'ishe, Anne Ursule W'eka, Marie France Alika and Rose Michelle Aghishwe;

My sisters and brothers, nieces and nephew, uncles and aunts, cousins, friends and in-laws.

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ABBREVIATIONS

%Em.	Percentage emergence
%Inc.	Percentage incidence
ALS	Angular Leaf Spot
ANOVA	Analysis of Variance
ANT	Anthracnose
AUDPC	Area Under the Disease Progress Curve
BCr	Backcross resistant
BCs	Backcross susceptible
CaCO3	Calcium Carbonate
CBB	Common Bacterial Blight
CFU	Colony-forming unit
CIAT	International Center for Tropical Agriculture
CIMMYT	International maize and wheat improvement centre
CIP	International Potato centre
CV	Coefficient of Variation
DAI	Days after planting
df	Degree of freedom
DR Congo	Democratic Republic of Congo
DTF	Days to 50% flowering
DTM	Days to 75% maturity
F_1	First filial generation
F_2	Second filial generation
F_3	Third filial generation
FAOSTAT	Food and Agriculture Organization Statistical
FS	Final Score
g	grams
GoK	Government of Kenya
HSW	Hundred seed weight
INERA	Institut National pour l'Etude et la Recherche Agronomiques
KALRO	Kenya Agricultural and Livestock Research Organization
KARI	Kenya Agricultural Research Institute
Kg/ha	Kilograms per hectare
LSD	Least Significance Difference
NPP	Number of pod per plant
ns	No significant difference
NSP	Number of seed per pod
PBS	Phosphate Buffered Saline
pH	Potential of hydrogen
RCBD	Randomized Complete Block Design
USAID	United States Agency for International Development
Xap	*Xanthomonas axonopodis* pv. *Phaseoli*
YDCA	Yeast Dextrose Carbonate Agar
χ^2	Chi-square

ABSTRACT

Foliar diseases have been reported to cause 45 to 100% of grain losses in common bean. However, conventional management strategies are not effective and sustainable to combat the bean yield losses. The use of host plant resistance is a more effective strategy to reduce losses. The objective of this study was to contribute to improved common bean productivity through a) Screening bean germplasm to identify sources of resistance to multiple diseases and b) determination of the genetics of resistance to the common bacterial blight resistance in common bean. To identify sources of resistance to multiple diseases, twenty four common bean lines were evaluated in the field at the Kenya Agricultural and Livestock Research Organization (KALRO)-Kakamega and Lugari during the short rains 2016 and long rains 2017. The trial was laid out in a randomized completed block design replicated three times in a 12 x 2 arrangement within the block. Data was collected on agronomic traits, disease incidence and severity and yield and yield related traits of common bean. The data was subjected to analysis of variance to determine the differences among the traits. Results showed significant variations among genotypes in their reaction to the fungal and bacterial diseases' intensity. Significant differences were also observed among genotypes for the percentage of emergence, days to 50% flowering and days to 75% maturity, number of pod per plant, 100-seed weight and grain yield. All the 24 bean lines evaluated showed moderate resistance to angular leaf spot. The genotypes Red34, KK15, Cal5B, Cal137, GLPX92, Cal6, Red45 and Cal33 were resistant to anthracnose while Red34, KKBC05/32, KK071, GLP2, Ciankui, RWR2245 and Cal6 were resistant to common bacterial blight. The genotypes Cal139A, Red16 and Red13 recorded the highest grain yield. In determining the genetics of resistance to the

common bacterial blight, three generations namely F_1, F_2 and backcrosses were developed from two parents namely VAX3 and MCM2001, resistant and susceptible respectively to common bacterial blight. Both parents and progenies were planted in the screenhouse at KALRO- Kakamega. The plants were inoculated and assessed for common bacterial blight disease severity/intensity. Chi square test was used to compare the Mendelian segregation ratios and heterosis was also calculated. Parental line VAX3 presented resistant reactions to common bacterial blight, while all the plants from the parental line MCM2001 were susceptible. All the F_1 plants from crosses between VAX3 and MCM2001 were resistant to common bacterial blight. The F_2 populations revealed segregation pattern following a 3:1 genetic ratio for resistance and susceptibility respectively implying that resistance to common bacterial blight was governed by a single dominant gene. The plants generated from the backcross with the resistant parent VAX3 were resistant to common bacterial blight with 1:0 genetic ratios for resistance and susceptibility while the plants generated from backcross with susceptible parent MCM2001 showed 50% of resistance and 50% susceptibility with an expected ratio of 1:1. Thus, the resistant parents VAX3 could be utilized to develop common bean varieties that are resistant to common bacterial blight. The percentage values from mid-parent heterosis had negative values which increased the resistance from about 75 to 80% compared to the resistant parent. The values from better parent heterosis remained constant compared to the resistant parent VAX3. The progeny F_1 increased the resistance to common bacterial blight compared to the resistant parent VAX3. The best performing genotypes for resistance to the multiple diseases could be tested under more diverse environments for release to the farmers to increase bean productivity in Kenya.

CHAPTER ONE

INTRODUCTION

1.1. Background

Common bean (*Phaseolous vulgaris* L.) is the most essential legume consumed worldwide (Nga'yu-Wanjau, 2013) and is grown on all the continents, except for Antarctica (Gicharu *et al*., 2013). In Africa, the common bean production is estimated to be 2.6 million metric tons on 4.2 million hectares equivalent to 619 kg per hectare (Katungi *et al.*, 2010). The common bean crop is cultivated widely in subtropical and tropical zones (Blair, 2010). Sub-Saharan Africa produces approximately 3.5 million metric tons ha^{-1} with 62% being produced in eastern and central Africa regions namely Tanzania, Burundi, Uganda, DR Congo, Kenya and Rwanda (Katungi *et al.*, 2010). Per capita common bean consumption, in central and eastern Africa, exceeds 40 kg per annum (Nga'yu-Wanjau, 2013).

In eastern and central Africa, common beans are grown primarily for home consumption and usually in intercrop with cereals, banana, roots and tubers (Wortmann *et al*., 1998; Kandala *et al*., 2011). Approximately 70% of the people live in rural areas and about 40 million people depend on agriculture for their livelihoods (Christiaensen *et al*., 2010). In 2014, DR Congo was ranked first on the Global Hunger Index, while the level of production in agriculture has fallen to 40 percent since 1990 (Kandala *et al*., 2011). In spite of this, in 2006, the agriculture-oriented sector contributed around 45% of the total Gross Domestic Product, decreasing in 1997 to about 10% (Blair *et al*., 2010). The average food consumption per day is approximately below 1,500 kilocalories per individual and this is below the minimum of 1,800 per individual required to maintain good health (Kandala *et al*., 2011).

Common bean is widely grown as a major staple food in east and central Africa (Hotz and McClafferty, 2007). It is the crop which the output and the commercialization could be a potential factor for the improvement of the livelihoods in rural areas (Njingulula, 2012). It is recognized as a capital source of human food calories and protein followed by maize and cassava (Kelly and Vallejo, 2004). It's essentially the most consumed food with about 300 grams per person per day in east and central Africa (Katungi, 2010). Beans are also cultivated mainly by women on small pieces of land in rural areas. It is considered as a complete food due to the high quality content and its complex nutrients. It is eaten as cooked green leaves and grains either fresh or dry, but more often in mixed dishes to complement cereals and starchy tubers. With such recipes with a high rate of consumption diversified, it provides a unique source of protein (65%), calories (32%) and trace elements that are essential for food security, nutrition and health, especially among the vulnerable infants, adolescents and pregnant women (Kabutbei, 2014). Thus, bean is considered to be meat for the poor (Katungi, 2010).

1.2. Problem statement

Common bean production is declining with yields being less than 0.5 t/ha compared to the expected yield of 1.5 t/ha (Hillocks *et al.*, 2006; FAOSTAT, 2013). Its production has declined by 20 % from over 0.5 million tons in 2006 to below 0.3 million tons in 2008 (Akibode, 2011). That translates to a decrease from 6 bags/ha in 2006 to 2 bags/ha in 2008 (ICRISAT, 2013). In Kenya, yields are still low at 400kg/ha, which is below the potential yield of 1350-1980 kg/ha according to KALRO (Mbugua, 2016). The low common bean yield in this region is attributed to a number of factors namely abiotic stresses like drought, soil infertility, high

temperatures, excessive and erratic rainfall, nutritional disorders and biotic factors such as diseases and insect-pests (Otsyula *et al*., 1998; Wagara and Kimani, 2007). Among the major foliar diseases that limit bean production include angular leaf spot, anthracnose and common bacterial blight are prevalent in east and central Africa (Kimiti *et al*., 2009). These foliar diseases have been reported to cause 45 to 100% of losses in common bean (Mahasi *et al*., 2010). With these high losses of yield, the farmers have difficulty in cultivating the common bean thus they have progressively abandoned it in favor of other crops (Katungi, 2010). These diseases are considered major biotic stresses due to the lack of improved disease resistant varieties with farmer preferred characteristics. The problem is further compounded by the fact that small-scale farmers, who are the principal common bean growers in east and central Africa, use farmers' own saved seeds that serve as primary inoculums for the development and spread of the disease epidemics (Njingulula, 2012). Conventional management strategies namely poor farming practices like continuous cropping without rotation and use of farm saved seeds by farmers are some of the factors that have been identified to cause major disease epidemics of common bean (Mahasi *et al*., 2010).Thus, these conventional management strategies are not effective and sustainable. The use of host plant resistance is a more effective strategy to decrease losses (Kimani *et al*., 2005).

1.3 Justification

Breeding bean varieties that are resistant to major production constraint like diseases would have a greater impact on the livelihood of the people. There is need to identify bean genotypes with resistance to the major diseases. The new resistant varieties have also to be accepted and cultivated by the farmers, and should exhibit high resistance to diseases, high yield and tolerance to other environmental stresses. They must be

profitable and have good characteristics than local variety (Gilligan, 2012). Therefore, breeding of common bean varieties with resistance to common bacterial blight, angular leaf spot and anthracnose will play a pivotal role, in combination with other control methods, in the development of an effective integrated strategy for disease management.

1.3. Objectives

The main objective of this study was to contribute to improved common bean productivity through development of germplasm resistant to angular leaf spot, anthracnose and common bacterial blight.

1.3.1 Specific objectives

1) To identify common bean genotypes with resistance to angular leaf spot, anthracnose, common bacterial blight and high yield.

2) To determine the genetics of resistance to common bacterial blight.

1.4. Hypotheses

1. Resistance to major foliar diseases is identified through selection of suitable common bean genotypes
2. The resistance to common bacterial blight disease is controlled by a single gene with dominant effect

CHAPTER TWO

LITERATURE REVIEW

2.1. Origin, distribution and botany of common bean

The common bean (*Phaseolus vulgaris L*.) originated from wild growing vines and is diversified in the Andes and the highlands of Middle America (Chacon *et al*., 2005; Gichangi *et al.,* 2012). It was domesticated in two regions distributed from Mesoamerican gene pool and the Andean gene pool (Gichangi *et al*, 2012). The domestication of common bean has changed the phenology, morphology and the form of the plant. The modification is visible also on the seed size, growth habit, maturity and seed retention (Beebe *et al*., 2014). Therefore, the dissimilarity among the cultivated and wild common bean is due to the seed size, pod size and the presence of edible parts such as the dry seed and green immature pod (Oshone *et al.,* 2014).

Phaseolus vulgaris L is the scientific name of common bean. It's within the legume family with a taxonomic hierarchy namely as Order is Fabales, Family is Fabaceae, Genus is *Phaseolus L*., and the Species is *Phaseolus vulgaris L*. The genus *Phaseolus* is diverse with around 80 wild and cultivated species, but it remains the most commonly cultivated species (Purseglove, 1968; Porch, 2013). Common bean is a multipurpose diploid (2n = 2x = 22) self-pollinated crop and the most widely grown pulse in eastern and central Africa (Stoetzer, 1984; Gichangi *et al.*, 2012).

Cultivation of common bean in Africa though widespread is mainly concentrated in East and Central African region (Katungi, 2010). Kenya is the principal producer of common bean in terms of area cultivated, followed by Uganda and Tanzania (Katungi, 2010). Though, Uganda occupies the first place in terms of production, then

Kenya followed by Tanzania (Balcha and Tigabu, 2015). The climate of common bean ranges from temperate to sub-tropical with defined wet and dry seasons. Production of common bean is high in areas where precipitation is moderate rather than in dry areas or areas with excessive rainfall (Beebe *et al*., 2014). Common bean is cultivated twice a year in eastern and central Africa and sowing seasons starts from March to April and from September to October, but in Ethiopia the long season is June to August (Katungi, 2010). Beans are grown in various cropping systems. Approximately 74% of bean area is mainly cultivated with bananas, maize, sorghum or millet, roots and tubers (Muthii, 2014).

2.2 Agronomic and yield parameters of common bean

Common bean crop is epigeal and requires around six to eight days under favourable environment to be germinated. The seeds harvested generally at physiological maturity do not have any dormancy (Amanullah and Muhammad, 2011). According to Taddale (2006), the seeds with small sizes tend to germinate and grow very fast than the large seeded ones at high temperature (28°C). At low temperature around 12°C, Kacharo (2009) showed that large seeded genotypes tend to germinate more rapidly than small seeded ones hence the adaptation of seed types to different environments. Germination of common bean does not occur when the temperature is below 8°C and they need to be planted preferably in warmer soils with more than 18°C (Amanullah and Muhammad, 2011).

Initiation of flowering and podding are highly temperature sensitive. Mulanya (2016) reported that both day-neutral and short day sensitive cultivars of common beans respond to temperature change in a similar way, with days to flowering hastened by higher temperatures. Mulanya (2016) postulated that by changing the rate of flower

bud development and presumably of pod growth and temperature affects the duration of flowering and seed filling and thus timing of maturity. Amanullah and Muhammad (2011) reported that beans grow optimally at temperatures between 20°C and 24°C. In South Africa, temperatures below 20°C reduce crop growth rate while temperatures of 15°C to 20°C after flowering damage tissue, delay maturity and affect pod filling. Kacharo (2009) observed that mean temperatures between 16 to 24°C during the growth and development stages have been associated with principal areas of bean production.

The specific yield component namely number of pods per plant have the major influence on the yield of common beans because it integrates the number of seed per pod and hundred seed weight (Amanullah and Muhammad, 2011). Similar observations have been made in soybeans by Narayan **(**2013) who found a positive correlation between the leaves per plant and numbers of pods per plant, and between seed size and leaf size (area of individual leaves).

2.3 Constraints to common bean production

Common bean is the crop which is adapted to intercropping with other different crops and its growth has a short cycle. Common bean has susceptibility to various abiotic and biotic constraints (Frahama *et al*., 2014). Low soil fertility and drought are among the major abiotic stresses. The common bean crop shows failed growth especially under dry land conditions with prevalent drought (Darkwa *et al.,* 2016). The cold at the beginning and at the end of growing season in the highlands (above 2000 m) and the low temperatures below 15°C may also reduce the bean productivity (De Ron *et al*., 2016).

The weeds also limit the performance of beans because of the competition for nutrients, water, light, space (Thuijsman, 2017). The best management of weed control may be realized by weeding three weeks after planting and repeating it every three weeks until physiological maturity (Thuijsman, 2017). As reported by Martelloni *et al.* (2016) the yield of common bean could be increased if chemical and mechanical weed control with minimum or no tillage was used. The different insect pests' species which attack common bean during the growing period and after harvesting are among the major biotic stresses. In east and central Africa, the main pests consist of foliage beetles **(***Epilachna varivestis Mulsant)*, bean fly *(Ophiomyia phaseoli*), black aphid (*Aphis fabae*), striped beetle *(Epicauta vittata)* and flower thrips *(Frankliniella bispinosa Morgan)* (Odogwu *et al*., 2014).

Among the biotic stresses, diseases are also principal constraints which contribute to yield losses in common bean. These diseases are classified into different groups such as bacterial, fungal and viral in nature. All these types of diseases are considered significant (Lunze *et al*., 2012). These diseases include common bacterial blight (*Xanthomonas axonopodis* pv. *phaseoli*), angular leaf spot (*Phaeisariopsis griseola),* floury leaf spot (*Mycovellosiella phaseoli*), rust (*Uromyces appendiculatus*), and bean common mosaic virus, which are more important in high temperature and low altitude environment (Pamela *et al.,* 2014). In low temperature and high altitude environment, the anthracnose (*Colletotrichum lindemuthianum*), aschochyta blight *(Phoma exigua*), the halo blight (*Pseudomonas savastanoi pv. phaseolicola*) and root rots (*Fusarium* spp, *Pythium* spp, *Rhizoctonia* spp, *Sclerotinia* spp and *Macrophomina* spp) are considered as more significant diseases (Pamela *et al.,* 2014).

2.3.1 Diseases of common bean

Common bean diseases are considered one of the major agronomic constraints in common bean production in Africa (Katungi, 2010). Diseases such as halo blight, rust, bean common mosaic virus, ascochyta blight, root rots, anthracnose, angular leaf spot and common bacterial blight are devastating to common bean production (Nga'yu-Wanjau, 2013).

Halo blight (*Pseudomonas savastonoi* pv. *phaseolicola)* is prevalent often from high altitude to mid altitude lands. It appears at temperatures varying between 16 and 20°C and at the presence of moisture, during the cloudy environment (Howard and Schwartz 2014). The disease survives in common bean seeds and remains for more than four years (Arnold *et al.*, 2011). The primary symptoms become visible as negligible water-soaked pinprick spots on the back of leaf. The infected surfaces of the leaves are encircled by the spots which progressively change the color into yellow green appearing as a halo (Fernandez-Sanz *et al.*, 2016). The white exudates are produced on the pods, stems and petioles which show symptoms of water soaked lesions (Howard and Schwartz, 2014). The disease causes losses of approximately 43% of the total production in the favorable environment (Howard and Schwartz, 2014).

Common bean rust *(Uromyces appendiculatus)* occurs worldwide and severally, the infected plants are visible and severe during the pre-flowering and flowering period (Odogwu *et al.*, 2014; Pamela *et al.*, 2014). The primary symptoms appear as negligible pale spots which turn to yellow with a small dark centre (Odogwu *et al.*, 2014). These lesions increase and turn to brick-red rust spores during the summer in

order to spread the pathogen (Pamela *et al.*, 2014). The disease causes yield losses ranging from 18-100% (Souza *et al.*, 2014).

The bean common mosaic virus is among the early seed-borne viruses which attack common bean plant (Feng *et al*., 2014). The virus causes the plant to wrinkle and the leaves are malformed with mottling. Trifoliolate leaves affected with this virus are irregular in form and show green and light yellow color upon shredding (Feng *et al*., 2014). The dark necrotic lesions are occasionally found on the leaves, petioles and roots. The small dark necrotic spot can develop on the pods and on the leaves (Li *et al*., 2014). This virus can cause significant yield losses of 50 to 100% in the host crop plants (Li *et al*., 2014).

Ascochyta blight *(Didymella rabiei)* appears more in Africa (Nene, 1982; Nganga *et al*., 2017) and particularly Uganda, Kenya, Rwanda, Tanzania, eastern of DR Congo, Burundi and Zambia where the environment is humid and cool (Ahmed *et al*., 2016). The first symptoms become visible on the leaves as dark grey to black lesions. Later the infected surface is surrounded by the concentric shaped rings around the black pycnidia (Ahmed *et al*., 2016). The disease has been reported to cause yield losses of upto 100% in chickpea on susceptible cultivars and upto 10% on resistant ones (Nganga *et al*., 2017).

Root rots are caused by a complex of different pathogens including *Fusarium* spp, *Pythium* spp, *Rhizoctonia* spp, *Sclerotinia* spp and *Macrophomina* spp. It produces spherical sporangia containing structure and oospores which act as the survival structure and primary inoculum (Lodhi and Khanzada, 2013). *Rhizoctonia solani*

infects the root tissues by means of sclerotia or mycelia which survive in the soil for longer periods to cause damping off (Naseri, 2014). *Fusarium solani* also causes root rots infection. The identification could be done by the presence of small reddish lesions on the taproot and the part called hypocotyl which forms the brownish color. This discoloration can be seen on the internal part of the stem starting from the root. Favourable weather conditions such as high humidity, lead to formation sclerotia which are globally shaped (Lodhi and Khanzada, 2013). Symptoms of root rots include stunting, yellowing of leaves, brown discoloration of the tap root system, damping off and wilting (Naseri, 2014). Yield losses due to root rot are approximately around 70% in the commercial population cultivars but the disease can also lead to the high yield losses when the populations are susceptible and growing under favorable environmental conditions for the development of the disease (Naseri, 2014).

