MULTIPLE DISEASE RESISTANCE AND AGRONOMIC PERFORMANCE OF INTER-RACIAL BEANS DEVELOPED THROUGH MARKER-ASSISTED GAMETE SELECTION

BY

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DECLARATION

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

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This thesis is dedicated to my beloved wife Henriette Bisimwa and to my two children Jeanne d'Arc and Gamaliel for their sacrifice and love.

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LIST OF ABBREVIATIONS AND ACRONYMS

AFBE : African bean environment

ALS : Angular leaf spot

AMMI : Additive Main-effects and Multiplicative Interaction

ANOVA : Analysis of variance

ASV : AMMI stability value

AUDPC : Area under disease progression curve

AYT : Advanced yield trial

BCMNV : Bean common mosaic necrosis virus

BCMV : Bean common mosaic virus

CBB : Common bacterial blight

CGIAR : Consultative Group for International Agriculture Research

CIAT : International Center for Tropical Agriculture

CV : Coefficient of variation

DRC : Democratic Republic of Congo

EABREN : East African Bean Research Network

ECABREN : East and Central Africa Bean Research Network

FAO : Food and Agriculture Organisation of the United Nations

G x E : Genotype by environment interaction

GGE : Genotype main effect plus genotype by environment interaction

GLP : Grain Legume Project

IYT : Intermediate yield trial

KALRO : Kenya Agricultural and Livestock Research Organization

KNBS : Kenya National Bureau of Statistics

LSD : Least significant difference

NARL : National Agricultural Research Laboratories

NARS : National Agricultural Research System

NGO : Non-Governmental Organization

PABRA : Pan-Africa Bean Research Alliance

PDA : Potato dextrose agar

PYT : Preliminary yield trial

RCBD : Randomized complete block design

RESAPAC : Réseau d'Amélioration de Phaseolus en Afrique Centrale

SABREN : Southern Africa Bean Research Network

SSD : Single seed decent

UNDP : United Nations Development Programme (UNDP)

UoN : University of Nairobi

USA : United States of America

ABSTRACT

Common bean (*Phaseolus vulgaris* L.) is the most important legume crop and the main source of dietary protein for urban and rural populations in Eastern and Central Africa. However, its productivity in this region is among the lowest in the world due to the presence of many biotic and abiotic production limiting factors. Diseases and pests are the most economically important biotic stresses. Although several diseases attack common bean, angular leaf spot, anthracnose, common bacterial blight, bean common mosaic virus and the root roots are the most damaging leading to substantial economic losses. Breeding for multiple resistance is the most practical, cost-effective and sustainable approach to cope with production limiting biotic factors since there is no additional investment by farmers. Broadening the genetic base of existing commercial cultivars through inter-racial crosses provides a unique opportunity for effective selection of improved progeny with better agronomic potential. This study was a continuation of a marker-assisted gamete selection programme initiated by the University of Nairobi Legume Breeding Research Programme in 2009 to determine whether this breeding procedure was effective in pyramiding genes for resistance to bean major diseases in Eastern Africa into susceptible, but popular, large- and small-seeded bean varieties. The specific objectives of this study were to: i) Determine the agronomic potential of 16 inter-racial and inter-gene pool populations and select the most promising small- and medium-seeded lines; ii) Determine yield stability and genotype x environment interactions of elite lines, and iii) Validate $F_{1.8}$ elite lines for multiple resistance to root rots, common bacterial blight, angular leaf spot, bean common mosaic virus and anthracnose using natural epiphytotics and artificial inoculations.

For the first objective, 16 populations were advanced from $F_{1.3}$ to $F_{1.5}$ generation at Kabete Field Station of the University of Nairobi between 2013 and 2016. The $F_{1.6}$ generation was subsequently evaluated at Mwea Research Station of the Kenya Agricultural and Livestock Research Organization (KALRO). Data were collected on seed yield and yield related parameters. The field disease score for target diseases was recorded using the CIAT standard system for bean germplasm evaluation. GenStat 15th edition software was used for analysis of variance (ANOVA) using generalized linear additive model. Fisher's Least Significant Difference (LSD) test was used for mean separation. Results on agronomic performance revealed significant differences for seed yield among populations, commercial checks and donor parents

(*P<0.05*). Although the performance of the populations was not consistent over generations and across sites, crosses involving the commercial variety KATB9 were generally high yielding and superior for most agronomic traits. Population KMA13-32 (KATB9 x Mex54 / G2333 // RWR719 / BRB191) with a mean seed yield of 2,844 kg ha^{-1}, out-yielded all the other populations, commercial varieties and donor parents used as checks. The number of pods per plant (r=0.85***) and the seed yield per plant (r=0.97***) were the most positively correlated to seed yield per ha, suggesting that these two traits can be used as indirect selection criteria for grain yield. Inter-racial populations showed low to moderate infection levels in all the generations (1.0 to 5.0) while commercial checks were moderate to highly susceptible to most of the pathogens (3.1 to 9.0). From the $F_{1.6}$ generation, 92 progeny rows from single plant selections belonging to five market classes (19 small reds, 12 pintos, 13 red kidneys, 16 red mottled and 32 mixed colors) were selected for further testing.

For the second objective, 92 $F_{1.7}$ lines representing five major market classes were evaluated in three locations (Mwea, Kabete and Tigoni) representing low, medium and high altitude agro-ecological conditions. Data were collected on seedling emergence rate, plant vigor, days to flowering, flower color, growth habit, days to maturity, number of pods per plant, number of seeds per pod, 100-seed mass, seed yield and the harvest index. Prevalent diseases were assessed using the CIAT standard system for bean germplasm evaluation. In addition to ANOVA, the AMMI (additive main-effects and multiplicative interaction) model was used to separate the additive variance from the G x E interaction and to determine the stability of the genotypes across locations using the PCA scores (IPCA1 and IPCA2) and the AMMI stability values (ASV). G x E effects were significant (*P<0.05*) for all the traits and market classes implying that the tested lines responded differently to variation in agro-ecological conditions, resulting in inconsistent ranking of genotypes across the three sites. The high altitude Tigoni site (2,130 masl) with a mean grain yield of 4,010.2 kg ha^{-1} was the most favorable environment for common bean cultivation, while the low altitude Mwea site (1,150 masl) with a mean yield of 771.6 kg ha^{-1} was the lowest yielding environment. AMMI analyses showed that seed yield varied significantly (*P<0.001*) among genotypes and test sites regardless of the market class. The red kidney market class had the best mean yield (2,299.5 kg ha^{-1}) while the lowest seed yield (1,599.3 kg ha^{-1}) was recorded on mixed color market class. The three major factors (genotype, environment, and G x E) contributed the most to the yield variability (87.8%) regardless of the

market class. Of these, environment factors were largest source of variability (74.2%). The interaction between the genotype and environment was high for the small reds and the mixed colors (17.6% and 26.7%, respectively) suggesting that tested lines were not stable and should, therefore, be selected and recommended to specific environments. From ASV, the higher yielding lines were also the most unstable across sites. Among tested lines, only KMA13-22-21 and KMA13-29-21 combined high yield potential and wider adaptation across the three agro-ecological conditions.

For the third objective on multiple disease resistance validation, pathogens were isolated from diseased bean plants from various parts of central Kenya, multiplied on appropriate media and used to inoculate the elite high yielding lines previously identified using the AMMI model. Data on disease incidence and severity were collected at 14^{th}, 21^{st} and 28^{th} days after inoculation using 1-9 CIAT scale. ANOVA and AUDPC (Area Under Disease Progression Curve) were used for data analysis. Results showed that five of the 26 elite lines possessed multiple resistance to five pathogens; eight genotypes were resistant to four pathogens; nine genotypes were resistant to three pathogens; three possessed resistance to two pathogens and one was resistant to one pathogen. However, there were no significant correlations in the reaction of tested genotypes to the seven diseases (angular leaf spot, bean common mosaic virus, common bacterial blight, anthracnose, *Pythium* root rot, *Fusarium* root rot and *Rhizoctonia* root rot) used in this study, except the significant correlation ($P<0.05$) existing between the reaction of genotypes to bean common mosaic virus and the angular leaf spot (r=0.39*). This suggested that resistance genes for those pathogens were inherited independently.

The presence of transgressive genotypes combining high yield potential (with a mean grain yield advantage of 17.5% over parental cultivars), stability across locations and high resistance to major diseases confirmed the effectiveness of inter-racial crosses and marker-assisted gamete selection for common bean improvement.

Keywords: Gene pyramiding, market class, *Phaseolus vulgaris*, stability analysis, yield potential

CHAPTER 1: INTRODUCTION

1.1. Background information

Common bean (*Phaseolus vulgaris* L) is the most important grain legume for human consumption worldwide (Broughton *et al.*, 2003; Beebe, 2012). After Latin America (with 5.5 million metric tonnes of production per year), the African continent is the second major common bean producer in the world with approximately 2.5 million metric tonnes. Countries like Tanzania, Uganda, Kenya, Democratic Republic of Congo (DRC), Rwanda and Burundi are the major contributors to the African production (Wortmann *et al.*, 1998; FAO, 2018), and among which Kenya is the largest producer in the region (Beebe *et al.*, 2013). More than 200 million persons depend on it in sub-Saharan Africa as a source of food and income (Mukankusi *et al.*, 2011; Mutuku *et al.*, 2016; PABRA, 2017). Common bean is a source of dietary protein (20-25%), complex carbohydrate, micronutrients (Fe, Zn, Ca, Cu, Mn, and Mg), vitamins (folate) and amino acids (lysine and methionine) for over 300 million persons in tropical and subtropical regions (Liebenberg and Pretorius, 1997; Welch *et al.*, 2000; Graham *et al.*, 2007; Blair *et al.*, 2010). Among Eastern African countries, Kenya (western regions) and Rwanda record the highest per capita consumption per year (approximately 60 kg) (Buruchara, 2007; Beebe *et al.*, 2013). Pulses contribute up to 20% of per capita total protein intake in Kenya among which the dry bean is the most important (Kimani and Karuri, 2001; Kimani *et al.*, 2005a; FAO, 2013; Kimani *et al.*, 2014).

Despite the importance of common bean in Eastern and Central Africa, its seed yield is still among the lowest in the world. The average yield in the region is approximately 0.5 t ha^{-1} (FAO, 2018) whereas higher yields are being reported in other parts of the world (1 to 3 t ha^{-1} for bush beans and up to 5 t ha^{-1} for climbing genotypes) (Hillocks *et al.*, 2006; Ronner *et al.*, 2017). In fact, bean productivity is severely constrained by abiotic stresses (especially drought and low soil fertility) (Kimani *et al.*, 2005b; Lunze *et al.*, 2011), biotic stresses especially plant diseases and pests, poor adaptation of introduced crops to local conditions, socio-economic factors such as low and timely access to external inputs especially seed of improved cultivars and fertilizers (Kimani *et al.*, 2005b; Kimani, 2014).

Several biotic factors contribute to the low grain yield reported in Eastern Africa. These include viruses, bacteria, fungi diseases and insect pests (Singh and Schwartz, 2010; Pereira *et al.*, 2013; Okii *et al.*, 2017). About 200 pathogens are known to attack the common bean, but less than a dozen can cause substantial economic losses (Mwesigwa, 2009). The major biotic constraints to productivity in Eastern and Central Africa include angular leaf spot (*Pseudocercospora griseola* (Sacc.) Crous and Braun) (Wagara, 2004; Wagara *et al.*, 2004; Leitich *et al.*, 2016), anthracnose (*Colletotrichum lindemuthianum* (Sacc. and Magn.)(Gathuru and Mwangi, 1991; Pastor-Corrales, 2005; Kiryowa *et al.*, 2016), root rots (*Pythium spp, Fusarium spp, Rhizoctonia spp,* etc.)(CIAT, 2003; Nzungize *et al.*, 2011a; Buruchara *et al.*, 2015), bean common mosaic and necrotic viruses (BCMV/BCMNV) (Omunyin *et al.*, 1995; Kapil *et al.*, 2011; Mutuku *et al.*, 2016), and common bacterial blight (CBB) caused by *Xanthomonas axonopodis* pv. *phaseoli* (Wortmann *et al.*, 1998; Kimani *et al.*, 2005b; Belete and Bastas, 2017). These pathogens lead to significant bean seed yield losses ranging from 20% to as high as 80-100% (Singh and Schwartz, 2010; Blair *et al.*, 2010; Mahuku *et al.*, 2011; Olango *et al.*, 2017). Wortmann *et al.* (1998) estimated the annual production losses caused by angular leaf spot at 281,300 t; anthracnose at 247,400 t; root rot at 179,800 t; common bacterial blight at 145,900 t and bean common mosaic virus at 144,600 t in Eastern Africa.

Although the decrease in seed yield due to biotic and abiotic factors can be managed by the use of fertilizers in combination with other appropriate cultural management, chemical and irrigation technologies; associated costs are not practical for the widespread low-input systems in Sub-Saharan Africa. An integrated system based on improved crop varieties with genetic resistance/tolerance to stresses and appropriate agronomic and post-harvest control measures is most likely the most efficient approach for enhancing crop productivity for resource-poor farmers in Southern, Central and Eastern Africa (Fizgerald and Lindow, 2013; Kimani, 2014). In addition, relying on chemicals to reduce production and post-harvest losses due to pathogens and insect pests (Wasonga *et al.*, 2010) decreases the market value as the produce may not meet the European market requirements related to the amount of chemical residues in food (Kimani *et al.*, 2002). Harmful effects on humans, animals and environment, the emergence of pesticide-resistant strains and the economic implications are the other drawbacks of the excess chemical utilization in agriculture.

1.2. Problem statement

In developing countries, the dry bean is predominantly produced by smallholder, resource-poor farmers who can hardly afford alternative disease management strategies. In Kenya for example, common bean is grown by small-scale farmers who find the application of pesticides costly (Mwaniki *et al.,* 2002). The development through plant breeding of resistant cultivars is the most environmentally harmless, cheapest and most practical approach for disease management for these farmers. This will greatly reduce the need for chemicals hence increasing returns on farmers' investment (Kimani and Mwang'ombe, 2007; Ddamulira *et al.,* 2015).

Despite the fact that bean breeding in Kenya started in mid-1970's (Kimani *et al.,* 1990; 2014), more work on improving marketable bean varieties is needed. In the development of improved dry bean varieties in Eastern and Central Africa, four key challenges are encountered. These are the occurrence of new pathogens of major diseases such as root rots, anthracnose, angular leaf spot (Leitich *et al.,* 2016; Mwaipopo *et al.,* 2017) ; identification and deployment of new sources of resistance to the emerging pathotypes (Ddamulira *et al.,* 2014a; Kijana *et al.,* 2017; Mukankusi *et al.,* 2018); broadening the genetic base of existing breeding populations to enhance genetic potential for important agronomic traits (Kimani *et al.,* 2005b; Okii *et al.,* 2014) and improving efficiency of breeding methodology (Kimani *et al.,* 2005b) which is defined by Ceccareli (2015) as the relation between the number of cultivars approved and the number of crosses done, the response to selection, and the ratio between the benefit and the cost. In addition, the creation of improved cultivars in Kenya has usually focused on conventional breeding methods (Kimani and Mwang'ombe, 2007) which lead to a longer duration for a variety development (approximately 12 years) and strong dependence on erratic weather conditions.

Yield of common bean in farmers' fields is often affected by several biotic constraints. Thus, breeding for one constraint will not result in a significant change (Kimani *et al.,* 2005b; Okii *et al.,* 2017). In addition, breeding for one trait at a time is expensive and time-consuming; hence justifying a need for a multiple constraint breeding method (Singh, 1994). Gamete selection procedure is more appropriate because it allows simultaneous selection for multiple traits (Beaver and Osorno, 2009). Compared to other breeding methods such as bulk, pedigree, backcross, single seed descent and their modifications, the gamete selection permits identification of promising populations and families and consistent yield assessments in early

generations and thus, helping to avoid wastage of scarce resources and time (Singh, 1994). However, gamete selection as originally proposed by Singh (1994) and further developed and validated by Singh *et al.* (1998); Asensio *et al*. (2006); and Terán and Singh (2009) is largely based on phenotyping for agronomic traits under field and greenhouse conditions. The hypothesis that the use of markers can improve the efficiency and precision of gamete selection has not been tested (Kimani *et al.*, 2010). In addition, there is limited literature on the use of molecular markers in gamete selection in Eastern Africa.

1.3. Justification

These issues listed above were the main focus of marker-assisted breeding programme at the University of Nairobi since 2009. The University of Nairobi Bean Research Programme initiated studies to determine whether marker-assisted gamete selection could be effective in pyramiding genes for resistance to bean major diseases in Eastern Africa (mainly ALS, anthracnose, CBB, BCMV and *Pythium* root rot) and introducing these genes into susceptible, but popular, large- and small-seeded bean varieties (Kimani *et al.,* 2012; Musyimi, 2014; Njuguna, 2014). To attend that objective, the programme sought firstly to determine and characterize the current pathogenic variation of those major bean disease races and their distribution in Kenya. A survey conducted from 2010 to 2013 in 35 districts across major bean growing regions of Kenya showed variability in pathogen races and their geographic distribution across surveyed areas (Njuguna, 2014; Musyimi, 2014). The two main pathogen groups (Andean and Mesoamerican) were also reported.

To control these major diseases, sixteen small- and medium-seeded bean populations were generated from inter-racial crosses involving six sources of resistance (Mex54, G10909, G2333, RWR719, AND1062, and BRB191) and four susceptible but high yielding and popular commercial varieties (KATB1, KATB9, GLP585, and GLP92). In these crosses, Mex54 (Namayanja *et al.,* 2006) and G10909 (Mahuku *et al.,* 2003; Vallejo and Kelly, 2009) were exploited to provide genes of resistance to angular leaf spot; G2333 for anthracnose resistance (Melotto and Kelly, 2000; Awale and Kelly, 2001; Miklas and Kelly, 2002). AND1062 (Mukalazi *et al.,* 2001) and RWR719 (Otsyula *et al.,* 2003; Nzungize *et al.,* 2011a) were used for their resistance to *Pythium* root rot whereas BRB191 was the source of resistance to BCMV (CIAT, 2003). The susceptible commercial varieties (KATB1, KATB9, GLP585 and GLP92)

were mainly chosen based on their high yield potential, seed quality, earliness, high marketability and adaptation to agro-ecological conditions of Eastern Africa (Kimani *et al.,* 2012; Ruraduma *et al*., 2016; Binagwa *et al.,* 2017). Male gametes with requisite resistance genes were then identified using markers SAB-3 for anthracnose (Garzon *et al.,* 2008); SH-13 for angular leaf spot; SW-13 for bean common mosaic virus (Melotto *et al.,* 1996; Sharma *et al.,* 2008; Wani *et al.,* 2017) and PYAA-19 for *Pythium* root rot (Namayanja *et al.,* 2014). These male gametes were thereafter used to construct the F_1 with susceptible varieties following gamete selection breeding method (Singh, 1994). A total of 16 populations were developed. The segregating $F_{1.1}$ and $F_{1.2}$ populations were then tested for resistance to these diseases and other agronomic attributes in the field at Kabete and Tigoni in 2012 and 2013 under natural disease infestation (Njuguna, 2014). Progenies were thereafter advanced following gamete selection procedure up to $F_{1.5}$ during 2014 and 2015.

The present study, which is a continuation of this breeding programme, aimed at advancing the segregating populations to pure lines and selecting for multiple disease resistance, marketable grain types and other agronomic traits. This was achieved by grouping lines into market classes based mainly on seed color, shape and size. Subsquently, a multilocation testing was conducted to determine the effects of the genotype by environment interactions on seed yield and seed yield stability across contrasting environmental conditions. Due to limitations of evaluating disease resistance in the open field, a greenhouse evaluation was conducted to validate the multiple disease resistance of those advanced lines to major diseases for which they were previously marker-selected in early generations.

1.4. Objectives

1.4.1. Overall objective

The general objective of this study was to contribute to the increased availability of improved bean varieties combining high grain yield potential and multiple resistance to major diseases of Eastern and Central Africa.

1.4.2. Specific objectives

1. Determine the agronomic performance of intra- and inter-gene pool bean populations and select small- and medium-seeded lines with market preferred traits.
2. Analyse stability and genotype-environment interaction effects on seed yield of the $F_{1.7}$ elite lines across different locations of Kenya.
3. Validate the resistance of the selected $F_{1.8}$ elite lines to infections by root rots, common bacterial blight, angular leaf spot, bean common mosaic virus and anthracnose pathogens using natural epiphytotics and artificial inoculation.

1.5. Hypotheses

1. There are no differences in grain yield and other agronomic traits among the inter- and intra-gene pool bean populations.
2. Elite bean lines selected using molecular markers are not stable across different locations of Kenya.
3. Marker-assisted gamete selection was not effective in combining yield potential, market preferred grain characteristics and multiple disease resistance in elite bean lines.

CHAPTER 2: REVIEW OF LITERATURE

2.1. Introduction

This chapter gives an overview of breeding common bean for multiple disease resistance with emphasis on major Eastern African common bean diseases such as angular leaf spot, anthracnose, common bacterial blight, *Pythium* and *Fusarium* root rots and bean common mosaic viruses. It provides a brief description of the centers of domestication (origin), distribution, taxonomy and the genetic diversity of the common bean. The production and the major production limiting factors of the common beans in the Eastern and Central Africa, with an emphasis on Kenya are also discussed. The taxonomy, epidemiology and symptoms and seed yield losses due to the major bean diseases are briefly described. The pathogenic variability of these economically important diseases, potential sources of resistance, and common bean breeding strategies including a review of the methods of breeding for multiple disease resistance are also discussed briefly. Among those breeding strategies, the gamete selection method which allows the accumulation of favorable alleles into a single genotype is highlighted at the end this review. Bean breeding for disease resistance in Eastern and Central Africa since the 1970s is briefly reviewed.

2.2. Origin, distribution and common bean genetic diversity

The genus *Phaseolus* is of American origin where its first domestication took place in two different regions dispersed from the southern regions of Peru to north-western parts of Argentina (Andean gene pool) and from northern Mexico to Colombia (Middle American gene pool also referred to as Mesoamerica gene pool) (Koenig and Gepts, 1989; Chacon *et al.,* 2005; Bitocchi *et al.,* 2013; Schmutz *et al.,* 2014). The genus comprises approximately 70 wild-growing species which are found only in the American continent (Gepts, 2001; Bitocchi *et al.,* 2017). Among them, only five specifically *P. vulgaris* L. (common bean), *P. lunatus* L. (Lima bean), *P. acutifolius* A. Gray (tepary bean), *P. polyanthus* Greenmann (year-long bean) and *P. coccineus* L. (scarlet runner bean) were domesticated (Broughton *et al.,* 2003; Mamidi *et al.,* 2011; Bitocchi *et al.,* 2017). Covering more than 85% of areas dedicated to all *Phaseolus* species production worldwide (Singh, 2001), the common bean is the most widely grown. The domestication of *Phaseolus vulgaris* occurred in the highland areas of Latin America

approximately 7000 years ago (Mamidi *et al.,* 2011) from where the introduction to other parts of the world took place. Cultivars from both the Andean and the Middle America gene pools were introduced to lowlands of the South America and to the African continent (Gepts and Debouck, 1991). Andean cultivars became predominant in Europe, Africa and northeastern United States of America (USA), while the cultivars from the Middle American gene pool were predominant in the southwestern USA (Gepts and Debouck, 1991). The fact that the common bean domestication took place in the two different regions resulted in two distinct gene pools (Singh *et al.,* 1991b; Chacon *et al.,* 2005; Schmutz *et al.,* 2014) as the characteristics of the two zones and selection under domestication were different (Kwak and Gepts, 2009). Due to the domestication process of the common bean; morphological, phenological, biochemical and molecular attributes of the plant were altered (Gaut, 2014). This affected mainly attributes like the growth habit, seed size, seed retention and time to maturity. For example, the Andean gene pool comprises large-seeded beans (>40 g 100-seed mass) while the Middle American gene pool is made of small- (<25 g 100-seed mass) and medium-seeded beans (25 to 40 g 100-seed mass) (Singh, 2001; Asensio-S.-Manzanera *et al.,* 2006). Selection during the domestication process focused on particular traits resulting in smaller and denser plants with short internodes. It suppressed climbing ability, favored fewer and thicker stems and larger leaves (Debouck, 1991). The final outcome from that selection process was common bean genotypes with determinate and indeterminate compact growth habit. It is essential to note that the diversity of cultivated common bean cultivars parallels the diversity of their wild bean ancestors. However, the changes in pod and the seed size were the major distinct differences between the wild ancestors and the cultivated common bean, resulting in diversity (Gaut, 2014). Based on their morphological, agronomic, adaptive and molecular characteristics, the two cultivated bean gene pools were further divided in six races; these comprise three races from Middle American gene pool (Durango, Jalisco and Mesoamerica) and three races from Andean South American gene pool (Chile, Nueva Granada and Peru)(Singh *et al.,* 1991a; Beebe *et al.,* 2000; Kwak *et al.,* 2012). Small-seeded beans which were used for this study are of the Mesoamerican race while the medium-seeded beans belong to the Jalisco race (Singh *et al.,* 1991a).

The bush bean which is the most predominant in Africa can reach up to 60 cm tall with most of its pods held above the ground. It is a relatively short season crop, maturing in 90 days in a tropical climate and yielding between 700 and 2000 kg ha^{-1}. If supported, climbing beans may

grow 2 to 3 m tall. Climbing beans take longer to mature (100 to 120 days) at mid-elevations and their yield can be as high as 5000 kg ha^{-1} (Buruchara, 2007; Ronner *et al.,* 2017).

Common bean is a seed-propagated, true diploid (2n = 2x = 22) and self-pollinated crop (Arumuganathan and Earle, 1991; Schmutz *et al.,* 2014). From the genomic perspective, it contains a relatively small genome when compared to rice. It has approximately 450 to 650 million base pairs per haploid (Broughton *et al.,* 2003; McClean *et al.,* 2004; Schmutz *et al.,* 2014). Although there is an out-crossing rate below 5%, common bean is a predominantly self-pollinated species except in some tropical locations where the rate of out-crossing can be important (Ibarra-Perez *et al.,* 1997; Grahić *et al.,* 2013). Despite the fact that the inter-specific crossing is very uncommon in nature, the hybridization between *P. vulgaris* and *P. coccineus* occurs (Broughton *et al.,* 2003).

As a warm-season crop, the common bean does not tolerate frost and exposure to very low temperatures at any stage of its growth. Although high temperatures do not have an effect on the common bean when proper soil water is present, they tend to inhibit pollination such that when they reach more than 30°C, seed set is significantly reduced or flowers and buds shedding is favored, which results in a significant seed yield decrease (Fageria *et al.,* 1997; Beebe *et al.,* 2013; Rao *et al.,* 2017). For better yields, the crop requires moderate amounts of precipitation (300 to 600 mm) but adequate soil moisture is crucial during and immediately after the flowering stage. Dry conditions are suitable for maturation of the crop and for harvesting as late rains affect the seed quality and thus lower the quality and bean market value (Gomez, 2004).

2.3. Common bean production in Eastern Africa

Common bean is the main grain legume cultivated in the African continent when considering both the area under cultivation and the amount consumed (CIAT, 2005; PABRA, 2017). In Eastern, Central and Southern Africa, it is produced under a diversity of cropping systems, very often in association with the major staple crops such as maize, banana, roots and tubers, sorghum or millet (Allen and Edje, 1990; Kimani *et al.,* 2005b) and most often under rainfed low-input systems. It offers an affordable source of protein and provides an important source of income to both rural and urban households in Eastern Africa (Mkandawire *et al.,* 2004; PABRA, 2017). It is the most important legume in the pulses category of Kenya's agricultural commodities and occupies the second place as food crop after the maize (Kimani *et al.,* 2005b). Total production

has increased mainly due to the expansion of cultivated lands. Grain yield per unit area has gradually decreased over time so that bean yields obtained in farmers' field represent only 20 to 30% of the genetic potential of the crop (Nderitu *et al.*, 1997; Wortmann *et al.*, 1998; FAO, 2018). These low yields are attributed to several constraints, among which the most important are diseases, insect pests, soil depletion and sporadic water stress (Kimani *et al.*, 2005b; Lunze *et al.*, 2011; Kimani, 2014). Both Andean gene pool (accounting for 61% of cultivars) characterized by large-seeded beans and the Middle American gene pool (small-seeded beans) are found in the African continent (CIAT, 2005). With regard to production quantity and the area under cultivation, five Eastern African countries i.e. Tanzania, Kenya, Uganda, Rwanda, and Burundi were ranked among the 20 highest producers of common bean in the world (Table 2.1).

Table 2.1. Bean production and harvested area of Eastern Africa countries for the period of 2008 to 2016

Country	Year	Harvested Area (ha)	Production (10^3 t)	Country	Year	Harvested Area (ha)	Production (10^3 t)
Burundi	2008	215,000	189,661	Rwanda	2008	336,577	308,000
	2009	220,000	207,272		2009	345,851	326,532
	2010	225,203	201,551		2010	319,252	327,497
	2011	236,764	200,673		2011	341,819	331,166
	2012	340,752	205,944		2012	479,899	432,857
	2013	338,130	225,003		2013	480,012	438,236
	2014	380,592	251,761		2014	465,865	415,259
	2015	355,685	282,978		2015	503,546	434,077
	2016	208,522	371,892		2016	513,137	437,673
DRC	2008	209,316	113,240	Uganda	2008	651,000	912,000
	2009	211,165	114,239		2009	616,000	925,000
	2010	213,030	115,237		2010	633,000	949,000
	2011	438,749	238,124		2011	653,889	915,445
	2012	452,953	247,196		2012	669,000	869,607
	2013	451,488	248,075		2013	672,273	941,182
	2014	452,372	248,957		2014	674,290	1,011,435
	2015	432,301	238,290		2015	674,964	1,012,446
	2016	403,365	222,694		2016	670,737	1,008,410
Kenya	2008	641,936	265,006	Tanzania	2008	749,540	570,750
	2009	960,705	465,363		2009	868,310	773,720
	2010	689,377	390,598		2010	1,208,690	867,530
	2011	1,036,738	577,674		2011	737,661	675,948
	2012	1,056,046	622,759		2012	1,265,404	1,199,267
	2013	1,083,604	714,492		2013	1,151,376	1,113,541
	2014	1,052,408	615,992		2014	1,114,393	1,114,500
	2015	1,243,882	765,000		2015	1,124,710	1,201,922
	2016	1,171,710	728,160		2016	1,118,406	1,158,039

Source: FAO (2018)

The average bean yield in the region is around 0.5 t ha^{-1}, although potential yields of 1.5 to 3.0 t ha^{-1} can be realized with improved varieties, proper crop and farming practices under reliable rainfed conditions (Mkandawire *et al.*, 2004; FAO, 2018). Yields in Kenya are still very low and unstable, fluctuating between 0.4 and 0.6 t ha^{-1} (Table 2.2). This could be attributed to the intensification of drought, insect pests and diseases (Katungi *et al.*, 2009), limited access and use of improved varieties and poor farming practices (Kimani *et al.*, 2005a; Kimani, 2014).