Angular leaf spot *(Phaeisariopsis griseola)* is a serious pathogen of common beans which occurs in East and Central African region especially in Kenya, Kivu Province of the DR Congo, Rwanda, Tanzania, Uganda, Burundi and Ethiopia (Mongi, 2016). Among the biotic and abiotic constraints, angular leaf spot is rated as the second most essential common bean disease (Huang and Han, 2014). The disease development and infection is caused by moderate temperatures of 20°C to 25°C and in humid environments (Perseguini *et al*., 2016). The symptoms are usually visible at late flowering or early filling of pod. The symptoms of disease caused the lesions on leaf, pods, petioles and branches and the severe infected leaves get defoliated (Mongi, 2016). The pods which are affected by the disease have particular symptoms like circular spots with reddish brown centers (Schmutz *et al*, 2014). Yield losses of between 50 to 90% have been reported (Mongi, 2016).

Anthracnose *(Colletotricum lindemuthianum)* is also the most essential and widespread disease of the common bean (Rava *et al*., 1994; Barcelos *et al*., 2014; Mohammed *et al.,* 2013). Anthracnose is predominant in eastern Africa region such as Kenya, Uganda, Ethiopia, Burundi, Tanzania, Rwanda and DR Congo. These common bean yield losses arise from poor seed germination, poor seedling vigor, seed abortion, pod abortion and loss of photosynthetic area (Mohammed *et al.,* 2013). When infected seed is used during sowing, the growing seedlings develop with dark brown to black sunken lesions on the stems, pods, leaves and cotyledons (Amin *et al.,* 2014). Under moist environments, small pink masses of spores, occur on the foliage lesions and are generally linear. As the disease progresses, discolouration appears on the upper leaf surface. Symptoms are not often present on the leaves and may be even neglected when recording data in the field. The symptoms are more visible on the pods (Amin *et al.,* 2014). Anthracnose can reduce losses of grain yield up to 95-100% particularly on susceptible varieties under favourable conditions and also when infected seed is used (Perseguini *et al*., 2016).

Common bacterial blight *(Xanthomonas axonopodis* pv. *phaseoli)* is widespread throughout African countries that grow common bean. It is prevalent in areas with high humidity and warm to high temperatures (Akhavan *et al*., 2013). Common bacterial blight causes damage on foliage and on the pods. Symptoms are initially visible as small, lesions on the leaves. The infected parts, such as the pods, have slightly embedded, circular areas, soaked in water (Belete and Bastas, 2017). The lesions later expand and merge into dark brown irregularly shaped lesions surrounded

by a narrow yellow halo. The infected pods produced yellow masses of bacterial ooze in humid conditions (Akhavan *et al*., 2013). The extent of yield loss and quality is dependent on environmental situations, the level of susceptibility of the genotypes in use and pathogen pressure (Belete and Bastas, 2017). The losses of yield due to common bacterial blight disease are estimated between 45-75% (Osdaghi and Zademohamad, 2016).

2.3.2 Management of the major foliar diseases of common bean

Integrated pest management approach is the most suitable strategy to control the major common bean diseases (Belachew *et al*., 2015). This method includes cultural control, chemical control using seed treatment followed by foliar spraying, and the use of host plant resistance. The main successful method of control of major diseases on common bean is the integration of cultural practices with insecticides and host plant resistance (Oshone *et al*., 2014).

Cultural management is important in controlling common bean foliar diseases. An effective management strategy is the planting of certified disease-free seeds. The diseases epidemics can effectively be reduced through employing crop rotation (Souza *et al.,* 2012). Farmers are advised to use crop rotation in their farming practices between two seasons with alternative no-legumes crop such as potatoes, cassava, sweet potatoes, maize, onions, garlic and vegetable as they are affordable for small scale resource poor farmers and also eliminate the host for the potential vector (Mohammed *et al.,* 2013). Eliminating weeds, intercropping and rogueing of volunteer common beans will reduce disease intensity (Souza *et al.,* 2012). Although pathogen-free seed should be used whenever possible, its use does not guarantee a clean crop, since plants with no symptoms can be colonized by causal agents and the

pathogen can systematically invade seed via vascular tissues (Mick *et al*., 2015). Therefore, certified pathogen free seed may still be contaminated with the pathogen. Thus, clean seed can be obtained by growing common bean seed in areas that are unfavorable for pathogen development (Mohammed *et al.,* 2013). The integration of seed treatment, soil solarization, and foliar sprays at the recommended rates are effective in reducing bean disease epidemics (Pamela *et al.,* 2014). Because of unavailability as well as high cost of the chemicals for subsistence farmers, chemical control against pathogen is not economical for example lindane and endosulfans are unavailable and very expensive (Kadaari, 2015). Thus, the chemical method would be an effective strategy if coupled with the use of moderately resistant varieties (Pamela *et al.,* 2014).

The host plant resistance approach is more beneficial compared to other control strategies (Pamela *et al.,* 2014). It is technically and economically the most practical and attractive method for the effective management of common bean diseases (Pamela *et al.,* 2014; Ssekandi *et al.,* 2015), although, this has been complicated by the presence of several strains or races of most pathogens, and the fact that plants resistant to one race may be susceptible to another. Even if using resistant varieties is the most effective, cheaper, and easiest method for farmers to adopt, the possible breakdown of resistance due to the adaptation and evolution of the pathogen is the major disadvantage of its utilization (Schwartz and Singh, 2015).

2.4 Genetics of resistance to major foliar diseases of common bean

Selection of elite varieties by the breeders through visual screening of the characteristics is of economical significance. However, the reproducibility and heritability of the parameter under consideration needs to be put into consideration (Singh and Schwartz, 2010). Thus, the use of molecular markers in common bean breeders' has contributed to accurate improvement during crosses and enabled breeders to develop germplasm with superior traits (Singh and Schwartz, 2010).

2.4.1 Genetics of resistance to angular leaf spot in common bean

The angular leaf spot caused by *Phaeoisariopsis griseola* is controlled by major genes, which could be dominant or recessive genes, duplicated or acting singly and which can interact in an additive manner with or with no epistasis (Keller *et al.,* 2015). A single recessive gene was found to condition inheritance to angular leaf spot (Borges *et al*., 2012). The involvement of major and minor genes in controlling resistance to angular resistance of leaf spot has been reported in bean research (Keller *et al.,* 2015). Borges *et al*. (2012) identified several sources of angular leaf spot resistance namely BAT 1432, A 152, A 75, BAT 76, A 140, A 175, A 229, G5686, BAT 431, BAT 1458 and MAR 1, MAR 2. These elite bean lines have been used as dependable markers for identifying new races of the pathogen (Keller *et al.,* 2015).

2.4.2 Genetics of resistance to anthracnose in common bean

Ferreira *et al*. (2013) highlighted the inheritance of resistance to anthracnose and the high intensity of variability that existed within the pathogen. Improvement for resistance to specific gene pathogen recognition systems needs the classification of

resistant plants, which could then be crossed with the best genotypes (Strange and Scott, 2005). Most of the previously catalogued resistance genes in bean breeding section have the Middle American origin. About 10% of anthracnose resistance genes were from Andean origin like the Co-14, Co-12, Co-15, Co-13 and Co-1 locus (Sousa *et al*., 2015; Goncalves-Vidigal *et al*., 2015).

The identification of supplementary sources of resistance from both gene groups will play a very critical role in developing resistant varieties of beans. Further on, the identification and cataloguing of those resistance genes will enable the effective transfer of the resistance using marker assisted selection and gene pyramiding to develop bean varieties with durable resistance (Ferreira *et al*., 2013).

2.4.3 Genetics of resistance to common bacterial blight of common bean

Breakdown of resistance to common bacterial blight resistance in common beans occurs due to linkage drag associated with undesirable characteristics, variability of the pathogen and the various genes which are conditioned by resistance in either the plant foliage, pods and seeds (Zhu *et al.,* 2016). Most of the disease resistance is quantitative and are affected by the environment making the phenotyping of genotypes difficult (Viteri and Singh, 2014). This is further compounded by the fact that there is differential reaction of organs of the plant like leaves, pods and seeds to the common bacterial blight disease thus complicating breeding efforts for resistance (Miklas *et al.,* 2017). Resistance breeding efforts are also curtailed by instability because after more than a dozen generations of selfing, common bacterial blight resistant genotypes segregate (Zhu *et al.,* 2016). Thus, to maintain high levels of common bacterial blight resistance, evaluations should be made under replicated trials

and the plant selected must be completely immune under high disease stress in each generation (Viteri and Singh, 2014).

The heritability of resistance may vary from low to moderately high depending on the type of population involved (Miklas *et al.,* 2017). Molecular marker studies have inventoried around 22 quantitative trait loci (QTLs) for resistance to common bacterial blight located on 11 chromosomes among diverse common bean genotypes (Viteri and Singh, 2014). The environmental conditions, genetic background, pressure of disease and certain agronomic traits influence the expression of quantitative trait loci (Zhu *et al.,* 2016). Thus, marker assisted selection may be used in introgression of the genes into the adapted common bean varieties.

Common bacterial blight resistance is also controlled by a single major gene with a large effect allele and additional 18 minor genes with small effect alleles (Miklas *et al.,* 2017). Singh and Schwartz (2010) also reported an interaction between negative epistasis and quantitative trait loci for resistance. Negative correlations between resistance quantitative trait loci and agronomic parameters have also been identified.

2.5 Breeding methods used on common bean

The main objective in any breeding is to improve particular traits of interest without compromising other traits possessed by the genotype (Cláudio de Faria *et al.,* 2017). Breeding of common bean has been emphasized on biotic and abiotic constraints and has been achieved by the use of selective resistance genes from donor parents (Asfaw *et al*., 2012). In the improvement of autogamous plants, bulk or population, pedigree or genealogical, single seed descent and backcross breeding methods have been used (Cláudio de Faria *et al.*, 2017).

Pedigree selection called genealogical method has been widely by bean breeders to generate improved lines. This allows selection for qualitative characteristics in the early generations from F_2 to F_4 while the later generations like F_5 to F_7 could be used to select for quantitative traits like yield (Singh and Miklas, 2015). Each segregated plants' population are independently selected and evaluated and this should be done within the representative zone and at the time of planting to avoid developmental variation (Pontes Júnior *et al*., 2016). Pedigree breeding method has been used in Brazil to obtain eight news cultivars of common bean (Sarah *et al*., 2010).

Bean breeders also use the single seed descent method to retain genetic variation while advancing the populations to higher generations (Pontes Júnior *et al*., 2016). This present method is widely used in soybean breeding. In beans, the Single pod descent method is generally where the generation are advanced by a pod as opposed to the use of a seed from each plant (Singh and Miklas, 2015). According to Pontes Júnior *et al*. (2016), the single pod descent caters for the sampling losses which arise from the segregation of advanced generations. In Brazil, seven news cultivars of common bean were developed through the single seed descent method in combination with the bulk method (Sarah *et al*., 2010).

Bulk breeding method is used by bean breeders when multiple generations are grown each year and breeders intend to advance common bean populations rapidly. This method is most employed for crosses between market materials and elite cultivars where little segregation for seed type will be expected (Singh and Schwartz, 2010). The bulk breeding method was hypothesized in the early 20^{th} century where plants from the F_2 were harvested in bulk and a seed sample drawn to generate an F_3

generation. This was then repeated for more generations and the plants were harvested individually to increase families which were then evaluated with duplication to obtain superior genotypes (Pontes Júnior *et al*., 2016).

The backcross method is applied when the breeders seeks to introgress new disease resistance into superior common beans genotypes (Singh and Miklas, 2015). An elite genotype (recurrent parent) is improved by introducing genetic material from a donor parent (Pontes Júnior *et al*., 2016). This involves repeated crossing of the hybrid generation with the recurrent parent and the selection of segregates heterozygous for the desired trait (Pontes Júnior *et al*., 2016). Backcross also reduces population size (Singh and Miklas, 2015) enabling easy handling of the population.

The inbred lines method is widely used on individual plants' selection in the original line, followed by the assessment of the progeny population (Singh and Miklas, 2015). The inbred populations selected form segregation lines due to mutations, natural crosses or mechanical seed mixture. The selection of inbred lines through the partnership of Embrapa Rice and Beans CIAT led to the development of new varieties (Sarah *et al*., 2010).

Gamete selection method is a breeding procedure that allows screening and selection of desirable dominant and codominant alleles through hybridization and production of last multiple-parent F_1 hybrids (Pontes Júnior *et al*., 2016). With an increasing need to improve at once multiple characteristics in common bean, gamete selection presents a method that permits identification of promising populations and families and offers reliable yield evaluations in early generations (Schwartz and Singh, 2015).

According to Singh and Miklas (2015), recurrent selection consists of performance of re-selection generation after generation, crossing of selected lines to realize genetic recombination. Therefore, this method is a continual procedure and cyclical, which involves the generation of populations, their evaluation, selection and crossing of superior lines, aiming at a superior frequency of favourable alleles, and, thus, a better expression of the characteristic under selection (Pontes Júnior *et al*., 2016). Through recurrent selection, the yields of a genotype could not only be determined by a new plant, but by mostly favourable mixture of existing genes in a collection of new plants. Abreu *et al*. (2004) used this method to develop the line BRSMG Talisman, resultant from a partnership project of Embrapa Rice and Beans, UFLA, UFV and EPAMIG.

2.6 Mating designs used to develop common bean hybrids

In breeding of crops, there are different types of mating designs used widely by breeders and geneticists to develop the new populations. Acquaah (2012) described various types of mating designs used in plant breeding program such as polycross, bi-parental progenies, top cross, Diallel (I, II, III, IV), Line × tester design and North Carolina (I, II, III). In all this forms of mating designs, the individual is taken at random and crossed to generate progeny which are connected to each other as full-sibs or half-sibs.

Complete diallel mating design is generally used in many crops. It allows mating in all the possible combinations among the parents and involves reciprocals and the selfs (Fasahat *et al*., 2016). This is the most widely used mating design in getting genetic

information (Fasahat *et al*., 2016). This mating design is much abused due to the fact that it uses two models for analysis; namely the fixed models and random (Schlegel, 2010). Diallel mating designs are widely used in the genetic improvement of many crop species (Gonçalves-Vidigal *et al.,* 2015). Griffings (1956) proposed the several methods for diallel analyses. Among these methodologies, Gonçalves-Vidigal *et al.* (2015) method has been employed in determination of gene action on diverse characteristics. Apart from dominance and additive gene actions, this approach is good to detect epistasis. Edith *et al*. (2010) used this design in three snap bean genotypes namely Morlane, Monel and Amy and two dry common bean genotypes namely GLPX 92 and GLP 20. The dry common bean genotypes were incorporated in order to assess their potential in the breeding of snap bean. Through a complete diallel, the genotypes generated revealed that the best bean combinations involved Amy for pod diameter, Morlane, for pod length and GLP 20 for pod weight.

Line x tester is an expansion of the top cross mating design proposed by Kumar *et al*. (2015). This design is usually used for more than one tester. According to Kumar *et al*. (2015), this design involves hybridization between lines (female) and broad based testers (Males) female x male = female/male hybrids. It has been used mostly in soybean breeding. Chandrakanti (2016) reported that 8 diverse genotypes of soybean namely RSC 10-04, RSC 10-17, , RSC 10-30, RSC 10-46, JS 97-52, JS 335, JS 93-05 and NRC 37 were mated in a Line x tester mating design where 4 genotypes were used as lines and the other 4 genotypes used as testers in Raipur (India) to identify best combiners.

According to Acquaah (2012), the North Carolina Design I is the best mating design used both in theoretical as well as practical plant breeding application. This design is usually employed in estimation of the additive and dominance variances. It is also used in assessment of half- and full-sib recurrent selection (Acquaah, 2012). The plant breeders Ortiz and Golmirzaie (2004) in La Molina and San Raman determined the proper selection approach for improvement of quantitative genetics of tuber yield in tetrasomic potato. In a quantitative study using hundred hybrid off springs generated through a NCDI from a heterogeneous CIP breeding population, several clones which were male sterile were identified. The NCD is easy to handle, however, the NCDI is not of practical use in breeding species that are unable to produce enormous quantity of seed.

North Carolina Design II is a type of mating design whereby every male parent mates with every female parent. North Carolina Design II is normally used in estimation of the degree of the genetic variance as well as degree of dominance (Fasahat *et al*., 2016). It is also used in estimation of general combining ability and specific combining ability of inbred lines (Odogwu *et al.,* 2016). This design is mostly used in breeding of common bean (Fasahat *et al*., 2016). In Rwanda, breeding studies have indicated genetic variability in dry beans for tannin content, cooking time, protein percentage and water absorption. The improvement of 16 genotypes (8 males and 8 females) of beans for these traits was done using the North Carolina Design II. To reduce the number of mating required, two sets were formed. Within each set, each male parent was crossed to four females, resulting in a total of 16 crosses per set. From the evaluation, five crosses were the best combiners for the traits under study (James *et al*., 1997).

In North Carolina design III, each male is mated to both inbred parents of original cross. It consists of 2m cross where m is number of male. This design is able to test epistasis, dominance and additive variances. This is more powerful and involves $P_{2,}$ F_1 and F_2 plants during crossing. Variance is separated into two portions due to male and the male cross with the female (Acquaah, 2012). It is also called as triple test cross because a third tester is incorporated in this (Fasahat *et al*., 2016).

CHAPTER THREE

RESISTANCE OF COMMON BEAN GENOTYPES TO MAJOR FOLIAGE DISEASES

3.1 Abstract

Diseases of common bean cause yield losses estimated between 45 to 100%. The use of host plant resistance is a more effective strategy to reduce losses. The objective of this study was to identify common bean genotypes with resistance to major common bean diseases and high yield. Twenty four common bean genotypes from the Kenya Agricultural and Livestock research Organization (KALRO)-Kakamega, local markets in Kakamega, Harvest Plus Rwanda and Egerton University were evaluated in the field at KALRO-Kakamega and Lugari over two seasons. Data was collected on severity and incidence of foliar diseases, emergence, days to 50% flowering and 75% maturity, number of pod per plant, number of seed per pod, 100-seed weight and grain yield. The diseases were scored using a 1 to 9 scale. Data was subjected to analysis of variance to determine the differences among the traits for the different bean genotypes**.** There were significant variations among the genotypes in response to diseases, emergence, days to 50% flowering and days to 75% maturity, number of pod per plant, 100-seed weight and grain yield. Significant and positive correlations were observed between final severity scores of anthracnose, angular leaf spot and common bacterial blight with their corresponding incidences. All the 24 lines evaluated showed moderate resistance to angular leaf spot. Genotypes Red34, KK15, Cal5B, Cal137, GLPX92, Cal6, Red45 and Cal33 were resistant to anthracnose while Red34, KKBC05/32, KK071, GLP2, Ciankui, RWR2245 and Cal6 were resistant to common bacterial blight. Genotypes Cal139A, Red16 and Red13 recorded the highest grain

yield. Thus, the best performing genotypes with resistance to foliar diseases could be used as donors to improve the adapted bean varieties in Kenya.

3.2 Introduction

Common bean is a very popular legume food crop worldwide and it's affected by fungal, bacterial and viral diseases (Ochilo *et al*., 2013). These diseases not only affect the common bean yields but also reduce the bean storability and marketability (CGIAR, 2012). The average of common bean production is estimated at 1300 kg ha^{-1} on smallholder farms and 1700 kg ha^{-1} on commercial farms in contrast to a production potential of 3000 to 4000 kg ha^{-1} in research fields (Blair *et al*., 2012).