Table 2.2. Bean production and consumption trends in Kenya for the period between 2006 and 2016

Year	Area harvested (ha)	Yield (kg ha^{-1})	Production (10^3 t)	Value ($\$10^3$)	Consumption (10^3 t)	Surplus/ Deficit (10^3 t)
2006	995,391	534.3	531,800	303,476.5	460,000	71,800
2007	846,327	507.9	429,839	240,404.1	524,400	-94,561
2008	641,936	412.8	265,006	234,863.0	624,036	-359,030
2009	960,705	484.4	465,363	350,748.9	-	-
2010	689,377	566.6	390,598	246,146.3	-	-
2011	1,036,738	557.2	577,674	403,230.0	614,000	-36,326
2012	1,056,046	589.7	622,759	469,572.7	698,000	-75,241
2013	1,083,604	659.4	714,492	511,228.0	-	-
2014	1,052,408	585.3	615, 992	531,882.6	652,000	-36,008
2015	1,243,882	615.0	765,000	602,463.0	801,000	-36,000
2016	1,171,710	621.4	728,160	541,923.8	765,000	-36,840

Source: Ministry of Agriculture (2009); KNBS (2013; 2016; 2018); FAO (2018)

In Kenya, the medium and highland regions of the country which experiences more reliable precipitations and suitable temperatures are considered to be the main growing areas of bean production. These comprise parts of Nyanza and Rift Valley, Central, Eastern and Western highlands which account for approximately 75% of the annual bean cultivation (Katungi *et al.*, 2009).

2.4. Major bean market classes in Eastern Africa

Several bean market classes are grown in Eastern Africa. These include mainly pinto, small red, red kidney, red mottled, black, navy (white), yellow, greyish green, beige, speckled sugar, tan brown, tan red, etc. Their distribution depends on seed color and size preferences of each people, and thus, making a difference in price on local and regional markets. Red kidney and red mottled

market classes are extensively grown in the African Great Lakes region (Rwanda, Burundi and DRC) with some climbing varieties. These are also very popular in Kenya and Uganda. Small red, navy and yellow bean market classes are popular in Kenya, Uganda, Tanzania and Ethiopia. Although high yielding and resistant to several diseases, black beans are less preferred by farmers and consumers in Eastern Africa, except some people in Uganda and Southern Ethiopia. The importance of yellow bean is increasing in Eastern Africa and fetches high prices. Some major market classes are presented in Figure 2.1.

Pinto beans

Red mottled beans

Dark red kidney beans

Black beans

Small red beans

Red kidney beans

Speckled sugar beans

Navy beans

Yellow beans

Figure 2.1. Major bean market classes in Eastern Africa

2.5. Common bean production constraints in East Africa

Several researchers have reviewed the literature on common bean production constraints in Eastern Africa (Wortmann *et al.,* 1998; Kimani *et al.,* 2005b; Olango *et al.,* 2017). These constraints comprise abiotic and biotic stresses that are responsible for the yield decrease of the common bean and consequently resulting in famine and poverty. Table 2.3 summarizes losses associated with major biotic and abiotic constraints to bean production in Africa.

Table 2.3. Yield losses due to major constraints to bean production in sub-Saharan Africa in thousands of tonnes year^{-1}

Constraint	Eastern Africa	Southern Africa	Sub-Saharan Africa
Angular leaf spot	281.3	93.5	384.2
N deficiency	263.6	125.2	389.9
Anthracnose	247.4	69.8	328.0
P deficiency	234.2	120.4	355.9
Bean stem maggot	194.4	96.4	297.1
Root rot	179.8	31.0	221.1
CBB	145.9	69.8	220.4
BCMV	144.6	29.9	184.2
Aphids	136.3	58.9	196.9

N=nitrogen, P=phosphorus, CBB=common bacterial blight, BCMV=bean common mosaic virus
Source: Wortmann *et al.* (1998).

2.5.1. Major bean diseases in Kenya and sources of resistance

The main disease constraints include angular leaf spot (ALS), anthracnose, root rot, bean common mosaic virus (BCMV) and common bacterial blight (CBB) (Wortmann *et al.,* 1998; Kimani *et al.,* 2005b). These are the responsible for lower yields in many bean growing areas of Kenya and Eastern Africa in general. When the environmental conditions are favorable for disease development, crop losses can be as high as 80 to 100% on susceptible bean cultivars (Mahuku *et al.,* 2011). Studies carried out all over Kenya where beans are intensively grown, have indicated the presence of pathogenic variation of these common bean diseases.

2.5.1.1. Angular leaf spot

Considered as one of the most important biotic constraints for common bean production, the ALS which is caused by a fungus *Pseudocercospora griseola* (Syn. *Phasaeiosariopsis griseola* Sacc.), is found in both tropical and subtropical areas where it causes severe harm (Aggarwal *et al.,* 2004). Its incidence and severity have increased in most common bean growing regions

(Stenglein *et al.,* 2003; Ddamulira *et al.,* 2014b; Kijana *et al.,* 2017). The disease attacks all aerial parts of the plant especially the leaves and pods. It causes dark grey to brown lesions on the leaves which are often delimited by the veins, giving them a characteristic angular appearance. The tissue surrounding the lesion may become chlorotic, and under severe infection lesions will coalesce and may lead to premature defoliation. In primary leaves the disease causes circular lesions (Borges *et al.,* 2013), although some virulent pathotypes have been reported to cause circular lesions on the trifoliate leaves (Crous *et al.,* 2006). Pod symptoms consist of circular to elliptical red-brown lesions which will result in shriveled seeds of reduced size and poor quality. The disease-causing agent is favored by the alternate of dry-wet and warm-cool weather conditions with an optimum temperature for pathogen development of about 24ºC (Stenglein *et al.,* 2003). Greater yield losses of more than 80% can be reached depending on the cultivar genetic background and the pathogenicity of its causal agent, and if weather conditions are conducive for the pathogen development (Singh and Schwartz, 2010; Mahuku *et al.,* 2011).

Pathogenic variation in *Pseudocercospora griseola* was reported as early as 1950's when Brock (1951) found indications of virulent differences between 13 Australian isolates. Pathogenic diversity in *P. griseola* has also been reported by several other authors (Stenglein *et al.,* 2003; Sartorato, 2004; Wagara *et al.,* 2004; Silva *et al.,* 2008). The first report of a systematic collection and race-typing of *P. griseola* isolates in Kenya using the international bean differentials identified 44 races from 100 isolates obtained in five districts (Wagara, 2004). In Kenya, the disease prevalence ranging from 65 to 80% was revealed by a survey carried out in various areas such as Kiambu, Machakos, Embu, Taita Taveta and Kakamega (Mwang'ombe *et al.,* 2007). The prevalence was higher at altitudes ranging between 963 and 2322 m above sea level, leading to the conclusion that the ALS is highly prevalent and severe in all traditionally bean growing areas of Kenya. Leitich *et al.* (2016) identified 42 isolates from the bean growing areas of Western Kenya and characterized them into 6 pathotypes, including 30:26, 31:10; 33:23, 63:7, 63:11, and 63:63) by use of 12 differential cultivars. The pathotype 63:63 was the most virulent across the surveyed areas. Resistance was associated with Mesoamerican small-seeded cultivars GLP585 and KK22 while the Andean large-seeded lines were highly susceptible. New races of *P. griseola* were recently identified in Kenya in a country-wide survey covering 12 agro-ecological zones that included Upper Highland, Lower Highland, Upper Midland and Lower Midland (Njuguna, 2014). Fifty-seven (57) isolates were collected from thirty-five districts and

tested for pathogenicity using 12 differentials (Don Timoteo, Bolon Bayo, Montcalm, G05686, Amendoin, G11796, BAT 332, PAN72, Cornell 49-242, Mex54, Flor de Mayo and G02858). Twenty-three races of *P. griseola* were then identified. Only 11 races were found in two or more districts. Race 63-63 was the most virulent and responsible of angular leaf spots on all the 12 differential cultivars. The race 63-55 was the most frequent (10 of 57 isolates) and widely distributed among the surveyed regions. Races 63-55, 63-63, 63-54 and 63-35 were the most dominant in surveyed areas. Two new races (31-31 and 63-31) were reported for the first time in Kenya. The virulence phenotype revealed that 45 isolates studied were of the Mesoamerican group and only 12 were Andean, suggesting co-evolution of the pathogen with *P. vulgaris* in this host-pathogen interaction.

According to Chacon *et al.* (2005), the two *P. griseola* pathogenic sets seem to have co-evolved with both common bean gene pools (Middle American also referred to as Mesoamerican and Andean) and consequently the two major groups of *P. griseola* are defined as, Andean (*Pseudocercospora griseola* f. griseola) and Mesoamerican (*Pseudocercospora griseola* f. mesoamericana) (Crous *et al.,* 2006; Saparrat *et al.,* 2009). The Andean groups of *P. griseola* attack only the Andean bean cultivars whereas the Mesoamerican counterparts attack not only the Mesoamerican beans but also large-seeded beans of the Andean gene pool. The last was also found to be more aggressive and more virulent (Mahuku *et al.,* 2002b). In addition to the two, the Afro-Andean group was later discovered. It is an African group of *P. griseola* having similar characteristics to the Andean group (Wagara *et al.,* 2004). The latter was likely a result of recombination, mutation and climatic adaptation of the Andean group to African climatic conditions (Mahuku *et al.,* 2002b). Due to this, it was recommended that the strategy to develop new cultivars with resistance to ALS will necessitate a thorough understanding of the genetic variation of the pathogen and the transfer of genes conferring resistance from one gene pool to cultivars belonging to the other gene pool (Pastor-Corrales and Jara, 1995; Njuguna, 2014).

As the ALS-causing agent is highly variable, many sources of resistance are required to control the disease (Mahuku *et al.,* 2003; Ddamulira *et al.,* 2015). Sources of resistance to both Andean and Mesoamerican groups were identified in cultivated cultivars, secondary common bean gene pools (*P. coccineus* and *P. polyanthus*) as well as wild and weedy *P. vulgaris* (Mahuku *et al.,* 2003). However, the level of resistance is low in cultivated genotypes compared to the secondary

gene pools. Among well described sources of resistance to ALS, there are A75, A229, A152, A140, A175, BAT332, BAT76, BAT1458, BAT1432, BAT431, G05686, G10474, G10909, AND277, MAR2, Mex54, Cornell 49-242 (Souza *et al.*, 2016). In Uganda, the landrace U00297 showed a strong and consistant resistance to major ALS pathotypes and were recommended for breeding programme to improve resistance in commercial cultivars. Other genotypes with good resistance were AND277 and G5686 (Ddamulira *et al.*, 2014). In eastern DRC, a recent study identified four sources of resistance in locally cultivated cultivars using virulent Andean and Mesoamerican isolates. These comprised ARA4, CODMLV059, MLV224/94B, LSA144, and Mex54 (Kijana *et al.*, 2017). In Kenya, resistance to ALS was associated with Mesoamerican small-seeded cultivars GLP585 and KK22 (Leitich *et al.*, 2016).

A total of nine genes have been identified to confer resistance to ALS. These genes include *Phg-1*^{a}, *Phg-2*^{2}, *Phg-3*^{2}, and *Phg-4*^{2} for cultivar AND227, *Phg-2*, *Phg-5* and *Phg-6* for Mex54 and MAR2 has *Phg-4* and *Phg-5* resistance genes (Caixeta *et al*., 2005). *Phg-1* was found on chromosome Pv01, *Phg-2* on Pv08, and *Phg-3* on Pv04, *Phg-4* on Pv04 and *Phg-5* on Pv010 (Gonçalves-Vidigal *et al.*, 2013; Souza *et al.*, 2016).

2.5.1.2. Anthracnose (*Colletotrichum lindemuthianum*)

Anthracnose is among the major seed-borne fungal diseases of common bean in subtropical and tropical areas, due to relatively cool and humid weather which favors the *C. lindemuthianum* development (Pastor-Corrales *et al.*, 1995; Kiryowa *et al.*, 2016; Zuiderveen *et al.*, 2016). There is high disease prevalence throughout bean growing areas of Africa where the severity of yield losses depends on the plant developmental stage when the infection occurs. Seed losses are much higher (reaching up to 100%) when the disease occurs earlier in the crop developmental stage where susceptible cultivars are grown (Opio *et al.*, 2001). The pathogen longevity in the seed is reported to be high and could reach 3 to 5 years and thus the growers who keep seed from the previously grown crop (like those in most parts of Kenya); most probably contribute to the carryover and spread of the disease (Tesfaye, 2003; Ferreira *et al.*, 2013).

The pathogenic variability of *C. lindemuthianum* was first reported by Barrus (1911) and since then, several races have been discovered worldwide (Gathuru and Mwangi, 1991; Kelly *et al.*, 1994; Sharma *et al.*, 2007; Padder *et al.*, 2009). Alzate-Marin *et al.* (2007) for example, identified a total of 50 *C. lindemuthianum* pathotypes in Brazil between 1994 and 2002. Mahuku

and Riascos (2004) identified 90 races from 200 isolates collected on Mesoamerican and Andean varieties from Mesoamerican and Andean areas. Approximately 182 races have been currently identified worldwide using 12 differential cultivars (Padder *et al.,* 2017).

Gathuru and Mwangi (1991) characterized 36 isolates collected from nine districts of Kenya, cultured and inoculated on bean differentials: Cornell 49-242, Michelite, Perry Marrow, Michigan Dark Red Kidney, Emerson 847, Kaboon, Processor and Canadian Wonder. Eleven isolates were grouped as beta, eight as gamma, five as epsilon, two as delta and one as alpha. Nine isolates did not fit in any of the known races. The cultivar Cornell 49-242 was found resistant to all isolates. The cultivar Kaboon was found susceptible to the majority of isolates. So far, seven races namely 17, 2, 38, 23, 1, 55 and 485 have been reported in Kenya (Gathuru and Mwangi, 1991; Ombiri *et al.,* 2002). In a country-wide survey conducted by Musyimi (2014), covering western, Rift Valley, central, eastern and coastal regions of Kenya; 31 isolates were characterized into 12 pathogenic races of *C. lindemuthianum*. Of the 12 races identified, seven (1, 2, 17, 23, 38, 55 and 485) had been previously identified, while five (65, 73, 81, 87 and 89) were new. Races 65 (8 of 31 isolates) and race 73 (4 of 31 isolates) were the most frequent in surveyed regions.

Different single, duplicate or complementary dominant genes have been shown to confer genetic resistance to some *C. lindemuthianum* pathotypes (Young and Kelly, 1996) and are present in many germplasm accessions (Sharma *et al.,* 2007; Kiryowa *et al.,* 2016). Many sources of resistance to *C. lindemuthianum* have been established from which Mex222, PI207262, G2333, Mex227, AB136, G2641, Cornell 49-242, TU, G811, and Ecuador 299 are the well-documented (Graham and Ranalli, 1997; Musyimi, 2014; Kiryowa *et al.,* 2016). In Kenya, Musyimi (2014) found that cultivars G2333 and AB136 were highly resistant to all the 31 isolates of *C. lindemuthianum* collected from western, Rift Valley, central, eastern and coastal regions of Kenya. The other sources of resistance used for other pathogens namely G10909 and Mex54 (for ALS), AND1062 and RWR719 (for *Pythium* root rot) and VAX6 (for CBB) and four commercial cultivars namely New Rosecoco, Kenya Umoja, GLP1004 and Canadian Wonder showed high compatibility with most of the races. Musyimi (2014) suggested that differential varieties AB136 and G2333 can be used in breeding programmes in Kenya as they were resistant to all the identified races.

The major disadvantage in the use of resistant cultivars to control the *C. lindemuthianum* is the breakdown of resistance caused by the adjustment of the pathogen to the host resistance. Moreover, the sources of resistance for a given race may not be successful against all races (Sharma *et al.,* 2007) as the pathogen responsible for the anthracnose is highly variable (Balardin and Kelly, 1998; Mahuku and Riascos, 2004; Alzate-Marin *et al.,* 2007). Thanks to its three resistance genes (*Co-4*^{2}, *Co-5*, and *Co-7*), the cultivar G2333 is resistant to almost all the described races of the *C. lindemuthianum* (more than 90% of the races) apart from some races (e.g., 3481, 3545, 3977, and 3933) to which it is very susceptible (CIAT, 1995; Young *et al.,* 1998; Vallejo and Kelly, 2009; Kiryowa *et al.,* 2016). Zuiderveen *et al.* (2016) while testing 230 Andean cultivars from different market classes and seed sizes collected all over the Americas, Europe and Africa; found that twenty-eight of those genotypes were carrying resistance to seven of the eight races used in screening. Only the the cultivar Uyole98 was resistant to all the eight races of anthracnose (7, 39, 55, 65, 73, 109, 2047, and 3481), making it the most suitable source of resistance to be exploited in breeding programmes. Major QTLs were located at the chromosomes Pv01, Pv02, and Pv04 while the minor ones were on Pv10 and Pv11. The resistance to *C. lindemunthianum* was attributed to a single dominant gene *Co-1* on Pv01. From 11 independent resistance genes (Co-genes) found in common bean for resistance to *C. lindemuthianum*; 10 were from Mesoamerican germplasm whereas only one was from Andean germplasm (Alzate-Marin *et al.,* 2007). Due to continuous occurrence of new races of *C. lindemuthianum* causing the anthracnose, the utilization of specific resistance genes in common bean breeding is not always providing durable resistance as the new occurring races are able to overcome the resistant germplasm. This calls for continual identification of sources of resistance to that pathogen and the introgression of genes conferring resistance into existing varieties (Mahuku *et al.,* 2002a; Kiryowa *et al.,* 2016).

2.5.1.3. Bean common mosaic virus (BCMV) and bean common mosaic necrotic virus (BCMNV)

These are seed-borne diseases and the most important viral diseases in terms of both damage caused and the spatial distribution worldwide (Miklas *et al.,* 2000; Kapil *et al.,* 2011; Mwaipopo *et al.,* 2018). Aphids contribute a lot to their transmission. The first identification of strains was by Drijfhout *et al.* (1978) who identified two serotypes (A and B) on international differential which were causing the temperature insensitive necrosis and mosaic symptoms on differential

cultivars carrying I and II resistance genes (Huang and Chang, 2005; Worrall *et al.*, 2015). These strains have now been regrouped as two different viral species of potyvirus based on their peptide profiles and nucleotide sequence data and named as BCMV (Serotype B) and BCMNV (Serotype A) (Huang and Chang, 2005). Practically, it is very difficult to differentiate the two viruses in the field due to the high resemblance of symptoms developed by some strains of both viruses (Gibbs *et al.*, 2008; Kapil *et al.*, 2011). The degree of pathogenic variability of the virus is known to be very high (Kapil *et al.*, 2011; Worrall *et al.*, 2015; Mwaipopo *et al.*, 2017).
Omunyin *et al.* (1995) reported on the pathogenicity groups occurring in Kenya and was able to differentiate 14 virus isolates into four pathogroups. These pathogroups included: the necrotic strain VI from Kakamega, Naivasha, Nyahururu, Murang'a, Thika and Kabete; the non-necrotic strain V from Kabete and two potentially new groups, one necrotic strain from Nyeri and another non-necrotic strain from Subukia in Nakuru. More recently, Mangeni *et al.* (2016) characterized three virus isolates X, Y, and Z from 15 sub-counties of western Kenya using 7 differential cultivars. That study revealed the presence of three pathogroups including PG IV, PG VI, and PG VII among which PG IV and PG VII were occurring for the first time in the region.

Several sources of genes conferring resistance to this potyviruses include BelNeb RR-1 and BelNeb RR-2 with the *bc-1*^{2} and *bc-2*^{2} genes that provide resistance to BCMV and BCMNV (Mukeshimana *et al.*, 2005; Worrall *et al.*, 2015). Other sources of resistance include BRB29, BRB32, and BRB191 that condition resistance to BCMNV (CIAT, 2003). The independence existing among the resistance genes could be perceived as an opportunity for the utilization of gene pyramiding as an approach for durable resistance breeding. The combination by bean breeders of the dominant I gene with recessive *bc* genes confers durable resistance to all known strains of BCMV and BCMNV (Kelly *et al.*, 2003; Worral *et al.*, 2015).

2.5.1.4. Root rots of common bean

The bean root rots is caused by complex pathogens including *Pythium*, *Sclerotium, Macrophomina, Aphanomyce* species, *Fusarium solani* pv. *phaseoli* and *Rhizoctonia solani* (Abawi and Pastor-Corrales, 1990; Nakedde *et al.*, 2016; Paparu *et al.*, 2018). Root rots are among the most destructive diseases in Eastern and Central Africa where common beans are intensively cultivated (Otsyula *et al.*, 2003; Nzungize *et al.*, 2011a; Paparu *et al.*, 2018). *Pythium* species are spread worldwide (Paul, 2004) but the bean root rot caused by them is a recent

problem in the Eastern and Central African regions and which is, unfortunately, increasing in importance (Otsyula *et al.,* 2003; Mukankusi *et al.,* 2011; Buruchara *et al.,* 2015). The *Pythium* fungus lasts in the soil for many years as oospores germinate to produce zoospores that attack the root and lower stem (Rusuku *et al.,* 1997). The *Pythium*-inducing agents generate many zoospores which allow them to quickly and constantly re-infect growing roots in susceptible varieties (Rusuku *et al.,* 1997). *Fusarium* root rot which is caused by *Fusarium solani* f.sp. *phaseoli*, is another major cause of root rot disease causing serious harm to the common bean production in Eastern and Central Africa resulting in seed yield losses of up to 84% (Mukankusi, 2008; Obala *et al.,* 2012; Paparu *et al.,* 2018). High seed yield losses of approximately 70% have been reported in popular commercial cultivars of Rwanda and Kenya, but under favorable environmental conditions for the pathogen development, complete yield losses are possible on susceptible cultivars (Tusiime, 2003; Otsyula *et al.,* 2003). Infected tissues become elongated, spongy, and water-soaked and discolored with many cavities. Furthermore, the yellowing of lower leaves (comparable to nitrogen deficiency), stunting, leaf browning and plant wilt and death are other characteristic symptoms of the disease (Ampaire, 2003).

Resistance to *Fusarium solani* is believed to be much more complex as it is controlled by two or more genes (Schneider *et al.,* 2001; Romans-Aviles and Kelly, 2005; Mukankusi *et al.,* 2011; Obala *et al.,* 2012), while, the *Pythium ultimum* resistance is only conditioned by a single dominant gene, marked by a dominant SCAR marker-PYAA19^{800} (Otsyula *et al.,* 2003; Mahuku *et al.,* 2005; Otsyula, 2010). The genetic resistance to *Fusarium* root rot is quantitative in nature (Miller and Burke, 1985; Schneider and Kelly, 2000) and therefore it is strongly affected by the environmental conditions (Schneider *et al.,* 2001).

In Eastern and Central Africa, the use of resistant cultivars is considered as the most efficient and practical control option against the *Pythium* root rot of bean (Otsyula *et al.,* 2003; Nzungize *et al.,* 2011a) but for the durability in use of resistant varieties, the diversity of causal agents has to be taken into account. *Pythium* species pathogenic to beans in Kenya have been characterized, which is crucial for effective epidemiological studies. Buruchara *et al.* (2004) characterized 134 *Pythium* isolates collected from different bean growing areas of Kenya and Rwanda which are affected by the root rot and was able to identify 22 species of *Pythium*. Nineteen of the 22 species were discovered from Rwanda and among them; the *Pythium ultimum* was the most

frequent (Buruchara *et al.,* 2004). In Kenya the isolates were collected from Trans-Nzoia, Kakamega, Vihiga, Kisii, Meru, Embu, Kirinyaga, Murang'a, Kiambu and Nairobi districts and a species distribution map established (Buruchara *et al.,* 2004). The Kenyan isolates were characterized into 15 species among which *P. vexans* was the most frequent, followed by *P. torulosum, P. irregular* and *P. sp.* (Buruchara *et al.,* 2004). In Rwanda at the other hand, *Pythium* agents that belong to a range of species have been reported to cause root rots (Nzungize *et al.,* 2011a) and these comprised *Pythium vexans, P. ultimum, P. indigoferae, P. torulosum,* and *P. cucurbitacearum* among others. Binagwa *et al.* (2016) reported 11 species of *Pythium* in Tanzania which included *P. aphanidermatum, P. splendens, P. ultimum, P. attrantheridium, P. graminicola, P. oligandrum, P. dissotocum, P. irregurale, P. camurandrum, P. paroecandrum* and *P. acanthophoron* with high incidence reported in areas with an acidic soil pH (5 to 6).

Until recently, no resistant genotypes to bean root rot were identified and commercial bean varieties released in Kenya, Uganda and Rwanda were highly susceptible to *Pythium* root rot (Otsyula *et al.,* 2003). Previous screenhouse and field screening have identified few sources of resistance to *Pythium* root rot within *P. vulgaris* (Otsyula *et al.,* 2003). These sources of resistance genes to *Pythium* root rot included RWR719, AND1062, and MLB49-89A that were selected through a greenhouse evaluation conducted at Kawanda in Uganda and were found to be some of the most resistant (Otsyula *et al.,* 2003; Buruchara, 2007). RWR719 and MLB49-89A showed also resistance to bean root rots in field evaluation carried out in Rwanda, Kenya and Uganda (CIAT, 2000; Otsyula *et al.,* 2003). After screenhouse and farmers' field conditions, cultivars MLB-49-89A, MLB-48-89A, RWR719, AND620 and SCAM80-cm/15 were selected as effective sources of resistance to *Pythium* root rot while MLB-49-89A, RWR719, Vuninkingi, Hoima Kaki, G2333, SCAM 80/15, Umgeni, MLB-48-89A, G1459 and G4795 were selected as sources of resistance to *Fusarium* root rot. *P. acutifolius* and *P. lunatus* and interspecific lines of *P. coccineus* and *P. acutifolius* provide important sources of resistance to bean root rots (Mukankusi, 2015).

2.5.1.5. Common bacterial blight

Common bacterial blight (CBB) which is caused by a seed-borne pathogen *Xanthomonas axonopodis* pv. *phaseoli* (Smith 1897) (Vauterin *et al.,* 1995), is reported as the major bacterial disease of common bean (Alladassi *et al.,* 2017). It is widely spread and found from the tropical

to the temperate bean growing areas (Yoshii, 1980; Singh, 2001; Miklas *et al.,* 2017). According to studies carried out by Wortmann *et al.* (1998), the CBB is ranked as the fourth most destructive bean disease in Africa. The CBB is systemic (Burkholder, 1921) and transmitted through the seeds (Aggour *et al.,* 1989) which plays a major role in the spread of CBB-causing agent (Weller and Saettler, 1980). Relative humid and warm growing conditions favour disease development resulting in high losses on susceptible cultivars (Miklas *et al.,* 2017). There is a huge accumulation of bacterial populations in susceptible cultivars which move more rapidly through vascular tissue in contrast to resistant varieties (Singh and Muñoz, 1999). The CBB causes 20 to 60% yield losses depending on the disease pressure, ecological conditions, and the grown genotype (Singh and Miklas, 2015). In Africa yield losses of 220,000 tonnes year^{-1} are reported; of these 146,000 tonnes are lost in Eastern Africa (Wortmann *et al.,* 1998). Moreover, severe CBB affects negatively the seed quality including the seed size, shape, color, and the germination capacity. Pod quality is also reduced. Thus, the marketability of diseased seed and its delivery out of the growing area can be restricted (Marquez *et al.,* 2007; Harveson and Schwartz, 2007). More than six distinct genotypes of common bacterial blight causing agent have been identified worldwide using differential cultivars and tepary bean genotypes (Mahuku *et al.,* 2006; Singh and Miklas, 2015).

As there is no adequate chemical control of CBB available, breeding for resistance is thought to be the most effective and durable control measure (Fourie *et al.,* 2011; Alladessi *et al.,* 2017), and is essential to all other CBB control approaches, including integrated disease-and-crop management practices. Compared to the levels of resistance found in some scarlet runner beans (*P. coccineus*), the resistance to CBB in common bean is moderate. Much higher levels of resistance to CBB have been identified in tepary bean (*P. acutifolius*) (Marquez *et al.,* 2007) suggesting the necessity of hybridization between *P. vulgaris* and its relatives (*P. acutifolius* and *P. coccineus*) for the development of CBB-resistant varieties (Singh *et al.,* 2001; Singh and Miklas, 2015). Cultivars NE2-14-8, VAX3, NE14-09-78, BAC-6, XAN-159, Montana 5, Wilk-2, HAB- 52, BAC-6, VAX6, VAX4 and PR 0313-58 and NE17-14-29 were identified and used to confer resistance to susceptible commercial cultivars (Arnaud-Santana *et al.,* 1994; Miklas *et al.,* 2003; Ferreira *et al.,* 2004; Mahuku *et al.,* 2006 ; Zapata *et al.,* 2011; Muimui *et al.,* 2011; Tryphone *et al.,* 2012; Alladessi *et al.,* 2017; Miklas *et al.,* 2017). Other sources of resistance to

CBB were recently reviewed by Singh and Miklas (2015). The CBB resistance conditioned by a single dominant gene was previously reported by Zapata *et al.* (2011); Muimui *et al.* (2011) and Tryphone *et al.* (2012) while the resistance found by Miklas *et al.* (2003) in Montana 5 was polygenic. Similar findings were reported by Arnaud-Santana *et al.* (1994). To date, only three major-effects QTL are used in marker-assisted selection for CBB resistance breeding and these include BC420 on Pv06, SAP6 on Pv10, and SU91 on Pv08 (Singh and Miklas, 2015).

2.6. Methods and strategies in breeding beans for disease resistance

The general objective of a breeding programme is to develop cultivars with improved characteristics without affecting other desirable traits possessed by the cultivar. Breeding for disease resistance has been one of the key objectives in bean improvement programmes (Beaver and Osorno, 2009; Singh and Schwartz, 2010). Common bean breeding programmes follow several methods. These include the pedigree selection which is the commonly used method in the development of improved varieties. The single seed descent (SSD) is a method used to shorten the breeding cycle and offers a means to maintain genetic variability when advanced-generation lines are developed. The bulk selection method is used to quickly advance bean populations when several generations have to be grown per year and is, therefore, the most suitable for crosses among elite lines within a market class where insignificant segregation for seed color and size is expected. The recurrent selection allows the accumulation of favorable alleles through recombination in each cycle of selection. The backcross method is often used to transfer and incorporate simply inherited traits. The participatory plant breeding approach is mainly used in developing countries; where it allows the participation of farmers in the development, evaluation and selection of bean lines. The more recently developed method is the gamete selection, which allows concurrent selection for multiple traits. These methods have been largely reviewed by Beaver and Osorno (2009). Among these, backcross, gamete selection, pedigree, recurrent selection methods and their modifications are the most widely used in common bean breeding programmes for disease resistance (Singh and Schwartz, 2010; Singh and Miklas, 2015). More than any other breeding objective, the marker-assisted selection has been successfully and widely used in breeding for biotic stresses (Miklas *et al.*, 2006; Beaver and and Osorno, 2009). Kelly and Miklas (1998) suggested that molecular markers can increase precision in pyramiding of resistance genes and accelerate the development of bean cultivars with more durable resistance.

This review will be focusing mainly on the gamete selection procedure which was used in the population development of materials used in this study.

2.6.1. Gamete selection for multiple constraint resistance

The common bean yield is often affected by several constraints, and thus, breeding for one will not result in a significant change (Kimani *et al.*, 2005b; Okii *et al.*, 2017). Breeding for one trait at a time, is also expensive and time-consuming; hence justifying a need for a multiple constraint breeding method (Singh, 1994). Gamete selection procedure is more appropriate as it allows concurrent bean selection for multiple traits (Beaver and Osorno, 2009). It was first described by Singh (1994) as a breeding procedure that permits screening and selection of desirable dominant and codominant alleles during hybridization and directly after creation of final multiple-parent F_1 hybrids. Compared to other breeding methods such as bulk, pedigree, backcross, single seed descent and their modifications, which involve managing and advancing considerable amounts of undesirable genotypes; the gamete selection permits identification of promising populations and families and consistent yield assessments in early generations and thus, helping to avoid wastage of scarce resources and time (Singh, 1994). It also maximizes the efficiency, usage and reduces costs of molecular markers. Gamete selection breeding procedure proposed by Singh (1994) was modified to include application of molecular markers by University of Nairobi Bean Research Programme in 2009. The marker-assisted gamete selection at the University of Nairobi is presented in Table 2.4.

Table 2.4. Marker-assisted gamete selection scheme at the University of Nairobi

Generations	Achievements
Parents	Selection of desirable and contrasting parental genotypes and determine the combining ability.
Single crosses	Development of single crosses between selected parents
Double crosses	Making double-cross males by combining two single crosses
Identification of male gametes for the final cross	Screening of male gametes for desirable trait genes with molecular markers. SAB-3 was used for anthracnose, SH-13 for ALS, SW-13 for BCMV and PYAA-19 for *Pythium* root rot. Selected single plants are to be utilized for the creation of final multiple-parent crosses with commercial varieties using plant-to-plant paired hybridization.
F_1	Evaluating the final F_1 for successful introgression of desirable dominant and codominant alleles and harvest seeds in separate envelopes. The same markers described above were once again used at F_1 to facilite pyramiding genes of resistance to target pathogens.
$F_{1.2}$-$F_{1.6}$	Evaluation of progenies from single plants in a multilocational replicated trials in contrasting environments. Uniformity in growth habit, flower color, seed traits and maturity are checked. Identifying high yielding populations and discarding undesirable populations.
$F_{1.7}$-$F_{1.9}$	Preliminary, Intermediate and Advanced yield trials (PYT, IYT, and AYT). Group and grow materials in complementary nurseries based on seed characteristics and discard inferior, susceptible and undesirable lines.
$F_{1.10}$-$F_{1.12}$	National Performance Trials using replicated yield trials in contrasting agro-ecological conditions to identify genotypes to be released to farmers.

Successful application of the gamete selection method has been reported by Singh *et al.* (1998); Asensio-S.-Manzanera *et al.* (2005; 2006); Singh *et al.* (2008); Terán and Singh (2009). However, gamete selection as originally proposed by Singh (1994) and further developed and validated by Singh *et al.* (1998); Asensio *et al.* (2006); and Terán and Singh (2009) is largely based on phenotyping for agronomic traits under field and greenhouse conditions. The hypothesis that the use of markers can improve the efficiency and precision of gamete selection

has not been tested (Kimani *et al.*, 2010). In addition, there is limited literature on the use of molecular markers in gamete selection.

In fact, the efficiency of breeding methods has improved with the latest progress in marker technology that permits breeders to manage the gene of interest and control the genetic background. Many markers linked to resistance genes for most important diseases in Eastern Africa have been identified (Musyimi, 2014; Njuguna, 2014). This included sequence characterised amplified regions (SCAR) linked to genes for resistance to angular leaf spot, anthracnose, common bacterial, *Pythium* root rot and bean common mosaic virus (Buruchara, 2007; Garzon *et al*., 2008). Many of these SCAR markers including SAB-3 for resistance genes to anthracnose, SH-13 for angular leaf spot, SW-13 for bean common mosaic virus and PYAA19 for *Pythium* root rot resistance genes are already being utilized in Kenya, Uganda, and Tanzania (Buruchara *et al*., 2011; Kimani *et al.*, 2012). The marker technology presents an opportunity to speed up the variety creation with more precision and thus reduces time to release of improved cultivars (Miklas *et al*., 2006). The use of markers in the gamete selection method and other conventional approaches for bean breeding could allow accelerating, augmenting precision and efficiency, and making easy the pyramiding of desirable genes. It was in that perspective that the marker-assisted gamete selection programme was initiated at the University of Nairobi in 2009. It was based on premise that the incorporation of markers on gamete selection procedure can improve the efficiency and precision of pyramiding genes for resistance to major diseases in Eastern Africa. Milestones and major achievements of that breeding programme in the early generations have been reported by Njuguna (2014); Musyimi (2014) and University of Nairobi Bean Research Programme (2016). The present work is a continuation of that breeding programme and is reporting on advanced generations ($F_{1.3}$ to $F_{1.8}$) for the period of 2013 to 2018.

2.7. Bean breeding for disease resistance in Kenya and Eastern Africa since the 1970s

2.7.1. Before 1985

Bean improvement in Kenya started in the late 1970s with a collaborative green legume programme between the University of Nairobi, the Dutch government and the Ministry of Agriculture (Kimani *et al.*, 2014). Research work was based at National Horticultural Research Station in Thika (Green Legume Project GLP) and at Kabete Field Station of the University of Nairobi (Mukunya and Keya, 1978). Initially this work was started at Kabete where a collection

of 1,250 accessions (local and introduced) were tested for yield and resistance to major diseases (Mukunya and Keya, 1978). From their findings, halo blight resistance and other resistances were associated with small red beans. Introduced materials were more susceptible to rust than the local ones. Several lines combining high yield potential and tolerance to diseases were identified. Among these were NB16, NB86, NB627, NB549, NB1181, NB84 and NM683. Among them, NB84 recorded the highest yield (2,400 kg ha^{-1}). These materials were evaluated at GLP Thika and several lines were released in 1984 including GLP2 (Rosecoco, a red mottled), GLP92 (Mwitemania, a pinto), GLP1004 (Mwezi Moja), GLP24 (Canadian Wonder, a dark red kidney), GLP585 (Wairimu or Red haricot, a small red) and GLP1127 (New Mwezi Moja). At the same period (in the early 1980s), FAO/UNDP Grain Legume Project initiated a bean breeding programme at Katumani. That programme released three cultivars in 1998 (KATB1, KATB9 and KATB2) and two others in 2001 (KATX-56 and KATX-69). In collaboration with CIAT, KALRO-Kakamega developed and released three root rot tolerant cultivars (KK 8 or SCAM 80/15 CM, KK 15 or MLB 49-89a; KK 22 or RWR 719), which were adapted to agro-ecological conditions of western Kenya (Kimani *et al.,* 2014). The main objectives of these programmes were to increase the common bean seed yield by developing cultivars with tolerance to biotic and abiotic production limiting factors.

2.7.2. From 1985 to 2000

Networking was embraced. There were creation of regional networks for the institutionalisation and support to participatory approaches in bean breeding as well as to ensure that research outcome was shared across national boundaries. To do so, two networks were formed in the mid-1980s following the coming of CIAT scientists in the region (Kimani *et al.,* 2005b). The East African Bean Research Network (EABRN) included national programmes of Uganda, Sudan, Kenya, Tanzania, Mauritius, Ethiopia and Madagascar and the RESAPAC (Réseau d'Amélioration de Phaseolus en Afrique Centrale) which comprised the DRC, Rwanda and Burundi. RESAPAC and EABRN were combined in 1995 to form the East and Central Africa Bean Research Network (ECABREN), responsible for nine countries (DRC, Uganda, Rwanda, Burundi, Kenya, Northern Tanzania, Sudan, Madagascar, and Ethiopia). During the same period, the SABRN (Southern Africa Bean Research Network) was created and was constituted of the national programmes of Malawi, Zambia, southern Tanzania, Zimbabwe, Mozambique, Angola,

South Africa, Botswana, Lesotho, Swaziland and Angola. These organisations offered an opportunity for the exchange of information, materials, and technologies. Technologies created in one region were utilized in other areas with similar conditions (Kimani *et al.,* 2005b). From 1985 to 2000, the Pan-African Bean Research Alliance (PABRA), in partnership with National Agricultural and Extension Services (NARES) and Non-Government Organisations (NGOs), had formulated and implemented many solutions, strategies, and approaches with the purpose of reducing the constraints encountered by the bean smallholder farmers. The main approach for improving bean yields in small-scale farms was to provide varieties with superior yield potential through the introduction, testing, and dissemination of varieties with genetic tolerance or resistance to the main biotic and abiotic constraints, as well as disseminating appropriate farming practices that alleviate the effects of these constraints (Kimani *et al.,* 2005b). The specific solutions proposed and implemented were to:

- Develop and make available seed of cultivars with high yield potential
- Develop and make accessible integrated pest and disease control measures
- Develop and make accessible soil management practices to enhance soil fertility in rural areas
- Develop and make accessible less labour-intensive technologies for soil management

With respect to pest and diseases, the following advances were achieved:

a. Germplasms with reliable resistance to diseases and pests

The project has released several germplasms to the national programmes within the 15 years. These either came from the CIAT headquarters in Colombia or were reconstituted as an outcome of further testing by project scientists in Africa in partnership with NARS scientists. From 1985 to 1996, 349 international bean nurseries (IBN) and international bean yield adaptation nurseries (IBYAN), 150 constraint nurseries, and over 3000 segregating populations and advanced lines were disseminated to NARS in Africa (Strachan *et al.,* 1999). Another 300 segregating multiple-constraint populations with specific combinations of resistance for Africa were disseminated in 1997, 1998, and 1999 (H. Gridley, personal communication). These comprised populations with multiple disease resistance to angular leaf spot, anthracnose, bean common mosaic virus, and common bacterial blight and with tolerance to low soil fertility (Kimani *et al.,* 2005b). Nurseries with resistance/tolerance to bruchids and bean stem maggot were disseminated to a small number of NARS for further testing (K. Ampofo, personal communication). Genotypes with tolerance to

low soil nitrogen and to phospate- and acidity-related problems and with resistance to root rot and angular leaf spot were sent to the multiple-constraint breeding programme based at the University of Nairobi (C. Wortmann and R. A. Buruchara, personal communication). Most of these lines were later utilized as parents in the crossing programme (Kimani *et al.,* 2005b).

Considerable progress in developing bean cultivars responsive to the needs of smallholder farmers was made by the Pan African Bean Research Alliance (PABRA) with its NARS partners and other stakeholders. A record 188 distinct varieties were released and have contributed significantly to improvements in the livelihoods of resource-poor rural communities through increased availability of food and household income, savings in cooking time, reduced wood fuel consumption, gender equity, and empowerment of women and other vulnerable groups (Kimani *et al.,* 2005b).

b. Cultivars resistant to diseases and pests

Resistant cultivars to one or more diseases were released by one or more NARS. For example, Awash 1 with resistance to rust was released in Ethiopia in 1989. Raozin'Alaotora, released in Madagascar in 1995, was resistant to rust, ascochyta, and angular leaf spot. CAL 143, released in Malawi, was tolerant to angular leaf spot. Vunikingi, a climber genotype and resistant to *Fusarium* root rot, was released in Rwanda in 1985. Uyole 98, released in Tanzania, was resistant to anthracnose. K131, released in Uganda and Zambia, was resistant to bean common mosaic virus and bean common mosaic necrosis virus (Kimani *et al.,* 2005b).

Following aspects were recommended by the PABRA programme for increasing bean yields and guiding breeding priorities in member countries:

- The use of marker-assisted selection for important traits, such as resistance to anthracnose, rust, common bacterial blight, etc. to increase the efficiency of the breeding programme.
- Multiple-constraint breeding, an alternative to yield improvements *per se*, is incorporating resistance to yield-reducing traits. Future breeding strategies should focus on reducing these losses by incorporating as many resistance genes in popular cultivars as possible. In several cases, many production constraints are limiting, and introducing resistance to one will not lead to a considerable change. Resistance to several constraints

is particularly essential for smallholder, resource-poor farmers who have a limited ability to improve the production environment (Kimani *et al.*, 2005b; Mahuku *et al.*, 2009).

- Broadening the genetic base by introducing the Mesoamerican gene pool genotypes, which are known to be high yielding and possess genes of resistance to major diseases of Andean gene pool beans in Africa (Welsh *et al.*, 1995).

2.7.3. From 2000 to date

Since 2000 dry bean breeding programmes in Eastern Africa adopted the market-led strategy to develop new cultivars targeting particular markets (Kimani *et al.*, 2005b). Dry bean breeding for multiple disease resistance in Eastern Africa involved the collection of local germplasm and introductions from CIAT and regional germplasm collections. These materials comprised segregating populations and advanced breeding lines which allowed a subsequent development of new segregating populations from simple and multiple crosses (Kimani *et al.*, 2008). Among large-seeded types, around 15 red mottled varieties with multiple resistance to angular leaf spot, anthracnose, BCMV, halo blight and common bacterial blight were released in six Eastern African countries between 2003 and 2008 (Kimani *et al.*, 2008). During the same period, 12 red kidney bean varieties with multiple resistance to ALS, anthracnose, BCMNV, BCMV, halo blight and CBB was released in Eastern Africa countries (Tanzania, DRC, Kenya, Ethiopia, Madagascar, Uganda, and Rwanda)(Kimani *et al.*, 2008). Also, eight new speckled sugar varieties were released in Kenya, Uganda, Ethiopia and DRC between 2003 and 2008. Among small- and medium-seeded types, eight small red varieties with multiple resistances to ALS, halo blight, and rust were released in Ethiopia, Kenya and Madagascar between 2003 and 2008. Eighteen varieties of other colors such as brown, tan and yellow with multiple resistance to diseases were released in five Eastern African countries (Kimani *et al.*, 2008). PABRA released a total of 146 improved bean varieties from 2003 to 2008. During 2009 to 2011, PABRA released 67 varieties with resistance to two or more stress factors, 13 of which were released for high Fe and Zn content, and 14 varieties released for specific niche markets (canning, snap and dry beans) (Buruchara *et al.*, 2011).

In Kenya, four early maturing sugar bean cultivars (New Rosecoco, Miezi Mbili, Kenya Speckled Sugar, and Kenya Early) developed by the University of Nairobi Bean Research Programme, were released by the Ministry of Agriculture in 2008. This programme had released

several other varieties with different attributes. These included three climbing beans in 2008. The programme subsequently developed biofortified bean varieties (Kimani *et al.*, 2016). In 2011, four biofortified bush bean varieties (Rosecoco Madini, Kenya Mauwa, Kenya Almasi, and Kenya Cheupe), and three climbers (Kenya Afya, Kenya Majano, Kenya Madini) were released and gazetted by the Ministry of Agriculture.

The programme embarked on the development of canning beans at the request of the canning industry in 2011. Four canning beans (Kenya Cheupe, Kenya Salama, Kenstar, Kenya Mamboleo) were released in 2015. Recently in 2018, three other varieties with niche markets were released. These included one canning bean (Kenya Dark Red Kidney) and two snap bush beans (Kenya Amboseli and Kenya Safari). These releases represent future directions of bean research as described by Kimani *et al.* (2005b). Kimani *et al.* (2014) reported that bean cultivars developed in Kenya has been shared in 33 countries from Africa, Asia, North and South America, Australia and Europe.

Binagwa *et al.* (2018) reported the release of seven new varieties in Tanzania by the Selian Agricultural Research Institute (SARI) in January 2018. These include two early maturing varieties (SELIAN13 and SELIAN12); three white canning beans (SELIAN09, SELIAN10, and SELIAN11) and two micronutrient-dense varieties (SELIAN14 and SELIAN15). These varieties are expected to improve the livelihood and health of farmers as well as to contribute to Tanzania slogan of industrialization.

2.8. Genotype by environment interaction and stability analysis

2.8.1. Definition of concepts

Adaptation refers to characteristics that enable a bean variety to produce high yields in a particular climatic environment. Wide adaptation is desired in varieties of beans that are to be grown over large geographic areas in which the agro-climatic conditions will vary. Because bean varieties and germplasms produced by breeding programmes are distributed widely throughout the tropical and subtropical bean production areas, wide adaptation is an important objective in the variety improvement programmes.

Stability refers to the consistency with which a variety produces satisfactory yields in local area in which weather and disease conditions vary from year to year. The yield stability is crucial in any plant breeding programme as individuals are affected by the environment where and when

they are grown. Screening for stability will, therefore, require that a variety is tested at several locations within the area over several seasons.

The phenotype of a given individual is a combination of both genotypic (G) and environmental (E) effects, resulting in an inconsistent performance across locations. The expression **genotype** refers to the genetic composition of an individual. **Environment** refers to biophysical factors that have an effect on the growth and development of a genotype.

Genotype by environment interaction (G × E) is when two different genotypes respond to environmental variation in different ways. The G × E study is especially important in countries with various agro-ecologies. Significant G × E interaction is a consequence of variations in the extent of differences among genotypes in diverse environments (called as a qualitative or rank changes) or variations in the comparative ranking of the genotypes (called as a quantitative or absolute differences between genotypes).

2.8.2. Stability analysis in bean breeding

In bean breeding programmes, a large number of genotypes are tested for many generations within contrasting environments before release for seed multiplication and distribution to growers (Corrêa *et al.,* 2015). Because environmental conditions for testing are distinct, the genotype and environment interaction (G x E) affects the agronomic performance (seed yield and yield components), making necessary to analyze its magnitude and stability of genotypes across environments (Ashango *et al.,* 2016; Tadesse *et al.,* 2017). These estimates allow the assessment of the real impact of selection and ensure high reliability in the genotype recommendation for a specific place or environment groups (Correa *et al.,* 2016). A multi-location testing of genotypes is, therefore, useful during the selection process because it provides information on specific or broader adaptation for a given genotype. Another key reason for the G x E analyses in bean breeding in Africa is that lines adapted to an African bean environment (AFBE) can be grown in similar areas in other parts of Africa (Wortmann and Allen, 1994). Due to differences among growing regions, breeding might be more effective if it was AFBE based. Therefore, we hope that lines developed through the current breeding programme in the AFBE of Kenya could be adapted and disseminated in African areas with similar agro-ecological conditions.

2.8.3. Determination of G x E effects and stability analysis

Several methods are used for the G x E analysis of cultivars by plant breeders. These are based on analysis of variance or on non-parametric, regression, multivariate analysis or mixed models. Among the multivariate methods, the additive main effect and multiplicative interaction (AMMI) model is the most commonly used for G x E analysis (Gauch and Zobel, 1997; Gauch *et al.*, 2008). This method has been effective because it captures a large portion of the G x E sum of squares; it clearly separates main and interaction effects and often provides meaningful interpretation of data to support a breeding programme such as genotype stability. AMMI uses ANOVA to test the main effects of genotypes and environments, and PCA to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G × E interaction, with a minimum number of degrees of freedom (Zobel *et al.*, 1988). The AMMI model is as follows:

$$y_{ger}=\mu+\alpha_g+\beta_e+\Sigma\lambda_n y_{gn}\delta_{en}+\rho_{ge}+\varepsilon_{ger} \qquad (1)$$

Where Y_{ger} is the yield of genotype g in the environment e for replicate r ; μ is the grand mean; αg is the genotype mean deviations; β_e is the environment mean deviation; n is the number of PCA axes retained in the model, λ_n is singular value for PCA axis n; y_{gn} is the Genotype eigenvector values for PCA axis n ; δ_{en} is the environment eigenvector values for PCA axis n ; ρ_{ge} represents the residuals and ε_{ger} is for error.

The stability of genotypes across locations can be determined using the PCA scores (IPCA1 and IPCA2). The IPCA score near zero reveals more stable genotypes, while large values indicate more responsive and less stable genotypes. AMMI's stability value for the grain yield is estimated as shown as follows (Purchase, 1997):

$$\text{ASV}=\sqrt{\left[\frac{\text{SS IPCA 1}}{\text{SS IPCA 2}}(\text{IPCA 1 Score})\right]^2+(\text{IPCA 2 Score})^2} \qquad (2)$$

Where ASV is the AMMI stability value, SS IPCA 1 and SS IPCA 2 are the sum of squares of IPCA 1 and 2, respectively and IPCA is the interaction principal component analysis. Thus, lowest ASV indicates a wide adaptation of specific genotypes for certain environments and vice-versa.

AMMI and GGE biplots are commonly constructed to determine adaptation and stability of genotypes across test environment. From this analysis, genotypes located near the biplot origin are considered as widely adapted, while genotypes located far are specifically adapted. All the genotypes with positive IPCA1 scores respond positively to the environment having positive IPCA1 scores, and are, therefore, adapted to that particular environment (Samonte *et al.*, 2005).

CHAPTER 3: AGRONOMIC PERFORMANCE OF INTER-RACIAL SMALL- AND MEDIUM-SEEDED BEAN POPULATIONS

ABSTRACT

Broadening the genetic base of existing breeding populations is crucial for increasing the variability and the chance of finding more promising genotypes. The objectives of this study were to: i) Evaluate the agronomic performance and other traits of $F_{1.3}$ to $F_{1.6}$ generations from 16 inter-racial small- and medium-seeded populations selected in early generations using markers linked to genes for disease resistance, and ii) Identify with respect to market classes, the most promising $F_{1.6}$ genotypes to be advanced for further testing and release. Experimental trials were carried out from 2013 to 2015 at Kabete Field Station of the University of Nairobi for the $F_{1.3}$ to $F_{1.5}$ generations. The $F_{1.6}$ experiment was conducted at Mwea Research Station of Kenya Agricultural and Livestock Research Organization (KALRO) in 2016. Regardless of the generation, a randomized complete block design (RCBD) with three replications was used. Data on plant vigor, growth habit, days to flowering, flower color, days to physiological maturity, number of pods per plant, number of seeds per pod, 100-seed mass, seed color, seed uniformity, field disease score, seed yield per plant and per hectare were collected. Analysis of variance (ANOVA) and Fisher's least significant difference (LSD) test were performed on the quantitative data to compare and separate means for the different populations and lines within those populations. Pearson's correlation coefficient was used to determine the relationship between seed yield and other agronomic traits. Results revealed significant differences for all the traits among populations, commercial checks and donor parents ($P<0.05$). Although, the populations were not consistent over generations and across sites, crosses involving the commercial variety KATB9 were high yielding and superior for most of agronomic traits. At the $F_{1.6}$ generation, which was used for the final selection before separating the lines by market classes, the population KMA13-32 from KATB9 x Mex54 / G2333 // RWR719 / BRB191 crosses, out-yielded all the other populations and all checks with a mean seed yield of 2,844 kg ha^{-1}. Other high yielding populations were KMA13-31 (2,504 kg ha^{-1}) and KMA13-30 (2,248 kg ha^{-1}), respectively from KATB9 x Mex54 / G2333 // AND1062 / BRB191 and KATB9 x G10909 / G2333 // RWR719 / BRB191 crosses. However, these three populations were not significantly different from the best check variety KATB9 (2,385 kg ha^{-1}). All other crosses were either statistically equal or lower than the commercial checks. Seed yield ha^{-1} was significantly

and positively correlated to the number of pods per plant (r=0.8530***), to the number of seeds per pod (r=0.2970***) and to seed yield plant^{-1} (r=0.9724***). However, seed yield ha^{-1} was negatively correlated to plant vigor (r=-0.2167***) and to 100-seed mass (r=-0.1657**). The number of pods per plant and the seed yield per plant could be, therefore, adopted by breeders as indirect selection criteria for seed yield. Inter-racial populations showed low to moderate infection levels by major bean diseases in all the generations (1.0 to 5.0), compared to commercial checks which were moderate to highly susceptible to most of the pathogens (3.1 to 9.0). In $F_{1.6}$ generation, 92 genotypes (from single plants) belonging to five market classes (19 small reds, 12 pintos, 13 red kidneys, 16 red mottled and 32 mixed colors) were selected for further testing regardless of the populations they originated from. The presence of transgressive genotypes in most of the populations, combining high yield potential and multiple disease resistance at any generation, confirmed the effectiveness of inter-racial crosses to improve the seed yield of common bean and the resistance to major bean diseases in Eastern Africa.

Keywords: Gamete selection, inter-racial population, generation, market class, yield potential

3.1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important food legume in the tropics (Polania *et al.,* 2016) where it is the main source of dietary protein (Zupin *et al.,* 2017). Over 200 million people in Africa, especially women and children living in rural areas and poorer urban communities depend on it for quality food (rich in protein, vitamins, energy, and micronutrients) and household income (PABRA, 2017). In Eastern Africa, which covers more than 60% of bean growing areas in Africa, bean consumption can be as high as 60 kg per capita per year in countries like Rwanda or in western Kenya (Buruchara, 2007; Beebe *et al.,* 2013).

Despite its importance, bean yields in Eastern and Central Africa are among the lowest in the world, with an average yield of 0.5 t ha^{-1} (FAO, 2018) compared to potential yield in Eastern Africa of 1 to 3 t ha^{-1} commonly reported in experimental sites, and up to 4 t ha^{-1} reported in the USA (Hillocks *et al.,* 2006; Kiptoo *et al.,* 2016). The low yields have been attributed to biotic (especially diseases and pests) and abiotic constraints, climate variability, limited use of external inputs due to socio-economic factors, and poor adaptation of introduced varieties to local

conditions (Kimani *et al.,* 2005b; Beebe, 2012; Beebe *et al.,* 2013; Kimani, 2014). Although losses due to biotic and abiotic stresses can be reduced by use of fertilizers in combination with other appropriate cultural management, chemical and irrigation technologies, associated costs are not practical for the widespread low-input systems in Sub-Saharan Africa (Fizgerald and Lindow, 2013; Kimani, 2014).

Plant breeding can contribute to meeting the demand for food and feed by developing high yielding genotypes that adapt to agricultural production ecosystems (Bertoldo *et al.,* 2014). Hybridization is commonly used in common bean improvement to obtain segregating populations with high productivity, sufficient levels of genetic variability, and other desirable characteristics (Ceolin *et al.,* 2007). Therefore, populations that are unpromising for breeding should be discarded as soon as possible to prevent wastage of time and resources in evaluating underperforming lines (Menezes *et al.,* 2016).

Broadening the genetic base of existing breeding populations to enhance the genetic potential for important agronomic traits is crucial in the East and Central Africa (Kimani *et al.,* 2005b) because it increases the variability and the chance of finding more promising genotypes in the segregating materials (Singh, 2001). Inter-racial and inter-gene pool crosses are, therefore, important to create a useful genetic variation for maximizing gains from selection, broadening the genetic base of commercial cultivars and making efficient use of available resources (Welsh *et al.,* 1995). In fact, there are several reasons for the growing interest of combining Andean and Middle American (Mesoamerican) genotypes, including enlarging genetic base for more durable and increased levels of resistance to both biotic and abiotic factors affecting bean production. Also combining the higher yielding Middle American to its large-seeded Andean counterparts stems from a greater market demand for large-seeded beans in Africa and South America (Welsh *et al.,* 1995; Sichilima *et al.,* 2016). In addition, there is an urgency to stabilize and improve yield because of limited resources available to farmers, the occurrence of new strains of major diseases, low soil fertility and drought (Welsh *et al.,* 1995; Singh *et al.,* 2002; Singh and Schwartz, 2010).

The common bean yield is often affected by a range of constraints, and thus, breeding for one will not result in a significant change (Kimani *et al.,* 2005b; Okii *et al.,* 2017). Breeding for one trait at a time, is also expensive and time-consuming; hence justifying a need for a multiple

constraint breeding method (Singh, 1994). Gamete selection procedure is more appropriate as it allows concurrent selection for multiple traits (Beaver and Osorno, 2009). Compared to other breeding methods such as bulk, pedigree, backcross, single seed descent and their modifications, the gamete selection permits identification of promising populations and families and consistent yield assessments in early generations and thus, helping to avoid wastage of scarce resources and time (Singh, 1994). This method should be, therefore, encouraged in Eastern Africa where it is not widely used in breeding for multiple constraints. Although not common (Singh *et al.,* 1998; Asensio *et al*., 2006; Terán and Singh, 2009), the incorporation of molecular markers in gamete selection method can speed up, improve the efficiency and precision of multiple constraint breeding instead of relying on phenotyping for agronomic traits (Kimani *et al.*, 2010).

The overall objective of this study was to contribute to the development of high yielding bean cultivars with multiple disease resistance in East and Central Africa. The specific objectives were to: i) Evaluate the agronomic performance and other traits of $F_{1.3}$ to $F_{1.6}$ generations from 16 inter-racial small- and medium-seeded populations selected in early generations using markers linked to genes for disease resistance, and ii) Identify with respect to market classes, the most promising genotypes to be advanced for further evaluation and release.

3.2. MATERIAL AND METHODS

3.2.1. Experimental site

Field experiments for $F_{1.3}$ to $F_{1.5}$ were conducted at Kabete Field Station of the University of Nairobi from 2013 to 2015. The $F_{1.6}$ experiment was carried out at Kirogo Research Station of Kenya Agricultural and Livestock Research Organization (KALRO) in Mwea Constituency, Kirinyaga County during 2016 short rain season (from October 2016 to February 2017).