Diseases have been identified as one of the main constraints contributing to low bean yields (Nga'yu-Wanjau, 2013). Among the fungal diseases on common bean, bean anthracnose and angular leaf spot are very significant in eastern Africa. Both halo blight and common bacterial blight are widespread and are among the most important bacterial disease (Belete and Bastas, 2017). According to Parsa *et al*. (2016), majority of these bacterial and fungal diseases are seed borne and their nature under epidemic conditions can lead to devastating effect both on quantity and quality of produce. Losses due to common bacterial blight affect both quality and quantity of yield losses estimated at 45 - 75% (Akhavan *et al.*, 2013). The amount of yield loss depends on the intensity of the disease, environmental conditions that favour the onset and progress of the disease, and the degree of susceptibility of the cultivars (Belete and Bastas, 2017). It was estimated that each 1% increase in common bacterial blight severity causes yield loss of about 10.5 - 78 kg ha^{-1}, depending on the season and crop growth stage (Akhavan *et al*., 2013). Late blight is commonly seed borne and can overwinter in seed and infested bean straw and can survive in seed for over 15 years

(Belete and Bastas, 2017). Under fairly high temperatures (25-35°C), high rainfall and humid conditions (Akhavan *et al*., 2013), the bacteria cause most severe disease. Angular leaf spot disease causes premature and severe defoliation which result in shrunken seeds, shriveled pods and causes losses of grain yield of 50 - 80% of the total production (Pamela *et al.*, 2014). Ddamulira *et al*. (2014) conducted a survey on angular leaf spot in Uganda and found that the average incidence varied from 65% to 80%. According to Pamela *et al.* (2014), every 10% increase in angular leaf spot severity results in 7.9% yield loss. Angular leaf spot is mostly found at an altitude varying between 963 to 2300 m. Therefore, angular leaf spot is highly prevalent and severe in eastern Africa (Nga'yu-Wanjau, 2013). Common bean anthracnose causes yield losses of up to 100% when susceptible genotypes are used and is favoured by relatively humid and cool environments (Mohammed *et al.,* 2013). Common bean production is significantly reduced due to the pathogen because of lower seed germination and seedling vigour, premature plant death and poor yield. The occurrence of favourable weather in East Africa for the pathogen infection and spread enhance the colonization of the plant by the pathogen (Mohammed *et al.,* 2013). The use of infected seeds at planting also helps to spread the disease (Schmutz *et al.,* 2014).

Smallholder common bean farmers mostly rely on insecticides and fungicides to reduce yield and post-harvest losses related with diseases (Amin *et al*, 2014). The use of chemicals makes the common bean seeds less marketable due to the maximum chemical remains set by the internationals markets (Lamichhane *et al*., 2016). Sustained use of chemicals also leads to emergence of disease resistant pathogen races, increased production cost and negative results on the human health and

environmental conditions (Knezevic *et al.,* 2017). Cultural methods like crop rotation, removal of plant debris, intercropping, regulation of planting dates, use of resistant varieties can decrease diseases intensity (Deeksha *et al.,* 2009). The use of host plant resistance is by far the most economical and ecologically sustainable approach in controlling common bean diseases.

Screening more bean genotypes is necessary to identify new bean varieties with resistance to major foliar diseases and high yield. This will supplement or replace the existing ones with new sources of resistance to anthracnose, common bacterial blight and angular leaf spot, and high yield. These new sources of resistance will have a positive impact on common bean improvement in eastern and central Africa. Thus, the objective of this study was to evaluate common bean genotypes for resistance to anthracnose, common bacterial blight and angular leaf spot, and high yield for introgression into the adapted but susceptible common bean genotypes.

3.3 Materials and Methods

3.3.1 Description of common bean germplasm

The common bean materials used in this study were twenty four genotypes from the Kenya Agricultural and Organization Livestock Research (KALRO)-Kakamega, local markets in Kakamega, Harvest Plus Rwanda and Egerton University (Table 3.1).

Table 3.1: Common bean genotypes used in the study and their reaction to diseases

Genotypes	Source	Reaction to disease
KKRILO5/RED 45	KALRO-Kakamega	Resistant to CBB, anthracnose and root rot
KKRILO5/Cal194	KALRO-Kakamega	Resistant to bean root rot and BCMNV, moderate resistant to ALS and anthracnose, susceptible to halo blight
KKRILO5/Cal137	KALRO-Kakamega	Resistant to bean root rot
KKRILO5/Cal33	KALRO-Kakamega	Resistant to bean root rot and BCMNV, moderate resistant to ALS and anthracnose, susceptible to CBB, BCMV, halo blight
GLPX92	KALRO-Kakamega	Resistant to halo blight
GLP585	KALRO-Kakamega	Resistant to BCMV
Cal51A	KALRO-Kakamega	Resistant to bean root rot
KK15	KALRO-Kakamega	Resistant to bean root rot and BCMNV, moderate resistant to ALS and anthracnose, susceptible to CBB and halo blight
KKRILO5/Cal139A	KALRO-Kakamega	Resistant to bean root rot
GLP2	Kakamega	Susceptible to bean stem maggot

Genotypes	Source	Reaction to disease
	local market	
KKRILO5/Cal5B	KALRO-Kakamega	Resistant to bean root rot
KK071	KALRO-Kakamega	Resistant to bean root rot
RWR2245	Harvest Plus Rwanda	Tolerant to ALS, Ascoshyta, Anthracnose and BCMV
Cal6	KALRO-Kakamega	Resistant to bean root rot
KK06/110	KALRO-Kakamega	Resistant to bean root rot
KK072	KALRO-Kakamega	Resistant to bean root rot
KKRILO5/RED16	KALRO-Kakamega	Resistant to bean root rot and BCMV, moderate resistant to ALS and anthracnose, susceptible to CBB,BCMV
KK06/29B	KALRO-Kakamega	Resistant to bean root rot
CIANKUI	Egerton University	Susceptible to bean stem maggot
KKRILO5/Red13	KALRO-Kakamega	Resistant to bean root rot and BCMNV, moderate resistant to ALS and anthracnose, susceptible to

Genotypes	Source	Reaction to disease
		CBB,BCMV and halo blight
KKBCO5/32	KALRO-Kakamega	Resistant to bean root rot
KK8	KALRO-Kakamega	Resistant to bean root rot and BCMNV, moderate resistant to ALS and anthracnose, susceptible to CBB,BCMV and halo blight
Red34	KALRO-Kakamega	Resistant to bean root rot, CBB and anthracnose
KKRILO5/Cal97A	KALRO-Kakamega	Resistant to bean root rot

K-K**:** KALRO-Kakamega; **Source:** KARI-Kakamega, 2008 and 2011; Otsyula, 2010

3.3.2 Description of experimental sites

The experiment was carried out at two sites namely Kenya Agricultural and Livestock Research Organization (KALRO) - Kakamega and Lugari in Kakamega County across two seasons (Table 3.2).

Table 3.2: Description of the study sites

Site	Latitudes	Longitudes	Altitudes	Soils	Mean annual	
					Temperature (°C)	Rainfall (mm)
Kakamega	00° 17' N	34° 47' E	1,250-2000m.	well drained, deep dark red friable nitisols	18.5-21.0	1600-2000;bimodal: long rains: April-June, short rains: August-November
Lugari	0°25′ and 1°N	4° 28′ and 35° E	1300 - 1800m.	Fertile, well drained, dark brown sandy loam to red oxisols.	17.7-25.5	1000-1600mm;bimodal:long rain: March-September, short rain:October-November

Source: Jaetzold *et al.*,2009

3.3.3 Experimental design and layout

The experiment was conducted in the field between September and December 2016 and between March and June 2017 at KALRO – Kakamega and at farmers' field in Lugari. Each of the 24 genotypes was planted in a plot measuring 2m x 1.5m plots with four rows at spacing of 50 cm x 10 cm. The experiment was set-up in a randomized complete block design (RCBD) with three replications. The distance between replication was 1m and between plots was 0.5m. Diammonium Phosphate (DAP) fertilizer was used at planting at a rate of 50kg/ha (Niyuhire *et al*., 2017) and

bean fly was managed by weekly application of Diazon pesticide at a rate of 395l/ha from emergence until flowering. The plants were subjected to natural disease infection. Data collected were percentage emergence, days to flowering and maturity, incidence and severity of angular leaf spot, anthracnose and common bacterial blight, number of pod per plant and seed per pod, hundred seed weight and yield.

3.3.4 Determination of agronomic parameters

The agronomic parameters assessed included days to 50 % emergence, plant stand, days to 50 % flowering, days to 75 % maturity. Days to 50% emergence involved counting the number of plants germinated to 50% germination relative to the number of seeds sown per plot. The plant stand was recorded by counting the number of plants per plot until maturity. Days to 50 % flowering was taken as the date when 50% of plants per plot flowered. Days to 75 % maturity was recorded as the number of days for each plot when a set of plants per plot attained 75% maturity.

3.3.5 Assessment of incidence and severity of the foliage diseases

The foliar diseases assessed included angular leaf spot, anthracnose, and common bacterial blight. The percentage disease incidence was obtained by counting the number of plants which showed the symptom per plot divided by the total number of plants per plot then multiplying by one hundred (Equation 3.1).

$$Disease\ incidence = \frac{\text{Number of infected plants/plot}}{\text{Total number of plant observed/plot}} \text{x}100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots Equation\ 3.1$$

Disease severity was evaluated by referring to CIAT standard evaluation scale (Table 3.3). The diseases were assessed when the first symptoms appeared on the plants and

this was repeated weekly until maturity of the bean crop. In each plot, sixteen plants were randomly chosen as sample for assessment of foliar diseases.The area under the disease progress curve (AUDPC) was calculated from the disease observations using computer programme developed at CIMMYT and it was done by using the weekly data on severity.

$$AUDPC = \sum_{t=1}^{n-1} \left(\frac{yi + yi + 1}{2} \right) (\text{ti} + 1 - \text{ti}) \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \text{Equation 3.2}$$

Where, Nt =total number of observations, y*i* = injury intensity at the *i*th observation, *t* = time at the *i*th observation (Wilcoxson *et al*., 1975; Sitta *et al*., 2017

Table 3.3 Evaluation of the disease severity using the CIAT standard scale

Scoring scale	Category	Symptoms ALS	Symptoms ANT.	Symptoms CBB
1-3	Resistant	1= No visible symptoms	1= No visible symptoms	1=No visible symptoms
		3=Presence of a few small nonsporulating lesions that cover approximately 2% of the leaf or pod surface	3=Presence of very small lesions, mostly on the primary vein of the leafs lower side or on the pod, that cover approximately 1% of the surface area	3=Approximately 5% of the leaf surface area covered with a small lesions. Pods are generally free of lesions.
3-5	Intermediate			
		5=Presence of several, generally small lesions with limited sporulation that cover approximately 5% of the leaf or pod surface area	5=Presence of several small lesions on the petiole and secondary veins of the leaf's lower side. On the pods, small round lesions, with or without reduced sporulation, cover approximately 5% of the pod surface area.	5=Approximately 5% of the leaf surface area covered by small lesions that are beginning to coalesce and sometimes encircled by yellow halos resulting in minor blight. Lesions on the pods are generally small and not coalescing.
7-9	Susceptible	7=Abundant and generally large sporulating lesions that cover approximately 10% of the leaf or pod surface area.	7=Presence of numerous enlarged lesions on the lower side of the leaf. Necrotic lesions are can also be observed on the upper leaf surface and on the petioles. On the pods the presence of medium-sized lesions are evident but also some small and large lesions generally with sporulation and that cover approximately 10% of pod surface area may be found.	7=Approximately 10% of the leaf surface area covered with medium and large lesions which are usually accompanied by yellow halos and necrosis. Lesions on pods are large and coalescing and often show bacterial exudates.

Scoring scale	Category	Symptoms ALS	Symptoms ANT.	Symptoms CBB
		9=Severe disease symptoms resulting in premature leaf fall and death	9=Severe necrosis on 25% or more of the plant tissue is evident as a result of lesions on the leaf, petioles, stem and even on the growing point which often results in death of much of the plant tissues. The presence of numerous, large, sporulating, sunken cankers can result in pod malformation, low seed number and death of the pod.	9=More than 25% of the leaf surface area with large coalescing and generally necrotic lesions resulting in defoliation. Lesion on pods coalescence to cover extensive areas, exhibit abundant bacterial exudation which sometimes causes pod malformation and empty pods.

Source: Schoonhoven and Pastor-Corrales, 1987

3.3.6 Assessment of yield and yield components

The bean yield and its related components included the number of plant at harvest, mean number of pods, mean number of seeds per pod, hundred seed weight and yield per plot. Data on number of pods per plant and seeds per pod were recorded at harvesting time. Ten plants per plot were selected randomly to determine the number of pods. Seeds were sun dried and hundred seeds and yield per plots were measured. The weight obtained per plot was calculated in extrapolation in hectares according to the following formula (Equation 3.3)

$$\frac{\text{Yield}}{\text{ha(Kg)}} = \frac{\frac{\text{Weight}}{\text{plot}}}{\text{Plot area}} \text{x ha area} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \textit{Equation } 3.3$$

3.3.7 Statistical data analysis

All the data were analyzed using GENSTAT 15th edition statistical software and the genotype means separated based on Fischer's Protected Least significant differences (LSD) at 5% probability level (Gomez and Gomez, 1984).

ANOVA model

$$Yij = \mu + ti + rj + eij \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots . Equation 3.4$$

Where,

µ = the overall mean, *r*j = *j*th replication effect, *t*i = ith treatment effect, and, *e*ij = error term.

All the data for disease, agronomic and yield traits were subjected to GENSTAT 15thEdition for correlation among the traits (Pearson, 1895).

$$r = \frac{\Sigma(X-\bar{X})(Y-\bar{Y})}{\sqrt{\Sigma(X-\bar{X})^2}\sqrt{(Y-\bar{Y})^2}} \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots \textbf{\textit{Equation 3.5}}$$

Where,

$\bar{X}$=mean of X variable; $\bar{Y}$=mean of Y variable

3.4 Results

3.4.1 Evaluation of common bean for the different traits at KALRO Kakamega

3.4.1.1 Analysis of variance for the agronomic traits during the short rains season 2016 and long rains season 2017 at KALRO Kakamega

Analysis of variance for agronomic traits of common bean genotypes showed significant differences ($p<0.05$) among the traits; emergency percentages, days to flowering and days to maturity in both seasons (Table 3.4.a). Significant differences ($p<0.05$) among sites were observed for all the agronomic traits (Table 3.4b). There was a significant seasonal difference for days to flowering and days to maturity. The interaction of genotype by season showed significant differences in emergency percentages and days to flowering while days to maturity did not show differences between the seasons.

Table 3.4a: Analysis of variance showing the means squares for the agronomic traits at KALRO-Kakamega during short rains 2016 and long rains 2017

Source of variation	df	Short rains 2016			Long rains 2017		
		%Em.	DTF	DTM	%Em.	DTF	DTM
Replication	2	351.1	0.375	0.292	60.4	2.26	0.4306
Genotype	23	1107.8*	3.864*	23.690*	169.3*	8.80*	17.4976*
Error	46	57.8	0.462	0.422	160.6	0.92	0.59
Total	71						

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype and season, %Em. =percentage of emergence, DTF=Days to 50% flowering, DTM= Days to 75% maturity.

Table 3.4b: Combined Analysis of variance showing the means squares of agronomic traits at KALRO-Kakamega short rains 2016 and long rains 2017

Source of variation	df	KALRO-Kakamega		
		%Em.	DTF	DTM
Replication	2	125.2	1.13	0.7
Genotype	23	632.6*	10.6*	40.1*
Season	1	585.8^{ns}	134.2*	0.34^{ns}
GxS	23	644.5*	2.1*	1.10^{ns}
Error	94	113	0.70	0.49
Total	143			

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype and season, %Em. =percentage of emergence, DTF=Days to 50% flowering, DTM= Days to 75% maturity.

3.4.1.2 Mean performance of the bean genotypes based on the agronomic traits

During the short rains season, Red13 showed the highest emergence percentages. Genotype KK072 was the earliest flowering genotype while the latest was Red34. With regard to maturity, genotype KK15 was the earliest while genotype Ciankui was the latest in maturity (Table 3.5).

During the long rains season, genotype Cal194 showed the highest percentage of emergence of 86.1 while GLP585 had the lowest emergency percentage (50.8). Genotype KKBC05/32 flowered earliest and the genotype GLP585 was the latest in flowering. Genotype KK15 matured earliest compared to the genotype Ciankui was latest in maturity.

Table 3.5: Percentage emergence, days to flowering and maturity for common bean genotypes planted at KALRO-Kakamega during 2016 short rains and 2017 long rains

Genotypes	**Short rains 2016**			**Long rains 2017**		
	% Em.	**DTF**	**DTM**	**% Em.**	**DTF**	**DTM**
Cal137	69.8	39.0	80.0	71.4	36.0	80.0
Cal139A	80.2	42.3	85.0	75.8	38.3	84.7
Cal194	78.6	42.0	82.0	86.1	41.0	82.3

Genotypes	Short rains 2016			Long rains 2017		
	% Em.	DTF	DTM	% Em.	DTF	DTM
Cal33	81.8	41.0	82.0	81.0	39.7	82.0
Cal51A	73.8	39.0	80.0	66.7	37.0	81.3
Cal5B	42.9	41.0	85.0	80.9	39.3	84.7
Cal6	78.2	41.7	82.7	77.4	39.7	83.0
Cal97A	78.6	41.3	85.0	79.0	39.7	85.0
Ciankui	40.1	42.0	86.0	68.3	39.0	84.7
GLP2	83.7	39.7	86.0	73.0	38.3	83.0
GLP585	88.5	42.0	82.0	50.8	43.0	82.0
GLPX92	42.5	40.0	85.0	74.2	38.3	84.7
KK06/110	81.0	41.3	86.0	75.8	38.3	86.0
KK06/29B	78.2	42.0	81.3	80.9	40.3	82.3
KK071	9.9	41.0	86.0	75.8	38.7	85.7
KK072	88.9	39.0	85.0	71.4	38.3	83.7
KK15	81.0	41.3	75.0	77.8	38.7	75.7
KK8	85.7	41.0	86.0	75.0	39.7	86.0
KKBC05/32	75.8	40.7	79.3	72.6	36.0	80.0
Red13	89.7	41.7	82.0	79.4	41.0	82.3
Red16	75.0	41.7	83.7	82.1	40.7	83.7
Red34	68.3	42.7	86.0	86.1	41.0	86.0
Red45	74.6	42.3	85.3	82.5	40.3	85.0
RWR2245	84.9	39.3	84.7	84.1	36.3	85.0
Grand mean	72.14	41.0	83.4	76.2	39.1	83.3
LSD (5%)	12.5	1.12	1.07	20.8	1.6	1.3
CV (%)	10.5	1.7	0.8	16.6	2.4	0.9

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; %Em. =percentage of emergence; DTF=Days to 50% flowering; DTM= Days to 75% maturity.

At Kakamega short and long rains combined, the results of mean performance for the agronomic traits are presented in table 3.6. The genotype emergence percentages ranged from 42 in KK071 to 84.5in Red13. Genotype Cal137 flowered earliest compared to genotype GLP585 which flowered latest. Genotype KK15 matured earliest while the genotype KK8 matured latest.

Table 3. 6: Percentage emergence, days to flowering and maturity for common bean genotypes planted at KALRO-Kakamega combined over seasons

Genotypes	KALRO-Kakamega		
	%Em.	DTF	DTM
Cal137	70.6	37.5	80.5
Cal139A	78.0	40.3	85.3
Cal194	82.3	41.5	82.7
Cal33	81.4	40.3	82.5
Cal51A	70.2	38.0	81.2
Cal5B	61.9	40.2	85.3
Cal6	77.8	40.7	83.3
Cal97A	78.8	40.5	85.5
Ciankui	54.2	40.5	85.7
GLP2	78.4	39.0	83.8
GLP585	69.6	42.5	82.5
GLPX92	58.3	39.2	85.2
KK06/110	78.4	39.8	86.5
KK06/29B	79.6	41.2	82.3
KK071	42.9	39.8	86.3
KK072	80.2	38.7	84.5
KK15	79.4	40.0	76.2
KK8	80.4	40.3	86.7
KKBC05/32	74.2	38.3	80.2
Red13	84.5	41.3	82.7
Red16	78.6	41.2	84.2
Red34	77.2	41.8	86.5
Red45	78.6	41.3	85.7
RWR2245	84.5	37.8	85.5
Grand mean	74.2	40.1	83.8
LSD (5%)	17.23	1.36	1.14
CV (%)	14.3	2.1	0.85

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; % Em. =percentage of emergence; DTF=Days to 50% flowering; DTM= Days to 75% maturity.

3.4.1.3 Incidence and severity of foliar diseases during the 2016 short rains, 2017 long rains and combined seasons at Kakamega

3.4.1.3.1 Analysis of variance for incidence and severity of foliar diseases

In both season, significant differences ($p<0.05$) was shown for the traits common bacterial blight severity and incidence of anthracnose a common bean genotypes (Table 3.7a). However, area under disease progress curve showed significant differences ($p<0.05$) in common bacterial blight. During 2017 long rains, bean

genotypes evaluated showed significant differences ($p<0.05$) in severity of angular leaf spots, common bacterial blight plus, incidence of common bacterial blight and also area under disease progress curve (Table 3.7b). Under combined seasons, the area under the disease progress curve of angular leaf spot and anthracnose showed significant differences. The genotype showed significant seasonal difference for all the diseases traits at $p<0.05$ except the severity of angular leaf spot and incidence of anthracnose. The interaction of genotype and season showed significant differences ($p<0.05$) in incidence of common bacterial blight (Table 3.7c).

Table 3. 7a: Analysis of variance showing the means squares for foliar diseases traits at KALRO-Kakamega during 2016 short rains

Source of variation	df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	11.56	5.17	1.17	4949.8	651.6	165.3	12600.4	6504	3634.4
Genotype	23	1.56^{ns}	1.60^{ns}	4.50*	403.9^{ns}	426.1*	137.3^{ns}	781.5^{ns}	1529.9^{ns}	2629*
Error	46	0.83	1.05	0.82	208.7	105.3	53.4	683.4	539.7	785.5
Total	71									

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

Table 3.7b: Analysis of variance showing the means squares for foliar diseases traits at KALRO-Kakamega during 2017 long rains

Source of variation	Df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	0.17	5.39	1.72	2718.9	549.5	200.5	1472	1512.9	2801.2
Genotype	23	1.04*	1.27^{ns}	7.61*	280.3^{ns}	477.2^{ns}	930.5*	258*	869.6^{ns}	2247.3*
Error	46	1.04	0.98	0.50	153.2	216.5	68.1	428.8	636.6	541.5
Total	71									

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease

Source of variation	Df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB

progress curve calculated from the weekly ALS, ANT and CBB severity scores.

Table 3. 7c: Combined Analysis of variance showing the means squares for foliar diseases traits at Kakamega 2016 short rains and 2017 long rains

Source of variation	df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	6.9	0.03	1.86	7500.8	351	353.4	1091.5	2630.3	6141.4
Genotype	23	2.2^{ns}	2.14^{ns}	8.34*	656.9*	777.1*	688.4*	1008.5^{ns}	1761.3^{ns}	4293.9*
Season	1	10.0^{ns}	61.36*	21.77*	396.1*	486^{ns}	103.4*	1133.4^{ns}	3822.3*	1792.1*
G x S	23	0.40^{ns}	0.72^{ns}	1.60^{ns}	27.3^{ns}	126.1^{ns}	379.4*	142^{ns}	529^{ns}	582.4^{ns}
Error	94	1	1.22	1.07	180.7	175.5	59.7	611.4	690.2	655.6
Total	143									

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

3.4.1.3.2 Mean performance of the bean genotypes based on foliar diseases traits

The current findings showed that, the genotypes Cal137, Cal194, Cal5B, Cal6, Ciankui, GLP2, GLPX92, KK071, KKBC05/32, Red13, Red34 and RWR2245 during short rains season 2016 at KALRO-Kakamega were resistant to common bacterial blight with the scores ranged from 2.3 to 3.0. The incidence of anthracnose ranged from 4.0 to 54.1%. The area under the disease progress curve of common bacterial ranged from 70 in GLP2 to 163.3 in Red13 (Table 3.8a).

Table 3. 8a: Incidence and severity of diseases of common bean at KALRO-Kakamega during the short rains 2016

Genotypes	Final severity			% Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	3.7	3.0	3.0	33.2	21.9	14.3	101.3	91.3	102.0	MR	R	R
Cal139A	5.0	3.7	4.3	50.8	7.0	16.1	142.0	86.7	126.0	MR	MR	MR
Cal194	4.3	3.7	3.0	48.8	12.4	16.5	136.7	90.3	86.3	MR	MR	R
Cal33	5.0	3.0	5.0	46.4	5.8	15.6	139.0	80.7	142.7	MR	R	MR
Cal51A	5.0	4.3	4.3	48.3	25.2	10.6	138.0	126.0	109.3	MR	MR	MR
Cal5B	4.3	3.0	3.0	51.4	23.3	10.1	120.0	79.3	74.7	MR	R	R
Cal6	4.3	4.3	3.0	42.6	10.1	7.6	120.0	102.3	84.3	MR	MR	MR
Cal97A	5.0	4.3	3.7	38.4	10.5	9.7	122.3	111.3	92.7	MR	MR	R
Ciankui	3.7	5.0	2.3	69.2	54.1	15.4	103.3	147.3	68.7	MR	MR	R
GLP2	4.3	4.3	3.0	37.1	6.9	4.9	126.0	109.3	78.7	MR	MR	MR
GLP585	5.0	4.3	5.0	35.1	24.9	18.1	137.7	130.7	157.3	MR	MR	R
GLPX92	6.3	3.0	3.0	59.5	20.3	26.2	136.3	73.7	91.3	MR	R	MR
KK06/110	4.3	5.0	5.0	50.1	30.8	19.9	120.0	147.3	142.7	MR	MR	MR
KK06/29B	4.3	3.7	4.3	71.6	12.7	14.1	130.7	101.3	120.0	MR	MR	R
KK071	5.7	4.3	3.0	75.2	31.4	34.3	146.0	99.7	78.7	MR	R	MR
KK072	5.7	4.3	4.3	49.7	6.6	16.6	155.7	109.3	132.7	MR	MR	S
KK15	5.7	2.3	7.0	33.0	4.0	15.8	118.7	62.7	168.0	MR	S	MR
KK8	5.0	4.3	5.7	44.5	10.3	12.3	148.7	111.3	128.7	MR	MR	R
KKBC05/32	5.0	3.7	3.0	43.6	8.1	6.0	148.7	97.3	80.7	MR	R	MR
Red13	5.7	5.0	3.0	35.9	11.3	13.6	155.7	126.0	96.0	MR	R	R
Red16	4.3	4.3	6.3	43.7	22.7	24.3	120.0	130.7	162.0	MR	MR	MR
Red34	5.7	3.0	3.0	43.6	13.8	11.5	159.7	89.3	94.0	MR	R	R
Red45	3.7	3.7	3.7	49.2	14.7	22.6	116.7	97.3	108.0	MR	MR	MR
RWR2245	4.3	4.3	3.0	59.1	36.1	8.5	147.3	130.7	91.3	MR	R	R
GM	4.81	3.9	3.9	48.3	17.7	15.2	132.9	105.5	109.0			

Genotypes	Final severity			% Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
LSD (5%)	1.5	1.7	1.5	23.7	16.9	12.0	43.0	38.18	41.51			
CV (%)	19.0	26.2	23.1	29.9	58.0	48.1	19.7	22.0	22.7			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant, S=Susceptible.

During the long rains season at KALRO-Kakamega, the results showed that all the genotypes assessed were moderately resistant to angular leaf spot with the scores ranging from 4.3 to 6.3. The genotypes Cal137, Cal5B, Cal6, KK071, KK072, KKBC05/32, Red34 and GLP2 were resistant to common bacterial blight with the scores ranging from 2.3 to 3. The incidence of common bacterial blight ranged from 10.3 to 67.1%. The area under the disease progress curve of common bacterial ranged of 70 in GLP2 to 163.3 in Red13 genotype and of angular leaf spot ranged from 119 in Cal137 to 158.7 in Red34 genotypes (Table 3.8b).

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Table3. 8b: Incidence and severity of diseases of common bean planted at KALRO-Kakamega during 2017 long rains

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	5.0	2.3	3.0	48.5	28.1	22.4	119.0	81.7	109.7	MR	R	R
Cal139A	5.0	3.0	4.3	59.7	19.4	24.2	130.7	74.7	126.0	MR	R	MR
Cal194	5.0	3.0	7.0	57.4	24.9	62.3	137.7	84.0	137.7	MR	R	S
Cal33	5.7	2.3	7.0	50.3	13.3	67.1	137.7	53.7	147.0	MR	R	S
Cal51A	5.7	2.3	4.3	62.5	26.2	18.8	147.0	81.7	105.0	MR	R	MR
Cal5B	5.7	1.7	3.0	62.3	6.3	18.2	135.3	46.7	84.0	MR	R	R
Cal6	4.3	2.3	3.0	52.4	15.6	15.8	126.0	63.0	86.3	MR	R	R
Cal97A	5.7	3.0	4.3	47.3	23.0	17.8	135.3	88.7	95.7	MR	R	MR
Ciankui	4.3	3.7	4.3	72.0	66.3	23.5	126.0	100.3	93.3	MR	MR	MR
GLP2	5.0	3.0	2.3	52.3	19.4	10.3	128.3	86.3	70.0	MR	R	R
GLP585	5.0	2.3	4.3	53.2	23.0	26.3	147.0	81.7	130.7	MR	R	MR
GLPX92	5.7	2.3	3.7	69.1	11.1	34.3	154.0	58.3	107.3	MR	R	MR
KK06/110	4.3	2.3	5.0	56.8	26.1	28.0	123.7	70.0	144.7	MR	R	MR
KK06/29B	5.0	2.3	3.7	81.6	19.3	22.2	140.0	67.7	107.3	MR	R	MR
KK071	5.7	3.0	3.0	83.9	19.7	42.6	151.7	60.7	84.0	MR	R	R
KK072	5.7	2.3	3.0	57.2	13.3	31.4	147.0	70.0	128.3	MR	R	R
KK15	5.7	2.3	7.0	52.0	10.7	64.3	133.0	58.3	158.7	MR	R	S
KK8	5.7	2.3	7.0	57.4	13.4	58.8	147.0	67.7	147.0	MR	R	S
KKBC05/32	5.7	3.7	3.0	55.7	20.5	14.2	144.7	86.3	86.3	MR	MR	R
Red13	6.3	3.7	7.0	52.6	23.8	52.4	154.0	93.3	163.3	MR	MR	S
Red16	5.7	3.7	7.0	53.6	35.2	50.1	142.3	107.3	158.7	MR	MR	S
Red34	6.3	1.0	3.0	49.2	0.0	19.9	158.7	35.0	95.7	MR	R	R
Red45	4.3	2.3	3.7	59.4	19.4	30.7	121.3	70.0	107.3	MR	R	MR
RWR2245	5.7	2.3	3.7	65.3	34.9	16.7	137.7	63.0	112.0	MR	R	MR
GM	5.3	2.6	4.6	58.8	21.4	32.2	138.5	72.9	116.1			
LSD (5%)	1.7	1.63	1.2	20.3	24.0	13.6	34.03	41.5	38.2			

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
CV (%)	19.1	38.0	15.6	21.0	68.9	25.6	14.9	34.6	20.0			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant, S=Susceptible.

With combined seasons at KALRO Kakamega, KK15, Cal51A, KK8, Cal5B, GLP585, KK072 and Red16 showed moderately resistant responses. The incidence of angular leaf spot ranged from 39.8 to 57.3%. The incidence of anthracnose ranged from 8.7 to 48%. The area under the disease progress curve of common bacterial blight ranged from 74.4 in GLP2 to 163.4 in KK15 genotype while the incidence of common bacterial blight ranged from 7.1 to 56.1% (Table 3.8c).

Table 3.8c Combined Incidence and severity of diseases for bean genotypes at KALRO-Kakamega 2016 short rains and 2017 long rains

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	4.3	2.7	3.0	43.1	17.3	33.1	110.2	86.5	105.9	MR	R	R
Cal139A	5.0	3.3	3.0	48.2	33.3	21.0	136.4	80.7	126.0	MR	MR	R
Cal194	4.7	3.3	2.3	48.3	18.9	40.9	137.2	87.2	112.0	MR	MR	R
Cal33	5.3	2.7	3.0	42.7	20.7	43.7	138.4	67.2	144.9	MR	R	R
Cal51A	5.3	3.3	4.0	50.3	20.0	24.6	142.5	103.9	107.2	MR	MR	MR
Cal5B	5.0	2.3	3.3	47.5	20.6	19.9	127.7	63.0	79.4	MR	R	MR
Cal6	4.3	3.3	2.7	46.5	11.9	12.9	123.0	82.7	85.3	MR	MR	R
Cal97A	5.3	3.7	3.0	44.7	25.6	15.2	128.8	100.0	94.2	MR	MR	R
Ciankui	4.0	4.3	2.3	48.3	48.0	15.3	114.7	123.8	81.0	MR	MR	R
GLP2	4.7	3.7	2.7	39.8	28.7	11.4	127.2	97.8	74.4	MR	MR	R
GLP585	5.0	3.3	3.3	44.1	25.5	21.6	142.4	106.2	144.0	MR	MR	MR
GLPX92	6.0	2.7	3.0	52.9	23.2	23.5	145.2	66.0	99.3	MR	R	R
KK06/110	4.3	3.7	3.0	45.7	22.1	20.0	121.9	108.7	143.7	MR	MR	R
KK06/29B	4.7	3.0	2.7	55.8	29.4	15.4	135.4	84.5	113.7	MR	R	R
KK071	5.7	3.7	3.0	57.3	21.3	28.0	148.9	80.2	81.4	MR	MR	R
KK072	5.7	3.3	3.3	46.4	18.4	26.1	151.4	89.7	130.5	MR	MR	MR
KK15	5.7	2.3	4.3	44.4	13.0	56.1	125.9	60.5	163.4	MR	R	MR
KK8	5.3	3.3	3.7	48.4	18.2	46.1	147.9	89.5	137.9	MR	MR	MR
KKBC05/32	5.3	3.7	1.3	43.4	26.0	7.1	146.7	91.8	83.5	MR	MR	R
Red13	6.0	4.3	2.3	46.8	27.5	43.1	154.9	109.7	129.7	MR	MR	R
Red16	5.0	4.0	3.3	49.0	32.1	43.0	131.2	119.0	160.4	MR	MR	MR
Red34	6.0	2.0	2.0	44.3	8.7	12.5	159.2	62.2	94.9	MR	R	R
Red45	4.0	3.0	3.0	44.8	26.6	23.0	119.0	83.7	107.7	MR	R	R
RWR2245	5.0	3.3	2.0	53.0	34.1	10.5	142.5	96.9	101.7	MR	MR	R
GM	5.1	3.3	2.9	47.3	23.8	25.6	135.7	89.2	112.6			
LSD (5%)	1.63	1.79	1.67	21.79	21.48	12.52	40.09	42.59	41.51			
CV (%)	19.9	33.8	24.0	25.1	67.8	32.6	18.2	29.5	22.7			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant.

3.4.1.4 Common bean yield and yield components during the 2016 short rains, 2017 long rains and combined seasons at Kakamega

3.4.1.4.1 Analysis of variance for Common bean yield and yield

The findings revealed that during 2016 short rains, the genotypes did not show significant variations for the number of pod per plant and seed per pod. Hundred seed weight and yield of genotypes were significantly different ($p<0.05$) during short rains season at Kakamega (Table 3.9a). During 2017 long rains, the genotypes did not show significant variations for all the yield and yield components except the hundred seed weight ($p<0.05$). The average number of pod per plant, hundred seed weight and yield during the short rains 2016 and 2017 long rains combined analysis at KALRO-Kakamega showed significant ($p<0.05$) variation. However, the genotypes did not differ in the number of seed per pod among seasons (Table 3.9b).

Table 3. 9a: Analysis of variance showing the means squares for the yield and yield components traits at KALRO-Kakamega during 2016 short rains and 2017 long rains

Source of variation	Df	Short rains				Long rains			
		NPP	NSP	HSW(g)	Yield (Kg/ha)	NPP	NSP	HSW(g)	Yield (Kg/ha)
Replication	2	7.0	4.05	1.34	708757	20.51	0.08	4.8	107080
Genotype	23	23.6^{ns}	4.26^{ns}	75.72*	591889*	24.93^{ns}	0.86^{ns}	90.4*	483987^{ns}
Error	46	12.7	2.75	2.02	64840	13.28	0.35	6.3	267041
Total	71								

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

Table 3.9b: Combined Analysis of variance showing the means squares for the yield and yield components traits for KALRO-Kakamega short rains and long rains seasons

Source of variation	df	KALRO-Kakamega			
		NPP	NSP	HSW(g)	Yield (Kg/ha)
Replication	2	25.0	1.93	5.6	1372
Genotype	23	34.3*	2.52^{ns}	156.8*	7993*
Season	1	315.0*	27.2*	969.7*	517646*
GxS	23	14.19^{ns}	2.60^{ns}	9.3^{ns}	27648^{ns}
Error	94	12.76	1.56	4.1	17684
Total	143				

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.1.4.2 Mean performance for common bean yield and yield component at Kakamega

Results of mean performance for the yield and yield component in KALRO-Kakamega during the long and short rain seasons are presented in table 3.10. During the short rains season, common bean 100-seed weight ranged from 17.1g in GLP585 to 37.7g in GLP2 genotype. Genotype Cal33 had the highest yield while genotype KK071 had the lowest. During the long rains season, 100-seed weight ranged from 20g in GLP585 genotype to 44.7g in RWR22 45 genotypes. At combined 2016 short rains and 2017 long rains at Kakamega, genotype Red16 had the highest number of pod per plant while the genotype KK071 had the lowest. The genotype RWR2245 recorded the highest 100-seed weight of 40.3g while GLP585 had the lowest 100-seed weight of 18.6g. The genotype Red13 had the highest yield compared to genotype KK071 which had the lowest yield (Table 3.11).

Table 3.10: Pod per plant, seed per pod, hundred seed weight and yield for common bean Genotypes planted at KALRO-Kakamega during 2016 short rains and 2017 long rains

Genotypes	Short rains				Long rains			
	NPP	NSP	HSW (g)	Yield (Kg/ha)	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal137	7.3	3.8	34.7	1385.5	12.2	4.4	36.3	1250.1
Cal139A	12.4	4.4	36.4	1480.0	14.7	3.9	41.4	2368.0
Cal194	12.3	6.0	32.5	1668.0	13.3	4.6	35.1	1766.0
Cal33	11.6	6.1	34.3	1963.0	13.3	4.1	40.6	1749.0
Cal51A	10.4	4.5	25.2	931.0	9.2	3.9	29.7	940.0
Cal5B	16.9	7.0	29.2	846.0	12.2	3.3	40.2	1453.0
Cal6	10.1	6.1	26.1	1525.0	13.9	4.3	29.3	1304.0
Cal97A	11.2	5.3	28.6	847.5	16.4	3.7	31.2	2098.0
Ciankui	6.9	3.9	34.6	522.0	11.4	2.9	38.1	1238.4
GLP2	7.8	4.3	37.7	1572.0	9.7	4.2	42.2	1755.0
GLP585	10.8	4.7	17.1	1011.0	17.5	5.5	20.0	1224.0
GLPX92	9.1	3.6	24.6	551.0	16.9	4.4	29.1	1478.0
KK06/110	9.0	6.1	33.5	1588.0	15.2	4.2	38.1	1717.0
KK06/29B	9.1	4.8	35.3	1329.5	14.1	3.9	38.6	2060.5
KK071	8.2	2.6	30.3	145.0	7.1	4.0	39.8	913.0
KK072	6.3	3.5	36.8	1237.0	11.8	4.3	39.6	1164.0
KK15	8.3	3.9	25.6	1051.0	10.3	5.0	31.0	1903.0
KK8	9.9	5.1	31.6	1480.5	15.8	3.8	37.1	1563.0
KKBC05/32	9.5	4.3	35.6	1419.0	13.3	4.3	40.2	1799.0
Red13	12.8	6.4	28.5	1701.0	18.7	4.3	35.1	2191.5
Red16	16.3	6.3	28.4	1630.0	15.9	4.8	37.1	2094.0
Red34	9.2	6.9	27.2	1301.5	10.8	4.1	36.0	1491.0
Red45	12.8	6.0	28.5	1172.0	16.4	4.7	32.8	2099.0
RWR2245	14.8	5.6	36.0	1785.0	14.0	3.8	44.7	1625.0
GM	10.5	5.0	30.8	1255.9	13.5	4.2	35.7	1635.1
LSD (5%)	5.9	2.7	2.4	418.5	6.0	1.0	1.2	849.3
CV (%)	33.8	32.9	4.6	20.3	27.0	14.1	7.0	31.6

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

Table 3.11: Combined means for Pod per plant, seed per pod, hundred seed weight and yield for common bean genotypes planted at KALRO-Kakamega short rains and long rains seasons

Genotypes	Kakamega			
	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal137	9.8	4.2	35.5	1317.5
Cal139A	13.5	3.9	38.9	1924

Genotypes	Kakamega			
	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal194	12.8	4.4	33.8	1717
Cal33	12.5	4.5	37.5	1856
Cal51A	9.8	4.2	27.4	935.5
Cal5B	14.5	3.8	34.7	1149.5
Cal6	12	4	27.7	1414.5
Cal97A	13.8	3.9	29.9	1472.5
Ciankui	9.2	3.6	36.4	880
GLP2	8.7	4.3	39.9	1663.5
GLP585	14.1	5.5	18.6	1117.5
GLPX92	13	4.4	26.9	1014.5
KK06/110	12.1	4	35.8	1652.5
KK06/29B	11.6	4.8	37	1694.5
KK071	7.6	4.5	35	529
KK072	9.1	4.6	38.2	1200.5
KK15	9.3	5.1	28.3	1477
KK8	12.9	3.9	34.3	1521.5
KKBC05/32	11.4	4.5	37.9	1609
Red13	15.8	4.5	31.8	1946
Red16	16.1	4.7	32.8	1862
Red34	10	4.1	31.6	1396
Red45	14.6	4.8	30.6	1635.5
RWR2245	14.4	3.7	40.3	1705
GM	12	4.3	33.4	1445.4
LSD (5%)	5.79	2.02	3.28	681.8
CV (%)	29.7	27.1	6.1	29.1

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.2 Evaluation of common bean genotypes for the different traits at Lugari during the short rains season 2016 and long rains season 2017

3.4.2.1 Analysis of variance for the agronomic traits during the short rains season 2016 and long rains season 2017 at Lugari

Analysis of variance for agronomic traits evaluated at Lugari in short rains season 2016 and long rains season 2017 are presented in table 3.12a. Bean genotypes evaluated showed significant differences for all agronomic traits i.e percent emergency, days to flowering and days to maturity in short rains season. Significant differences were observed among genotypes for all agronomic traits except days to flowering during the long rains season. At combined Lugari short rains 2016 and long rains 2017, significant differences among genotypes were observed for all the agronomic traits at $p<0.05$. There were significant seasonal differences for all the agronomic traits at $p<0.05$. For the interaction of genotype and sites, percent emergency showed significant differences while days to flowering and to maturity did not show any differences between the sites (Table3.12b).