Kabete Field Station is located at 01°15'S; 036°44'E and at 1820 masl. The station experiences mean bimodal precipitation of 1059 mm per year. Temperatures range from 12.3°C to a mean maximum temperature of 22.5°C. The soils are humic nitisols, very deep, well-drained, friable clay with acid humic topsoil, dark reddish brown. The pH is about 5.0 to 5.4 and a mean sunshine of 6.6 hours per day. Kabete Field Station is located in the African Bean Environment I (AFBE 1), which is characterized by sub-humid highland (>1500 masl) of high potential at low

latitude; high available moisture (> 400 mm), acidic pH and bimodal rains (Wortmann and Allen, 1994). Most of the bean diseases occur naturally at Kabete and, therefore, suitable for disease screening. It is the main testing site of the University of Nairobi Bean Research Programme with critical research infrastructure and is, therefore, more cost effective and convenient.

Kirogo Research Station is located on coordinates 0°38'S; 37°22'E and at an elevation of approximately 1150 m above sea level. This research station experiences a bimodal rainfall regime with an annual mean of 850 mm. Long rains occur from March to May while short rains are between October and December. The mean annual maximum and minimum temperatures recorded at the station are 28.6°C and 15.6°C, respectively. It has vertisol soils with an acidic pH of about 5.1 (Ndungu *et al.,* 2004; Wahome *et al.,* 2011; NARL, 2016). Mwea represents a sharply contrasting bean growing environment region and AFBE 8. This AFBE is characterized by semi-arid conditions, mid-altitude (1000 to 1500 masl), low latitudes, low available moisture (<400 mm), acidic pH and bimodal rains (Wortmann and Allen, 1994). Excellent facilities such as reliable irrigation and fast crop growth facilitating rapid evaluation justified its choice in this study.

3.2.2. Plant materials

In 2013, a total of 768 lines from 16 $F_{1.3}$ inter-racial populations (making 48 lines per population) and 10 commercial checks and donor parents were grown at Kabete Field Station. In 2014, 463 lines selected from the previous generation were advanced as $F_{1.4}$ generation. In 2015, 279 selected lines were evaluated as $F_{1.5}$ at Kabete Field Station. A total of 239 genotypes were evaluated at Kirogo Research Station during the 2016 short rain season for the $F_{1.6}$ generation. These included 229 $F_{1.6}$ lines from 16 inter-racial common bean populations and 10 parental genotypes used as checks (Table 3.4).

These populations were derived from crosses made among sources of resistance to angular leaf spot, anthracnose, root rots, common bacterial blight, and bean common mosaic virus and susceptible commercial varieties (Kimani *et al.,* 2012; Njuguna, 2014).

Sources of resistance

In these crosses, Mex54 (Namayanja *et al.,* 2006) and G10909 (Mahuku *et al.,* 2003; Vallejo and Kelly, 2009) were used as source of resistance to angular leaf spot; G2333 to anthracnose

(Melotto and Kelly, 2000; Awale and Kelly, 2001; Miklas and Kelly, 2002); RWR719 (Otsyula *et al.,* 2003; Nzungize *et al.,* 2011) and AND1062 (Mukalazi *et al.,* 2001) to *Pythium* root rot while BRB191 (CIAT, 2003) was used for its *bc-3* resistance genes that confer resistance to bean common mosaic virus (Table 3.1).

Mex54 has medium-sized seed, with an indeterminate growth habit and has been previously identified as resistant to most African *P. griseola* races (CIAT, 1996). Mex54 has been found to contain a single dominant gene for resistance to angular leaf spot (Nietsche *et al.,* 2001; Mahuku *et al.,* 2004; Namayanja *et al.,* 2006).

G10909 is a medium red-seeded climbing bean genotype from the highlands of Guatemala that was identified as having high levels of resistance to *P. griseola* under field conditions (Pastor-Corrales *et al.,* 1998) and under greenhouse conditions using *P. griseola* pathotypes of diverse origin (Mahuku *et al.,* 2003).

The Mexican landrace, G2333 commonly referred as Umubano, has been widely used as a source of resistance to *Colletotrichum lindemuthianum*, the causal agent of anthracnose (Young and Kelly, 1996; Vallejo and Kelly, 2009). G2333 carries three characterized naturally-occurring gene pyramid for anthracnose resistance: *Co-4*^{2}, *Co-5* and *Co-7* (Pastor-Corrales *et al.,* 1995; Young *et al.,* 1998). The most effective gene in this pyramid is *Co-4*^{2}, which conferred resistance to 33 out of 34 different races of *C. lindemuthianum* collected from 9 different countries in the Americas (Balardin *et al.,* 1997).

RWR719 is a late maturing small red-seeded variety of Mesoamerican gene pool which is resistant to all species of *Pythium* (Otsyula *et al.,* 2003; Nzungize *et al.,* 2011a). AND1062 is a medium maturing and the only large-seeded variety resistant to *Pythium* (Mukalazi *et al.,* 2001). These genotypes are known to possess resistance to *Pythium* which is controlled by a single dominant gene (Otsyula *et al.,* 2003; Nzungize *et al.,* 2011a). RWR719 and AND1062 have been proposed as donors for resistance against the virulent and predominant *Pythium spp*. in breeding programmes to create common bean varieties resistant to bean root rot and adapted to Eastern and Central Africa (Otsyula *et al.,* 2003).

The red mottled Andean genotype BRB191 was utilized due to its *bc-3* resistance genes that confer resistance to bean common mosaic virus (CIAT, 2003).

Susceptible commercial parents

GLP92, GLP585, KATB9 and KATB1 were used as susceptible parents. They were mainly chosen because of their seed quality, high marketability, seed yield potential and good adaptation to agro-ecological conditions of Eastern Africa (Kimani *et al.,* 2012; Njuguna, 2014).

KATB1 is a high yielding, early maturing, and determinate variety, resistant to rust but susceptible to angular leaf spot and anthracnose. It is recommended for semi-arid areas where rainfall is below 250 mm per season, preferably at higher altitudes between 1000 m and 1800 m above sea level. Seeds are bold, round and deep yellow in color (Kimani *et al.,* 2012).

KATB9 is a drought tolerant, compact and bushy genotype with a yield potential ranging between 1400 and 1900 kg ha^{-1}. It is preferred for its dark red seeds, low flatulence and sweet taste (Kimani *et al.,* 2012). The two genotypes KATB1 and KATB9, basing to their early maturity, seed type, color, structure, taste and marketability are highly demanded by bean traders in the East African countries (Ruraduma *et al*., 2016; Binagwa *et al.,* 2017).

GLP585 Wairimu or Red haricot bean is a small-seeded commercial variety with good marketability traits and potentially a high yielder. It is adapted especially in altitudes ranging between 1500 and 2000 m above sea level and matures in 2.4 to 3 months. It has bright red seeds. It is susceptible to angular leaf spot, anthracnose and root rot diseases but resistant to common bean mosaic virus (Kimani *et al.,* 2012).

GLP92 Mwitemania is a late maturing (85 to 95 days), indeterminate, semi-spreading, high yielding pinto bean (1200 kg ha^{-1}). It is resistant to halo blight but susceptible to bean common mosaic virus, rust, anthracnose and angular leaf spot (Kimani *et al.,* 2012). It has wide adaptability to various agro-ecological zones from low to high rainfall areas and hence recommended for all bean-growing areas except for those notorious for bean common mosaic virus (Kimani *et al.,* 2012). Seeds are round and broad with brown flecks on cream background. The major characteristics of these parental genotypes are summarized in Table 3.1.

Table 3.1. Major characteristics of parental bean lines used in population development

Genotypes	[1]Gene pool	Seed color	[2]Growth habit	[3]Reaction to diseases					Markers	References
				ALS	ANT	RR	BCMV	CBB		
Donor parents										
G2333	M	Red	IV	R	R	S	S	S	SAB3 SAS13 $SBB14^{1150/1050}$	Young and Kelly, 1996; Vallejo and Kelly, 2009
Mex54	M	Cream beige	IV	R	S	S	S	S	$OPE4^{708}$	Queiroz *et al.*, 2004
G10909	M	Red	IV	R	S	S	S	S	$SH13^{520}$	Mahuku *et al.*, 2011
RWR719	M	Red	I	S	S	R	S	S	$PYAA19^{800}$	Muhuku, 2005; Otsyula *et al.*, 2003
AND1062	A	Red Kidney	I	S	S	R	S	S	$PYAA19^{800}$	Muhuku, 2005; Otsyula *et al.*, 2003
BRB191	A	Red Mottled	I	S	S	S	R	R	$SW13^{690}$	Sharma *et al.*, 2008
Susceptible parents										
GLP585	M	Red	I	S	S	S	S	S	N/A	
GLP92	M	Pinto	II	S	S	S	S	S	N/A	
KATB1	M	Green	I	S	S	S	S	S	N/A	
KATB9	M	Red	I	S	S	S	S	R	N/A	

[1]A=Andean, M=Mesoamerican, [2]I=determinate, II=indeterminate bush, erect stem and branches, III=indeterminate bush with weak and prostrate stem and branches, IV=indeterminate climbing habit with weak, long and twisted stem and branches, [3]R=resistant, S=susceptible, ALS=angular leaf spot, ANT=anthracnose, BCMV=bean common mosaic virus, RR=*Pythium* root rot, CBB=common bacterial blight

All the six donor parents and four selected commercial cultivars were subjected to phenotypic evaluation that involved artificially inoculating the plants (21 days-old seedlings) with known races of the pathogens, in the greenhouse conditions. Results obtained are presented in Table 3.2.

Table 3.2. Reaction of 10 parental bean lines to inoculation with target disease pathogens

Genotypes	Angular leaf spot	Anthracnose	Common bacterial blight	*Pythium* root rot	Bean common mosaic virus
G10909	1.0	1.0	7.4	5.2	7.9
Mex54	1.0	1.0	5.7	4.7	6.3
G2333	1.0	1.0	5.0	6.6	5.4
RWR719	5.5	1.0	4.0	1.0	4.2
AND1062	6.6	8.1	4.0	1.0	4.8
BRB191	4.0	8.4	2.0	1.0	3.0
GLP585	5.4	4.3	5.3	5.7	3.7
GLP92	6.6	2.5	6.7	6.1	5.0
KATB1	6.5	9.0	4.1	7.1	6.8
KATB9	7.4	8.8	2.6	6.9	6.8

Source: Musyimi (2014) and Njuguna (2014)

The assessment of the disease severity was done 21 days after inoculation using a 1-9 scale developed at CIAT (1-3 highly resistant, 3.1-5 resistant, 5.1-7 susceptible and 7.1-9 highly susceptible) (Schoonhoven and Pastor-Corrales, 1987). Table 3.2 showed that G2333, Mex54 and G10909 were resistant to angular leaf spot and anthracnose. RWR719 was resistant to *Pythium* root rot and anthracnose. BRB191 showed resistance to common bacterial blight, *Pythium* root rot and the bean common mosaic virus. The test confirmed which parents were resistant to what disease, setting a solid base for population development and breeding for resistance.

Population development

Populations under study were developed from crosses made between 2009 and 2010 at Kabete Field Station of the University of Nairobi (Njuguna, 2014; UoN Bean Research programme, 2016). Development of populations involved making single crosses in the first round of crossing. The single crosses were subsequently combined into double crosses during the second round of crossing. Male gametes with requisite resistance genes were then identified using markers SAB-3 for anthracnose (Garzon *et al.,* 2008); SH-13 for angular leaf spot; SW-13 for bean common mosaic virus (Melotto *et al.,* 1996; Sharma *et al.,* 2008; Wani *et al.,* 2017) and PYAA-19 for *Pythium* root rot (Namayanja *et al.,* 2014). Lines with these male gametes were thereafter used to construct the F_1 in the final cross of the double-cross gamete to the commercial varieties (Singh, 1994). Selection started in F_1 instead of F_2 in normal cases. A total of 16 populations were developed. The segregating F_1 and $F_{1.2}$ populations were then evaluated for agronomic attributes and tested for resistance to target diseases under natural disease infestation in the field at Kabete and Tigoni in 2011 and 2012 (Njuguna, 2014). Molecular markers were used to screen the male gametes and the segregating F_1. $F_{1.2}$ progenies were thereafter advanced following gamete selection procedure up to $F_{1.6}$ during the period of 2013 to 2016 (Table 3.3). The breeding scheme used to develop these populations is summarized in Figure 3.1.

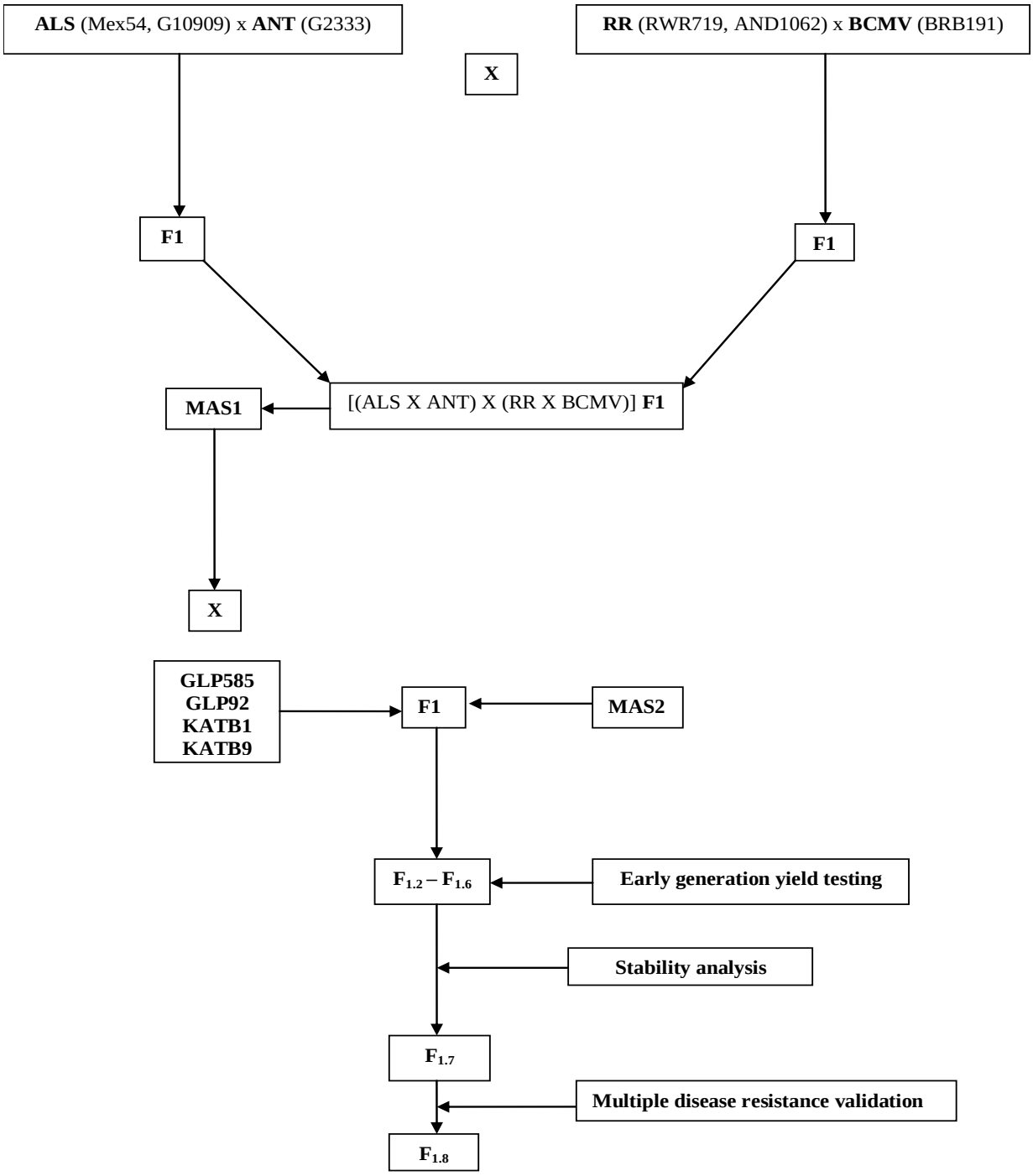


Figure 3.1. Marker-Assisted Gamete Selection Breeding Scheme at the University of Nairobi

Table 3.3. Milestones of marker-assisted gamete selection used for the simultaneous improvement of resistance to angular leaf spot, anthracnose, *Pythium* root rot and bean common mosaic virus disease in common bean at the University of Nairobi from 2009 to date

Year	Generations	Achievements
Before 2009	Parents	Resistant genotypes were selected for their resistance genes; Mex54 and G10909 for angular leaf spot; G2333 for Anthracnose; AND1062 and RWR719 for *Pythium* root rot and BRB191 for bean common mosaic virus.
2009-2010	Single crosses	Single crosses were developed between genotypes carrying resistance genes to angular leaf spot and anthracnose (Mex54/G2333, G10909/G2333), and between *Pythium* root rot and bean common mosaic virus (AND1062/BRB191, RWR719/BRB191).
2010-2011	Double crosses	Four double cross males were produced by combining two single crosses: (Mex54/G2333) and (AND1062/ BRB191); (Mex54 /G2333) and (RWR719/BRB191); (G10909/G2333) and (AND1062/BRB191) and (G10909/G2333) and (RWR719/BRB191).
2010-2011	Identification of male gametes for the final cross	Male gametes were screened for desirable resistance genes with molecular markers i.e. SH-13 for angular leaf spot, SAB-3 for anthracnose, PYAA-19 for *Pythium* root rot and SW-13 for bean common mosaic virus. Selected single plants were utilized for the production of final multiple-parent crosses with commercial varieties (GLP585, GLP92, KATB1 and KATB9) using plant-to-plant paired hybridization.
2011-2012	F_1	Evaluation of the final F_1 for successful introgression of resistance genes in the field at Kabete against angular leaf spot, anthracnose, *Pythium* root rot and bean common mosaic virus and, agronomic traits. As the F_1 was segregating, markers were used for the second time to select specific desirable combinations.
2012-2013	$F_{1.2}$	Early generation yield testing at Kabete and Tigoni were conducted for identifying high yielding populations and discarding undesirable populations.
2013-2016	$F_{1.3}$-$F_{1.6}$	Further testings of segregating populations for yield potential and creation of market classes to switch from segregating populations to pure lines were conducted at Kabete and Mwea. Single plant selection was performed at $F_{1.6}$ and the seed was increased at Mwea Research Station in 2016.
2017-2018	$F_{1.7}$	Seed yield stability analysis and evaluation of the effects of G x E on seed yield of elite lines across three agro-ecological environments. These were Mwea (low altitude), Tigoni (high altitude) and Kabete (medium altitude). Five market classes were evaluated at this stage.
2017-2018	$F_{1.8}$	Field and greenhouse validation of the multiple disease resistance of the elite lines for angular leaf spot, root rot, bean common mosaic virus, common bacterial blight and the anthracnose.

Source: Njuguna (2014); Musyimi (2014); UoN Bean Research programme (2016).

The pedigree of the 16 small- and medium-seeded inter-racial populations evaluated and their genealogy are given in Table 3.4.

Table 3.4. Genealogy of segregating inter-racial bean populations used for this study from $F_{1.3}$ to $F_{1.6}$ generations

Population	Pedigree (cross)	No of lines evaluated per generation			
		$F_{1.3}$	$F_{1.4}$	$F_{1.5}$	$F_{1.6}$
KMA13-17	GLP585 x G10909 / G2333 // AND1062 / BRB191	48	33	4	3
KMA13-18	GLP585 x G10909 / G2333 // RWR719 / BRB191	48	31	1	1
KMA13-19	GLP585 x Mex54 / G2333 // AND1062 / BRB191	48	28	5	5
KMA13-20	GLP585 x Mex54 / G2333 // RWR719 / BRB191	48	32	2	2
KMA13-21	GLP92 x G10909 / G2333 // AND1062 / BRB191	48	29	29	26
KMA13-22	GLP92 x G10909 / G2333 // RWR719 / BRB191	48	33	27	27
KMA13-23	GLP92 x Mex54 / G2333 // AND1062 / BRB191	48	24	23	22
KMA13-24	GLP92 x Mex54 / G2333 // AND1062 / BRB191	48	26	24	19
KMA13-25	KATB1 x G10909 / G2333 // AND1062/ BRB191	48	32	22	24
KMA13-26	KATB1 x G10909 / G2333 // RWR719 / BRB191	48	30	18	16
KMA13-27	KATB1 x Mex54 / G2333 // AND1062 / BRB191	48	27	27	26
KMA13-28	KATB1 x Mex54 / G2333 // RWR719 / BRB191	48	30	15	13
KMA13-29	KATB9 x G10909 / G2333 // AND1062 / BRB191	48	30	24	23
KMA13-30	KATB9 x G10909 / G2333 // RWR719 / BRB191	48	31	16	13
KMA13-31	KATB9 x Mex54 / G2333 // AND1062 / BRB191	48	23	20	5
KMA13-32	KATB9 x Mex54 / G2333 // RWR719 / BRB191	48	24	22	4
Total		**768**	**463**	**279**	**229**

3.2.3. Methods

Experimental design and crop management

The $F_{1.3}$ generation was grown at Kabete Field Station on 14th October 2013 during the short rain season in a replicated trial with 3 replications. This experiment involved 768 lines from inter-racial populations and 10 parents. Progenies and the parents were grown on single rows of 3 m long spaced by 50 cm while spacing within rows was 10 cm. Recommended management practices were carried out including the application of diammonium phosphate (DAP) fertilizer at a rate of 80 kg ha^{-1}, three weedings and the application of Confidor (200 g l^{-1} Imidacloprid) to control whiteflies and leaf miner.

The $F_{1.4}$ generation experiment involving 463 lines from 16 inter-racial population and 10 parental genotypes was conducted at Kabete during the 2014 short rain season for the period of October 2014 to February 2015. The experiment was carried out under a randomized complete block design (RCBD) with three replications. Each progeny was grown on two 3-meter rows

spaced as described on $F_{1.3}$ generation. The same management practices, as for $F_{1.3}$ generation, were carried out including the application of DAP fertilizer, three weedings and the Confidor to control whiteflies and leaf miner.

The same experimental design as for $F_{1.4}$ generation was used in the 2015 short rain season for the $F_{1.5}$ generation which involved the evaluation of 279 lines grouped in 16 populations. Once again, parental genotypes were included in the experiment. The $F_{1.5}$ generation experiment was also conducted at Kabete Field Station. Regardless of the generation, water was supplied to plants through irrigation, in addition to rainfall.

In $F_{1.6}$ generation, the families, which were still segregating, were evaluated in a preliminary yield trial at Mwea during the 2016 short rain season (from October 2016 to February 2017). Selection for agronomic performance and other market-demanded traits were conducted both among and within populations. The study materials were grouped into three sets; set I were the populations, set II the progenies (lines) and set III were individual plants within progeny rows. The trial was laid out in a randomized complete block design (RCBD) with three replications. A total of 229 $F_{1.6}$ genotypes and 10 progenitors were planted on 14th October 2016. Each progeny row (line) was grown on two 4-meter rows with a seed rate of 10 seeds m^{-1} and a row spacing of 0.5 m. Control genotypes (commercial checks and donor parents) were included in each set and were each planted on two 4-meter rows spaced as described above. Populations, progeny rows and controls were randomly allocated to the sets (Vilela *et al.*, 2009). Diammonium phosphate (DAP) at a rate of 80 kg ha^{-1} was applied at planting. Weeding was carried out three times: two weeks after seedling emergence, before flowering and after podding. Confidor (200 g l^{-1} Imidacloprid) was used to control whiteflies and leaf miner.

At maturity, single plant harvests were made from segregating lines within families/populations to increase homozygosity and progression to pure lines in subsequent generations. Lines were considered to be nearly homozygous when they showed one-grain type i.e. one seed color.

Grouping beans in market classes

Harvested single plant samples from $F_{1.6}$ generation were processed at Kabete Field Station of the University of Nairobi. Samples were grouped into major market classes. The market classes were grouped based mainly on seed color, size and shape. All genotypes were grouped into five

major market classes including red kidney, red mottled, small red, pinto and mixed color (containing beans of little commercial importance: black, green, tan brown and tan red).

With respect to market classes, nurseries were formed by regrouping lines with the same grain type. From those nurseries, 15% of materials were first selected based mainly on seed yield per plant after the ranking of means. Further selection was based on the standard appearance of commercial grain: uniformity in seed color, regular seed shape and morphological appearance which resulted in a final selection intensity of 5% for materials used in further evaluations (Ranalli *et al.,* 1991; Ahmed, 2016; Carvalho *et al.,* 2017). Bush beans were also separated from climbing types as their management and requirements are different.

Data collection

CIAT standard system for the evaluation of bean germplasm was used in data collection regardless of the generation (Schoonhoven and Pastor-Corrales, 1987). Data were taken on single plant in each plot for each trait:

- Growth habit: was determined at R6 and R9 growth stages. Plants were classified into four types; I (determinate), II (indeterminate, upright), III (indeterminate, prostrate) and IV (climbing).
- Days to flowering were measured as the number of days after planting to stage R6 when at least 50% of the plants have one or more flowers.
- Days to maturity were measured in days-after-planting and coinciding with the initiation of developmental stage R9 when at least 75% of the plants have reached physiological maturity. Genotypes were thereafter grouped into 3 maturity categories: 85 to 94 (early maturity); 95 to 104 (medium maturity) and 105 to 115 (late maturity) (Liebenberg, 2002).
- Flower color was determined by visual observation in the field during the flowering stage.
- Vegetative adaptation (plant vigor) was assessed when plants reached their maximum development at R5. Scale: 1= Excellent, 3= Good, 5= Intermediate, 7= Poor, and 9= very poor vigor.

- Uniformity was evaluated visually by observing the plants in the field, flower color and seed color using 1-9 scale, where 1 to 3= Very uniform, 3.1 to 5= Uniform, 5.1 to 7= intermediate, and 7.1 to 9 as segregating.
- The number of pods per plant was the mean number of pods per plant, obtained by counting the total number of pods of every single plant in the row.
- The number of seeds per plant was obtained by counting the seed in each of 10 pods randomly taken from a lot of pods harvested from every single plant.
- Seed size was expressed as the weight in grams of 100 randomly chosen seeds from seeds harvested from every single plant. Seeds were categorized as small (<25 g 100-seed mass); medium (25 g to 40 g 100-seed mass) and large (>40 g 100-seed mass). Seeds were dried to constant moisture up to a moisture content of 13% humidity before weighing.
- Seed yield (kg ha^{-1}): The mean seed yield (g) obtained in each row was extrapolated to the yield per hectare.
- Field disease score for each of the five major diseases was obtained by using the 1-9 CIAT scale: 1-3 being resistant, 3.1-6 intermediate resistant and 6.1-9 susceptible (Schoonhoven and Pastor-Corrales, 1987).

3.2.4. Statistical analysis

For $F_{1.3}$ to $F_{1.5}$ generations, available data were analyzed only at populations' level to assess differences among populations for seed yield and other agronomic traits. Analysis of variance (ANOVA) and Fisher's least significant difference (LSD) test using Genstat 15^{th} and Statistix version 8.0 softwares were performed on quantitative data to compare and separate means for the different populations. For the $F_{1.6}$ generation, in addition to analysis at populations' level, ANOVA for all lines (including $F_{1.6}$ populations, donors and commercial varieties) was conducted to determine whether there were significant differences among them for each trait. This was followed by computation of means for populations, and then lines within populations, i.e. based on the genetic structure of the study genotypes. At $F_{1.6}$ generation, the LSD test facilitated two key comparisons:

i) Populations level: This separation allowed comparisons among population means and comparisons among populations and commercial checks and donor parents;

ii) Lines within populations: This separation allowed orthogonal comparisons among lines, check varieties and donor parents.

Pearson's correlation coefficient was performed to determine the relationship between the seed yield and other agronomic traits. Qualitative data (flower color, seed color, growth habit) were summarized in frequencies for each population and lines within populations.

3.3. RESULTS

3.3.1. $F_{1.3}$ Generation of segregating inter-racial bean populations grown at Kabete

3.3.1.1. Agronomic performance of the $F_{1.3}$ inter-racial bean populations

The section below summaries the agronomic performance and disease reaction of 16 $F_{1.3}$ inter-racial populations grown in 2013 short rain season for the period of 14th October 2013 to February 2014 at Kabete Field Station.

Table 3.5 presents data on plant vigor, days to flowering, days to maturity, and the number of seeds per pod of the 16 $F_{1.3}$ populations. There were no significant differences among $F_{1.3}$ populations for the plant vigor (*P>0.05*). All the populations had good vigor (3.1 – 5.0). Compared to checks and donor parents, there were significant differences (*P<0.05*) as some donor parents (AND1062, BRB191, and G2333) showed better plant vigor (1.0 – 3.0) than the inter-racial populations. Commercial checks were either statistically equal or less vigorous than $F_{1.3}$ populations (4.3 – 6.7).

There were no significant differences among $F_{1.3}$ populations for the days to flowering (*P>0.05*). Populations' means for days to flowering ranged from 40.4 days (KMA13-22) to 41.8 days (KMA13-32). However, differences were significant when comparing the populations to commercial checks and donor parents (*P<0.05*). Donor parents BRB191 (31.8 days), AND1062 (34.3 days) and commercial checks KATB1 (36.9 days), KATB9 (38.4 days) flowered the earliest compared to all the populations, other commercial checks and donor parents. RWR719 which flowered in 52.2 days was the last to flower compared to all populations, checks and donor parents (Table 3.5).

There were no significant differences among the $F_{1.3}$ populations for days to maturity. However, differences were significant when comparing the populations to commercial checks and donor parents (*P<0.05*). The populations' range was from 89.7 days (KMA13-25) to 93.2 days (KMA13-32). Commercial checks KATB1 (73.6 days), KATB9 (76.2 days), GLP585 (83.6 days) and donor parents BRB191 (74.9 days), AND1062 (79.0 days) and G10909 (87.5 days) were early maturing compared to all $F_{1.3}$ populations. RWR719 was the last to mature compared to all populations and checks (102.2 days) (Table 3.5).

There were no significant differences among populations for the number of seeds per pod. Donor parents G10909 (7.4 seeds pod^{-1}) and G2333 (7.4 seeds pod^{-1}) had more seeds compared to all checks and other donor parents while the commercial checks KATB1 (4.8 seeds pod^{-1}) and KATB9 (4.9 seeds pod^{-1}) produced the least number of seeds per pod (Table 3.5).