Table3. 12a: Analysis of variance for the means squares for the agronomic traits at Lugari during short rains 2016 and long rains 2017

Source of variation	df	Short rains 2016			Long rains 2017		
		%Em.	DTF	DTM	%Em.	DTF	DTM
Replication	2	634.3	4.50	0.29	328.0	195.29	0.72
Genotype	23	968.6*	20.01*	23.69*	170.9*	7.89^{ns}	21.18^{*}
Error	46	106.2	1.27	0.42	71.4	7.21	0.56
Total	71						

*= Significant difference at 5%, ^{ns}= no significant, df= degree of freedom, G x S = Interaction of Genotype and season, %Em. =percentage of emergence, DTF=Days to 50% flowering, DTM= Days to 75% maturity.

Table 3.12b: Combined analysis of variance for the means squares for the agronomic traits at Lugari short and long rains seasons

Source of variation	df	Lugari		
		%Em.	DTF	DTM

Replication	2	637.06	79.65	0.97
Genotype	23	497.43*	17.87*	44.44*
Season	1	3195.7*	5329*	345.34*
GxS	23	642.07*	10.03^{ns}	0.43^{ns}
Error	94	93.8	6.70	0.48
Total	143			

*= Significant difference at 5%, ^{ns}= no significant, df= degree of freedom, G x S = Interaction of Genotype and season, %Em. =percentage of emergence, DTF=Days to 50% flowering, DTM= Days to 75% maturity.

3.4.2.2 Mean performance for the agronomic traits

Results of the mean performance for agronomic traits in Lugari during the long and short rain seasons are presented in table 3.13 and combined seasons in table 3.13. During the short rains season, genotype KK06/110 recorded the highest percentage of emergence of 65.9 while GLPX92 had the least emergency percentage. Genotype GLP2 flowered earliest compared to genotype KK071 which flowered latest. Genotype KK15 matured earliest while the genotype Ciankui matured latest. During the long rains season, genotype Red45 recorded the highest percentage of emergence of 90.5 while the genotype Cal137 had the least emergency percentage. Genotype KK15 matured earliest compared to the genotype KK8 which matured latest. At combined Lugari' short and long rains season, genotype KK8 recorded the highest percentage of emergence of 72.4 while GLPX92 had the least emergency percentage. Genotype GLP2 flowered earliest compared to genotype Cal194 which flowered latest. Genotype KK15 matured earliest while the genotypes Ciankui, GLP2, KK06/110, KK071, KK8 and Red34 matured latest (Table 3.14).

Table 3.13: Percentage emergence, days to flowering and maturity for common bean genotypes planted at Lugari during 2016 short rains and 2017 long rains

Genotypes	**Short rains 2016**	**Long rains 2017**

	%Em.	DTF	DTM	%Em.	DTF	DTM
Cal137	44.8	55.7	84.0	58.3	43.0	81.0
Cal139A	48.8	56.0	89.0	76.6	44.3	86.0
Cal194	44.4	59.0	86.0	87.7	47.0	83.0
Cal33	55.6	55.0	86.0	66.7	44.7	83.0
Cal51A	40.5	55.0	84.0	73.0	42.7	81.0
Cal5B	10.3	56.7	89.0	68.7	44.3	86.0
Cal6	61.1	50.3	86.7	70.6	44.3	83.7
Cal97A	26.2	58.7	89.0	79.8	45.0	86.0
Ciankui	7.1	57.3	90.0	70.6	42.7	86.7
GLP2	53.2	50.0	90.0	71.8	40.7	84.7
GLP585	48.4	54.7	86.0	69.1	44.3	83.0
GLPX92	7.1	54.0	89.0	65.5	43.0	85.7
KK06/110	65.9	52.3	90.0	69.5	43.7	87.0
KK06/29B	57.5	57.0	85.3	65.9	45.7	82.3
KK071	21.0	60.0	90.0	79.0	43.0	87.0
KK072	54.8	56.7	89.0	69.8	41.0	85.3
KK15	52.4	56.7	79.0	65.5	43.7	76.7
KK8	64.3	58.7	90.0	80.6	43.7	87.3
KKBC05/32	41.7	54.0	83.3	76.6	42.3	80.3
Red13	61.5	58.0	86.0	65.5	43.3	83.0
Red16	45.2	55.7	87.7	77.8	46.3	84.7
Red34	29.0	57.7	90.0	75.4	46.7	87.0
Red45	27.8	58.7	89.3	90.5	42.3	86.3
RWR2245	56.0	54.3	88.7	65.5	42.3	86.0
Grand mean	42.7	55.9	87.4	72.5	43.8	84.3
LSD (5%)	16.9	1.85	1.07	13.9	4.4	1.23
CV (%)	24.1	2.0	0.7	11.7	6.1	0.9

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; % Em. =percentage of emergence; DTF=Days to 50% flowering; DTM= Days to 75% maturity

Table 3.14: Percentage emergence, days to flowering and maturity for common bean genotypes planted at Lugari combined over seasons

Genotypes	Lugari		
	%Em.	DTF	DTM
Cal137	51.6	49.3	82.0
Cal139A	62.7	50.2	87.0
Cal194	66.1	53.0	84.0
Cal33	61.1	49.8	84.0
Cal51A	56.7	48.8	82.0
Cal5B	39.5	50.5	87.0
Cal6	65.9	47.3	84.7
Cal97A	53.0	51.8	87.0
Ciankui	38.9	50.0	88.0

Genotypes	Lugari		
	%Em.	DTF	DTM
GLP2	62.5	45.3	88.0
GLP585	58.7	49.5	84.0
GLPX92	36.3	48.5	87.0
KK06/110	67.7	48.0	88.0
KK06/29B	61.7	51.3	83.3
KK071	50.0	51.5	88.0
KK072	62.3	48.8	87.0
KK15	58.9	50.2	77.0
KK8	72.4	51.2	88.0
KKBC05/32	59.1	48.2	81.3
Red13	63.5	50.7	84.0
Red16	61.5	51.0	85.7
Red34	52.2	52.2	88.0
Red45	59.1	50.5	87.3
RWR2245	60.7	48.3	86.7
Grand mean	57.6	49.8	85.4
LSD (5%)	15.7	4.19	1.12
CV (%)	16.8	5.2	0.8

LSD: Least significant difference; CV (%): Percentage of coefficient of variati
% Em. =percentage of emergence; DTF=Days to 50% flowering; DTM= Days
75% maturity

3.4.2.3 Analysis of variance showing the mean squares for the incidence and severity of foliar diseases at Lugari site

3.4.2.3.1 Analysis of variance for incidence and severity of foliar diseases

The genotypes did not differ significantly ($P<0.05$) for severity of angular leaf spot and anthracnose except the severity of common bacterial blight. Incidence of angular leaf spot and anthracnose did not show significant differences ($P<0.05$) among genotypes except the incidence of common bacterial blight. The area under the disease progress curve of angular leaf spot and anthracnose did not show significant differences ($P<0.05$) among genotypes except for the area under the disease progress curve of common bacterial blight (Table 3.15a). In long rains seasons at Lugari, significant differences among genotypes were recorded for the severity of angular leaf

spot, anthracnose and the area under the disease progress curve of angular leaf spot and anthracnose while no significant difference were recorded for severity of common bacterial blight, all diseases incidence and area under the disease progress curve of common bacterial blight at $p<0.05$ (Table 3.15b). At combined Lugari 2016 short rains and 2017 long rains, no significant differences among genotypes evaluated were observed for all the diseases traits at $p<0.05$. There were significant seasonal differences for all the diseases traits at $p<0.05$ except the severity of common bacterial blight and the area under disease progress curve of common bacterial blight. The interaction of genotype and season did not show significant differences among genotypes for all the diseases traits at $p<0.05$ (Table 3.15c).

Table 3.15a: Analysis of variance of the means squares for foliar diseases traits at Lugari during the short rains 2016

Source of variation	df	Final severity			%Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	6.00	3.17	1.39	128.1	464.2	11.18	2818.1	2442.7	614.5
Genotype	23	1.14^{ns}	0.67^{ns}	2.49^{*}	108.4^{ns}	194.6^{ns}	43.72^{*}	460.4^{ns}	693^{ns}	1683.5*
Error	46	0.90	0.56	1.22	166.4	140.7	21.41	331.9	673.4	964.6
Total	71									

*= Significant difference at 5%, ^{ns}= no significant, df= degree of freedom, G x S = Interaction of Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

Table 3.15b: Analysis of variance of the means squares for foliar diseases traits at Lugari during 2017 long rains

Source of variation	df	Final severity			%Incidence					
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	1.56	0.67	0.72	33.1	1196.8	175.2	2291.4	1962	143.6
Genotype	23	1.22*	1.25^{*}	2.05^{ns}	73.3^{ns}	318.4^{ns}	474.5^{ns}	359.3^{*}	751.1*	962.8^{ns}
Error	46	0.80	0.90	1.30	38.32	277.8	394.9	379	819.4	974.5
Total	71									

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of

Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

Table 3.15c: Combined analysis of variance of the means squares for foliar diseases traits at Lugari 2016 short rains and 2017 long rains

Source of variation	Df	Final severity			%Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	6.8	0.8	2.03	138.7	1573	137	5044.8	611	654.7
Genotype	23	1.7^{ns}	1.2^{ns}	2.58^{ns}	136.1^{ns}	467^{ns}	350.3^{ns}	691.8^{ns}	834.3^{ns}	1933.4^{ns}
Season	1	58.8*	9.0*	2.25^{ns}	7506.2*	239.2*	6132.6*	10574.7*	17755.6*	6574.5^{ns}
G x S	23	0.6^{ns}	0.8^{ns}	1.96^{ns}	45.6^{ns}	46.1^{ns}	168^{ns}	128^{ns}	609.7^{ns}	713^{ns}
Error	94	0.9	0.8	1.23	100.7	206.7	204.8	349.3	811.2	951.1
Total	143									

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

3.4.2.3.2 Mean performance for the disease incidence and severity at Lugari

The results during the short rains season revealed that all the genotypes were resistant to common bacterial blight except the genotypes KK15, KK8, Red16, Cal33 and KK072 which were moderately resistant to common bacterial blight. The incidence of common bacterial blight had a range of 0.5 to 16%. The area under the disease progress curve of common bacterial had a range of 56 (KKBC05/32) to 165.7 (KK15) (Table 3.16a).

Table3.16a: Incidence and severity of diseases for common bean at Lugari during 2016 short rains

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	3	3.7	2.3	22.8	11.3	3.3	102	122.7	79.3	R	MR	R
Cal139A	3	3.7	3	20.4	34.5	9.6	96	122.7	105	R	MR	R
Cal194	4.3	3	2.3	23	7.3	5.2	116	100	79.3	MR	R	R
Cal33	3	3.7	3.7	20.6	15.8	3.5	102	120.7	112	R	MR	MR
Cal51A	3	3	3	35.1	8.7	5.6	102	102	105	R	R	R
Cal5B	2.3	3	3	13.9	22.4	8.2	77.3	100	105	R	R	R
Cal6	3.7	2.3	3	24.3	7.7	4.8	107	77.3	95.7	MR	R	R
Cal97A	4.3	2.3	3	31.7	16.4	4.4	119	79.3	102.7	MR	R	R
Ciankui	3	3	2.3	11.4	17.3	3.5	75.7	100	81.7	R	R	R
GLP2	2.3	3	2.3	18	25.6	3.1	79.3	91.3	81.7	R	R	R
GLP585	3	3	3	29.3	21.7	8.8	102	102	102.7	R	R	R
GLPX92	3	3	2.3	20.4	22.9	3.2	86.3	102	79.3	R	R	R
KK06/110	3	3	3	11.5	13.4	3.9	102	102	102.7	R	R	R
KK06/29B	3	4.3	3	23.5	38.7	4.8	81.7	143.3	105	R	MR	R
KK071	3	3	3	16.4	18.8	5.3	100	102	105	R	R	R
KK072	3	3.7	3.7	18.8	10.9	6	102	122.7	114.3	R	MR	MR
KK15	3.7	3.7	5.7	24.8	10	16	109	112	165.7	MR	MR	MR
KK8	5	3.7	5	28.6	21.1	13.7	123	122.7	144.7	MR	MR	MR
KKBC05/32	3	3	1.7	15.2	19.1	0.5	96	102	56	R	MR	R
Red13	3.7	3.7	2.3	20.2	12.3	3.3	107	122.7	81.7	MR	MR	R
Red16	3.7	3.7	4.3	25.6	16.7	12.8	109	122.7	133	MR	MR	MR
Red34	3	3	2.3	18.3	12.2	4.3	102	98	81.7	R	R	R
Red45	3	3	3	22.7	27.8	7.2	102	102	102.7	R	R	R
RWR2245	3	3.7	2.3	16.5	20.9	2	102	102	79.3	R	MR	R
GM	3.2	3.3	3	21.4	18.1	5.9	100	107.3	100.1			
LSD (5%)	1.6	1.23	1.81	21.2	19.5	7.6	29.9	42.7	51.05			
CV (%)	29.2	23	36.4	60.4	65.7	77.8	18.2	24.1	31			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant.

Table 3.16b: Incidence and severity of diseases for common bean at Lugari during long rains 2017

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	3.7	1.7	3.7	37.7	6.5	43.8	105	46.7	93.3	MR	R	MR
Cal139A	3.7	3	3	36.8	47.1	17.7	105	105	105	MR	R	R
Cal194	5	2.3	2.3	39.2	12.9	19.5	123.7	81.7	79.3	MR	R	R
Cal33	4.3	3	2.3	35.2	28.1	20.2	112	102.7	81.7	MR	R	R
Cal51A	5	2.3	5	38.1	13.7	30.4	114.3	81.7	109.7	MR	R	MR
Cal5B	4.3	3	3.7	32.8	34.9	21.6	114.3	91	107.3	MR	R	MR
Cal6	3.7	1.7	2.3	40.7	8.3	10.1	109.7	58.3	79.3	MR	R	R
Cal97A	5.7	3	3	42	28.2	12.5	140	77	102.7	MR	R	R
Ciankui	3.7	3	2.3	24.5	29.7	7.2	95.7	102.7	70	MR	R	R
GLP2	3.7	3	3	27.3	38	12.5	102.7	98	81.7	MR	R	R
GLP585	4.3	2.3	3.7	35	28	16.9	116.7	81.7	105	MR	R	MR
GLPX92	5.7	3	3.7	36.6	35.4	12.7	126	98	95.7	MR	R	MR
KK06/110	4.3	2.3	3	34.7	18	12	128.3	81.7	93.3	MR	R	R
KK06/29B	5	2.3	2.3	30	39.5	8.5	107.3	74.7	81.7	MR	R	R
KK071	4.3	2.3	3	30.7	22.9	13.4	109.7	70	98	MR	R	R
KK072	4.3	3	3	35.6	23.4	20.8	119	93.3	102.7	MR	R	R
KK15	5	2.3	3	36.7	15.3	48	130.7	70	88.7	MR	R	R
KK8	5	2.3	2.3	39.5	22.9	33.5	133	70	93.3	MR	R	R
KKBC05/32	5	3.7	1	31.1	31.5	0	109.7	95.7	35	MR	MR	R
Red13	5	4.3	2.3	41	31.3	33.8	128.3	107.3	79.3	MR	MR	R
Red16	5	3.7	2.3	44.4	29.1	35.8	128.3	105	81.7	MR	MR	R
Red34	5	2.3	1.7	39.4	17.3	5.1	121.3	79.3	58.3	MR	R	R
Red45	4.3	2.3	3	30.2	33.9	15.4	114.3	81.7	95.7	MR	R	R
RWR2245	3.7	3.7	1.7	30.2	33.3	4.2	116	98	58.3	MR	MR	R
GM	4.5	2.6	2.8	35.4	26.2	19	117.2	85.5	86.5			
LSD (5%)	1.5	1.56	1.88	10.17	27.4	32.7	32	47.05	51.3			
CV (%)	19.8	34.5	41.1	17.3	63.6	55.2	16.6	33.5	36.1			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant.

For the combined short and long rains, only the genotype GLP2 was resistant to angular leaf spot with the score of 3.0. The genotypes Cal6, Ciankui, GLP2, KK071, KKBC05/32 and Red34 were resistant to common bacterial blight. The incidence of

anthracnose had a range of 7 to 35.7% and of common bacterial blight had the range of 3.3 to 19.8%. The area under the disease progress curve of anthracnose had a range of 67.8 for Cal6 to 115 for Red13 and of common bacterial blight had a range of 45.5 for KKBC05/32 to 127.2 for KK15 (Table 3.16c).

Table 3.16c: Combined Incidence and severity of diseases for bean genotypes at Lugari 2016 short rains and 2017 long rains seasons

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	3.3	2.7	3.7	28	16.6	8.8	103.5	84.7	86.3	MR	R	MR
Cal139A	3.3	3.3	4.3	35.6	20.8	12.8	100.5	113.9	105	MR	MR	MR
Cal194	4.7	2.7	4.7	35.9	9.9	10.8	119.9	90.9	79.3	MR	R	MR
Cal33	3.7	3.3	5.3	33.5	10.8	9.6	107	111.7	96.9	MR	MR	MR
Cal51A	4	2.7	5	41.7	16.9	8.1	108.2	91.9	107.4	MR	R	MR
Cal5B	3.3	3	3.7	32.7	22.8	9.1	95.8	95.5	106.2	MR	R	MR
Cal6	3.7	2	3	33.5	8.9	6.2	108.4	67.8	87.5	MR	R	R
Cal97A	5	2.7	4	35	13.5	7	129.5	78.2	102.7	MR	R	MR
Ciankui	3.3	3	3	40.3	35.7	9.4	85.7	101.4	75.9	MR	R	R
GLP2	3	3	3	27.6	16.3	4	91	94.7	81.7	R	R	R
GLP585	3.7	2.7	5	32.2	23.3	13.5	109.4	91.9	103.9	MR	R	MR
GLPX92	4.3	3	4	40	21.6	14.7	106.2	100	87.5	MR	R	MR
KK06/110	3.7	2.7	5	30.8	22.1	11.9	115.2	91.9	98	MR	R	MR
KK06/29B	4	3.3	4	47.5	25.7	9.4	94.5	109	93.4	MR	MR	MR
KK071	3.7	2.7	3	45.8	25.1	19.8	104.9	86	101.5	MR	R	R
KK072	3.7	3.3	4.7	34.2	8.8	11.3	110.5	108	108.5	MR	MR	MR
KK15	4.3	3	7	28.9	7	15.9	119.9	91	127.2	MR	R	S
KK8	5	3	6.3	36.6	15.7	13	128	96.4	119	MR	R	MR
KKBC05/32	4	3.3	3	29.4	13.6	3.3	102.9	98.9	45.5	MR	MR	R
Red13	4.3	4	4.7	28.1	11.8	8.5	117.7	115	80.5	MR	MR	MR
Red16	4.3	3.7	6.7	34.7	19.7	18.5	118.7	113.9	107.4	MR	MR	MR
Red34	4	2.7	3	31	13	7.9	111.7	88.7	70	MR	R	R
Red45	3.7	2.7	3.7	35.9	21.2	14.9	108.2	91.9	99.2	MR	R	MR
RWR2245	3.3	3.7	3.7	37.8	28.5	5.3	109.4	105	68.8	MR	MR	MR
GM	3.9	3	4.3	34.9	17.9	10.6	108.6	96.6	93.3			
LSD (5%)	1.49	1.43	1.8	16.26	23.31	23.2	30.3	46.17	50			
CV (%)	23.7	29.4	38.3	35.1	64.9	84.7	17.2	29.5	33.1			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were assessed based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT

and CBB severity scores, R= resistant, MR= moderately resistant, S= susceptible.