Table 3.5. Plant vigor, days to flowering and to maturity and seeds pod^{-1} of $F_{1.3}$ segregating inter-racial bean populations grown at Kabete in 2013

Populations	Vigor		Days to flowering		Days to maturity		Seeds pod^{-1}	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range
KMA13-17	4.1	1.0 – 9.0	41.5	34.0 – 47.0	93.1	74.0 – 108.0	6.0	3.7 – 7.0
KMA13-18	3.9	1.0 – 7.0	41.1	32.0 – 51.0	91.5	72.0 – 117.0	6.4	4.7 – 7.7
KMA13-19	3.7	1.0 – 9.0	40.5	32.0 – 51.0	90.1	72.0 – 117.0	6.1	3.7 – 8.0
KMA13-20	3.6	1.0 – 9.0	41.3	32.0 – 51.0	90.9	72.0 – 117.0	6.3	4.0 – 7.7
KMA13-21	4.1	1.0 – 8.0	41.0	32.0 – 52.0	91.0	72.0 – 109.0	6.2	3.7 – 7.7
KMA13-22	3.5	1.0 – 8.0	40.4	32.0 – 50.0	90.2	72.0 – 119.0	6.4	4.0 – 7.7
KMA13-23	3.4	1.0 – 9.0	40.8	32.0 – 51.0	92.1	72.0 – 121.0	6.3	3.7 – 7.7
KMA13-24	3.7	1.0 – 9.0	40.8	31.0 – 50.0	90.2	72.0 – 109.0	6.2	3.7 -7.7
KMA13-25	3.8	1.0 – 9.0	40.8	32.0 – 55.0	89.7	72.0 – 111.0	6.3	4.0 – 7.7
KMA13-26	3.8	1.0 – 9.0	40.6	31.0 – 51.0	89.7	73.0 – 109.0	6.3	3.7 – 7.7
KMA13-27	3.6	1.0 – 9.0	41.1	32.0 – 51.0	91.8	71.0 – 109.0	6.3	4.3 -7.7
KMA13-28	3.7	1.0 – 8.0	41.1	33.0 – 49.0	89.9	71.0 – 115.0	6.3	4.3 – 7.7
KMA13-29	3.6	1.0 – 8.0	41.1	31.0 – 51.0	91.7	72.0 – 108.0	6.1	3.7 – 7.7
KMA13-30	3.7	1.0 – 9.0	41.5	32.0 – 51.0	91.5	72.0 – 109.0	6.3	3.0 – 7.7
KMA13-31	4.0	1.0 – 9.0	40.7	32.0 – 51.0	90.5	72.0 – 109.0	6.5	4.3 – 7.7
KMA13-32	4.1	1.0 – 9.0	41.8	32.0 – 53.0	93.2	73.0 – 109.0	6.4	3.7 – 7.7
Checks and donor parents								
AND1062	1.7		34.3		79.0		5.7	
BRB191	1.0		31.8		74.9		5.7	
G10909	3.7		43.0		87.5		7.4	
G2333	2.7		47.3		94.9		7.4	
GLP585	6.3		44.6		83.6		6.4	
GLP92	6.7		44.3		91.0		6.3	
KATB1	4.3		36.9		73.6		4.8	
KATB9	4.3		38.4		76.2		4.9	
Mex54	4.0		42.5		92.2		6.5	
RWR719	4.3		52.2		102.2		6.9	
Mean	3.8		41.0		81.0		6.3	
$LSD_{0.05}$	1.4		4.0		5.8		0.8	
CV (%)	61.4		13.2		16.3		17.3	

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold

Table 3.6 shows that there were no significant differences among populations for the number of pods per plant (Table 3.6). Pods per plant varied from 24.6 (KMA13-24) to 31.4 (KMA13-27). However, there were differences among populations and commercial checks and donor parents (*P<0.05*). $F_{1.3}$ inter-racial populations had more pods than most of the commercial checks and

donor parents. Donor parents G10909 (36.3) and G2333 (35.0) recorded the highest number of pods per plant, higher than all populations and commercial checks and other donor parents. The lowest number of pods per plant was recorded on commercial checks KATB1 and KATB9 (11 pods plant^{-1}).

There were no significant differences among $F_{1.3}$ populations for the 100-seed mass. All the populations were medium-seeded (29.7 to 34.3 g 100-seed mass). Differences were, however, significant when comparing populations' means to commercial checks, and donor parents. Donor parents BRB191 (62.2 g) and AND1062 (50.4 g) recorded the highest 100-seed mass. They were the only large-seeded genotypes among all populations, commercial checks and donor parents while the donor parent RWR719 was the only small-seeded (20.7 g 100-seed mass).

Table 3.6 shows that there were highly significant differences among $F_{1.3}$ populations and among the $F_{1.3}$ populations, commercial checks and donor parents for the seed yield plant^{-1} (*P<0.001*). KMA13-30 recorded the highest seed yield per plant among populations (58.5 g) while the lowest mean was recorded on KMA13-29 (28.9 g). Compared to commercial checks and donor parents, $F_{1.3}$ populations were globally higher yielding than most of the checks and donor parents.

Table 3.6. Pods plant^{-1}, 100-seed mass and seed yield plant^{-1} among $F_{1.3}$ segregating inter-racial bean populations grown at Kabete in 2013

Populations	Pods plant^{-1}		100-seed mass (g)		Seed yield plant^{-1} (g)	
	Mean	Range	Mean	Range	Mean	Range
KMA13-17	28.4	9.0 – 56.0	29.9	14.8 – 44.1	47.2	17.8 – 83.5
KMA13-18	27.3	5.0 – 61.0	31.8	15.3 – 71.9	47.7	6.1 – 107.9
KMA13-19	27.4	3.0 – 66.0	34.3	14.7 – 71.3	57.5	7.3 – 106.2
KMA13-20	29.1	4.0 – 61.0	31.3	14.9 – 60.3	51.0	7.0 – 96.3
KMA13-21	28.1	4.0 – 67.0	32.2	61.1 – 61.3	50.7	15.3 – 116.7
KMA13-22	28.3	9.0 – 63.0	31.2	12.5 – 76.8	51.9	11.3 – 84.3
KMA13-23	27.5	7.0 – 51.0	32.7	17.0 – 74.1	49.5	20.9 – 114.1
KMA13-24	24.6	5.0 – 55.0	31.2	17.0 – 61.6	39.1	20.5 – 108.6
KMA13-25	30.5	3.0 – 63.0	32.3	15.0 – 54.4	52.9	8.1 – 103.3
KMA13-26	25.6	5.0 – 56.0	29.7	15.1 – 67.1	43.9	9.1 – 143.0
KMA13-27	31.4	9.0 – 58.0	30.9	14.5 – 72.3	56.9	12.3 – 132.4
KMA13-28	28.0	11.0 – 55.0	30.6	17.0 – 52.0	55.0	20.1 – 97.6
KMA13-29	29.3	2.0 – 75.0	31.4	15.0 – 66.8	28.9	13.4 – 145.8
KMA13-30	29.4	8.0 – 62.0	33.0	17.0 – 52.0	58.5	5.7 – 97.7
KMA13-31	28.2	6.0 – 63.0	32.5	15.4 – 67.5	56.0	23.1 – 132.8
KMA13-32	29.3	4.0 – 62.0	31.4	14.7 – 68.4	51.5	13.6 – 116.3
Checks and donor parents						
AND1062	14.8		50.4		54.1	
BRB191	12.4		62.4		56.4	
G10909	36.3		32.6		25.0	
G2333	35.0		29.7		37.1	
GLP585	24.8		27.0		40.2	
GLP92	28.9		30.1		21.6	
KATB1	11.1		34.2		18.9	
KATB9	11.8		36.1		22.7	
Mex54	30.5		36.2		44.2	
RWR719	19.8		20.7		19.7	
Mean	27.9		31.8		44.2	
$LSD_{0.05}$	7.1		4.9		11.4	
CV (%)	53.9		41.6		76.5	

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold

Table 3.7 shows that there were significant differences among $F_{1.3}$ populations for seed yield ha^{-1} (*P<0.05*). The trend was the same when comparing populations to commercial checks and donor parents. Among populations, KMA13-24 recorded the highest seed yield (2,002.2 kg ha^{-1}). Other higher yielding populations were KMA13-17 (1,806.4 kg ha^{-1}) and KMA13-29 (1,769.3 kg ha^{-1}). The lowest yield among populations was recorded on population KMA13-23 (1,144.4 kg ha^{-1}). When comparing populations to commercial checks and donor parents, only BRB191 (3,102.7 kg ha^{-1}) had significantly higher yields than all $F_{1.3}$ populations. All other commercial checks and

donor parents were statistically equal to $F_{1.3}$ populations. The lowest yield among populations and among populations, commercial checks and donor parents was recorded on commercial check KATB1 (937.5 kg ha^{-1}).

Table 3.7. Seed yield (kg ha^{-1}) among $F_{1.3}$ segregating inter-racial bean populations grown at Kabete in 2013

Populations	Seed yield (kg ha^{-1})		
	Mean	Range	Ranking
KMA13-17	1,806.4	625.0 – 3,035.7	5
KMA13-18	1,604.1	535.7 – 2,847.2	11
KMA13-19	1,482.1	721.1 – 2,500.0	15
KMA13-20	1,567.0	416.6 – 3437.5	12
KMA13-21	1,639.6	659.7 – 2,875.2	10
KMA13-22	1,558.0	511.4 – 4,218.8	13
KMA13-23	1,144.4	500.0 – 2,500.0	25
KMA13-24	2,002.2	437.5 – 3,171.3	4
KMA13-25	1,275.5	553.0 – 3,125.0	22
KMA13-26	1,514.6	625.0 – 2,842.7	14
KMA13-27	1,293.3	714.0 – 2,467.1	20
KMA13-28	1,290.3	480.8 – 2,291.7	21
KMA13-29	1,769.3	491.1 – 3,375.0	6
KMA13-30	1,306.8	511.4 – 3,187.5	19
KMA13-31	1,655.5	347.2 – 4,326.9	9
KMA13-32	1,243.4	458.3 – 2,554.7	24
Checks and donor parents			
AND1062	2,361.2		2
BRB191	3,102.7		1
G10909	1,431.6		16
G2333	1,675.6		8
GLP585	1,693.5		7
GLP92	1,369.4		17
KATB1	937.5		26
KATB9	1,358.0		18
Mex54	2,236.1		3
RWR719	1,269.5		23
Mean	1,536.8		
$LSD_{0.05}$	519.0		
CV (%)	74.4		

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold

3.3.1.2. Reaction of $F_{1.3}$ populations to major bean diseases in Eastern Africa

There were no significant differences among $F_{1.3}$ populations for their reactions to the angular leaf spot (ALS). All the populations were moderately resistant (3.0 – 5.0). Differences were, however, significant among populations and commercial checks and donor parents (*P<0.01*).

Donor parents Mex54 (2.1) and G10909 (2.6) showed resistance to angular leaf spot while all other parents were ranging from moderately resistant to highly susceptible. Commercial check GLP92 was the most susceptible to ALS (7.9) compared to all populations and parents (Table 3.8).

Table 3.8 shows that there were no significant differences among $F_{1.3}$ populations in their reactions to anthracnose. All the populations were moderately resistant to anthracnose (3.0 – 5.0). However, the differences were highly significant when comparing the reaction to anthracnose of $F_{1.3}$ populations and commercial checks and donor parents (*P<0.001*). Only the donor parent G2333 showed resistance to anthracnose (1.7) while all commercial checks and other donor parents were ranging from moderately resistant (4.6) to highly susceptible (8.4). The commercial check GLP92 showed the highest susceptibility to anthracnose (8.4).

There were no significant differences among $F_{1.3}$ populations for the reaction to the bean common mosaic virus (BCMV). They were all moderately resistant (3.0 – 5.0). The differences were, however, significant when comparing the populations to parental genotypes (*P<0.05*). Commercial checks and donor parents showed more susceptibility to BCMV than $F_{1.3}$ populations as they were ranging from 5.6 to 7.1, except the donor parent BRB191 which showed a high level of resistance to BCMV (2.9). Among checks and donor parents, AND1062 was the most susceptible (7.1) (Table 3.8).

There were no significant differences among populations and between populations and parental genotypes for their reactions to root rot disease. They all ranged from resistant (1.0 – 3.0) to moderately resistant (3.1 – 5.0).

Table 3.8. Disease score to major bean diseases of $F_{1.3}$ segregating inter-racial bean populations grown at Kabete in 2013

Population	ALS		Anthracnose		BCMV		Root rot	
	Mean	Range	Mean	Range	Mean	Range	Mean	Range
KMA13-17	3.8	2.3 – 6.7	4.5	2.3 – 7.3	4.7	1.3 – 8.3	3.4	2.0 – 6.3
KMA13-18	3.5	1.0 – 9.0	4.4	2.7 – 9.0	4.2	1.0 – 7.3	3.1	1.0 – 7.0
KMA13-19	3.6	1.0 – 9.0	4.1	2.0 – 9.0	4.4	1.0 – 8.7	3.3	1.0 – 8.0
KMA13-20	4.1	1.0 – 8.3	4.2	1.0 – 9.0	4.5	1.0 – 7.3	3.1	1.0 – 9.0
KMA13-21	3.6	2.3 – 8.7	4.1	1.7 – 9.0	4.6	2.0 – 9.0	3.9	1.0 – 8.7
KMA13-22	3.9	2.0 – 8.0	4.4	2.3 – 9.0	4.6	1.0 – 9.0	2.7	1.0 – 9.0
KMA13-23	4.0	1.0 – 8.0	4.5	2.0 – 7.7	4.7	1.3 – 9.0	2.8	1.0 – 7.0
KMA13-24	4.3	2.3 – 9.0	4.7	2.3 – 9.0	5.0	2.0 – 9.0	2.4	1.0 – 9.0
KMA13-25	3.8	2.3 – 9.0	4.8	3.0 – 9.0	4.7	2.0 – 9.0	3.2	1.0 – 9.0
KMA13-26	4.0	2.3 – 8.0	4.5	2.0 – 9.0	4.4	1.0 – 7.3	3.1	1.0 – 9.0
KMA13-27	4.9	2.0 – 9.0	5.0	2.7 – 9.0	4.6	1.0 – 8.0	2.4	1.0 – 6.0
KMA13-28	4.2	2.0 – 9.0	4.9	2.7 – 9.0	4.6	2.0 – 7.3	3.0	1.0 – 9.0
KMA13-29	3.6	2.0 – 9.0	4.0	2.0 – 9.0	4.5	1.0 – 9.0	3.6	1.0 – 9.0
KMA13-30	4.6	2.0 – 8.3	4.6	2.0 – 9.0	5.0	2.0 – 7.3	2.2	1.0 – 6.0
KMA13-31	4.5	2.3 – 9.0	4.8	2.0 – 9.0	5.1	2.0 – 9.0	2.6	1.0 – 9.0
KMA13-32	3.8	2.0 – 9.0	4.2	2.7 – 9.0	4.5	1.0 – 9.0	3.6	1.0 – 9.0
Checks and donor parents								
AND1062	7.0		6.7		7.1		1.2	
BRB191	5.8		5.4		2.9		1.5	
G10909	2.6		6.3		6.2		2.1	
G2333	3.9		1.6		5.6		2.4	
GLP585	6.8		7.7		6.5		4.5	
GLP92	7.9		8.4		6.5		4.3	
KATB1	6.1		6.7		6.3		3.8	
KATB9	5.9		6.7		6.0		3.8	
Mex54	2.1		4.6		5.9		3.1	
RWR719	7.2		6.3		5.6		1.0	
Mean	4.6		5.1		4.6		3.0	
$LSD_{0.05}$	1.9		2.1		1.4		1.8	
CV (%)	51.7		34.8		41.5		75.4	

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold

3.3.2. $F_{1.4}$ generation of segregating inter-racial bean populations grown at Kabete

3.3.2.1. Agronomic performance of the $F_{1.4}$ segregating inter-racial bean populations

This section summaries the agronomic performance and disease reaction of 16 $F_{1.4}$ inter-racial populations grown in 2014 short rain season for the period of October 2014 to February 2015 at Kabete Field Station.

There were highly significant differences (*P<0.001*) among $F_{1.5}$ populations for plant vigor, days to flowering and the seed yield (Table 3.9). Population KMA13-20 was the most vigorous (3.0)

compared to all the populations, commercial checks and donor parents. Populations KMA13-23 and KMA13-26 were the least vigorous among populations, but they were more vigorous when compared to the donor parent RWR719 (4.2) and the check variety KATB1 (4.6).

Populations KMA13-25 and KMA13-22 were the earliest to flower among populations (36.7 and 36.9 days after planting, respectively). They were, however, late compared to commercial checks KATB1 and GLP92 and the donor parent BRB191 which flowered in 30.4, 32.7 and 36 days after planting, respectively. KMA13-19, KMA13-18, and KMA13-32 took longest to flower among populations (39.4 and 39.1, respectively) but earlier than donor parents RWR719 (40.0 days), G2333 (39.7 days), and G10909 (39.5 days) (Table 3.9).

The highest seed yield was recorded on populations KMA13-29 (1,869.0 kg ha^{-1}) and KMA13-19 (1,865.0 kg ha^{-1}). These two populations were lower yielding compared to means recorded on donor parents AND1062 (2,139.8 kg ha^{-1}) and BRB191 (1,952.8 kg ha^{-1}). The least productive population was KMA13-24 (811.2 kg ha^{-1}) but which was higher compared to donor and commercial checks G10909 (507.0 kg ha^{-1}), KATB9 (528.2 kg ha^{-1}), and RWR719 (755.0 kg ha^{-1}). Crosses involving check varieties KATB9 (KMA13-29, KMA13-30, KMA13-31 and KMA13-32) and GLP585 (KMA13-17, KMA13-18, KMA13-19 and KMA13-20) were better yielding compared to the rest of the populations (Table 3.9).

Table 3.9. Agronomic performance of $F_{1.4}$ segregating inter-racial bean populations grown at Kabete in 2014

Populations	Vigor		Days to flowering		Seed yield (kg ha^{-1})	
	Mean	Range	Mean	Range	Mean	Range
KM13-17	3.3	3.0 – 5.0	38.2	35.0 – 40.0	1,294.6	375.0 – 2,921.8
KM13-18	3.5	3.0 – 7.0	39.1	33.0 – 40.0	1,637.2	250.0 – 3,550.0
KM13-19	3.0	3.0 – 3.0	39.4	33.0 – 40.0	1,865.0	446.4 – 3,687.6
KM13-20	3.6	3.0 – 7.0	38.5	29.0 – 45.0	1,487.0	325.0 – 3,484.8
KM13-21	3.7	3.0 – 5.0	37.6	31.0 – 45.0	1,678.8	388.8 – 3,972.2
KM13-22	4.0	3.0 – 6.0	36.9	21.0 – 45.0	1,181.2	152.2 – 3,975.0
KM13-23	4.1	3.0 – 6.0	38.4	31.0 – 45.0	877.2	125.0 – 2,551.8
KM13-24	4.0	3.0 – 5.0	37.9	31.0 – 45.0	811.2	95.2 – 2,800.0
KM13-25	4.0	3.0 – 7.0	36.7	31.0 – 45.0	1,403.4	261.4 – 3,138.8
KM13-26	4.1	3.0 – 5.0	37.3	31.0 – 45.0	900.0	125.0 – 3,218.8
KM13-27	4.0	3.0 – 6.0	37.9	31.0 – 43.0	1,080.2	125.0 – 3,375.0
KM13-28	3.7	3.0 – 5.0	37.8	31.0 – 43.0	1,610.4	450.0 – 3,307.6
KM13-29	3.4	3.0 – 6.0	38.4	31.0 – 45.0	1,869.0	318.2 – 4,600.0
KM13-30	3.2	3.0 – 4.0	37.6	31.0 – 40.0	1,581.4	263.8 – 3,944.4
KM13-31	3.6	3.0 – 5.0	38.6	31.1 – 45.0	1,701.4	551.8 – 4,516.2
KM13-32	3.6	3.0 – 5.0	39.1	31.0 – 45.0	1,031.6	100.0 – 2,975.0
Checks and donors parents						
RWR719	4.2		40.0		755.0	
AND1062	3.5		38.0		2,139.8	
BRB191	3.4		36.0		1,952.8	
G10909	3.5		39.5		507.0	
G2333	3.6		39.7		973.4	
GLP585	3.3		37.9		1,643.0	
GLP92	4.0		32.7		1,119.0	
KATB1	4.6		30.4		1,138.8	
KATB9	3.5		38.3		528.2	
Mex54	3.5		38.2		1,248.2	
Mean	3.7		38.0		1,308.3	
$LSD_{0.05}$	0.4		1.3		434.8	
CV (%)	19.7		8.1		59.3	

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold

3.3.2.2. Reaction of $F_{1.4}$ segregating inter-racial bean populations to major bean diseases in Eastern Africa

There were no significant differences among $F_{1.4}$ segregating populations and donor and commercial checks to major bean diseases (Table 3.10).

Table 3.10. Disease resistance of $F_{1.4}$ inter-racial bean populations grown at Kabete in 2014

Populations	Disease scores			
	ALS	**ANT**	**BCMV**	**CBB**
KM13-17	3.0	1.0	2.0	3.0
KM13-18	3.0	1.0	2.0	3.0
KM13-19	3.0	1.0	2.0	3.0
KM13-20	3.0	1.0	2.0	3.0
KM13-21	3.0	1.0	2.0	3.0
KM13-22	3.0	1.0	2.0	3.0
KM13-23	3.0	1.0	2.0	3.0
KM13-24	3.0	1.0	2.0	3.0
KM13-25	3.0	1.0	2.0	3.0
KM13-26	3.0	1.0	2.0	3.0
KM13-27	3.0	1.0	2.0	3.0
KM13-28	3.0	1.0	2.0	3.0
KM13-29	3.0	1.0	2.0	3.0
KM13-30	3.0	1.0	2.0	3.0
KM13-31	3.0	1.0	2.0	3.0
KM13-32	3.0	1.0	2.0	3.0
Checks and donor parents				
RWR719	3.0	1.0	2.0	3.0
AND1062	3.0	1.0	2.0	3.0
BRB191	3.0	1.0	2.0	3.0
G10909	3.0	1.0	2.0	3.0
G2333	3.0	1.0	2.0	3.0
GLP585	3.0	1.0	2.0	3.0
GLP92	3.0	1.0	2.0	3.0
KATB1	3.0	1.0	2.0	3.0
KATB9	3.0	1.0	2.0	3.0
Mex54	3.0	1.0	2.0	3.0
Mean	3.0	1.0	2.0	3.0
$LSD_{0.05}$	-	-	-	-
CV (%)	-	-	-	-

ALS: angular leaf spot; ANT: anthracnose; BCMV: bean common mosaic virus; CBB: common bacterial blight; CV: coefficient of variation; $LSD_{0.05}$: least significant difference at 5% P-value threshold

3.3.3. $F_{1.6}$ generation of inter-racial segregating bean populations grown at Mwea

The following section discusses the agronomic performance and other traits of 16 $F_{1.6}$ inter-racial populations grown in 2016 short rain season for the period of October 2016 to February 2017 at the Kirogo Research Station of Kenya Agricultural and Livestock Research Organization (KALRO)-Mwea, in Kirinyaga County. Results are presented at population level, lines within population level and the major market classes.

3.3.3.1. Populations' performance

Days to flowering and days to maturity of $F_{1.6}$ generation of inter-racial common bean population grown at Mwea

There were highly significant differences for days to flowering and days to maturity among populations (*P<0.001*) (Table 3.11). The range for days to flowering was between 34 and 47 days after seedling emergence whereas the range for days to maturity was between 81 and 106 days after seedling emergence. All the populations were early to medium maturing (88.9 to 97.8 days). The trend was the same for parental genotypes except the donor parent RWR719 (106 days), which was late maturing according to Liebenberg (2002) classification. From that classification, 85 to 94 days= early maturity; 95 to 104 days= medium maturity and 105 to 115 days= late maturity. Population KMA13-29 matured the earliest (88.9 days) even if lately compared to all the commercial checks. In the other hand, populations KMA13-32 (98 days) and KMA13-22 (96 days) took longest to mature compared to all other populations.

Table 3.11. Days to 50% flowering and 75% maturity among $F_{1.6}$ inter-racial populations of common bean grown at Mwea in 2016

Populations	Days to flowering		Days to maturity		Maturity category
	Mean	Range	Mean	Range	
KMA13-17	41.3	38.5 – 44.0	90.5	87.4 – 92.8	Early
KMA13-18	40.0	40.0 – 40.0	91.4	91.4 – 91.4	Early
KMA13-19	37.8	34.5 – 40.5	93.8	88.2 – 96.0	Early
KMA13-20	37.2	36.5 – 38.0	91.5	90.3 – 93.5	Early
KMA13-21	37.5	34.5 – 42.0	94.0	92.2 – 99.0	Early
KMA13-22	39.6	35.0 – 43.0	96.1	93.1 – 102.2	Medium
KMA13-23	42.3	38.0 – 48.0	94.2	90.8 – 99.1	Early
KMA13-24	40.5	34.5 – 48.0	94.8	91.0 – 103.2	Early
KMA13-25	37.3	33.5 – 46.0	92.7	89.7 – 97.0	Early
KMA13-26	41.3	38.0 – 48.0	90.4	88.2 – 95.7	Early
KMA13-27	40.7	35.0 – 45.5	94.1	92.5 – 99.4	Early
KMA13-28	37.8	34.0 – 43.0	91.3	88.3 – 95.1	Early
KMA13-29	39.5	36.0 – 43.0	88.9	86.1 – 92.0	Early
KMA13-30	38.1	35.0 – 42.5	94.6	90.1 – 98.9	Early
KMA13-31	38.1	37.0 – 40.0	93.2	89.0 – 100.8	Early
KMA13-32	42.4	40.0 – 45.5	97.8	95.2 – 107.3	Medium
Checks and donors					
AND1062	38.9		91.4		Early
BRB191	41.5		97.0		Medium
G10909	40.5		96.0		Medium
G2333	38.5		99.9		Medium
GLP585	38.2		81.2		Early
GLP92	34.2		88.5		Early
KATB1	36.2		83.0		Early
KATB9	35.5		86.2		Early
Mex54	38.5		92.2		Early
RWR719	46.9		105.8		Late
Mean	39.2		92.1		
$LSD_{0.05}$	4.1		6.8		
CV (%)	8.3		11.7		
P-value	<0.001		<0.001		

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Plant vigor

There were highly significant differences for plant vigor among populations (*P<0.001*) (Table 3.12). According to CIAT 1-9 scale, all our populations were ranging from good (3.0) to intermediate plant vigor (5.0). The best score is 1.0 (excellent) while the worst on this scale is 9.0 (very poor plant vigor).

Table 3.12. Plant vigor among $F_{1.6}$ inter-racial populations of common bean grown at Mwea in 2016

Population	Vigor score		Vigor category	Ranking
	Mean	Range		
KMA13-17	4.0	3.5 – 4.5	Good	3
KMA13-18	6.0	6.0 – 6.0	Intermediate	26
KMA13-19	4.9	4.0 – 7.0	Good	14
KMA13-20	4.0	4.0 – 4.0	Good	4
KMA13-21	4.7	3.0 – 7.0	Good	10
KMA13-22	4.8	3.0 – 7.0	Good	12
KMA13-23	4.9	3.5 – 7.0	Good	13
KMA13-24	5.6	4.0 – 7.5	Intermediate	23
KMA13-25	4.5	3.5 – 6.0	Good	8
KMA13-26	5.9	4.0 – 8.0	Intermediate	25
KMA13-27	5.0	3.5 – 8.0	Good	15
KMA13-28	4.2	3.5 – 5.0	Good	5
KMA13-29	5.2	4.5 – 7.0	Intermediate	21
KMA13-30	5.1	4.0 – 6.0	Intermediate	16
KMA13-31	4.3	3.5 – 5.0	Good	6
KMA13-32	4.5	4.0 – 5.0	Good	9
Checks and donors				
AND1062	4.5		Good	7
BRB191	5.3		Intermediate	22
G10909	5.9		Intermediate	24
G2333	5.2		Intermediate	19
GLP585	4.8		Good	11
GLP92	5.2		Intermediate	20
KATB1	5.1		Intermediate	17
KATB9	3.3		Good	1
Mex54	3.9		Good	2
RWR719	5.2		Intermediate	18
Mean	4.8			
$LSD_{0.05}$	1.4			
CV (%)	28.1			
P-value	<0.001			

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Flower color and growth habit

Flower color was either white or purple for all the populations (Table 3.13). Populations with white color represented 67.3% of genotypes. Only populations KMA13-17 and KMA13-20 carried lines having only white flowers (100% of genotypes) whereas only the population KMA13-18 carried 100% of genotypes with only purple flowers. All other populations had genotypes with mixed flower colors.

The populations showed both determinate and indeterminate growth habit (Table 3.13). About 87.1% of genotypes from all the populations were of indeterminate growth habit while only 12.9% of them were bush beans (determinate growth). All lines from population KMA13-17 showed determinate growth habit. In contrast, populations KMA13-18; KMA13-20; KMA13-28; KMA13-30; and KMA13-31 were entirely composed of plants with indeterminate growth habit.

Table 3.13. Flower color and growth habit among $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Population	Flower color (%)		Growth habit (%)	
	Purple	White	Determinate	Indeterminate
KMA13-17	0.0	100.0	100.0	0.0
KMA13-18	100.0	0.0	0.0	100.0
KMA13-19	18.2	81.8	30.0	70.0
KMA13-20	0.0	100.0	0.0	100.0
KMA13-21	37.7	62.3	1.9	98.1
KMA13-22	48.2	51.8	1.8	98.2
KMA13-23	35.0	65.0	28.6	71.4
KMA13-24	19.4	80.6	10.8	89.2
KMA13-25	31.9	68.1	2.1	97.9
KMA13-26	36.0	64.0	12.0	88.0
KMA13-27	38.0	62.0	2.0	98.0
KMA13-28	44.0	56.0	0.0	100.0
KMA13-29	21.7	78.3	2.2	97.8
KMA13-30	11.5	88.5	0.0	100.0
KMA13-31	10.0	90.0	0.0	100.0
KMA13-32	71.4	28.6	14.3	85.7
Mean	32.7	67.3	12.9	87.1

Pods per plant and seeds per pod

The number of pods per plant varied highly significantly among populations (*P<0.001*) (Table 3.14). Population KMA13-32 had the highest number of pods per plant (30.7) followed by populations KMA13-31 (26.2), KMA13-30 (24.8) and KMA13-29 (23.8). Population KMA13-17 had the least number of pods per plant (15.2). Only the population KMA13-32 had significantly more pods per plant than all the commercial checks and all other $F_{1.6}$ populations.

There were highly significant differences in the number of seeds per pod among populations (*P<0.001*) (Table 3.14). The highest number of seeds per pod were recorded on populations KMA13-18 (5.8) and KMA13-31 (5.8) but both were significantly lower than the commercial

checks KATB9 (6.5) and GLP585 (6.4) and the donor parent G2333 (6.3). The lowest number of seeds per pod was recorded on population KMA13-17 (4.2).

Table 3.14. Number of pods plant^{-1} and number of seeds pod^{-1} among $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Populations	Pods plant^{-1}			Seeds pod^{-1}		
	Mean	Range	Ranking	Mean	Range	Ranking
KMA13-17	15.2	10.9 – 16.3	25	4.2	3.9 – 4.3	26
KMA13-18	20.2	20.2 – 20.2	14	5.8	5.8 – 5.8	6
KMA13-19	19.4	13.7 – 28.0	16	5.2	4.2 – 6.0	12
KMA13-20	18.1	16.8 – 19.4	18	5.2	5.0 – 5.3	13
KMA13-21	16.8	11.6 – 21.2	22	4.8	3.3 – 5.9	21
KMA13-22	21.8	17.2 – 33.6	8	5.1	4.2 – 6.6	16
KMA13-23	23.4	13.9 – 38.3	7	5.0	4.0 – 6.4	19
KMA13-24	20.4	13.0 – 30.3	13	5.1	4.0 – 6.0	17
KMA13-25	20.6	15.4 – 26.3	12	5.2	4.0 – 7.1	11
KMA13-26	14.0	2.0 – 26.3	26	4.4	3.3 – 5.9	24
KMA13-27	19.0	14.1 – 27.0	17	5.0	4.1 – 6.0	18
KMA13-28	21.7	17.5 – 30.2	9	4.9	4.0 – 5.9	20
KMA13-29	23.7	14.8 – 32.9	6	4.7	3.8 – 5.6	22
KMA13-30	24.8	15.5 – 31.1	4	5.1	3.5 – 6.5	14
KMA13-31	26.2	24.1 – 29.5	3	5.8	5.3 – 6.1	5
KMA13-32	30.7	27.2 – 31.3	1	5.2	4.1 – 6.0	10
Checks and donors						
AND1062	17.4		20	5.1		15
BRB191	21.1		11	5.3		9
G10909	17.8		19	5.7		7
G2333	23.7		5	6.3		3
GLP585	19.7		15	6.4		2
GLP92	16.4		23	4.3		25
KATB1	17.3		21	6.0		4
KATB9	27.0		2	6.5		1
Mex54	15.3		24	4.6		23
RWR719	21.1		10	5.7		8
Mean	20.5			5.3		
$LSD_{0.05}$	7.5			0.9		
CV (%)	36.6			18.6		
P-value	<0.001			<0.001		

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Seed yield per plant and 100-seed mass

There were highly significant differences (*P<0.001*) for seed yield per plant among the populations (Table 3.15). The highest seed yield per plant was recorded on population KMA13-32 (45.5 g plant^{-1}). Other populations with high seed yield per plant included KMA13-31 (40.6 g

plant^{-1}) and KMA13-30 (36.0 g plant^{-1}). However, their seed yields per plant were not significantly different from KATB9, the best yielding commercial check (38.2 g plant^{-1}). All other crosses were either statistically equal to or lower than the commercial checks and donor parents.

There were highly significant differences in 100-seed mass among populations ($P<0.001$) (Table 3.15). The population KMA13-17 had the largest seeds (41.4 g 100-seed mass). It was the only large-seeded compared to all other populations from crosses. All the other crosses produced progenies that were medium-seeded with a 100-seed mass varying from 25 to 40 g. The donor variety G10909 had the smallest seeds (21.4 g 100-seed mass).

Table 3.15. Seed yield plant^{-1} and 100-seed mass among $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Populations	Seed yield plant^{-1} (g)			100-seed mass (g)			
	Mean	Range	Ranking	Mean	Range	Ranking	Class
KMA13-17	19.9	13.9 – 21.3	25	41.4	38.9 – 45.1	1	Large
KMA13-18	24.1	24.1 – 24.1	21	27.1	27.1 – 27.1	21	Medium
KMA13-19	28.3	20.6 – 40.1	12	28.2	23.4 – 30.4	17	Medium
KMA13-20	27.6	26.4 – 28.7	15	36.0	34.7 – 37.2	3	Medium
KMA13-21	24.5	16.6 – 40.7	20	30.5	22.6 – 34.7	9	Medium
KMA13-22	29.5	21.3 – 47.8	8	29.2	25.2 – 32.2	15	Medium
KMA13-23	32.1	22.9 – 50.1	6	29.9	24.4 – 35.4	12	Medium
KMA13-24	24.8	4.3 – 40.6	19	26.9	16.3 – 34.1	22	Medium
KMA13-25	30.3	22.7 – 46.6	7	31.7	26.5 – 38.5	6	Medium
KMA13-26	16.0	2.5 – 30.8	26	26.8	18.4 – 34.3	23	Medium
KMA13-27	25.9	0.6 – 40.6	18	30.3	23.9 – 36.9	11	Medium
KMA13-28	28.0	21.9 – 48.1	13	29.5	23.2 – 40.1	13	Medium
KMA13-29	28.8	18.0 – 42.7	9	31.5	22.0 – 40.6	7	Medium
KMA13-30	36.0	19.5 – 52.7	4	29.4	22.1 – 35.2	14	Medium
KMA13-31	40.1	36.6 – 43.3	2	27.2	24.4 – 29.4	20	Medium
KMA13-32	45.5	35.7 – 54.0	1	34.3	27.6 – 37.3	5	Medium
Checks and donors							
AND1062	27.6		16	45.5		4	Large
BRB191	28.4		11	40.4		10	Large
G10909	23.3		22	21.4		26	Small
G2333	32.5		5	28.4		16	Medium
GLP585	27.6		14	24.6		25	Small
GLP92	20.2		24	31.3		8	Medium
KATB1	26.3		17	27.6		19	Medium
KATB9	38.2		3	28.2		18	Medium
Mex54	22.3		23	37.4		2	Medium
RWR719	28.7		10	25.9		24	Medium
Mean	28.5			30.0			
$LSD_{0.05}$	11.2			4.9			
CV (%)	39.8			16.4			
P-value	<0.001			<0.001			

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Uniformity of seed color pattern

There were highly significant differences in uniformity of seed color among populations (*P<0.001*) (Table 3.16). Only population KMA13-17 has shown the uniformity (1.72) of seed color while all other populations ranged from segregating to intermediate uniformity. As the materials are from crosses involving multiple parents, the segregation for seed color was still observed. The most dominant seed color and its relative importance in terms of percentage for each of the 16 populations are presented in the Table 3.16.

Table 3.15. Degree of uniformity and major seed color patterns among $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Populations	Uniformity score			Major seed color patterns
	Mean	Range	Uniformity category	
KMA13-17	1.7	1.0 – 3.0	Uniform	Red mottled (67.3%)
KMA13-18	4.8	3.0 – 6.0	Intermediate	Large red (44.4%)
KMA13-19	3.6	3.0 – 6.0	Intermediate	Small red (55.8%)
KMA13-20	3.4	3.0 – 6.0	Intermediate	Red mottled (100%)
KMA13-21	5.0	3.0 – 6.0	Intermediate	Mixed color (46.1%)
KMA13-22	6.2	6.0 – 9.0	Segregating	Mixed color (46.9%)
KMA13-23	5.0	3.0 – 6.0	Intermediate	Mixed color (52.6%)
KMA13-24	5.1	3.0 – 6.0	Intermediate	Mixed color (41.0%)
KMA13-25	6.6	6.0 – 9.0	Segregating	Mixed color (33.0%)
KMA13-26	2.7	1.0 – 3.0	Uniform	Small red (21.0%)
KMA13-27	5.0	3.0 – 6.0	Intermediate	Mixed color (34.0%)
KMA13-28	5.6	3.0 – 6.0	Intermediate	Mixed color (40.4%)
KMA13-29	5.7	3.0 – 6.0	Intermediate	Mixed color (44.5%)
KMA13-30	5.1	3.0 – 6.0	Intermediate	Small red (46.0)
KMA13-31	5.0	3.0 – 6.0	Intermediate	Small red (64.0%)
KMA13-32	5.2	3.0 – 6.0	Intermediate	Mixed color (53.8%)
Checks and donors				
AND1062	1.0		Uniform	Red kidney
BRB191	1.0		Uniform	Red mottled
G10909	1.0		Uniform	Medium red
G2333	1.0		Uniform	Small maroon (red)
GLP585	1.0		Uniform	Small red
GLP92	1.0		Uniform	Pinto
KATB1	1.0		Uniform	Yellow/green
KATB9	1.0		Uniform	Medium red
Mex54	1.0		Uniform	Cream beige
RWR719	1.0		Uniform	Small red
Mean	4.4			
$LSD_{0.05}$	0.6			
CV (%)	27.0			
P-value	<0.001			

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Seed yield

There were highly significant differences for seed yield among populations (*P<0.001*) (Table 3.17). Seed yield among populations varied from 1,001 kg ha^{-1} for the population KMA13-26 to 2,844 kg ha^{-1} for the population KMA13-32. Population KMA13-32 out-yielded all the other populations, commercial checks and donor parents with a mean seed yield of 2,844 kg ha^{-1}. Other high yielding populations were KMA13-31 (2,504 kg ha^{-1}) and KMA13-30 (2,248 kg ha^{-1}). However, these were not significantly different from KATB9 (2,385 kg ha^{-1}), the best yielding

commercial check. All other crosses were either statistically equal to or lower than commercial checks and donor parents.

Table 3.16. Seed yield (kg ha^{-1}) among $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Population	Seed yield (kg ha^{-1})		Ranking
	Mean	Range	
KMA13-17	1,244	871.2 – 1,329.8	25
KMA13-18	1,505	1,505.0 – 1,505.0	21
KMA13-19	1,771	1,285.3 – 2,504.5	12
KMA13-20	1,722	1,652.8 – 1,794.9	15
KMA13-21	1,530	1,034.7 – 2,542.5	20
KMA13-22	1,847	1,331.4 – 2,987.0	8
KMA13-23	2,005	1,429.0 – 3,131.3	6
KMA13-24	1,550	266.6 – 2,535.9	19
KMA13-25	1,891	1,416.7 – 2,912.1	7
KMA13-26	1,001	156.3 – 1925.8	26
KMA13-27	1,617	662.7 – 2,540.3	18
KMA13-28	1,747	1,370.1 – 3,005.6	13
KMA13-29	1,799	1,123.7 – 2,669.1	9
KMA13-30	2,248	1,215.6 – 3,295.3	4
KMA13-31	2,504	2,286.7 – 2,705.5	2
KMA13-32	2,844	2,233.9 – 3,375.3	1
Checks and donors			
AND1062	1,722		16
BRB191	1,777		11
G10909	1,454		22
G2333	2,032		5
GLP585	1,725		14
GLP92	1,262		24
KATB1	1,643		17
KATB9	2,385		3
Mex 54	1,396		23
RWR 719	1,794		10
Mean	1,781		
LSD$_{0.05}$	698.8		
CV (%)	39.8		
P-value	<0.001		

CV: coefficient of variation; LSD: least significant difference at 5% P-value threshold.

Pearson's correlation coefficient between seed yield and other agronomic traits

Table 3.18 shows that seed yield was positively and significantly correlated to the number of pods per plant (r=0.8530***), number of seeds per pod (r=0.2970***) and the seed yield per plant (r=0.9724***). It was however negatively correlated to 100-seed mass (r=-0.1657**) and

to plant vigor (r=-0.2167***). One consequence of that correlation analysis is that seed yield per plant or pod number per plant are good indicators of seed yield in kg ha^{-1}. So, these two traits could be used to select lines for further evaluation.

Table 3.17. Pearson's correlation coefficients among seed yield and other agronomic traits in $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Parameters	Days to flowering	100-seed mass	Pods $plant^{-1}$	Seeds pod^{-1}	Yield $plant^{-1}$	Plant vigor
100-seed mass	0.1705**					
Pods $plant^{-1}$	0.0834^{ns}	-0.0083^{ns}				
Seeds pod^{-1}	0.0882^{ns}	-0.193***	0.2541***			
Yield $plant^{-1}$	0.0355^{ns}	-0.165**	0.8530***	0.2970***		
Plant vigor	0.1314**	0.285***	-0.0575^{ns}	-0.1351**	-0.2167***	
Seed yield	0.0355^{ns}	-0.165**	0.8530***	0.2970***	0.9724***	-0.2167***

^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

3.3.3.2. Line performance within $F_{1.6}$ inter-racial bean populations grown at Mwea in 2016

Population KMA13-17 Lines

There were significant differences for plant vigor (*P<0.001*), days to flowering (*P<0.01*), number of seeds per pod (*P<0.001*) and the 100-seed mass (*P<0.001*) among lines within the population KMA13-17. Among crosses, KMA13-17-25 was the most vigorous (3.5) but less vigorous than the best commercial check KATB9 (3.0). KMA13-17-25 was also the earliest to flower among crosses (38.5 days). GLP92 was the earliest to flower compared to all crosses and checks (34.3 days). The highest number of pods per plant among crosses was recorded on KMA13-17-25 (16.3 pods), but lower compared to most of the checks. The largest seeds (45.1 g 100-seed mass) were found on KMA13-17-01, larger than all crosses and checks (Table 3.19).

Table 3.18. Means of agronomic traits of lines within inter-racial bean population KMA13-17 grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-17-01	4.0	41.5	10.9	4.3	15.5	45.1	969.8
KMA13-17-17	4.5	44.0	12.3	3.9	13.9	39.2	871.2
KMA13-17-25	3.5	38.5	16.3	4.3	21.3	38.9	1,329.8
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.9	39.5	19.6	5.5	27.3	30.3	1,703.5
CV (%)	26.8	7.4	35.5	18.2	37.4	17.2	37.4
P-value	0.00**	0.00**	0.08^{ns}	0.00***	0.08^{ns}	0.00***	0.08^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-18 Lines

There were significant differences among lines within population KMA13-18 for days to flowering (*P<0.01*), the number of seeds per pod (*P<0.01*) and 100-seed mass (*P<0.001*). KMA13-18-12, the only line advanced from that population, was either equal or inferior to commercial checks and donor parents for those traits (Table 3.20).

Table 3.19. Means of agronomic traits of lines within population KMA13-18 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-18-12	6.0	40.0	20.2	5.8	24.1	27.1	1,506.3
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.9	39.1	19.9	5.6	27.7	29.6	1,730.2
CV (%)	23.8	7.4	33.8	17.8	34.2	19.4	34.2
P-value	0.17^{ns}	0.00**	0.28^{ns}	0.00**	0.28^{ns}	0.00***	0.28^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-19 Lines

There were significant differences among lines within population KMA13-19 for plant vigor (*P<0.05*), days to flowering (*P<0.01*), number of seeds per pod (*P<0.01*) and 100-seed mass (*P<0.001*). KMA13-19-15 and KMA13-19-12 were the most vigorous (4.0) and the earliest to flower (34.5 days) among crosses. KMA13-19-15 had, in addition, the highest number of seeds per pod (6.0) and the highest 100-seed mass (30.4 g). It was also the higher yielding (2,504.5 kg ha^{-1}) compared to all crosses and checks (Table 3.21).

Table 3.20. Means of agronomic traits of lines within population KMA13-19 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-19-02	7.0	40.5	16.1	5.0	21.4	23.4	1,338.5
KMA13-19-09	4.5	39.0	19.3	5.7	26.1	29.9	1,632.5
KMA13-19-12	4.0	34.5	19.8	4.2	20.6	28.7	1,285.3
KMA13-19-15	4.0	34.5	28.0	6.0	40.1	30.4	2,504.5
KMA13-19-16	5.0	40.5	13.7	5.2	38.2	29.5	2,386.7
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	5.0	38.6	19.8	5.6	27.8	29.5	1,738.6
CV (%)	22.7	7.2	33.7	17.5	33.2	18.9	33.2
P-value	0.02*	0.00**	0.20^{ns}	0.00**	0.16^{ns}	0.00***	0.16^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-20 Lines

There were significant differences among lines within population KMA13-20 for days to flowering (*P<0.01*), the number of seeds per pod (*P<0.01*) and the 100-seed mass (*P<0.001*). KMA13-20-03 was the earliest to flower (36.5 days) compared to KMA13-20-14 (38.0 days). These two lines were medium-seeded with respectively, 37.2 g and 34.7 g 100-seed mass (Table 3.22). They were statistically equal or inferior to commercial checks and donor parents for all the traits.

Table 3.21. Means of agronomic traits of lines within population KMA13-20 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1}	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-20-03	4.0	36.5	19.4	5.3	28.7	37.2	1,794.9
KMA13-20-14	4.0	38.0	16.8	5.0	26.4	34.7	1,652.8
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.9	38.7	19.8	5.6	27.8	30.0	1,735.9
CV (%)	24.3	7.4	34.5	17.6	34.9	18.1	34.9
P-value	0.08^{ns}	0.00**	0.33^{ns}	0.00**	0.42^{ns}	0.00***	0.42^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-21 Lines

There were significant differences among lines within population KMA13-21 for plant vigor (*P<0.05*), days to flowering (*P<0.05*), number of seeds per pod (*P<0.01*) and 100-seed mass (*P<0.01*). KMA13-21-03; KMA13-21-06; KMA13-21-11; KMA13-21-14 were the most vigorous (3.0) whereas KMA13-21-21 was the least vigorous (7.0) compared to all crosses and checks. KMA13-21-21 was however the earliest to flower among crosses (34.5 days) and was statistically equal to the earliest check variety GLP92 (34.3 days). KMA13-21-21 recorded the highest number of seeds per pod (5.9) compared to other lines. All the other crosses were either equal or inferior to checks and donor parents. All the crosses were medium-seeded, except the line KMA13-21-27 (22.6 g 100-seed mass) which was small-seeded. The highest value for 100-seed mass among crosses (34.7g) was recorded on KMA13-21-21 (Table 3.23).

Table 3.22. Means of agronomic traits of lines within population KMA13-21 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-21-03	3.0	38.0	18.9	3.9	40.7	32.3	2,542.5
KMA13-21-04	4.3	35.7	13.3	4.2	31.3	30.4	1,955.8
KMA13-21-06	3.0	40.5	20.9	5.6	25.7	31.9	1,608.7
KMA13-21-07	5.0	36.0	17.9	4.7	22.3	28.5	1,390.9
KMA13-21-09	5.0	37.5	13.8	5.1	19.9	30.7	1,242.9
KMA13-21-10	4.0	35.0	19.8	5.0	27.8	27.7	1,740.1
KMA13-21-11	3.0	36.0	18.0	4.0	29.0	34.0	1,814.7
KMA13-21-12	3.5	37.5	17.5	5.2	25.5	32.4	1,592.8
KMA13-21-13	4.0	40.5	11.6	3.8	21.6	33.0	1,350.0
KMA13-21-14	3.0	41.0	17.6	5.3	26.3	33.0	1,646.3
KMA13-21-21	4.0	39.5	18.0	5.9	25.6	30.4	1,597.3
KMA13-21-16	4.5	36.5	15.9	4.6	24.2	31.9	1,511.0
KMA13-21-17	4.5	37.5	12.1	5.6	17.6	31.7	1,100.8
KMA13-21-18	5.5	36.0	14.6	4.5	16.6	30.9	1,034.7
KMA13-21-19	5.5	35.5	14.6	4.9	23.4	34.0	1,461.6
KMA13-21-20	5.5	38.0	16.7	5.3	25.4	34.7	1,587.3
KMA13-21-21	7.0	34.5	11.7	3.3	17.0	33.7	1,061.8
KMA13-21-22	5.0	35.0	19.8	4.9	26.2	29.1	1,639.3
KMA13-21-23	5.5	36.5	19.3	5.8	26.1	25.6	1,633.0
KMA13-21-24	5.5	39.0	18.9	5.7	27.0	28.4	1,689.0
KMA13-21-25	5.0	35.0	19.0	4.6	27.9	31.9	1,744.5
KMA13-21-26	5.5	36.5	17.8	4.8	27.0	30.7	1,688.3
KMA13-21-27	5.5	42.0	14.7	5.1	18.1	22.6	1,133.4
KMA13-21-28	5.5	39.5	17.1	4.6	20.4	28.0	1,273.3
KMA13-21-29	5.5	38.5	19.3	4.5	18.9	28.3	1,181.7
KMA13-21-30	5.5	39.0	21.2	4.5	24.5	28.9	1,532.2
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.7	37.9	17.6	5.0	25.3	30.1	1,581.3
CV (%)	22.9	6.8	34.0	19.3	36.2	16.2	36.2
P-value	0.01*	0.01*	0.38^{ns}	0.00**	0.57^{ns}	0.00**	0.57^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-22 Lines

There were significant differences among lines within population KMA13-22 for plant vigor (*P<0.05*), days to flowering (*P<0.05*), the number of seeds per pod (*P<0.01*) and the 100-seed mass (*P<0.05*). The most vigorous plant was KMA13-22-30 (3.0) whereas KMA13-22-04 and KMA13-22-13 were the least vigorous (7.0). KMA13-22-06 and KMA13-22-07 were the earliest crosses to flower (35.0 days). The highest number of seeds per pod (6.6) was recorded on KMA13-22-30, higher compared to all crosses and checks. All the crosses were medium-seeded with the largest having 32.2 g 100-seed mass (Table 3.24).

Table 3.23. Means of agronomic traits of lines within population KMA13-22 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1}	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-22-01	5.5	40.5	18.4	6.2	24.9	29.4	1,556.0
KMA13-22-02	5.5	38.5	18.3	4.5	21.6	31.1	1,347.7
KMA13-22-03	4.5	36.5	18.3	5.2	29.4	32.2	1,837.2
KMA13-22-04	7.0	36.0	18.9	4.6	22.8	25.2	1,425.9
KMA13-22-05	6.5	36.0	18.1	5.6	21.3	28.5	1,331.4
KMA13-22-06	5.5	35.0	17.2	4.5	21.8	27.6	1,364.6
KMA13-22-07	5.0	35.0	21.8	4.7	28.2	26.9	1,764.3
KMA13-22-09	5.5	39.5	19.9	4.7	22.1	28.7	1,380.6
KMA13-22-10	4.5	39.0	21.8	4.2	23.5	28.7	1,470.3
KMA13-22-12	5.5	38.0	27.7	4.7	32.1	29.8	2,005.2
KMA13-22-13	7.0	41.5	22.5	5.6	26.6	29.2	1,659.7
KMA13-22-14	6.0	40.5	19.7	5.8	27.7	30.8	1,729.1
KMA13-22-15	5.0	42.0	22.8	4.5	32.0	28.7	2,000.5
KMA13-22-16	4.0	43.0	20.0	5.4	28.4	28.2	1,778.1
KMA13-22-17	4.5	39.5	20.9	5.3	24.5	28.9	1,533.5
KMA13-22-18	5.0	43.0	20.8	4.9	29.4	29.1	1,838.0
KMA13-22-19	4.5	50.5	23.8	4.3	30.7	32.1	1,916.8
KMA13-22-20	5.0	39.5	20.0	5.3	28.9	30.5	1,807.4
KMA13-22-21	5.0	37.0	20.9	5.3	33.6	29.8	2,099.6
KMA13-22-23	4.5	40.5	21.6	5.4	31.0	25.3	1,935.6
KMA13-22-24	4.5	43.0	20.7	5.0	28.3	28.9	1,770.7
KMA13-22-25	3.5	39.5	23.0	5.1	31.4	30.4	1,959.9
KMA13-22-27	4.5	43.0	20.1	6.0	29.6	27.0	1,852.6
KMA13-22-28	3.7	41.3	24.0	5.3	34.4	29.6	2,149.2
KMA13-22-29	3.5	43.0	25.7	5.4	46.1	27.8	2,881.6
KMA13-22-30	3.0	40.5	33.6	6.6	47.8	29.4	2,987.0
KMA13-22-32	4.0	37.0	23.6	4.8	33.4	31.7	2,088.9
KMA13-22-33	4.0	40.5	21.9	4.4	31.8	30.8	1,985.6
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.8	39.7	21.0	5.2	28.9	29.1	1809.6
CV (%)	23.7	6.9	27.2	16.9	28.2	16.8	28.2
P-value	0.03*	0.03*	0.35^{ns}	0.00**	0.12^{ns}	0.03*	0.12^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-23 Lines

There were significant differences among lines within population KMA13-23 for days to flowering (*P<0.01*), the number of seeds per pod (*P<0.01*) and the 100-seed mass (*P<0.05*). Most of the crosses were late flowering (from 38.0 for KMA13-23-06 to 48 days for KMA13-23-19). KMA13-23-11 had the highest number of seeds per pod (6.4) whereas only 4.0 seeds per pod were recorded on KMA13-23-18 and KMA13-23-22. All the crosses except KMA13-23-18 (24.4 g 100-seed mass) were medium-seeded. The highest 100-seed mass among crosses was recorded on KMA13-23-04 (35.4 g) (Table 3.25).

Table 3.24. Means of agronomic traits of lines within population KMA13-23 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1}(g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-23-03	4.5	43.0	20.5	4.5	30.4	33.9	1,900.3
KMA13-23-04	4.5	40.0	13.9	4.7	24.1	35.4	1,504.2
KMA13-23-05	4.5	45.5	15.8	5.3	23.8	32.9	1,487.4
KMA13-23-06	3.5	38.0	27.2	4.7	36.3	28.8	2,270.5
KMA13-23-07	4.0	45.0	24.6	5.0	37.6	29.3	2,352.8
KMA13-23-08	5.0	43.0	24.1	5.2	34.4	31.4	2,147.0
KMA13-23-09	4.5	42.0	22.5	5.0	32.3	31.1	2,019.1
KMA13-23-10	4.0	39.5	23.3	4.3	36.3	27.9	2,269.8
KMA13-23-11	4.0	42.5	23.7	6.4	40.7	31.2	2,542.5
KMA13-23-12	5.0	39.0	19.8	5.3	26.7	29.3	1,668.1
KMA13-23-13	5.0	40.5	21.7	5.6	31.0	27.9	1,935.4
KMA13-23-14	5.5	43.0	22.5	5.7	28.8	29.8	1,801.1
KMA13-23-17	6.0	45.5	38.3	5.3	50.1	28.0	3,131.3
KMA13-23-18	5.0	45.5	32.0	4.0	38.9	24.4	2,428.3
KMA13-23-19	4.5	48.0	28.4	5.7	32.1	28.9	2,003.4
KMA13-23-20	4.5	39.0	24.0	4.3	29.6	33.0	1,849.6
KMA13-23-21	5.5	41.5	21.1	4.6	29.4	32.1	1,839.2
KMA13-23-22	7.0	43.0	21.6	4.0	28.1	27.5	1,757.1
KMA13-23-23	5.5	39.0	29.9	5.4	31.6	27.5	1,971.9
KMA13-23-24	5.0	43.0	19.3	5.1	26.4	29.9	1,652.4
KMA13-23-25	4.0	42.5	20.8	5.3	30.3	31.2	1,893.5
KMA13-23-26	6.0	43.0	16.6	4.1	22.9	26.9	1,429.0
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.8	41.3	22.19	5.2	30.6	29.6	1,909.8
CV (%)	24.6	7.6	32.3	17.5	32.1	18.0	32.1
P-value	0.32^{ns}	0.00**	0.19^{ns}	0.00**	0.43^{ns}	0.02*	0.43^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-24 Lines

There were significant differences among lines within population KMA13-24 for days to flowering (*P<0.01*), the number of seeds per pod (*P<0.05*) and the 100-seed mass (*P<0.001*). KMA13-24-18 (34.5 days) was the earliest to flower among crosses whereas KMA13-24-08 (48 days) was the last flowering. KMA13-24-06 had the highest number of seeds per pod (6.0) whereas KMA13-24-24 (34.1 g 100-seed mass) had the largest seeds compared to all other crosses. The seed size was ranging from 16.3 g 100-seed mass for the line KMA13-24-18 to 34.1 g 100-seed mass for KMA13-24-24. KMA13-24-11 (2,535.9 kg ha^{-1}) was the best yielding cross but not significantly different from the best check KATB9. KMA13-24-18 was the lowest yielding compared to other lines and to check varieties (266.6 kg ha^{-1}) (Table 3.26).

Table 3.25. Means of agronomic traits of lines within population KMA13-24 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-24-01	4.0	39.0	18.5	4.4	20.6	31.9	1,289.0
KMA13-24-03	5.0	36.5	17.6	4.4	19.0	27.4	1,190.2
KMA13-24-04	5.5	41.5	14.4	5.0	18.9	28.3	1,179.7
KMA13-24-05	5.0	37.5	19.2	5.6	26.2	27.6	1,636.6
KMA13-24-06	5.0	37.5	17.4	6.0	26.0	26.9	1,627.8
KMA13-24-07	4.5	43.0	21.7	5.4	29.9	26.0	1,869.8
KMA13-24-08	6.0	48.0	20.7	5.5	27.2	27.2	1,700.3
KMA13-24-10	6.5	43.0	20.1	5.9	29.2	23.5	1,825.2
KMA13-24-11	7.5	45.5	30.3	5.3	40.6	28.0	2,535.9
KMA13-24-13	6.5	41.5	24.0	5.0	21.0	23.7	1,313.8
KMA13-24-14	6.5	39.0	23.6	4.8	27.8	25.4	1,740.4
KMA13-24-16	7.0	37.5	21.4	5.2	27.0	25.6	1,689.9
KMA13-24-17	6.0	38.0	22.3	5.3	26.3	24.6	1,646.2
KMA13-24-18	5.5	34.5	-	-	4.3	16.3	266.6
KMA13-24-19	5.5	45.5	13.0	4.0	13.8	25.6	862.7
KMA13-24-20	5.0	36.0	15.8	5.5	22.1	21.2	1,378.8
KMA13-24-21	4.0	41.0	28.4	5.2	33.8	27.5	2,111.5
KMA13-24-22	6.0	45.0	16.9	4.0	22.1	33.3	1,382.0
KMA13-24-23	5.0	42.0	16.7	5.3	24.7	33.4	1,544.3
KMA13-24-24	5.5	39.5	26.0	4.8	31.4	34.1	1,965.5
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	5.3	40.0	19.7	5.2	25.5	27.6	1,596.4
CV (%)	23.4	7.8	37.7	18.3	39.6	18.3	39.6
P-value	0.07^{ns}	0.00**	0.50^{ns}	0.02*	0.24^{ns}	0.00***	0.24^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-25 Lines

There were significant differences among lines within population KMA13-25 for days to flowering (*P<0.01*), the number of seeds per pod (*P<0.01*) and 100-seed mass (*P<0.01*) (Table 3.27). The earliest line to flower was KMA13-25-02 (33.5 days). It was also earlier than all checks and donor parents. KMA13-25-28 (7.1) and KMA13-25-07 (7.0) were the genotypes with the highest number of seeds per pod. The lowest number of seeds per pod was recorded on KMA13-25-26 (4.0), which was lower than all crosses, commercial checks and donor parents. All the genotypes from crosses were medium-seeded (26.5 to 38.5 g 100-seed mass) with the highest value recorded on KMA13-25-20 (38.5 g 100-seed mass).