3.4.2.4 Mean performance for the yield and yield component at Lugari

3.4.2.4.1 Analysis of variance showing the mean squares for yield and yield components

During the short rains, the genotypes did not show significant difference for yield and yield components (P<0.05). During the long rains, the genotypes did not show significant difference for the number of pod per plant and yield except for the number of seed per pod and hundred seed weight at (P<0.05) (Table 3.17a). With the combined season analysis, the genotypes showed significant differences for the number of pod per plant and seed per pod, and hundred seed weight. All yield and yield components were significant different among seasons at p<0.05 except the number of seed per pod. The interaction of genotype and season showed no significant difference for all the traits (Table 3.17b).

Table 3.17a: Analysis of variance of the means squares for the yield and yield components traits at Lugari during short rains 2016 and long rains 2017

Source of variation	Df	Short rains				Long rains			
		NPP	NSP	HSW(g)	Yield(Kg/ha)	NPP	NSP	HSW(g)	Yield (Kg/ha)
Replication	2	10.81	10.21	23.78	1018257	22.7	0.159	5.34	148411
Genotype	23	5.31^{ns}	4.85^{ns}	39.29^{ns}	31402^{ns}	22.6^{ns}	0.898*	89.61*	247357^{ns}
Error	46	3.6	1.93	57.28	29197	7.8	0.228	7.35	148693
Total	71								

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

Table 3.17b: Combined analysis of variance of the means squares for the yield and yield components traits at Lugari short and long rain season

Source of variation	df	Lugari			
		NPP	NSP	HSW (g)	Yield (Kg/ha)
Replication					
	2	5.6	5.5	19.2	8662
Genotype	23	15.1*	3.0*	84.4*	1172^{ns}
Season	1	3843.8*	4.6^{ns}	3251.2*	6207*
GxS	23	11.9^{ns}	2.7^{ns}	44.5^{ns}	1615^{ns}
Error	94	6.2	1.2	31.8	934
Total	143				

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.2.4.2 Mean performance of the different genotypes with regard to yield and yield components

During the long rains, the genotype KK06/29B had the highest number of seed per pod while the genotype RWR2245 had the lowest. The highest mean value for hundred seed weight was recorded for the genotype RWR2245 while the lowest mean value was for the genotype GLP585 (Table 3.18). With the combined season analysis, genotype Cal33 had the highest number of pod per plant while the genotype Cal139A had the lowest. The genotype KK06/110 had the highest number of seed per pod while the genotype KK071 had the lowest. The genotype RWR2245 recorded the highest 100-seed weight of 36g while GLP585 had the least 100-seed weight of 22.5g (Table 3.19).

Table3.18: Pod per plant, seed per pod, hundred seed weight and yield for common bean genotypes planted at Lugari during 2016 short rains and 2017 long rains

Genotypes	Short rains				Long rains			
	NPP	NSP	HSW (g)	Yield (Kg/ha)	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal137	2.8	3.4	25.4	124	14.1	3.9	33.8	1413
Cal139A	3.2	2.7	30.4	206	9.5	3.9	39.4	1825
Cal194	3.5	4.4	23.9	313	10.9	4.2	32	1771.5
Cal33	5.5	4.1	30.8	156	16.9	4.9	39.4	1527
Cal51A	3.4	5.8	22.7	177	10.9	4.5	30	1270
Cal5B	3.5	3.3	31.1	202	13.9	4.3	38.2	1699.5
Cal6	3.8	5.6	23.8	385	15.5	3.8	26.9	1263
Cal97A	3.2	3.3	23.5	146	17.5	4.2	30.1	1979
Ciankui	2.1	2.7	29.7	135	13.7	4.2	38.3	1354
GLP2	3.4	4.3	25.3	185	11.7	4.4	40.8	1364
GLP585	2.4	5.1	26.5	154	14.4	5.5	18.6	1340
GLPX92	8.7	4.3	22	533	13	4.4	29.3	946
KK06/110	4.2	6.7	25.9	234	18.2	3.8	36.7	1804.4
KK06/29B	3.8	4	27.7	202	16.4	5.7	36.8	1682
KK071	3.6	3.5	24.7	70	11.7	4.9	40.1	1090
KK072	3.2	4.3	23.6	112	18.4	5	38.5	1802
KK15	3.3	3.5	25.5	96	12.4	5.2	30.8	1645
KK8	2.6	2.1	25.4	161	13.5	4	35.3	1795
KKBC05/32	3.2	7.2	27.2	133	10.3	4.7	40.4	1391.5
Red13	5.2	5.2	26	110	15.4	4.6	35	1547
Red16	3.7	3.2	14.6	312	12	4.5	35.7	1741
Red34	4.2	2.9	23	219	16.8	4	34.6	950
Red45	4.1	3.2	20.8	191	18.2	4.9	32.7	1769
RWR2245	2.4	4.1	28.6	240	11.1	3.7	43.3	1348
GM	3.7	4.1	25.3	199.8	14	4.5	34.8	1513.2
LSD (5%)	3.12	2.3	12.4	280.8	4.59	0.78	4.5	633.8
CV (%)	51.3	33.8	29.9	65.5	19.9	10.7	7.8	25.5

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

Table3.19: Mean Pod per plant, seed per pod, hundred seed weight and yield for bean genotypes at Lugari combined over seasons

Genotypes	Lugari			
	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal137	8.5	3.6	29.6	768.5
Cal139A	6.3	3.6	34.9	1015.5
Cal194	7.2	5.2	28	1042
Cal33	11.2	5.1	35.1	841.5
Cal51A	7.2	5.2	26.3	723.5
Cal5B	8.7	5.1	34.7	950.5
Cal6	9.7	5.8	25.3	824
Cal97A	10.4	4.3	26.8	1062.5
Ciankui	7.9	3.3	34	744.5
GLP2	7.6	4.2	33	774.5
GLP585	8.4	4.9	22.5	747
GLPX92	10.9	4	25.7	739.5
KK06/110	11.2	6.4	31.3	1019
KK06/29B	10.1	4.4	32.2	942
KK071	7.6	3	32.4	580
KK072	10.8	3.9	31.1	957
KK15	7.9	3.7	28.2	870.5
KK8	8.1	3.6	30.4	978
KKBC05/32	6.7	5.7	33.8	762
Red13	10.3	5.8	30.5	828.5
Red16	7.9	4.7	25.2	1026.5
Red34	10.5	4.9	28.8	584.5
Red45	11.2	4.6	26.7	980
RWR2245	6.8	4.8	36	794
GM	8.9	4.6	30.1	856.5
LSD (5%)	4.02	1.74	9.14	495.6
CV (%)	28	25.1	18.7	35.7

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.3 Evaluation of common bean for the different traits in combined sites and seasons

3.4.3.1 Evaluation of agronomic traits in combined sites and seasons

3.4.3.1.1 Analysis of variance for the agronomic traits in combined sites and seasons

At combined sites and seasons, the genotypes showed significant differences for all the agronomic traits at $p<0.05$ (Table 3.20).

Table 3.20: Analysis of variance for the mean squares for agronomic traits at combined sites and seasons

Source of variation	df	%Em.	DTF	DTM
Replication	2	610.1	49.4	1.6
Genotype	23	989.3*	21.1*	84.3*
Environment	1	19761.8*	6854.3*	183.7*
Season	1	20599.0*	3577.2*	450.0*
G x E	23	140.8^{ns}	6.5^{ns}	1.3*
G x S	23	1082.9*	6.1^{ns}	0.2^{ns}
E x S	1	11945.5*	1886*	162.0*
G x E x S	23	203.7*	5.1^{ns}	0.2^{ns}
Error	190	103.9	3.1	0.49
Total	287			

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype and season, G x E = Interaction of genotype and environment, E x S = Interaction of environment and season, G x E x S = Interaction of genotype, season and environment, %Em. =percentage of emergence, DTF=Days to 50% flowering, DTM= Days to 75% maturity.

3.4.3.1.2 Mean performance of the bean genotypes based on the agronomic traits

The genotypes KK8 had the highest percentage of emergence and the genotype KK071 had the lowest. The genotype GLP2 flowered early while Cal194 flowered late and the genotype KK15 matured early while the latest was KK8 (Table 3.21).

Table 3.21: Mean performance of the genotypes with regard to the agronomic traits at Kakamega and Lugari during 2016 short rains and 2017 long rains

Genotypes	Combined sites and seasons		
	%Em.	DTF	DTM
Cal137	61.1	42.2	81.1
Cal139A	70.3	44.3	86
Cal194	74.2	46.1	83.2
Cal33	71.2	44.1	83.1
Cal51A	63.5	42.3	81.5
Cal5B	50.7	44.3	86
Cal6	71.8	43.3	83.9
Cal97A	65.9	45	86.1
Ciankui	46.5	44.3	86.6
GLP2	70.4	41.5	85.5
GLP585	64.2	45.3	83.1
GLPX92	47.3	42.9	85.9
KK06/110	73	43.1	87.1
KK06/29B	70.6	45.2	82.7
KK071	46.4	44.5	87
KK072	71.2	42.7	85.5
KK15	69.1	44.1	76.5
KK8	76.4	44.7	87.2
KKBC05/32	66.7	42.3	80.6
Red13	74	45.1	83.2
Red16	70	45.1	84.8
Red34	64.7	46	87.1
Red45	68.9	45	86.3
RWR2245	72.6	42	86
Grand mean	65.9	44	84.4
LSD (5%)	16.41	3.21	1.1
CV (%)	15.5	4.4	0.79

Genotypes	Combined sites and seasons		
	%Em.	DTF	DTM

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; % Em. =percentage of emergence; DTF=Days to 50% flowering; DTM= Days to 75% maturity.

3.4.3.2 Incidence and severity of foliar diseases at combined sites and seasons

3.4.3.2.1 Analysis of variance for incidence and severity of foliar diseases

At combined sites and seasons, the analysis revealed significant differences among the genotypes for all the traits except final severity for anthracnose, percentage incidence for angular leaf spot, and the AUDPC for anthracnose. Environment showed significant differences for all the traits except the final severity for anthracnose and AUDPC for common bacterial blight at $p<0.05$. For the genotype by environment interaction, only the percentage incidence for common bacterial blight showed significant differences (Table 3.22).

Table 3.22: Analysis of variance of the mean squares for foliar diseases traits across sites

Source of variation	df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Replication	2	8.4	0.3	3.9	4827	705.9	112.4	14534.8	596.3	5374.6
Genotype	233	2.8*	2.1^{ns}	8.6*	255.2^{ns}	616.5*	782.6*	1968.5*	1564.2^{ns}	4740.3*
Environment	1	100.3*	5.0^{ns}	14.7*	1118.5*	2518.9*	1623.2*	9316.1*	5403.3^{ns}	750.8*
Season	1	58.7*	58.7*	5.0^{ns}	4493.9*	490.5^{ns}	9045.4*	5308.7*	3894*	2673.3^{ns}
G x E	23	1.13^{ns}	1.2^{ns}	2.3^{ns}	21.8^{ns}	102.1^{ns}	401.7*	182.3^{ns}	518.8^{ns}	754.6^{ns}
G x S	23	0.44^{ns}	0.8^{ns}	2.2^{ns}	537.7*	627.7*	256.1^{ns}	620.9^{ns}	1140.6^{ns}	1487^{ns}
E x S	1	10.1^{ns}	11.7*	19.0*	280.9^{ns}	361.4^{ns}	277.8^{ns}	2392^{ns}	1937.5*	7615.8*
G x E x S	23	0.6^{ns}	0.61^{ns}	1.4^{ns}	51.1^{ns}	70.1^{ns}	145.6^{ns}	87.7^{ns}	620^{ns}	540.8^{ns}
Error	190	0.97	0.91	1.14	168.8	201.9	134.8	490.3	770.7	809.9
Total	287									

Source of variation	df	Final severity			% Incidence			AUDPC		
		ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, G x E = Interaction of genotype and environment, E x S = Interaction of environment and season, G x E x S = Interaction of genotype, season and environment, ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were evaluated based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores.

3.4.3.2.2 Mean performance of the bean genotypes based on foliar diseases traits

For the evaluation across sites and seasons of angular leaf spot, all the genotypes were moderately resistant with the scores ranging from 3.7 to 5.3. The incidence of anthracnose had a range of 10.4 to 43.1%. The genotypes Red34, KKBC05/32, KK071, GLP2, Ciankui, RWR2245 and Cal6 across sites were resistant to common bacterial blight. The area under the disease progress curve of common bacterial had a range of 64.5(KKBC05/32) to 145.3(KK15) while the incidence of common bacterial blight had a range of 5.6 to 40.1% (Table 3.23).

Table 3.23: Incidence and severity of diseases for common bean across KALRO-Kakamega and Lugari sites during 2016 short rains and 2017 long rains

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal137	3.9	2.7	3.4	37.1	17	23.4	106.8	85.6	96.1	MR	R	MR
Cal139A	4.3	3.3	3.8	43.2	28.3	17.7	118.4	97.3	115.5	MR	MR	MR
Cal194	4.7	3.1	3.7	43.3	15.3	28.9	128.5	89	95.7	MR	MR	MR
Cal33	4.7	2.9	4.4	39	16.8	30	122.7	89.5	120.9	MR	R	MR
Cal51A	4.8	3.1	4.6	46.9	18.8	18	125.3	97.9	107.3	MR	MR	MR
Cal5B	4.3	2.6	3.5	41.6	21.5	15.6	111.7	79.3	92.8	MR	R	MR
Cal6	4.1	2.8	2.9	41.3	10.7	10.3	115.7	75.2	86.4	MR	R	R

Genotypes	Final severity			%Incidence			AUDPC			Disease response		
	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB	ALS	ANT	CBB
Cal97A	5.2	3.3	3.6	40.8	20.8	11.9	129.2	89.1	98.5	MR	MR	MR
Ciankui	3.7	3.8	2.7	45.1	43.1	13	100.2	112.6	78.4	MR	MR	R
GLP2	4	3.4	2.9	34.9	23.7	8.4	109.1	96.2	78	MR	MR	R
GLP585	4.5	3.1	4.3	39.3	24.6	18.4	125.9	99	123.9	MR	MR	MR
GLPX92	5.3	2.8	3.6	47.7	22.6	20	125.7	83	93.4	MR	R	MR
KK06/110	4.1	3.3	4.2	39.8	22.1	16.8	118.5	100.3	120.9	MR	MR	MR
KK06/29B	4.4	3.1	3.5	52.5	27.9	13	114.9	96.8	103.5	MR	MR	MR
KK071	4.9	3.3	3	52.7	22.8	24.7	126.9	83.1	91.4	MR	MR	R
KK072	4.9	3.3	4.1	41.5	14.5	20.2	130.9	98.8	119.5	MR	MR	MR
KK15	5.1	2.6	5.9	38.2	10.6	40.1	122.9	75.8	145.3	MR	R	MR
KK8	5.2	3.2	5.3	43.7	17.2	32.9	137.9	92.9	128.4	MR	MR	MR
KKBC05/ 32	4.8	3.5	2.3	37.8	21	5.6	124.8	95.3	64.5	MR	MR	R
Red13	5.3	4.2	3.7	39.3	21.2	29.3	136.3	112.3	105.1	MR	MR	MR
Red16	4.7	3.9	5.3	43.3	27.2	33.2	124.9	116.4	133.9	MR	MR	MR
Red34	5.2	2.3	2.6	38.9	10.4	10.6	135.4	75.4	82.4	MR	R	R
Red45	3.9	2.9	3.4	41.2	24.5	19.8	113.6	87.8	103.4	MR	MR	MR
RWR2245	4.3	3.5	3	46.9	31.9	8.4	125.9	100.9	85.2	MR	R	R
GM	4.6	3.2	3.7	42.3	21.4	19.6	122.2	92.9	102.9			
LSD (5%)	1.6	1.6	1.71	20.9	22.9	18.7	35.66	44.71	45.83			
CV (%)	22.1	31.8	29.6	31.6	68.2	64.2	18.1	29.9	27.7			

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; ALS= angular leaf spot, ANT=Anthracnose, CBB=Common bacterial blight, ALS, ANT and CBB, FS=Final score of severity. The severity were evaluated based CIAT scale (1-9) where 1= asymptomatic plants and 9=complete plant death; % ALS, ANT and CBB incidence (%Inc.)= percentage of the number of plants with ALS, ANT and CBB infection, AUDPC=Area under the disease progress curve calculated from the weekly ALS, ANT and CBB severity scores, R= resistant, MR= moderately resistant.

3.4.3.3 Yield and yield components at combined sites and seasons

3.4.3.3.1 Analysis of variance for common bean yield and yield

Across the two sites and seasons, significant differences were observed among genotype, environment and environment and season interaction for most of the traits. For the genotype by environment interaction and the genotype by season interaction, no significant differences were observed for all the traits (Table 3.24).

Table 3.24: Analysis of variance of the mean squares for yield and yield components traits across sites

Source of variation	df	NPP	NSP	HSW(g)	Yield(Kg/ha)
Replication	2	11.2	3.0	20.9	648584
Genotype	23	28.4*	3.0^{ns}	220.8*	631898*
Environment	1	714.0*	4.8^{ns}	768.1*	24973574*
Season	1	3179.9*	7.4^{ns}	3886.0*	51552869*
G x E	23	21.9^{ns}	2.9^{ns}	20.4^{ns}	284743^{ns}
G x S	23	17.1^{ns}	2.5^{ns}	35.2^{ns}	256235^{ns}
E x S	1	978.1*	27.1*	334.9*	15700893*
G x E x S	23	9.0^{ns}	2.4^{ns}	18.6^{ns}	181759^{ns}
Error	190	9.6	1.4	17.8	137460
Total	287				

*= Significant difference at 5%, ^{ns}= no significant difference, df= degree of freedom, G x S = Interaction of Genotype by season, G x E = Interaction of genotype and environment, E x S = Interaction of environment and season, G x E x S = Interaction of genotype, season and environment, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.3.3.2 Mean performance for common bean yield and yield component at combined sites and seasons

At combined the sites and seasons, the genotype Red13 had the highest number of pod per plant while KK071 had the lowest number of pod per plant. The highest mean value for hundred seed weight was recorded from the genotype RWR2245 while the

lowest mean value on the genotype GLP585.The genotype Cal139A had the highest yield while KK071 had the lowest (Table 3.25).

Table 3.25: Pod per plant, seed per pod, hundred seed weight and yield for common bean genotypes combined of KALRO-Kakamega and Lugari during 2016 short rains and 2017 long rains

Genotypes	Combined sites and seasons			
	NPP	NSP	HSW (g)	Yield (Kg/ha)
Cal137	9.2	4	33.1	1097.9
Cal139A	10.7	3.8	37.3	1560.6
Cal194	10.6	4.7	31.5	1447
Cal33	12	4.7	36.5	1450.2
Cal51A	8.7	4.6	27	850.7
Cal5B	12.2	4.3	34.7	1069.9
Cal6	11.1	4.7	26.7	1178.3
Cal97A	12.4	4.1	28.7	1308.5
Gankui	8.7	3.5	35.4	825.8
GLP2	8.3	4.3	37.2	1307.9
GLP585	11.8	5.3	20.2	969.3
GLPX92	12.1	4.2	26.4	904.5
KK06/110	11.7	5	34	1399.1
KK06/29B	11	4.6	35.1	1393.5
KK071	7.6	3.9	34	549.4
KK072	9.8	4.3	35.4	1103.1
KK15	8.7	4.5	28.2	1234.4
KK8	10.9	3.8	32.7	1304.1
KKBC05/32	9.5	5	36.3	1270.2
Red13	13.6	5	31.3	1499
Red16	12.8	4.7	29.7	1527.8
Red34	10.2	4.4	30.5	1071.4
Red45	13.2	4.7	29.1	1373.3
RWR2245	11.4	4.2	38.6	1340.6
GM	10.8	4.4	32.1	1209.9
LSD	4.98	1.9	6.79	597.1
CV (%)	29.6	26.5	13.3	32.2

LSD: Least significant difference; CV (%): Percentage of coefficient of variation; GM=Grand mean; NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = hundred seed weight (gram), Yield (kg/ha) =Yield (kilogram per hectare).