Table 3.26. Means of agronomic traits of lines within population KMA13-25 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant $^{-1}$	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-25-01	5.0	40.5	24.4	4.1	29.8	32.0	1,862.8
KMA13-25-02	4.5	33.5	18.9	5.6	26.8	29.9	1,677.4
KMA13-25-03	5.0	34.0	21.0	4.9	26.3	30.3	1,645.5
KMA13-25-04	5.0	37.5	22.2	4.6	32.4	33.1	2,026.4
KMA13-25-05	4.0	38.0	21.6	5.0	31.2	34.8	1,947.3
KMA13-25-06	4.0	38.5	23.1	5.1	31.9	31.2	1,992.6
KMA13-25-07	3.5	36.0	20.6	7.0	34.0	32.5	2,124.5
KMA13-25-08	4.5	40.5	19.4	4.6	31.6	30.5	1,974.2
KMA13-25-09	4.0	46.0	25.7	6.5	46.6	29.0	2,912.1
KMA13-25-10	4.0	36.0	18.0	6.1	28.5	29.0	1,780.2
KMA13-25-13	4.0	37.0	21.1	5.3	27.1	27.9	1,696.7
KMA13-25-14	5.0	35.0	17.0	4.7	22.7	32.4	1,416.7
KMA13-25-17	4.0	35.5	15.4	5.3	35.3	35.6	2,208.0
KMA13-25-18	4.0	36.5	15.6	4.6	23.4	36.3	1,463.5
KMA13-25-19	4.0	35.5	21.6	5.6	27.2	28.0	1,701.3
KMA13-25-20	3.5	36.5	18.9	5.0	30.5	38.5	1,905.3
KMA13-25-21	5.5	35.5	16.4	4.8	24.1	33.7	1,507.2
KMA13-25-22	5.5	39.5	18.0	4.9	25.1	36.4	1,568.1
KMA13-25-23	4.0	36.0	26.3	4.3	33.1	32.8	2,066.7
KMA13-25-25	5.0	35.5	20.2	5.4	27.6	31.7	1,722.6
KMA13-25-26	5.5	36.0	20.0	4.0	28.5	27.0	1,779.3
KMA13-25-27	5.0	45.0	20.3	6.2	27.8	31.2	1,735.0
KMA13-25-28	6.0	38.5	19.6	7.1	30.7	28.7	1,917.5
KMA13-25-29	5.0	35.0	21.3	4.7	31.1	26.5	1,943.5
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR 719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.6	37.9	20.0	5.3	29.0	30.8	1814.3
CV (%)	27.0	7.5	30.1	17.9	30.7	16.1	30.7
P-value	0.47^{ns}	0.00**	0.78^{ns}	0.00**	0.65^{ns}	0.00**	0.65^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-26 Lines

There were significant differences among lines within population KMA13-26 for all the traits measured notably the plant vigor (*P<0.01*), days to flowering (*P<0.01*), the number of pods per plant (*P<0.01*), the number of seeds per pod (*P<0.001*), the seed weight per plant (*P<0.001*), the 100-seed mass (*P<0.01*) and the seed yield (*P<0.001*). The most vigorous genotypes among crosses were KMA13-26-01 and KMA13-26-16 (4.0) but less vigorous than the checks KATB9 (3.0) and Mex54 (3.8). KMA13-26-21 (35 days) was the earliest to flower compared to all other crosses. KMA13-26-33 and KMA13-26-11 (48 days) were the last to flower. Among crosses, KMA13-26-32 had the highest number of pods per plant (26.3) which was also higher compared to all the checks and donor parents. The lowest number of pods per plant was recorded on KMA13-26-11 (2.0). KMA13-26-04 and KMA13-26-32 recorded the highest number of seeds per pods (5.9) among crosses but which was lower compared to best checks and donor parents. The highest seed weight per plant among crosses was recorded on KMA13-26-32 (30.8 g) but lower compared to the best checks KATB9 (38.2 g) and G2333 (32.5g). The population KMA13-26 was small- and medium-seeded with the 100-seed mass varying from 18.4 to 34.3 g. Most of the lines from this population were poor yielding compared to most of checks and donor parents. The highest yield among crosses was recorded on KMA13-26-32 (1,925.8 kg ha^{-1}) whereas the lowest was on KMA13-26-11 (156.3 kg ha^{-1}) (Table 3.28).

Table 3.27. Means of agronomic traits of lines within population KMA13-26 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-26-01	4.0	42.0	14.1	5.0	17.1	32.1	1,070.6
KMA13-26-04	6.0	39.5	20.8	5.9	23.7	23.3	1,478.9
KMA13-26-05	7.0	39.0	20.0	4.8	21.7	28.0	1,358.6
KMA13-26-06	5.5	40.5	17.5	5.0	21.1	24.6	1,318.0
KMA13-26-08	5.0	39.0	15.0	4.3	17.6	34.3	1,100.1
KMA13-26-09	5.5	42.0	15.0	3.3	12.5	18.4	781.3
KMA13-26-11	6.0	48.0	2.0	4.0	2.5	26.3	156.3
KMA13-26-16	4.0	43.0	10.7	4.0	10.0	29.6	624.3
KMA13-26-21	6.0	35.0	8.0	4.0	12.0	26.8	749.1
KMA13-26-22	6.5	38.0	10.8	4.0	15.8	27.3	988.3
KMA13-26-23	7.0	38.0	15.6	3.7	16.5	25.5	1,028.3
KMA13-26-25	8.0	43.0	4.5	4.0	5.9	31.0	371.1
KMA13-26-28	6.0	42.0	12.4	4.0	12.9	23.1	804.6
KMA13-26-32	6.5	43.0	26.3	5.9	30.8	27.7	1,925.8
KMA13-26-33	6.0	48.0	17.9	4.6	20.6	24.7	1,287.6
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	5.5	40.4	16.1	4.9	20.6	27.7	1,288.1
CV (%)	21.5	7.4	39.9	20.0	44.8	21.6	44.8
P-value	0.00**	0.00**	0.00**	0.00***	0.00***	0.00**	0.00***

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-27 Lines

There were significant differences among lines within population KMA13-27 for plant vigor (*P<0.01*), the number of seeds per pod (*P<0.05*) and 100-seed mass (*P<0.01*). KMA13-27-31 and KMA13-27-19 were the most vigorous among crosses with a mean score of 3.5. The highest number of seeds per pod was recorded on KMA13-27-07 (6.0). Genotypes among this population were medium-seeded with mean 100-seed mass ranging from 25.3 to 36.9 g except the KMA13-27-01 (23.9 g) which was small-seeded. Compared to checks and donor parents, the crosses were either equal or inferior for those traits (Table 3.29).

Table 3.28. Means of agronomic traits of lines within population KMA13-27 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant^{-1} (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-27-01	4.5	40.0	16.7	5.2	21.4	23.9	1,336.8
KMA13-27-02	4.5	42.0	19.9	5.0	25.7	30.1	1,607.5
KMA13-27-03	4.5	37.5	16.6	5.3	10.6	26.7	662.7
KMA13-27-04	4.0	41.5	16.7	4.9	17.9	27.2	1,121.8
KMA13-27-05	6.0	43.0	16.3	4.8	25.9	28.3	1,616.7
KMA13-27-06	5.5	35.5	22.5	4.3	24.3	25.9	1,519.6
KMA13-27-07	8.0	45.5	27.0	6.0	40.6	27.8	2,540.3
KMA13-27-08	6.0	43.0	16.8	4.5	25.8	26.6	1,611.3
KMA13-27-09	5.0	37.5	20.6	5.7	26.9	27.8	1,683.3
KMA13-27-10	7.0	41.0	19.9	5.3	25.8	25.3	1,613.1
KMA13-27-11	5.5	45.0	17.4	4.8	20.1	31.5	1,259.2
KMA13-27-12	5.0	45.5	23.3	5.9	33.2	30.7	2,076.2
KMA13-27-13	4.5	39.0	26.8	5.2	39.0	34.5	2,434.5
KMA13-27-14	6.0	41.5	17.9	4.8	23.2	34.5	1,450.5
KMA13-27-16	4.5	38.0	16.9	4.5	24.4	28.5	1,527.0
KMA13-27-17	5.0	40.5	15.0	5.0	20.7	35.1	1,292.7
KMA13-27-18	5.5	36.0	22.7	4.5	28.5	33.7	1,779.8
KMA13-27-19	3.5	43.0	16.4	5.2	25.1	34.2	1,571.6
KMA13-27-20	4.0	37.0	15.2	5.5	22.7	31.7	1,419.1
KMA13-27-21	4.0	38.5	17.5	5.1	24.3	35.3	1,519.7
KMA13-27-23	5.0	43.0	14.8	4.6	21.9	31.0	1,369.6
KMA13-27-24	4.5	43.0	14.1	5.0	18.7	30.0	1,170.6
KMA13-27-25	5.0	42.0	17.7	4.1	27.5	32.1	1,719.7
KMA13-27-26	4.5	39.5	18.8	5.6	28.9	31.6	1,805.6
KMA13-27-27	4.5	42.5	23.5	5.1	33.9	27.3	2,120.5
KMA13-27-28	4.5	35.0	27.0	4.8	40.2	30.8	2,512.5
KMA13-27-31	3.5	42.5	18.4	5.9	26.5	36.9	1,654.5
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex 54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR 719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.9	40.2	19.2	5.2	26.5	30.0	1,657.3
CV (%)	21.6	8.4	35.5	18.0	38.9	16.8	38.9
P-value	0.00**	0.10^{ns}	0.75^{ns}	0.03*	0.58^{ns}	0.00**	0.58^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-28 Lines

There were significant differences among genotypes within population KMA13-28 for some traits including days to flowering (*P<0.05*), the number of seeds per pod (*P<0.01*) and the 100-seed mass (*P<0.001*) (Table 3.30). KMA13-28-24 was the earliest to flower compared to all other crosses, all checks and donor parents (34 days). KMA13-28-23 was the last to flower among crosses (43 days). The highest number of seeds per pod among crosses was recorded on the genotype KMA13-28-29 (5.9) but which was lower than many checks. Genotypes within this population were ranging from small-seeded (23.2 g 100-seed mass) to large-seeded beans (40.1 g 100-seed mass).

Table 3.29. Means of agronomic traits of lines within population KMA13-28 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-28-02	3.5	36.5	25.7	5.7	29.6	40.1	1,851.1
KMA13-28-03	4.0	39.0	25.3	4.6	31.8	28.2	1,986.6
KMA13-28-05	3.5	39.0	20.8	5.4	42.8	33.3	2,677.4
KMA13-28-07	4.0	38.5	17.5	4.9	32.4	31.6	2,023.6
KMA13-28-10	4.5	37.0	18.3	5.7	25.0	27.4	1,559.7
KMA13-28-13	4.0	38.0	24.1	4.6	27.8	31.1	1,740.3
KMA13-28-20	4.0	35.0	17.7	4.0	21.9	36.0	1,370.1
KMA13-28-21	4.0	37.5	30.2	5.2	48.1	25.0	3,005.6
KMA13-28-22	3.5	36.0	25.8	4.8	29.8	27.7	1,864.7
KMA13-28-23	5.0	43.0	26.0	4.0	24.8	26.6	1,547.7
KMA13-28-24	5.0	34.0	19.6	5.0	22.9	29.2	1,431.1
KMA13-28-28	5.0	42.5	19.3	4.5	25.3	27.5	1,578.9
KMA13-28-29	5.0	36.0	23.9	5.9	24.2	23.2	1,514.4
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.5	38.3	21.2	5.2	28.7	29.4	1,792.2
CV (%)	27.9	7.3	31.5	17.9	36.1	17.6	36.1
P-value	0.19^{ns}	0.01*	0.32^{ns}	0.00**	0.35^{ns}	0.00***	0.35^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-29 Lines

There were significant differences among lines within population KMA13-29 for the number of seeds per pod (*P<0.001*) and the 100-seed mass (*P<0.001*) (Table 3.31). The highest number of seeds per pod among crosses was recorded on KMA13-29-11 (5.6) but which was significantly lower than most of checks and donor parents. This population contained small-, medium- and large-seeded genotypes with mean values ranging from 22.0 to 40.6 g 100-seed mass.

Table 3.30. Means of agronomic traits of lines within population KMA13-29 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-29-01	4.5	36.0	22.4	4.7	26.7	24.1	1,671.6
KMA13-29-02	5.5	39.0	22.2	3.8	24.4	29.5	1,526.8
KMA13-29-04	5.5	39.5	14.8	4.3	28.7	30.3	1,790.6
KMA13-29-05	4.5	40.5	27.6	4.9	27.7	24.9	1,734.1
KMA13-29-09	6.0	42.5	18.7	5.0	21.6	29.4	1,347.9
KMA13-29-10	4.5	40.0	24.1	5.5	25.1	22.0	1,567.6
KMA13-29-11	6.5	38.5	18.8	5.6	18.7	28.0	1,171.1
KMA13-29-13	5.0	39.5	18.8	4.1	24.3	35.1	1,518.0
KMA13-29-15	5.5	38.0	18.2	3.8	23.8	36.6	1,488.9
KMA13-29-16	5.0	39.5	16.4	4.4	18.0	23.6	1,123.7
KMA13-29-18	5.0	41.0	23.7	5.0	26.3	40.3	1,641.5
KMA13-29-19	5.0	40.0	25.7	4.4	33.1	31.2	2,066.6
KMA13-29-21	6.0	43.0	23.3	4.7	28.2	34.2	1,765.2
KMA13-29-22	7.0	40.0	24.3	4.5	33.5	32.6	2,093.2
KMA13-29-23	5.0	38.0	25.4	5.1	32.5	30.6	2,032.4
KMA13-29-24	5.0	39.0	27.0	4.2	35.2	34.1	2,201.1
KMA13-29-25	5.0	40.0	27.0	4.0	36.0	30.1	2,252.9
KMA13-29-26	4.5	38.5	27.8	4.8	29.0	32.7	1,812.7
KMA13-29-27	6.0	36.0	28.0	4.7	22.2	33.2	1,386.7
KMA13-29-28	4.5	39.0	26.6	5.0	33.8	34.9	2,114.8
KMA13-29-29	5.0	39.0	23.3	5.0	34.4	40.6	2,152.7
KMA13-29-30	5.0	42.0	32.9	4.8	42.7	32.6	2,669.1
KMA13-29-31	5.5	39.5	23.2	5.0	27.6	32.2	1,722.3
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	5.1	39.3	22.2	4.9	28.1	30.7	1,756.1
CV (%)	24.9	7.2	33.6	18.7	37.4	17.3	37.4
P-value	0.46^{ns}	0.20^{ns}	0.47^{ns}	0.00***	0.79^{ns}	0.00***	0.79^{ns}

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-30 Lines

There were significant differences for days to flowering (*P<0.05*), the number of seeds per pod (*P<0.001*), seed weight per plant (*P<0.05*), 100-seed mass (*P<0.001*) and the seed yield per unit area (*P<0.05*) (Table 3.32). KMA13-30-30 was the earliest cross to flower (35 days) while KMA13-30-01(42.3 days) was the last. The highest number of seeds per pod was recorded on KMA13-30-15 (6.5) but which was statistically equal to the best check KATB9 and higher than all other checks and donor parents. The genotype KMA13-30-14 had the highest seed weight per plant (52.7g) and the highest seed yield per ha (3,295.3 kg ha^{-1}). The other high yielding genotypes were KMA13-30-02 (2,771.4 kg ha^{-1}), KMA13-30-07 (2,505.9 kg ha^{-1}), KMA13-30-16 (2,395.1 kg ha^{-1}) and KMA13-30-30 (2,434.9 kg ha^{-1}), all superior to the best yielding check variety KATB9 (2,384.7 kg ha^{-1}). All other lines were either equal or inferior to the best commercial check. All the genotypes from this population were medium-seeded with mean 100-seed mass ranging from 25.1 to 35.2 g 100-seed mass, except KMA13-30-21 which was a small-seeded line (22.1 g 100-seed mass).

Table 3.31. Means of agronomic traits of lines within population KMA13-30 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods plant^{-1}	Seeds pod^{-1}	Seed weight plant (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-30-01	4.5	42.5	20.7	5.2	29.4	28.6	1,840.1
KMA13-30-02	5.5	37.0	27.5	5.8	44.3	27.7	2,771.4
KMA13-30-07	6.0	35.5	26.1	5.0	40.1	33.7	2,505.9
KMA13-30-08	5.5	38.0	27.3	4.6	32.9	29.1	2,059.3
KMA13-30-13	4.5	35.5	26.1	5.0	34.1	25.8	2,131.2
KMA13-30-14	5.5	41.0	31.1	5.6	52.7	30.4	3,295.3
KMA13-30-15	4.5	36.5	23.2	6.5	26.4	25.1	1,648.0
KMA13-30-16	4.5	35.5	24.6	4.4	38.3	35.2	2,395.1
KMA13-30-18	4.5	38.5	25.3	5.9	35.8	31.6	2,236.8
KMA13-30-20	5.0	42.0	17.4	4.0	25.9	31.3	1,621.1
KMA13-30-21	6.0	39.0	15.5	3.5	19.5	22.1	1,215.6
KMA13-30-22	6.0	39.0	20.2	5.4	31.3	31.9	1,955.7
KMA13-30-30	4.0	35.0	25.3	5.8	39.0	27.8	2,434.9
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.9	38.5	21.9	5.3	31.5	29.1	1,969.2
CV (%)	22.6	7.7	28.6	17.1	29.4	17.8	29.4
P-value	0.17^{ns}	0.03*	0.08^{ns}	0.00***	0.02*	0.00***	0.02*

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-31 Lines

There were significant differences among genotypes within population KMA13-31 for the following traits: plant vigor (*P<0.05*), days to flowering (*P<0.05*), the number of seeds per pod (*P<0.01*), seed weight per plant (*P<0.05*), 100-seed mass (*P<0.001*) and the seed yield (*P<0.05*) (Table 3.33). KMA13-31-04 was the most vigorous genotype among crosses with a mean score of 3.5. However, it was less vigorous compared to the best check KATB9 (3.0). KMA13-31-04 and KMA13-31-06 flowered earlier than all other crosses in 37 days after planting but they are late compared to checks GLP2 (34.3 days) and KATB9 (35 days). The highest number of seeds

per pod was recorded on KMA13-31-06 (6.1) but which was lower compared to checks G2333 (6.3), GLP585 (6.4) and KATB9 (6.5). KMA13-31-03 recorded the highest seed weight per plant (43.3 g) and the highest seed yield per ha (2,705.5 kg ha^{-1}). Apart from the genotype KMA13-31-08 (2,286.7 kg ha^{-1}), all other genotypes in this population were higher yielding than the best check variety KATB9 (2,384.7 kg ha^{-1}). Genotypes in population KMA13-31 ranged from small- to medium-seeded with mean 100-seed mass varying from 24.4 g to 29.4 g.

Table 3.32. Means of agronomic traits of lines within population KMA13-31 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods $plant^{-1}$	Seeds pod^{-1}	Seed weight plant (g)	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-31-01	4.5	39.0	29.5	5.8	41.6	29.3	2,599.6
KMA13-31-03	4.0	37.5	25.8	6.0	43.3	24.4	2,705.5
KMA13-31-04	3.5	37.0	26.3	6.0	40.5	24.8	2,533.6
KMA13-31-06	4.5	37.0	25.4	6.1	38.4	29.4	2,401.7
KMA13-31-08	5.0	40.0	24.1	5.3	36.6	28.1	2,286.7
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.6	38.7	21.6	5.7	31.7	28.4	1,980.4
CV (%)	23.7	7.3	29.9	16.8	30.0	19.2	30.0
P-value	0.04*	0.01*	0.08^{ns}	0.00**	0.04*	0.00***	0.04*

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

Population KMA13-32 Lines

There were significant differences among lines within population KMA13-32 for days to flowering (*P<0.01*), the number of pods per plant (*P<0.05*), the number of seeds per pod (*P<0.01*), seed weight per plant (*P<0.01*), 100-seed mass (*P<0.001*) and the seed yield per ha (*P<0.01*) (Table 3.34). Crosses were globally late to flower (40 to 45.5 days) compared to checks and donor parents (34.3 to 46 days, most of them have flowered within 39 days). Crosses

recorded higher number of pods per plant (27.2 to 31.3) compared to commercial checks and donor parents (14.7 to 24.0). The number of seeds per pod for the crosses was either equal or inferior to commercial checks and donor parents. The genotype KMA13-32-28 was the best yielding (3,375.3 kg ha^{-1}) among all the crosses and all the checks and donor parents. The other higher yielding line was KMA13-32-26 (2,823.5 kg ha^{-1}) which was also superior to all checks and donor parents. Genotypes KMA13-32-24 (2,382.3 kg ha^{-1}), KMA13-32-22 (2,233.9 kg ha^{-1}) were not statistically different from the best check variety KATB9 (2,384.7 kg ha^{-1}). All the crosses were medium-seeded with mean values ranging from 27.6 g 100-seed mass for the genotype KMA13-32-22 to 37.3 g 100-seed mass for the genotype KMA13-32-26.

Table 3.33. Means of agronomic traits of lines within population KMA13-32 of bean grown at Mwea in 2016

Lines	Vigor	Days to flowering	Pods $plant^{-1}$	Seeds pod^{-1}	Seed weight $plant^{-1}$	100-seed mass (g)	Seed yield (kg ha^{-1})
KMA13-32-22	5.0	45.5	30.2	4.8	35.7	27.6	2,233.9
KMA13-32-24	4.5	43.5	27.2	6.0	38.1	34.2	2,382.3
KMA13-32-26	4.5	40.0	31.3	4.1	45.2	37.3	2,823.5
KMA13-32-28	4.5	40.5	28.0	6.0	54.0	37.1	3,375.3
Donors							
AND1062	4.6	38.9	17.4	5.1	27.6	35.5	1,723.8
BRB191	5.3	41.5	21.3	5.3	28.8	30.4	1,800.3
G10909	5.8	40.3	16.3	5.7	21.0	21.1	1,313.8
G2333	5.2	38.5	23.8	6.3	32.5	28.5	2,033.8
Mex54	3.8	38.5	14.7	4.6	22.4	37.4	1,397.9
RWR719	5.1	38.9	20.7	5.7	28.1	25.9	1,755.3
Checks							
GLP585	4.8	38.2	19.7	6.4	27.6	24.6	1,726.6
GLP92	5.3	34.3	16.4	4.3	20.2	31.3	1,263.1
KATB1	5.0	46.0	16.3	6.0	24.8	27.4	1,549.8
KATB9	3.0	35.0	24.0	6.5	38.2	27.7	2,384.7
Mean	4.7	40.0	22.1	5.5	32.0	30.4	2,000.0
CV (%)	25.6	7.4	29.4	17.3	29.3	17.7	29.3
P-value	0.19^{ns}	0.00**	0.02*	0.00**	0.00**	0.00***	0.00**

CV: coefficient of variation; ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively.

3.3.3.3. Market classes

From the 16 segregating bean populations, 8 market classes were identified. These were red kidney, red mottled, small red, black, mixed color, pinto, yellow and greyish green beans (Table 3.35). The most dominant market class was the mixed colors (31.1%) present in all the populations apart from KMA13-17 and KMA13-20. This group was mainly constituted by tan red and tan brown seed colors. The second most abundant market class was the small red (18.0%), dominant in populations KMA13-31 (64.0%); KMA13-19 (55.9%) and KMA13-30 (46.0%). Pinto (5.6%), yellow (3.2%) and greyish green beans (0.9%) were the least abundant market classes.

Table 3.34. Major market classes from 16 $F_{1.6}$ segregating bean populations grown at Mwea in 2016

Population	Market classes (%)							
	Red kidney	Red mottled	Small red	Blacks	Mixed color	Pinto	Yellow	Greyish green
KMA13-17	32.7	67.3	0.0	0.0	0.0	0.0	0.0	0.0
KMA13-18	44.4	0.0	0.0	33.3	22.2	0.0	0.0	0.0
KMA13-19	22.1	0.0	55.9	11.8	8.8	1.5	0.0	0.0
KMA13-20	0.0	100.0	0.0	0.0	0.0	0.0	0.0	0.0
KMA13-21	3.5	10.7	2.2	15.3	46.2	15.8	6.3	0.0
KMA13-22	1.3	3.2	9.2	20.5	46.9	17.2	1.6	0.0
KMA13-23	3.1	0.5	4.1	24.7	52.6	13.4	1.5	0.0
KMA13-24	9.6	11.1	5.0	7.1	41.4	25.2	0.5	0.0
KMA13-25	9.6	9.9	21.5	12.6	33.4	1.7	6.8	4.4
KMA13-26	14.3	11.8	21.0	12.6	18.5	13.4	5.0	3.4
KMA13-27	6.2	14.3	18.8	17.4	34.3	2.0	2.0	5.1
KMA13-28	9.6	4.1	6.2	30.8	40.4	1.4	5.5	2.0
KMA13-29	10.5	17.8	9.4	8.9	44.5	1.0	7.8	0.0
KMA13-30	3.2	8.7	46.0	5.6	28.6	3.2	4.8	0.0
KMA13-31	0.0	1.3	64.0	8.0	25.3	0.0	1.3	0.0
KMA13-32	0.0	12.8	25.6	0.0	53.8	0.0	7.7	0.0
Mean	10.6	17.1	18.0	12.3	31.1	5.6	3.2	0.9

Characteristics of the different lines selected for further evaluation

Major characteristics of genotypes selected and grouped by market class from those 16 $F_{1.6}$ bean populations are presented in Tables 3.36, 3.37, 3.38, 3.39 and 3.40. For further evaluation, 16 red mottled genotypes were selected mainly from the populations KMA13-24 (4 lines), KMA13-29 (3 lines) and KMA13-17, KMA13-28 and KMA13-32 (2 lines each). Thirteen red kidney nearly homozygous lines were selected from populations KMA13-19, KMA13-25 and KMA13-29

contributing 2 lines each. For small reds, 19 lines were selected. These were mainly from populations KMA13-30; KMA13-32 both contributed 4 lines each and KMA13-22, KMA13-23 and KMA13-32 with 2 lines each. Twelve pinto lines were selected for further testing. Six were from KMA13-22 and three from KMA13-23. Black, yellow and greyish green was added to mixed color from which a total of 31 genotypes were selected for further testing. This includes 19 tan browns and reds, 9 blacks, 1 greyish green and 1 yellow bean.