3.4.4 Pearson correlation coefficients among the different traits

At KALRO-Kakamega, days to flowering showed significant and negative correlation with HSW. The AUDPC for ALS showed significant and positive correlation with the final severity for the ALS. The final severity for the three diseases showed significant and positive correlation with the AUDPC for the same diseases (Table 3.26).

At Lugari, the percentage emergence had a significant and negative correlation with days to flowering and NPP. The days to flowering had a negative and significant correlation with NPP, HSW, and yield and percentage incidence for angular leaf spot. NPP showed significant and positive correlation with HSW, yield, and negative correlation with final severity and percentage incidence for ALS. The final severity for the three foliar diseases showed a positive and significant correlation with the three diseases (Table 3.27). Across the sites, the final severity for the three diseases had a significant and positive correlation with the AUDPC for the same diseases. The DTF had a negative correlation with NPP, HSW, yield and percent ALS (Table 3.28).

Table3.12: Correlations among the agronomic, disease and yield traits at KALRO-Kakamega

	%Em.	DTF	DTM	NPP	NSP	HSW	Yield	Final severity			AUDPC			%Incidence		
								ALS	ANT	CBB	ALS	ANT	CBB	/ALS	/ANT	/CBB
%Em.	-															
DTF	-0.09	-														
DTM	-0.14	0.12	-													
NPP	-0.04	0.02	0.06	-												
NSP	0.06	0.33*	-0.04	0.27*	-											
HSW	0.22*	-0.50*	0.18*	-0.01	-0.28*	-										
Yield	0.51*	-0.13	-0.08	0.20*	0.09	0.38*	-									
FS/ALS	0.08	-0.11	-0.05	0.02	-0.1	0.02	0.03	-								
FS/ANT	-0.01	0.23*	0.11	-0.13	0.13	-0.17*	-0.16	-0.15	-							
FS/CBB	0.24*	-0.03	-0.24*	0.16	-0.03	-0.07	0.24*	0.16	-0.16	-						
AUDPC/ALS	0.08	0.02	0.05	0.08	-0.06	-0.01	2	0.70*	0.03	0.09	-					
AUDPC/ANT	0.04	0.027*	0.09	-0.1	0.16	-0.22*	-0.1	-0.14	0.89*	-0.08	0.07	-				
AUDPC/CBB	0.25*	0.07	-0.21*	0.13	0.05	-0.1	0.24*	0.17*	-0.07	0.80*	0.17*	0.02	-			
%Inc.ALS	-0.09	-0.17*	0.15	0.08	-0.13	0.26*	-0.11	0.27*	-0.12	0	0.93*	0.23*	0.30*	-		
%Inc.ANT	-0.18*	-0.1	0.14	0.06	-0.17*	0.06	-0.16	-0.03	0.40*	-0.1	0.2*	0.93*	0.07	0.27*	-	
%Inc.CBB	0.02	-0.09	-0.09	0.26*	-0.1	0.16	0.16	0.25*	-0.22*	0.54*	0.27*	-0.06	0.87*	0.25*	0.05	-

*=Significant at 5%, ALS,ANT and CBB Severity were assessed based CIAT scale(1-9)where 1= asymptomatic plants and 9=complete plant death, AUDPC=Area under the disease progress curve calculated from the weekly ALS,ANT and CBB severity scores; ALS, ANT and CBB % Incidence= percentage of the number of plant with ALS, ANT and CBB infection, % Em. =percentage of emergency, DTF=Days to 50% flowering, DTM= Days to 75% maturity, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = Hundred seed weight (gram), Yield (kg/ha) = Yield (kilogram per hectare), ALS: Angular leaf spot, ANT: Anthracnose, CBB: Common bacterial blight, FS=Final score severity of ALS, ANT and CBB.

Table 3.13: Correlation analysis among the agronomic, disease and yield traits at Lugari

	%Em.	DTF	DTM	NPP	NSP	HSW	Yield	Final severity			AUDPC			%Incidence		
								ALS	ANT	CBB	ALS	ANT	CBB	/ALS	/ANT	/CBB
%Em.	-															
DTF	-0.67*	-														
DTM	-0.4*	0.44*	-													
NPP	0.57*	-0.76*	-0.38*	-												
NSP	0.28*	-0.22*	-0.29*	0.19*	-											
HSW	0.39*	-0.57*	-0.23*	0.50*	0.15	-										
Yield	0.63*	-0.79*	-0.41	0.80*	0.16*	0.54*	-									
FS/ALS	0.45*	-0.45*	-0.30*	0.49*	0.1	0.27*	0.50*	-								
FS/ANT	-0.08	0.25*	0.1	-0.26*	-0.09	-0.12	-0.24*	-0.15	-							
FS/CBB	0.04	0.06	-0.05	-0.1	-0.09	-0.24*	-0.04	-0.02	-0.02	-						
AUDPC/ALS	0.42*	-0.34*	-0.20*	0.37*	0.11	0.15	0.43*	0.81*	-0.15	0.08	-					
AUDPC/ANT	-0.17*	0.38*	0.19*	-0.35*	-0.08	-0.20*	-0.33*	0.24*	0.88*	0.02	-0.22*	-				
AUDPC/CBB	-0.03	0.18*	0.08	-0.17*	-0.11	0.27*	-0.11	-0.07	-0.02	0.92*	0.07	0.04	-			
%Inc.ALS	0.42*	-0.51	0.37*	0.49*	-0.01	0.30*	0.56*	0.62*	-0.23*	0.04	0.93*	0	0.32*	-		
%Inc.ANT	0.16	-0.19*	-0.07	0.23*	-0.02	0.27*	0.26*	0.03	0.42*	-0.14	0.05	0.94*	-0.06	0.07	-	
%Inc.CBB	0.26*	-0.39*	-0.37*	0.32*	0.04	0.18*	0.45*	0.24*	-0.19*	0.47*	0.34	-0.11	0.97*	0.32*	-0.04	-

*=Significant at 5%, ALS,ANT and CBB Severity were assessed based CIAT scale(1-9)where 1= asymptomatic plants and 9=complete plant death, AUDPC=Area under the disease progress curve calculated from the weekly ALS,ANT and CBB severity scores; ALS, ANT and CBB % Incidence= percentage of the number of plant with ALS, ANT and CBB infection, % Em. =percentage of emergency, DTF=Days to 50% flowering, DTM= Days to 75% maturity, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = Hundred seed weight (gram), Yield (kg/ha) = Yield (kilogram per hectare), ALS: Angular leaf spot, ANT: Anthracnose, CBB: Common bacterial blight, FS=Final score severity of ALS, ANT and CBB.

Table 3.14: Correlations analysis among the agronomic, disease and yield traits across KALRO-Kakamega and Lugari sites during 2016 short rains and 2017 long rains

	%Em.	DTF	DTM	NPP	NSP	HSW	Yield	Final severity			AUDPC			%Incidence		
								ALS	**ANT**	**CBB**	**ALS**	**ANT**	**CBB**	**ALS**	**ANT**	**CBB**
DTF	-0.62*	-														
DTM	-0.40*	0.56*	-													
NPP	0.43*	-0.61*	-0.30*	-												
NSP	0.21*	-0.14*	-0.20*	0.24*	-											
HSW(g)	0.38*	-0.52*	-0.15*	0.37*	-0.01	-										
Yield(Kg/ha)	0.65*	-0.61*	-0.39*	0.63*	0.16*	0.52*	-									
FS/ALS	0.42*	-0.53*	-0.34*	0.38*	0.06	0.24*	0.43*	-								
FS/ANT	0.06	0.06	0.04	-0.14*	0.06	-0.18	-0.12*	-0.08	-							
FS/CBB	0.28*	-0.29*	-0.29*	0.15*	0	-0.03	0.26*	0.26*	-0.04	-						
AUDPC/ALS	0.39*	-0.46*	-0.25*	0.33*	0.07	0.17*	0.38*	0.80*	0.02	0.28*	-					
AUDPC/ANT	-0.11	0.29*	0.20*	-0.26	0.04	-0.22*	-0.24*	-0.21*	0.86*	-0.09	-0.1	-				
AUDPC/CBB	0.20*	-0.1	-0.16*	0.05	0	-0.11	0.16	0.17*	-0.19	0.86*	0.23*	-0.07	-			
%Inc.ALS	0.34*	-0.60*	-0.29*	0.37*	0.07	0.34*	0.38*	0.57*	-0.05	0.28*	0.95*	0.07	0.41*	-		
%Inc.ANT	-0.02	-0.05	0.09	0.12*	-0.1	0.15*	0.04	-0.04	0.40*	-0.14*	0.09	0.94*	-0.02	0.1	-	
%Inc.CBB	0.26*	-0.41*	-0.33*	0.35*	0.06	0.23*	0.40*	0.35*	-0.16*	0.57*	0.41*	-0.1	0.93*	0.40*	-0	-

*=Significant at 5%, ALS,ANT and CBB Severity were assessed based CIAT scale(1-9)where 1= asymptomatic plants and 9=complete plant death, AUDPC=Area under the disease progress curve calculated from the weekly ALS,ANT and CBB severity scores; ALS, ANT and CBB % Incidence= percentage of the number of plant with ALS, ANT and CBB infection, % Em. =percentage of emergency, DTF=Days to 50% flowering, DTM= Days to 75% maturity, NPP=Number of pods per plant, NSP=Number of seeds per pod, HSW (g) = Hundred seed weight (gram), Yield (kg/ha) = Yield (kilogram per hectare), ALS: Angular leaf spot, ANT: Anthracnose, CBB: Common bacterial blight, FS=Final score severity of ALS, ANT and CBB.

3.5 Discussion

3.5.1 Percentage emergence, days to flowering and maturity

The weather conditions across the different sites affected the capacity of the genotypes to absorb water to maximize the rate of emergence. The weather conditions were favourable for flowering and maturity (Appendix1). For rapid and uniform emergence, bean seeds require warm soils with an optimum temperature of 26.6 °C, at flowering and 15.6°C to 29°C for maturity (Pattung *et al*., 2016). Geovani *et al.* (2016) reported that the percentage of emergence of castor bean seedlings was highly affected by environmental conditions like water salinity. De Ron *et al.,* (2016) worked on phenotypic response and seedling emergence of bean genotypes under diverse temperatures under open field and under controlled conditions and they observed that germination and seedling emergence increased with temperature in many crops such as legumes soybean, cowpea, peanut and chickpea. The variability with regard to percentage of emergence could be attributed to the capacity of genotypes to absorb water, presence of dry soil, unfavorable climate and unavailability of adequate soil moisture. The temperature, moisture, gases and light are the four major environmental factors which affect germination and emergence of common bean (Masangwa *et al*., 2017; Azimi *et al.,* 2014). According to Mohammed *et al*., (2013), temperatures varying between 13°C to 26 °C, with an optimal temperature of 17 °C and the relative humidity greater than 92% could favour conidial production and plant infection.

The differences in days to 50% flowering can be attributed to genetic variability among the genotypes. Ghanbari *et al*., (2013) reported that the variation in flowering may be

induced by either diseases or drought and negatively impact on grain yield. Research findings by Abubaker (2008) found no significant variations among plant population for the days to flowering of bush common beans. The duration of physiological maturity is usually affected by the temperature. The days to maturity among the dry beans in previous studies was within the range of 45 to 150 days and was dependent on the growth habit type and location (Fahad *et al*., 2014; Tadesse *et al*., 2014).

3.5.2 Incidence and severity of foliar diseases

The bean genotypes showed different responses to the foliar diseases implying there was a favourable environment for disease establishment and spread. Kimno *et al*., (2016) reported that common bacterial blight and angular leaf spot are more prevalent in high temperate and humid weather environments in East and Central Africa. Temperature, relative humidity and precipitation affect the occurrence of pests and diseases within a region (Belete and Bastas, 2017). This study observed that the genotypes reacted uniformly to the anthracnose disease. Similar results with regard to response to the angular leaf spot for Andean and Mesoamerican isolates have been reported (Mukamuhirwa *et al*., 2017; Leitich *et al*., 2016). The angular leaf spot development requires a relative humidity of 70-100% and a temperature range between 18 to 22°C for successful infection and sporulation (Olango *et al*., 2017). Environmental variations had an effect on the pathogen as lower infections were recorded across the different sites. According to Beebe *et al*., (2014), occasionally lower temperatures accompanied by limited free water on the surfaces of the bean plant might have contributed to lowering the pathogens' ability to infect and colonize its hosts. Yang and Hartman, (2015) who

conducted anthracnose resistance studies on soybean varieties reported non-significant variations among commercial bean lines for the traits he studied.

According to Barcelos *et al*., (2014), the anthracnose disease can result to total yield loss. Under favourable environments, the common bean yield losses arise from poor seed germination, poor seedling vigor, seed abortion, pod abortion and loss of photosynthetic area (Liu *et al*., 2013). According to Belete and Bastas, (2017), the greatest difficulty in common bacterial blight resistance breeding is the instability of resistance, frequently after a dozen generations of selfing due to the segregation of the resistant lines. Plant resistance genes have been shown to be affected by temperature, soil nutrient composition, humidity and light which are either high or low (Jorgensen, 2012). Akhavan *et al*., (2013) noted that the proper evaluation for resistance to common bacterial blight should be under hot and humid weather conditions. Olango *et al*., (2017) who worked on reaction of bean genotypes to *Pseudocercospora griseola* and the development of angular leaf spot among varieties showed no significant variation for the area under disease progressive curve. The disease evolution rate aids to verify whether disease progress in one treatment is faster than the other (Davidson, 2010). Mateen *et al*., (2015) reported that the wheat cultivars which show low area under disease progressive curve and terminal severity values have the best intensity of plant resistance. Mateen *et al*., (2015) also reported that the area under disease progressive curve is an excellent indicator of plant resistance under field environments. In addition, Shahin and El-Orabey (2015) reported that the area under disease progressive curve is the outcome of all aspects that

could be influenced by the development of the pathogen such as differences in genotypes, development of the disease and in environmental conditions.

3.5.3 Yield and yield components

High genetic variability was observed for yield and its components among the lines and this could be attributed to the relationship of genotypes and the capacity to absorb the nutrients (Darkwa *et al*., 2016). This was also dependent on the level of moisture during pod setting and grain filling (Asfaw *et al.,* 2012). Nduwarugira (2016) reported significant differences among bean cultivars for number of pods per plant. Ahmed and Kamaluddin, (2013) who worked on correlation and path analysis for agro-morphological traits reported significant variability for number of pods per plant. The number of pods per plant is a yield component with the largest influence on the common beans' yield as it includes other yield components like the number of seeds per pod and hundred seed weight (HSW) (Tadesse *et al*., 2014). All these traits are affected by the level of moisture during the pod setting and grain filling and also the soil characteristics (Acosta-gallegos *et al.,* 2007). Non significant variations for number of seed per pod were reported by Yoseph *et al*. (2014) and Idris (2008) who evaluated common bean varieties for yield and yield components. In this study, the bean genotypes showed variations in the hundred seed weight. Similar findings have been reported in previous studies (Zelalem, 2014; Safapour *et al*. 2011; Yoseph *et al*., 2014). The seed weight varies with the type of genotype and also the season and environment (Narayan, 2013). Yield is a quantitative trait and is conferred by various genes, which directly or indirectly influence its expression.

3.5.4 Correlations among the agronomic, disease and yield traits

Lateness in flowering of genotypes reduces the number of seeds per pod, the seed weight and yield. In this study, lateness in flowering decreased the intensity of angular leaf spot disease. Zongo *et al*., (2017) found out that the days to 50% flowering on groundnut showed a significant and negative correlation with yield and all the yield components. Other researchers reported similar findings (Zingore and Giller, 2012; Vishnuvardhan *et al.,* 2012; Mayeux and Ntare, 2001). Lemessa, *et al*. (2011) reported negative effect of foliar diseases namely angular leaf spot and common bacterial blight on bean and sunflower yield. The foliar diseases cause defoliation which limits the production of photosynthates and the photosynthetic leaf area hence low yields (Jesus Junior *et al*., 2003).

3.6 Conclusions

In conclusion, some of the best bean genotypes identified included genotype KK8 with better emergence; GLP2 genotype showed early flowering while KK15 genotype showed the earliest maturity. Genotypes Red34, KK15, Cal5B, Cal137, GLPX92, Cal6, Red45 and Cal33 were resistant to anthracnose while Red34, KKBC05/32, KK071, GLP2, Ciankui, RWR2245 and Cal6 were resistant to common bacterial blight. Genotypes Cal139A, Red16 and Red13 recorded the highest grain yield compared to the other materials. The Genotype Red13 had the highest pod number while RWR2245 genotype had the highest weight and Cal139 genotype had highest yield.

In general, incidence and severity increased with increasing infection levels among the genotypes. Usually, the genetic composition for each variety and their reaction to environmental factors like temperature, moisture, rainfall and soil nutrient are fundamental factors for the development of health crops.

CHAPTER FOUR

GENETICS OF RESISTANCE TO COMMON BACTERIAL BLIGHT DISEASE IN COMMON BEAN

4.1 Abstract

Common bacterial blight (*Xanthomonas axonopodis* pv *phaseoli)* is a seed-borne disease of common bean and causes severe yield losses of between 40 to 70%. The objective of this study was to determine the genetics of resistance to the common bacterial blight disease in common beans. In screen house, F_1, F_2 and backcrosses were generated from two parents namely VAX3 and MCM2001, resistant and susceptible to common bacterial blight respectively. Both parents and their progenies were inoculated and evaluated for severity and incidence of common bacterial blight. Chi-square test was used to compare the Mendelian segregation ratios and heterosis was calculated. Parental line VAX3 showed resistance to common bacterial blight, while the parental line MCM2001 was susceptible. All the F_1s from the crosses between VAX3 and MCM2001 were resistant. The F_2 populations revealed segregation in a 3:1 genetic ratio for resistance and susceptibility. These results showed that the resistance to common bacterial blight is controlled by a single dominant gene. All the plants generated from the backcross with resistant parent VAX3 were resistant to common bacterial blight with 1:0 genetic ratios for resistance and susceptibility while the plants generated from backcross with susceptible parent MCM2001 showed 50% of resistance and 50% susceptibility with an expected ratio of 1:1. The percentage values from mid-parent heterosis had negative values which increased the resistance by about 75 to 80% compared to the resistant parent. The values from better parent heterosis remained constant compared to the

resistant parent VAX3. Resistance to common bacterial blight is controlled by a single dominant gene. The progenies F_1 increased the resistance to common bacterial blight compared to the resistant parent VAX3. The resistant parents VAX3 could be utilized to improve common bean varieties that are susceptible to the common bacterial blight disease.

4.2 Introduction

Common bacterial blight (*Xanthomonas axonopodis* pv. *phaseoli)* is one of the major seed-borne diseases of common bean and is common in low to mid-altitude and warm environment (Belete and Bastas, 2017; Ribeiro *et al*., 2017). Yield losses estimated between 40 to 70% have been reported (Popovic *et al*., 2012). The magnitude of yield loss depends on the environmental conditions that favour the onset and progress of the disease, the intensity of the disease, and the level of susceptibility of the genotypes (Ribeiro *et al*., 2017).

Resistance of common bacterial blight in common bean is a quantitatively inherited character that shows low to moderate heritability and is controlled by an indefinite number of genes (Miklas *et al.*, 2017). Agoyi *et al.* (2016) determined that the number of genes correlated with resistance to common bacterial blight assorted depending on the parents used during the development of population and on the period at which the plants were assessed (Singh and Schwartz, 2010). Molecular marker studies have identified about 22 quantitative trait loci for resistance to common bacterial blight spread across all the 11 chromosomes in diverse common bean genotypes (Viteri and Singh, 2014).

Breeding for genetic resistance to common bacterial blight in common bean is delayed by the natural complex genetic nature of the host resistance, variation in host-pathogen relationship, pathogen variability, variation in quantitative trait loci expression, diverse genes controlling resistance in multiple plant tissues and linkage drag (Zhu *et al.*, 2016). Despite the fact that common bean lines with common bacterial blight resistance have been identified, their resistance is limited and does not afford the total defense from disease (CIAT, 2016). An additional obstacle of quantitative infection resistance is that the genetic loci are influenced by the environment (Viteri and Singh, 2014). Expression of quantitative resistance in different genetic contexts or ecological situations may differ and make the breeding efforts difficult (Miklas *et al.*, 2017). According to Singh and Schwartz, (2010), negative epistasis and quantitative trait loci for resistance have shown negative interactions with agronomic parameters. Mutlu *et al*. (2005) obtained negative correlations among resistance quantitative trait loci and agronomic parameters. The differential reaction of organs of the plant to common bacterial disease and a lack of correlation in response to the common bacterial blight and between leaves, pods and seeds further complicate breeding for resistance (Belete and Bastas, 2017).

Resistant genotypes can be developed by choosing for moderately horizontal than vertical resistance (Belarmino, 2015). Inheritance of resistance to common bacterial blight also depends on the genetic material used (Zapata *et al.*, 2011). Therefore, bean breeders require to constantly replace cultivars and frequently introgress new resistance genes into the cultivars under production (Belachew *et al*., 2015). It is also crucial to have durable sources of resistance to common bacterial blight. Thus, the objective of this study was to

determine the genetics of resistance to common bacterial blight disease in common beans.

4.3 Materials and Methods

4.3.1 Description of common bean germplasm

Two parental lines from CIAT used in this study were VAX3 and MCM2001 and their characteristics are shown in Table 4.1. VAX3 was used as the male parent while MCM2001 was used as the female parent.

Table 4.1: Description of genotypes used during the crossing

Parent	Entry	Source	Pedigree	Colour	Size	Reaction to CBB
P_1(♂)	VAX3	CIAT	VAX1 x XAN309	Red	Small	Resistant to common bacterial blight
P_2(♀)	MCM2001	CIAT	IVT831607 x RAB71	Red	Small	Susceptible to common bacterial blight

P_1 (♂) - male, P_2 (♀) - female**,** CIAT: International Center for Tropical Agriculture

4.3.2 Population development for inheritance study

The two parents' namely VAX3 and MCM2001 were used to generate F_1, F_2 and backcrosses. The parents namely P_1 and P_2 (Table 4.1) were planted in the screen house in the polyethylene bags filled with sterilized sandy soil mixed with manure with 3:2:1 as ratio. Two seeds were sown per bag and eight bags were used for each parent'. Planting was replicated three times to ensure synchronization of flowering between the male and female parents. Diammonium phosphate (DAP) fertilizer was applied two weeks after planting at the rate of 3g/bag. Pesticides were applied weekly until maturity. Crosses were done early morning between 6.00 to 10.00 am and late in the evening between 4.00 to 6.00 pm. The female parent was emasculated and then pollinated following the hooking method described by Bliss (1980). A fine-tipped curved forcep was used to open

and emasculate the female buds. The emasculated buds were pollinated by rubbing and hooking the female stigma with a pollen-dusted stigma from the male parent a day before flower opening. The pollinated female flowers were tagged using a small labelled watchmaker tag. Information carried on the labels included name of female and male, date of pollination and person who performed the cross. The pollinated flowers were monitored soon after crossing (three days later) to check for any abortions. To develop the F_2 and backcrosses populations, both parents P_1 and P_2 were used as males. The F_1 generated was used as the female parents. Two seeds were sown per bag with five bags for each parent male and female. A portion of F_1 plants were backcrossed to susceptible parent to generate the backcross susceptible population (BCs) whereas another portion was backcrossed to resistant parent to generate backcross resistant population (BCr).

4.3.3 Experimental design and layout

The experiment for the evaluation of the populations generated was conducted in the screenhouse between September 2016 and August 2017 at KALRO-Kakamega. The experiment was set-up in a completely Randomized Design (CRD) with one replication. Seeds of different generations namely the parents, F_1, F_2 and backcrosses populations were planted under screen house conditions in the polyethylene bags filled with sterilized soil sandy mixed with manure as follows: 60 seeds from each of the parents, 60 F_1 seeds, 300 F_2 seeds and 90 seeds from each of the backcrosses (BCr and BCs). Germinated seedlings were watered two times a day to provide a good environment for bacteria development (Karthik *et al.*, 2016). The plants were artificially inoculated with the common bacterial blight.

4.3.4 Preparation of *Xanthomonas axonopodis* pv. *phaseoli* inoculum and inoculation

Xanthomonas axonopodis pv. *phaseoli* was isolated from diseased tissues of common bean leaves showing clear symptoms of common bacterial blight. The diseased leaves were obtained from KALRO-Kakamega. Yeast Dextrose Calcium Carbonate Agar (YDCA) media (10g dextrose, 5g yeast extract, 10g Calcium carbonate, 400ml of agar, 5ml glycerol, 1000ml distilled water) was used to culture the pathogen. The diseased leaf samples were sterilized in 2% sodium hypochlorite solution for 3 minutes and rinsed in three changes of sterile distilled water. The sterilized tissues were then macerated in small amount (0.5 ml) sterile distilled water (Leta *et al*., 2017).

The extract was streaked on YDCA media and the plates incubated for 48 hours at 27^0C (CIAT, 2016). Colonies showing yellow colour characteristic for *Xanthomonas axonopodis* pv. *phaseoli*, mucoid and zone of hydrolysis formed around them were sub cultured and purified on fresh medium. Inoculum was harvested from 48 hours-old cultures by flooding with distilled water. The bacterial suspension was serially diluted in phosphate buffered saline (PBS) (0.01M; pH 7.2) to a concentration of 5×10^7 cfu / ml (CIAT, 2006; CIAT, 2016). Inoculation was done on 18 days old bean seedlings at second trifoliate leaves using the multiple needle inoculation technique (CIAT, 2016). A leaf on the plant was placed into the Petri dishes containing the bacterial inoculums (Mkandawire *et al*. 2004).

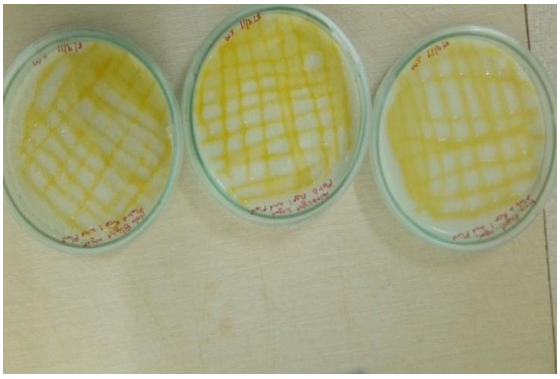

Plate 4.1 Colonies showing yellow colour characteristic for *Xanthomonas axonopodis pv. phaseoli*

Plate 4.2 Multiple needle inoculation technique

4.3.5 Assessment of common bacterial blight severity

Common bacterial blight symptoms were assessed after 4th, 8th and 12th days after inoculation and the level of infection compared between the resistant and susceptible parents as controls (Popovic *et al*., 2010). The evaluation of common bacterial blight was based on disease severity scale of 1 to 9 as shown on Table 3.3. To assess for disease, fifteen plants from each generation were selected randomly and evaluated by scoring three trifoliate leaves starting from the base to determine the intensity of reaction to the disease. The number of plants which showed symptoms per generation was scored for determination of the resistance or susceptibility of the population. Plants which scored

between 1 to 3 were resistant, 3 to 5 were moderately resistant and 7 to 9 were susceptible.

4.3.5 Data analysis

The chi-square method was used to test the goodness of fit of observed segregations to the expected phenotypic ratios obtained from the disease phenotypic reactions of the backcrosses generation and F_2 populations. Mendelian ratios were calculated by counting the number of plants with dominance and with recessive and which were converted in proportions. Probability values were calculated based on the actual number of resistant and susceptible plants in the screen house evaluation (Equation 4.1) (Snedecor and Cochran, 1989).

$$\chi^2 = \sum \frac{(Observed - Expected)^2}{Expected} \quad \text{.....Equation 4.1}$$

The performance of the progeny was estimated by relative heterosis (heterosis over the mid-parental value), heterobeltiosis (heterosis over the better parent) according to the equations (4.2; 4.3 and 4.4) suggested by Fonseca and Patterson (1968).

$$MPH = \frac{F_1 - MP}{MP} * 100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots Equation\ 4.2$$

$$BPH = \frac{F_1 - BP}{BP} * 100 \ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots\ldots Equation\ 4.3$$

Where,

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

MP= Mid parent; BP= Better parent during a cross; MPH= Mid parent heterosis; BPH= Better parent heterosis

4.4 Results

4.4.1 Reaction of common bean populations to inoculation with an isolate of *Xap* at KALRO-Kakamega at KALRO-Kakamega

All VAX3, F_1 and BCr showed severity score of 1 at 4^{th}, 8^{th} and 12^{th} days after inoculation (Table 4.2). All MCM2001, F_2 and BCs recorded the severity score of 3 at 4^{th} day after inoculation, severity score 5 after 8^{th} day after inoculation and severity score 7 at 12^{th} day after inoculation.

Table4.2: Evaluation of common bacterial blight severity after 4^{th}, 8^{th} and 12^{th} days after inoculation at KALRO-Kakamega

Parent/Cross	Generation	4DAI	8DAI	12DAI
VAX3	P_1	1	1	1
MCM2001	P_2	3	5	7
MCM2001 x VAX3	F_1	1	1	1
MCM2001 x VAX3	F_2	3	5	7
(MCM2001 x VAX3) x VAX3	BCr	1	1	1
(MCM2001 x VAX3) x MCM2001	BCs	3	5	7

P1: VAX3, P2: MCM2001, F_1: MCM2001 x VAX3, F_2: MCM2001 x VAX3, BCr (Backcross resistant): (MCM2001 x VAX3) xVAX3, BCs (Backcross susceptible): (MCM2001 x VAX3) x MCM2001, DAI: Day after inoculation.

All VAX3 plants showed resistant reactions to common bacterial blight, while all the MCM2001 plants were susceptible. All the F_1 plants from crosses between VAX3, resistant and MCM2001, susceptible variety showed resistance to common bacterial blight. The F_2 populations from the parents VAX3 and MCM2001 showed a segregation ration of 3:1 genetic ratio for resistance and susceptibility (Table 4.3). All the plants generated from the backcross with the resistant parent VAX3 showed resistance to

common bacterial blight with 1:0 genetic ratios for resistance and susceptibility while the plants generated from backcross with susceptible parent MCM2001 showed 50% resistance and 50% susceptibility with an expected ratio of 1:1 (Table 4. 3).

Table 4.3: Reaction of VAX3 and MCM2001 bean genotypes, their F_1, F_2 and backcrosses to inoculation with an isolate of *Xanthomonas axonopodis* pv *phaseoli* at KALRO-Kakamega

Parent/Cross	Generation	Number of plants		Phenotypic ratio	Chi-square (χ^2)
		Resistant	Susceptible		
VAX3	P_1	55	0	-	-
MCM2001	P_2	0	59	-	-
MCM2001 x VAX3	F_1	53	0	1:0	00^{ns}
MCM2001 x VAX3	F_2	202	76	3:1	0.81^{ns}
(MCM2001 x VAX3) x	BCr	84	0	1:0	00^{ns}
VAX3 (MCM2001 x VAX3) x MCM2001	BCs	48	36	1:1	1.71^{ns}

P_1:VAX3, P_2:MCM2001, F_1: MCM2001 x VAX3, F_2: MCM2001 x VAX3,
BCr (Backcross resistant): (MCM2001 x VAX3) xVAX3,
BCs (Backcross susceptible): (MCM2001 x VAX3) x MCM2001, ^{ns}: no significant difference.

4.4.2 Common bean parents and progenies F_1 and F_2 evaluated at KALRO-Kakamega

The percentage values from mid-parent heterosis had negative values which increased the resistance from about 75 to 80% compared to the resistant parent VAX3. The values from better parent heterosis remained constant compared to the resistant parent VAX3. Heterosis values estimated over mid parent (MP) and better parent (BP) for the diseases traits are presented in Table 4.4.

Table4.4: Severity of parents and F1 progenies; and the percentage of mid and better parent heterosis for common bacterial blight disease

No	VAX3	MCM2001	F_1 Progenies	MP	Heterosis	
	Severity				MPH	BPH
1	1	7	1	4	-75	0
2	1	7	1	4	-75	0
3	1	7	1	4	-75	0
4	1	7	1	4	-75	0
5	1	7	1	4	-75	0
6	1	9	1	5	-80	0
7	1	7	1	4	-75	0
8	1	7	1	4	-75	0
9	1	9	1	5	-80	0
10	1	9	1	5	-80	0
11	1	7	1	4	-75	0
12	1	7	1	4	-75	0
13	1	7	1	4	-75	0
14	1	9	1	5	-80	0
15	1	7	1	4	-75	0

MPH= Mid parent heterosis; BPH= Better parent heterosis; MP= Mid parent

4.5 Discussion and conclusion

All VAX3, F_1 and BCr obtained the severity score 1 at 4^{th}, 8^{th} and 12^{th} days after inoculation. All MCM2001, F_2 and BCs obtained the severity score 3 at 4^{th} day after inoculation, severity score 5 after 8^{th} day after inoculation and severity score 7 at 12^{th} day after inoculation. Alladassi *et al*., (2017) who worked on inheritance of resistance to common bacterial blight among four selected common bean populations and inoculated at 10^{th}, 21^{st} and 35^{th} day reported similar findings. Ribeiro *et al*., (2017) explained that the level of severity among genotypes to common bacterial blight can be explained by the occurrence of additive and non-additive effects, resulting in complex inheritance.

All the MCM2001 plants were susceptible and all the VAX3 plants were resistant. The F_1 were resistant to common bacterial blight suggesting that the resistance trait is dominant.

VAX3 has been reported to have resistance to common bacterial blight (Belete and Bastas, 2017). This line was developed by CIAT in Colombia and shows morphological and seed characteristics similar to that of the Middle American gene pool.

For the F_2 population, only one dominant gene was associated with resistance to common bacterial blight. The backcrosses to susceptible parent showed a segregation ratio of 1:1 and F_2 segregation ratio of 3:1 resistant to susceptible while all the backcrosses to VAX 3 had resistant individuals. The F_2 progenies showed segregation patterns varying from complete resistance to susceptibility. The phenotypic segregation of F_2 progenies for the reaction to *Xanthomonas axonopodis* pv. *phaseoli* segregated in the ratio of 3:1 ($\chi 2$ = 0.81; P>0.05) suggesting the presence of dominant genes controlling resistance to *Xanthomonas axonopodis* pv. *phaseoli* in VAX 3. These results corroborate with those of Muimui *et al*. (2011) who suggested that the resistance to common bacterial blight is governed by dominant genes in VAX 3 with the presence of good and high level of resistance to common bacterial blight. Chataika *et al*. (2011) and Miklas *et al*. (2006) reported that the resistance to common bacterial blight is quantitatively inherited with major gene effect. Jung *et al*. (1996) reported that the resistance to common bacterial blight has quantitative pattern of inheritance, and has differential leaf and pod reaction. The complex inheritance to *Xanthomonas axonopodis* pv. *phaseoli* makes the transfer of quantitatively inherited disease resistance genes into elite cultivars difficult (Popovic *et al*., 2012). Belete and Bastas (2017) stated that the nature of inheritance depends on the genotype used as the susceptible parent among other factors. For example, Silva *et al*. (2008) reported that the inheritance of resistance to common bacterial blight in plant

canopy and trifoliate leaves was governed by one major gene. In addition, it has been established that inheritance and gene action to *Xanthomonas axonopodis* pv. *phaseoli* is influenced by plant architecture which includes growth habit influencing disease severity (Ribeiro *et al*., 2017). Drijfhout and Blok (1987) crossed the resistant parent PI 319443 and the susceptible parent Oaxaca 88 and PI 313488 *P. acutifolius* population and they found that one dominant allele determined resistance in leaves and pods. However, Musana *et al*. (1993), who worked on 10 crosses derived from a parent with resistance and susceptible parent stated that the resistance to common bacterial blight was controlled by two or more genes. Similar findings were observed by Miklas *et al.* (2003) who showed that the inheritance of common bacterial blight resistance in Montana No5 was polygenic with at least a single major gene effect. The resistant parent VAX 3 can be used to improve common bean genotypes susceptible to common bacterial blight.

Mid parent heterosis improved the resistance to common bacterial blight compared to the parental line VAX3. The better parent heterosis remained constant in this study. Singh *et al.* (2009) observed higher percentages of heterosis for net head weight in cabbage. Fend *et al*., (2015) observed that some plant hybrids displayed superior growth over their parents. Hladni *et al.* (2007) also noted that heterosis does not appear in all hybrid arrangements of the F_1 generation and heterotic effects are diverse for different characters. Negative heterosis is advantageous as it shows the superiority of the progenies to either mid-parent or better-parent as a result of combined gene interactions. According to Dapp *et al*. (2015), F_1 progenies performed better than their parents in terms of biomass, yield or resistance to environmental challenges.

In conclusion, in the inheritance of resistance to common bacterial blight, the chi-square test revealed that the F_2 population fit the segregation ratio of 3:1 (resistant: susceptible) suggesting the involvement of a single dominant gene in controlling resistance to the common bacterial blight. The back cross (BC) progenies fit the segregation ratio of 1:1. Mid parent heterosis improved the resistance to common bacterial blight compared to the parental line VAX3.

CHAPTER FIVE

GENERAL DISCUSSION, CONCLUSION AND RECOMMENDATIONS

5.1 General discussion and conclusion

This study revealed differences among the genotypes with regard to the different traits evaluated implying that sufficient genetic variation exists within the bean germplasm evaluated. The obtained variation during flowering and maturity were attributed to the genotypes' diversity in growth habit, seed characteristics, maturity and adaptation. The response of the bean genotypes to the foliar diseases also showed high variation. The disease incidence and severity of common bean diseases is dynamic and can change with localities and environmental conditions especially those correlated with climate change and its variability (Mandizvo *et al*., 2016). Due to the effect of genotype by environment interaction, susceptibility or resistance may vary through years, sites or even seasons (Narayan, 2013). Also, the temperature and moisture conditions influence the rate of disease development (Darkwa, 2016). The yield components namely number of pods per plant have the major influence on the yield of common beans because it integrates the number of seed per pod and hundred seed weight (Amanullah and Muhammad, 2011). The late flowering of genotypes decreased the number of seed per pod, the seed weight and yield as shown by the correlation analyses. Lateness or earliness is a key trait affecting either resistance or susceptibility to the foliar diseases (Zingore and Giller, 2012; Vishnuvardhan *et al.,* 2012; Lemessa, *et al*., 2011).

In the inheritance of resistance to common bacterial blight, the chi-square test revealed that the F_2 population fit the segregation ratio of 3:1 (resistant: susceptible) suggesting the involvement of a single dominant gene in controlling resistance to the common bacterial

blight. Previous studies reported the role of one major gene in controlling resistance to the common bacterial blight **(**Tryphone *et al*., 2012). The back cross (BC) progenies fit the segregation ratio of 1:1. Belete and Bastas, (2017) stated that resistance to common bacterial blight could be conditioned by both minor and major genes. Thus, the nature of inheritance depends on the varieties used among other factors (Miklas *et al.*, 2017).

Mid parent heterosis improved the resistance to common bacterial blight compared to the parental line VAX3. Similar findings have been reported in previous studies (Nadeem *et al.*, 2015; Ibrahim, 2010; El-Bramawy and Osman, 2012). According to Wang *et al.*, (2014), the genetic materials of hybrid off springs are inherited from the two parents. In theory, no new genes are formed, so heterosis is probably caused by differences in gene expression or qualitative or quantitative modification (Wang *et al.*, 2014).

Some of the best bean genotypes identified included Genotype KK8 with better emergence; GLP2 genotype showed early flowering while KK15 genotype showed the earliest maturity. Genotypes Red34, KK15, Cal5B, Cal137, GLPX92, Cal6, Red45 and Cal33 were resistant to anthracnose while Red34, KKBC05/32, KK071, GLP2, Gankui, RWR2245 and Cal6 were resistant to common bacterial blight. Genotypes Cal139A, Red16 and Red13 recorded the highest grain yield. The genotype Red13 had the highest pod number while RWR2245 genotype had the highest weight and Cal139 genotype had highest yield.

5.2 Recommendations

1. This research work should be done across more sites and seasons to validate these results especially on the response of the bean genotypes to the foliar diseases.
2. Since a single dominant gene conditioned resistance to the common bacterial blight, bean improvement through recurrent selection can easily be achieved. However, this should be repeated in more seasons for validation.
3. The resistant parent VAX 3 could be utilized to improve bean genotypes that are susceptible to common bacterial blight.
4. A dissection of the quantitative trait loci would reveal the exact nature of the genes controlling the common bacterial blight resistance while mapping its genomic regions.

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APPENDIX

Appendix I: Precipitation (mm) and temperature (°C) data recorded at Kakamega Meteorological Weather Station for the short rains 2016 and long rains 2017

Year	2016 Short rain				2017 Long rain			
Month	September	October	November	December	March	April	May	June
Total precipitation (mm)	175	144	140	95	33	64	63	44
Average Temperature (°C)	19.9	20.5	20.6	20.5	22	20.5	19.5	19
Maximum temperature (°C)	28.1	28.9	28.8	28.9	29	26	24	23
Minimum temperature (°C)	11.7	12.2	12.4	12.1	15	15	15	15