Table 3.35. Characteristics of red mottled $F_{1.6}$ lines selected from 16 populations grown at Mwea in 2016

Line	Vigor	Days to flowering	Days to maurity	Pods plant^{-1}	Seed pod^{-1}	100-seed mass	Seed yield plant^{-1}	Seed yield (kg ha^{-1})
KMA13-17-17	3.0	40.0	96.0	12.3	3.9	39.2	15.9	993.8
KMA13-17-25	2.0	34.0	90.0	9.0	4.0	42.3	11.0	689.2
KMA13-20-14	4.0	41.0	97.0	20.2	5.0	34.6	35.8	2240.2
KMA13-24-05	5.0	38.0	94.0	13.6	5.2	29.2	21.2	1328.3
KMA13-24-11	6.0	43.0	99.0	30.2	5.2	27.9	40.6	2535.9
KMA13-24-16	6.0	42.0	98.0	29.2	6.3	26.6	33.8	2113.9
KMA13-24-17	4.0	43.0	99.0	32.3	6.3	26.0	38.2	2389.8
KMA13-25-03	4.0	35.0	91.0	25.0	5.0	26.9	28.8	1800.1
KMA13-27-25	6.0	36.0	92.0	18.4	4.6	30.9	23.0	1442.6
KMA13-28-03	3.0	42.0	98.0	20.4	5.0	29.7	27.6	1724.6
KMA13-28-13	3.0	38.0	94.0	17.2	4.8	31.1	27.8	1740.3
KMA13-29-05	4.0	38.0	94.0	31.0	5.0	29.6	36.8	2301.3
KMA13-29-21	6.0	43.0	99.0	35.7	4.4	35.6	43.5	2718.1
KMA13-29-24	5.0	36.0	92.0	22.7	3.7	33.7	29.3	1833.0
KMA13-32-24	5.0	48.0	104.0	26.2	5.5	35.4	37.6	2350.2
KMA13-32-28	2.0	38.0	94.0	28.0	6.0	37.0	54.0	3375.3
Test lines mean	4.2	39.7	95.7	23.2	5.0	32.2	31.6	1973.5
BRB191	5.3	41.0	97.0	21.1	5.3	40.4	28.4	1776.1
Overall mean	4.3	39.8	95.8	23.1	5.0	32.7	31.4	1961.9

Table 3.36. Characteristics of red kidney $F_{1.6}$ lines selected from 16 populations of bean grown at Mwea in 2016

Line	Vigor	Days to flowering	Days to maturity	Pods plant^{-1}	Seed pod^{-1}	100-seed mass	Seed yield plant^{-1}	Seed yield (kg ha^{-1})
KMA13-17-25	2.0	34.0	90.0	9.0	4.0	42.8	11.3	703.9
KMA13-19-12	4.0	35.0	91.0	26.6	4.8	31.2	30.7	1920.6
KMA13-19-16	5.0	41.0	97.0	13.7	5.2	32.0	44.7	2793.9
KMA13-20-03	4.0	38.0	94.0	29.0	5.2	39.7	46.3	2901.8
KMA13-21-11	3.0	35.0	91.0	13.4	3.6	37.4	21.4	1340.2
KMA13-25-03	4.0	33.0	89.0	17.0	4.9	33.8	23.9	1490.9
KMA13-25-20	2.0	35.0	91.0	15.9	3.9	43.0	26.3	1645.6
KMA13-26-32	5.0	38.0	94.0	25.6	4.8	37.9	36.0	2252.7
KMA13-27-31	4.0	42.0	98.0	20.3	6.7	42.0	30.3	1896.1
KMA13-28-02	2.0	36.0	92.0	12.6	6.1	44.1	21.9	1365.4
KMA13-29-28	5.0	42.0	98.0	30.8	5.2	37.3	40.2	2512.0
KMA13-29-30	3.0	36.0	92.0	33.8	4.6	41.8	44.7	2794.2
KMA13-30-22	5.0	35.0	91.0	29.5	5.2	32.7	42.4	2648.7
Test lines mean	3.7	36.9	92.3	21.3	4.9	38.1	32.3	2020.5
AND1062	4.5	38.0	94.0	17.4	5.1	45.5	27.6	1723.8
Mex54	3.9	38.0	94.0	15.3	4.6	37.4	22.3	1397.9
Overall mean	3.8	37.1	93.1	20.7	4.9	38.6	31.3	1959.2

Table 3.37. Characteristics of small red $F_{1.6}$ lines selected from 16 populations of bean grown at Mwea in 2016

Line	Vigor	Days to flowering	Days to maturity	Pods plant^{-1}	Seed pod^{-1}	100-seed mass	Seed yield plant^{-1}	Seed yield (kg ha^{-1})
KMA13-22-27	6.0	43.0	99.0	18.5	6.8	24.3	32.53	2032.9
KMA13-22-29	4.0	37.0	95.0	22.2	6.4	31.9	39.2	2451.9
KMA13-23-14	6.0	43.0	99.0	28.4	5.8	29.9	39.4	2460.3
KMA13-23-21	4.0	35.0	91.0	26.5	5.0	38.5	41.3	2582.1
KMA13-25-09	2.0	44.0	100.0	28.3	7.0	30.9	57.5	3594.2
KMA13-28-13	3.0	38.0	94.0	24.1	4.6	31.1	27.8	1740.3
KMA13-30-02	5.0	36.0	92.0	27.5	5.8	27.7	44.3	2771.3
KMA13-30-14	7.0	48.0	104.0	37.3	5.2	34.8	65.1	4071.4
KMA13-30-16	4.0	37.0	95.0	29.0	5.3	34.0	49.6	3100.9
KMA13-30-30	5.0	35.0	91.0	29.6	5.8	27.9	41.8	2613.8
KMA13-31-01	5.0	42.0	98.0	35.6	6.0	23.7	50.0	3128.1
KMA13-31-03	4.0	38.0	94.0	25.7	6.1	24.1	46.4	2899.4
KMA13-31-04	3.0	38.0	94.0	28.5	6.0	24.8	47.0	2937.7
KMA13-31-08	5.0	42.0	98.0	23.5	5.0	27.4	36.4	2273.7
KMA13-32-26	3.0	43.0	99.0	32.5	4.2	36.3	48.1	3007.1
KMA13-32-28	2.0	38.0	94.0	28.0	6.0	37.0	54.0	3375.3
Test lines mean	4.2	39.8	96.1	27.8	5.7	30.3	45.0	2815.0
GLP585	5.0	38.0	94.0	19.7	6.4	24.6	27.6	1725.0
KATB9	3.0	35.0	91.0	27.0	6.5	28.2	42.7	2666.0
G2333	5.0	38.0	94.0	23.7	6.3	28.4	32.5	2032.0
G10909	5.0	40.0	96.0	17.8	5.8	21.4	23.3	1454.0
RWR719	5.0	39.0	95.0	21.1	5.7	29.9	28.7	1794.0
Overall mean	4.3	39.4	95.6	26.4	5.8	29.4	31.0	1934.2

Table 3.38. Characteristics of pinto $F_{1.6}$ lines selected from 16 populations of bean grown at Mwea in 2016

Line	Vigor	Days to flowering	Days to maturity	Pods plant^{-1}	Seed pod^{-1}	100-seed mass	Seed yield plant^{-1}	Seed yield (kg ha^{-1})
KMA13-21-19	5.0	35.0	91.0	22.6	6.2	34.7	37.9	2368.4
KMA13-22-03	4.0	37.0	93.0	22.2	6.4	32.0	39.2	2452.0
KMA13-22-07	5.0	36.0	92.0	24.7	4.3	24.2	38.57	2410.4
KMA13-22-21	6.0	36.0	92.0	20.8	5.2	28.2	38.0	2372.9
KMA13-22-30	2.0	38.0	94.0	33.6	6.6	29.4	47.8	2986.9
KMA13-22-32	4.0	37.0	93.0	26.0	4.7	29.9	39.8	2484.9
KMA13-22-33	3.0	43.0	99.0	23.3	3.7	28.8	35.6	2225.2
KMA13-23-13	4.0	38.0	94.0	28.4	5.8	27.6	40.5	2530.4
KMA13-23-18	4.0	43.0	99.0	32.0	4.0	24.4	38.8	2428.3
KMA13-23-22	5.0	38.0	94.0	34.7	5.8	28.2	45.3	2831.4
KMA13-24-06	4.0	40.0	96.0	23.3	6.5	27.2	37.7	2354.7
KMA13-24-07	5.0	43.0	99.0	30.5	5.6	25.4	39.8	2489.8
Test lines mean	4.2	38.7	94.7	26.8	5.4	28.3	39.9	2494.6
GLP92	5.0	34.0	90.0	16.4	4.3	31.3	20.2	1262.0
Overall mean	4.3	38.3	94.3	26.0	5.3	28.6	38.4	2399.8

Table 3.39. Characteristics of mixed color $F_{1.6}$ lines selected from 16 populations of bean grown at Mwea in 2016

Line	Vigor	Days to flowering	Days to maturity	Pods plant^{-1}	Seed pod^{-1}	100-seed mass	Seed yield plant^{-1}	Seed yield (kg ha^{-1})
			Blacks					
KMA13-22-23	5.0	43.0	99.0	24.6	4.8	26.5	39.0	2439.5
KMA13-23-10	4.0	37.0	93.0	27.2	4.7	22.0	32.7	2046.8
KMA13-23-11	4.0	43.0	99.0	24.7	5.7	26.9	37.3	2334.4
KMA13-25-04	4.0	33.0	89.0	23.2	4.6	35.5	37.7	2359.4
KMA13-27-10	7.0	34.0	90.0	10.8	4.8	25.9	18.1	1131.8
KMA13-27-12	5.0	43.0	99.0	18.9	6.7	27.7	26.0	1626.1
KMA13-28-21	6.0	38.0	94.0	31.7	4.7	21.2	32.7	2044.2
KMA13-28-22	2.0	37.0	93.0	30.0	6.0	30.9	41.3	2582.1
KMA13-28-29	3.0	37.0	93.0	28.2	7.0	23.4	33.9	2119.5
Mean	4.4	38.3	94.3	24.4	5.4	26.7	33.2	2076.0
			Tan brown and tan red					
KMA13-21-23	5.0	36.0	92.0	21.7	5.2	25.8	32.4	2027.5
KMA13-22-16	3.0	43.0	99.0	24.4	5.8	32.0	39.4	2465.9
KMA13-22-32	4.0	37.0	93.0	21.1	4.9	33.6	27.1	1692.8
KMA13-23-09	5.0	42.0	98.0	26.2	5.0	30.7	35.9	2242.2
KMA13-23-20	4.0	42.0	98.0	29.5	4.5	41.1	43.9	2743.9
KMA13-24-10	6.0	43.0	99.0	31.6	6.6	22.0	43.7	2728.4
KMA13-25-01	5.0	38.0	94.0	23.5	4.5	35.9	31.1	1931.1
KMA13-27-13	5.0	35.0	91.0	42.0	5.0	33.4	59.3	3707.2
KMA13-27-14	7.0	35.0	91.0	29.2	5.0	35.9	38.1	2380.8
KMA13-27-27	5.0	37.0	93.0	40.0	6.2	30.2	61.5	3842.5
KMA13-28-05	4.0	37.0	93.0	25.5	5.6	33.3	42.8	2677.4
KMA13-28-13	3.0	38.0	94.0	24.1	4.6	31.1	27.8	1740.3
KMA13-29-19	5.0	43.0	99.0	31.0	4.2	35.3	35.1	2192.9
KMA13-29-21	6.0	43.0	99.0	35.7	4.4	35.6	43.5	2718.1
KMA13-30-07	6.0	35.0	91.0	27.9	4.6	29.3	34.9	2183.7
KMA13-31-06	5.0	36.0	92.0	24.2	6.8	27.2	39.7	2479.5
KMA13-32-22	2.0	48.0	104.0	30.2	4.8	27.6	35.7	2233.9
Mean	4.7	39.3	95.3	28.7	5.2	31.8	39.5	2469.9
			Yellow and greyish green					
KMA13-21-20	5.0	42.0	98.0	21.0	5.7	37.7	35.2	2199.4
KMA13-27-21	3.0	35.0	91.0	10.9	4.2	40.8	15.2	947.9
Mean	4.0	38.5	94.5	15.9	4.9	39.2	25.2	1573.6
KATB1	5.0	46.0	102.0	17.3	6.0	27.6	26.3	1643.0

3.4. DISCUSSION

Yield and yield components among populations, commercial checks and donor parents

Inter-racial and inter-gene pool populations were not consistent in yield over generations. In the $F_{1.3}$ generation for example, KM13-24 (2 t ha^{-1}) followed by KM13-17 (1.81 t ha^{-1}) and KM13-29 (1.77 t ha^{-1}) were the best yielding populations. In $F_{1.4}$ generation, KMA13-29 and KMA13-19 (1.87 t ha^{-1}) were the best. The trend was much different when the $F_{1.6}$ generation was grown at Mwea, population KMA13-32 (2.8 t ha^{-1}) was the best in terms of seed yield. The trend was similar for the commercial checks and donor parents as their ranking was also varying with site and season. BRB191 was the best in $F_{1.3}$ (3.1 t ha^{-1}), AND1062 in $F_{1.4}$ (2.1 t ha^{-1}) while the small red bean variety KATB9 was outstanding at the $F_{1.6}$ grown at Mwea (2.4 t ha^{-1}). The effects of generations are often confounded with the effects of the environment when they were grown. Thus, differences should not be attributed simply to genetic difference among populations, but rather to environmental differences in growing seasons (Borel *et al.*, 2013). The high variability in Kenyan weather conditions could, therefore, explain the high variability observed among populations across years.

Yield and yield components varied significantly among inter-racial populations. Crosses involving the parental genotype KATB9 (KMA13-29, KMA13-30, KMA13-31 and KMA13-32) were better yielding among inter-racial populations and most of the commercial checks and donor parents while populations having the yellow bean KATB1 as female parent were poor yielding. These findings are similar to those of Ragagnin *et al*. (2009) who observed genetic variability for seed yield and other qualitative traits among 40 multiple-parent families assessed. Inter-gene and inter-racial crosses usually result in high genetic variability which is important for common bean improvement (Borel *et al.*, 2013).

There were transgressive genotypes within most of the inter-racial populations for seed yield and yield related traits. The best yielding line within the population KMA13-32 had the highest seed yield (3.38 t ha^{-1}) followed by 3.29 t ha^{-1} for KMA13-30 , 3.13 t ha^{-1} for KMA13-23, and 3.01 t ha^{-1} for KMA13-28. The trend was the same for the number of pods per plant and the seed yield per plant. The overall mean for a given population was not always reflecting the true picture within the population as some populations, although with poor overall means, possessed individual lines with higher performance. The breeder should not, therefore, limit the selection at

the population level but should also detect and select those outstanding genotypes within poor yielding populations. The presence of transgressive genotypes from these inter-racial populations provides a hope of selecting better varieties from the present breeding programme. Welsh *et al.* (1995) showed that lines from inter-racial populations yield higher than lines from intra-racial populations. Similar findings were found by Njuguna (2014). This demonstrated the effectiveness of the inter-racial crosses to improve the seed yield of common beans. Singh *et al.* (2002), after studying the effects on seed yields of Andean intra-gene pool crosses and Andean-Middle America inter-gene pool crosses, concluded that the utilization of high yielding genotypes from both gene pools which are diverse and with positive general combining ability could maximize gains from seed yield selection. Welsh *et al.* (1995) and Singh and Urrea (1995) suggested the necessity to explore inter-gene pool and inter-racial crosses as a mean to create useful genetic variations and to broaden the genetic base of commercial cultivars as well as maximizing gains from selections. However, the high variability generated by inter-gene crosses, seldom leads to increase in seed yield compared to intra-gene crosses. This could be attributed to loss of favorable epistatic combinations which contribute to greater adaptation to the environments of origin of the two gene pools (Borel *et al.,* 2013). This could explain why some populations were lower yielding compared to commercial checks which are mainly from intra-gene crosses.

The high yielding parents were likely to give high yielding progenies. In fact, all crosses involving the commercial variety KATB9 from early generation (Njuguna, 2014) have shown outstanding yields. Populations KMA13-29, KMA13-30, KMA13-31 and KMA13-32 had an overall mean yield superior to other populations. As described by Kimani *et al.* (2012), KATB9 is a drought tolerant, compact and bushy genotype with a yield potential of between 1.4 and 1.9 t ha^{-1}. It could, therefore, have transmitted all these desirable traits to its progenies especially drought tolerance which has allowed them to adapt and give good yield during a drought period in which our trials were conducted.

Pearson's correlation coefficients among seed yield and yield components

Except for the plant vigor and the 100-seed mass which were negatively correlated to seed yield and the days to flowering which had not shown any significant correlation; all other parameters, such the number of pods per plant, the number seeds per pod, the seed yield per plant, were

positively correlated to seed yield. These findings are similar to those found by Welsh *et al.* (1995) and recently by Njuguna (2014). In fact, for the legume crops and common bean precisely, any factor favouring the number of pods per plant, the number of seeds per pod will consequently improve the seed yield per plant and per unit area (Rugheim and Abdelgani, 2012; Mekki, 2016; Mushagalusa *et al.*, 2016).

One consequence of the correlation analysis is that the seed yield per plant or pod number per plant are good indicators of grain yield in kg ha^{-1}. Thus, these two traits could be used by plant breeders as an indirect method for yield selection. In this study, there was no significant correlation between the days to flowering and the seed yield. However, Welsh *et al.* (1995) and Njuguna (2014), all working on inter-racial populations have found significant correlations but in a contrasting direction. For the first author, days to flowering was significantly positively correlated to yield whereas for Njuguna (2014), it was negatively correlated, a finding supported by Singh *et al.* (1992) and Perez-Vega *et al.* (2011). In water stressed environments, early maturing genotypes provide better yields than late ones (Rao *et al.*, 2017).

From the correlation, small-seeded genotypes yielded higher than large-seeded genotypes. Singh *et al.* (2002) reported approximately 40 to 60 % more yields from small-seeded genotypes compared to the large-seeded counterparts. Thus, there is a negative correlation between the 100-seed mass and the seed yield per unit area as supported by our findings and by Singh *et al.* (2002). Most of the small-seeded genotypes were of indeterminate growth habit compared to large-seeded which were mainly determinate in growth. Welsh *et al.* (1995) had demonstrated a highly significant correlation between growth habit and seed yield, showing that indeterminate genotypes yielded higher than determinate genotypes.

Reactions of inter-racial populations to target diseases

There were no significant differences among inter-racial populations in their reactions to angular leaf spot (ALS), bean common mosaic virus (BCMV) and anthracnose. All the populations were moderately resistant. Differences were, however, significant among populations and commercial checks and donor parents. Donor parents Mex54 and G10909 showed resistance to angular leaf spot confirming them as sources of resistance to ALS pathogen. All other parents were ranging from moderately resistant to highly susceptible. Commercial check GLP92 was the most susceptible to ALS and anthracnose. Among parents, only the donor parent G2333 showed

resistance to anthracnose. Commercial checks and donor parents showed more susceptibility to BCMV than inter-racial populations as they were ranging from 5.6 to 7.1, except the donor parent BRB191 which showed a high level of resistance to BCMV. BRB191 is also a good source of resistance to BCMV. Among checks and donor parents, AND1062 was the most susceptible. There were no significant differences among populations and among populations and parental genotypes for their reactions to root rot disease. They all ranged from resistant to moderately resistant. The low levels of disease infection recorded on tested populations could be attributed to inter-gene and inter-racial crosses performed between Andean and Mesoamerican cultivars as they allowed to broaden the genetic base and increased levels of resistance to both biotic and abiotic stresses (Welsh *et al.,* 1995; Singh *et al.,* 2002; Singh and Schwartz, 2010; Singh, 2013). In fact, the resistance genes to most of the pathogens attacking Andean cultivars (intensively grown in Eastern Africa) were associated with the small-seeded Mesoamerican cultivars (Okii *et al.,* 2017). This rendered the use of inter-gene pool and inter-racial crosses very crucial to control major diseases of common beans.

3.5. CONCLUSION

The presence of transgressive genotypes within most of the populations confirmed the effectiveness of inter-racial crosses to improve the seed yield of common beans. Some populations, even though with poor overall means, possessed individual lines which had much better performance than commercial and check varieties. The best yielding line within the population KMA13-32 had the highest seed yield (3.38 t ha^{-1}) followed by 3.29 t ha^{-1} for KMA13-30 , 3.13 t ha^{-1} for KMA13-23, and 3.01 t ha^{-1} for KMA13-28. Athough the seed yield was not consistant across locations and generations ($F_{1.3}$ to $F_{1.6}$), populations with KATB9 as female parent (KMA13-29, KMA13-30, KMA13-31 and KMA13-32) were highly performing compared to other populations and check varieties. The number of pods per plant and the seed yield per plant as the most strongly correlated with seed yield per unit area could be adopted by breeders as indirect selection criteria for seed yield. After final selection, KMA13-22 produced the highest number of superior lines (12), followed by KMA13-23, KMA13-27, KMA13-28 and KMA13-31 which contributed 9 genotypes each. No line was selected from KMA13-18. A total of 92 genotypes belonging to five major market classes (small red, pinto, red kidney, red mottled and mixed color) were selected for further evaluation. Inter-racial populations showed low to

moderate infection levels (1.0 to 5.0) while commercial checks were moderate to highly susceptible to most of the pathogens (3.1 to 9.0); confirming that the use of markers at early generations was effective in identifying and transferring resistance genes to susceptible varieties.

CHAPTER 4: YIELD STABILITY AND GENOTYPE X ENVIRONMENT INTERACTIONS OF INTER-RACIAL COMMON BEAN SELECTIONS

ABSTRACT

Determination of yield stability and genotype x environment interactions (G x E) is critical in identifying new cultivars with either specific or broad adaptation in target environments. The aim of this study was to assess the yield stability and G x E effects on the agronomic performance of 92 $F_{1.7}$ lines previously selected with molecular markers for multiple disease resistance from 16 inter-racial bean populations and grouped in five major market classes (pinto, red kidney, red mottled, small red and mixed color). Each market class was evaluated in three agro-ecological conditions (low-, medium- and high altitudes) in the central highlands of Kenya. The experimental design was simple lattice with four replicates. Data were collected on seedling emergence rate, plant vigor, days to flowering, flower color, growth habit, days to maturity, number of pods per plant, number of seeds per pod, 100-seed mass, seed yield, the harvest index and the field disease score using the CIAT standard system for evaluation of bean germplasm. Analysis of variance (ANOVA) and least significant difference (LSD) test were performed to compare and separate genotypes means using generalized linear model procedures. In addition, the AMMI (additive main-effects and multiplicative interaction) model was used to separate the additive variance from the G x E interaction and to determine the stability of genotypes across locations using the PCA scores (IPCA1 and IPCA2) and to calculate AMMI stability values (ASV). Results showed that effects due to interactions between the sites and the genotypes for all the traits and all the market classes were significant ($P<0.05$), implying that the advanced lines behaved differently from one site to another and their ranking varied significantly across the three sites. Lines grown in the high altitude site at Tigoni showed significantly higher mean values for all traits compared with low (Mwea) and medium altitude (Kabete) sites. Mean yield across sites varied from 1,518 to 2,748 kg ha^{-1} for pinto lines; 1,324 to 3,860 kg ha^{-1} for red mottled lines; 1,537 to 3,722 kg ha^{-1} for red kidney lines; 1,005 to 3,385 kg ha^{-1} for small red lines and from 1,010 to 3,718 kg ha^{-1} for mixed color lines. The seed yield per unit area was highly significantly and positively correlated to days to flowering (r=0.69***), days to maturity (r=0.71***), the number of pods per plant (r=0.85***), the number of seeds per pod (r=0.35***), the 100-seed mass (r=0.44***) and the harvest index (r=0.57***). The most important of those components regardless of the market class was the number of pods per plant

which could be used by breeders as an indirect selection criterion for seed yield. AMMI analyses showed that variability among genotypes across sites was highly significant (*P<0.001*) regardless of the market class. The treatments (genotype, environment, and genotype-environment interaction) accounted for more than 80% of the yield variability regardless of the market class. By partitioning the treatments' contribution for each market class, results showed that environment contributed the most to the variability compared to the genotypes and the interactions among genotypes and environments, with mean values of 86.4% (pintos), 84.8% (red kidneys), 82.3% (red mottled), 68% (small reds) and 49.5% (mixed colors). The effect of the environment was, therefore, responsible for the largest part of the variability. The interaction between the genotype and environment was high for the small reds and the mixed colors (17.6% and 26.7%, respectively), suggesting that tested lines were not stable and thus responded differently across locations. Those genotypes should, therefore, be selected and recommended to specific environments. From ASV, the higher yielding lines were also the most unstable across sites. Among advanced lines, only KMA13-22-21 (P5) and KMA13-29-21 (RM13) combined high yield potential and wider adaptation across the three agro-ecological conditions. KMA13-27-27 (MC10), KMA13-29-24 (RM14), KMA13-23-14 (SR3) and KMA13-25-9 (SR5) were adapted to both low- and highlands. KMA13-28-21 (MC28), KMA13-21-20 (MC32) and KMA13-30-22 (RK13) were adapted to medium and high altitudes. KMA13-30-16 (SR9) was the only line adapted to medium and low altitudes. All other higher yielding lines had specific adaptation and can only be recommended for one agro-ecological environment. Across sites, two pinto lines, four red kidney, 15 red mottled, nine small reds and two mixed color lines did better than their corresponding checks with yield advantages of 7.6% for pinto, 14.3% for red kidney, 71.5% for red mottled, 27.3% for small red and 34.9% for the mixed color market classes. Due to dry conditions not conducive to the pathogen developments, the effects of the target diseases on the growth and yield of the advanced lines were not significant.

Keywords: Inter-racial lines, grain yield, market class, AMMI model, Kenya

4.1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is probably the most important grain legume consumed in the world (Assefa *et al.,* 2015). Eastern Africa and Latin America are the major producers as well as consumers (Burachura *et al.,* 2011; Beebe, 2012). Six races of common bean which can be distinguished by morphological, agronomic, adaptive, and molecular characteristics have been identified (Singh *et al.,* 1991a). Three of these races (Durango, Jalisco, and Mesoamerica) belong to the Middle American or Mesoamerican gene pool. The other three races (Chile, Nueva Granada, and Peru) belong to the Andean South American gene pool (Singh *et al.,* 1991a; Beebe *et al.,* 2000; Kwak *et al.,* 2012). Small-seeded beans (<25 g 100-seed mass) belong to Mesoamerican race and are known to be adapted to relatively warmer tropical lowlands. Medium-seeded beans have a 100-seed mass of 25 to 40 g and belong to Durango race for the semi-climbers and Jalisco race for the climbers. They are as well adapted to tropical and subtropical environments (Singh, 2001). Small- and medium-seeded beans often have indeterminate growth habit and out-yield their large-seeded counterparts (>40 g 100-seed mass) from Chile and Nueva Granada races by as much as 500 to 2000 kg ha^{-1} (Singh *et al.,* 1991a; Singh *et al.,* 2002). In addition to their high yields, those small- and medium-seeded beans are known to be resistant to several diseases devastating the large-seeded beans such as angular leaf spot, anthracnose, rust, bean golden yellow mosaic virus and bean common mosaic virus and possess genes and high level of resistance to drought stress (Terán and Singh, 2002). However, large-seeded Andean beans are the most widely grown in Eastern Africa because they are preferred by farmers and consumers for their seed quality and often fetch higher prices (Singh *et al.,* 2002; Sichilima *et al.,* 2016).

The genetic base of common bean varieties grown in Eastern Africa needs to be broadened to enhance yield potential and resistance to diseases. Inter-racial and inter-gene pool crosses provide an important opportunity to create a useful genetic variation for maximizing gains from selection, broaden the genetic base of commercial cultivars and make efficient use of available resources (Welsh *et al.,* 1995; Singh, 2001). Despite of the limitations faced in developing inter-racial and inter-gene pool cultivars (notably the F_1 hybrid dwarfism, weakness, or incompatibility, problems in recovering desirable seed quality and adaption characteristics, and cripples or virus-like foliage symptoms), breeding programmes across the world have succeeded

through inter-racial and inter-gene crosses to develop genotypes combining desirable traits such as tolerance to production limiting factors (especially diseases, drought), seed quality and high yield potential (Kelly and Adams, 1987).

Common bean yields in Eastern and Central Africa are among the lowest in the world (0.5 t ha^{-1}) while the potential is between 1.5 to 3 t ha^{-1} for bush beans, and up to 5 t ha^{-1} for climbing beans)(Kaizzi *et al.,* 2012; Ronner *et al.,* 2017; FAO, 2018). The improvement of productivity requires effective and efficient selection for yield traits, in addition to biotic and abiotic factors, which cause bean production losses in the region (Wortmann *et al.,* 1998; Kimani *et al.,* 2005b; Okii *et al.,* 2017). In bean breeding programmes, a large number of genotypes are tested for many generations within contrasting environments before release for seed multiplication and distribution to growers (Corrêa *et al.,* 2015). Because environmental conditions for testing are distinct, the genotype and environment interaction (G x E) affects the agronomic performance (seed yield and yield components), making necessary to analyze its magnitude and stability of genotypes across environments (Ashango *et al.,* 2016; Tadesse *et al.,* 2017). These estimates allow the assessment of the real impact of selection and ensure high reliability in the genotype recommendation for a specific place or environment groups (Correa *et al.,* 2016). A multi-location testing of genotypes is, therefore, useful during the selection process because it provides information on specific or broader adaptation for a given genotype. Another key reason for the G x E analyses in bean breeding in Africa is that lines adapted to an African bean environment (AFBE) can be grown in similar areas in other parts of Africa (Wortmann and Allen, 1994). Due to differences among growing regions, breeding might be more effective if it was AFBE based. Therefore, we hope that lines developed through the current breeding programme in the AFBE of Kenya could be adapted and disseminated in African areas with similar agro-ecological conditions.

The specific objective of this study was to assess the yield stability and G x E effects on the agronomic performance of 92 advanced $F_{1.7}$ lines previously selected for multiple disease resistance using molecular markers. These lines originated from 16 small- and medium-seeded inter-racial bean populations, which were subsequently grouped in five market classes.

4.2. MATERIALS AND METHODS

4.2.1. Experimental sites

This study was conducted in 3 different agro-ecological zones, representing major bean growing environments in Kenya. The experiments were conducted during 2017 short rain season at KALRO-Mwea representing low altitude conditions, Kabete Field Station of the University of Nairobi, the medium altitude, and KALRO-Tigoni for the high altitude environments.

KALRO-Mwea is located on coordinates 0°38'S (latitude); 37°22'E (longitude) and at approximately 1150 masl. This research station receives mean precipitation of 850 mm per year with a bimodal distribution. The long rain season starts in March and ends in May. The short rain season usually starts in October to end in late December. Mean annual temperatures range from 15.6℃ to 28.6℃. Soils at this station are vertisols with an acidic pH of about 5.1 (Wahome *et al.,* 2011; NARL, 2016).

KALRO-Tigoni is located at coordinates 01°08'S; 036°40'E and at approximately 2130 msl. It receives bimodal rainfall of 1100 mm per year. Temperatures range from 12℃ to 24℃. Soils at Tigoni are humic nitisols with soil pH of approximately 4.6 (Njoki, 2013).

Kabete Field Station is located at 01°15'S; 036°44'E and 1820 masl. The station experiences mean bimodal precipitation of 1059 mm per year. Mean monthly temperatures range between 12.3℃ and 22.5℃ (Jaetzold *et al.,* 2006). The soils are humic nitisols, which are very deep, well-drained, friable clay with acid humic topsoil, dark reddish brown in colour. The pH is about 5.0 to 5.4 and a mean sunshine of 6.6 hours per day.

4.2.2. Plant materials

Study materials were 102 lines including 92 $F_{1.7}$ advanced small- and medium-seeded genotypes selected from 16 inter-racial populations, six donor parents and four commercial check varieties. The six donor parents were Mex54 and G10909 used as the source of resistance to angular leaf spot, G2333 to anthracnose, RWR719 and AND1062 to *Pythium* root rot, and BRB191 for bean common mosaic virus. The four commercial varieties were GLP92, GLP585, KATB9 and KATB1. These commercial varieties are susceptible to angular leaf spot, anthracnose, root rots, common bacterial blight and bean common mosaic virus but have high yield potential and good adaptation to agro-ecological conditions of Eastern Africa. The 92 $F_{1.7}$ lines were grouped in 5

market classes on the basis of their seed color, shape and size but regardless of the populations where they originated from. The 92 $F_{1.7}$ lines comprised of, 14 red kidney, 16 red mottled, 19 small reds, 12 pintos and 31 were of mixed colors including blacks, greyish green, tan red and tan brown, which may be of importance in niche markets. The five market classes were evaluated in separate trials and compared with appropriate commercial checks and donor parents. In these trials, AND1062 and Mex54 were used as checks for red kidney market class, BRB191 for red mottled, GLP585, KATB9, G2333, G10909 and RWR719 for small red; GLP92 (Mwitemania) for pintos, and KATB1 and Mex54 for the mixed colors (Table 4.1)

Table 4.1. List of genotypes advanced under the multi-site evaluation

Genotypes IDs	Lines	Populations[1]	Seed color
	Pinto lines		
P1	KMA13-21-10	KMA13-21	Pinto
P2	KMA13-21-19	KMA13-21	Pinto
P3	KMA13-22-3	KMA13-22	Pinto
P4	KMA13-22-7	KMA13-22	Pinto
P5	KMA13-22-21	KMA13-22	Pinto
P6	KMA13-22-30	KMA13-22	Pinto
P7	KMA13-22-33	KMA13-22	Pinto
P8	KMA13-23-13	KMA13-23	Pinto
P9	KMA13-23-18	KMA13-23	Pinto
P10	KMA13-23-22	KMA13-23	Pinto
P11	KMA13-24-6	KMA13-24	Pinto
P12	KMA13-24-7	KMA13-24	Pinto
GLP92*	GLP92^{M}	N/A	Pinto
	Red mottled lines		
RM1	KMA13-17-25	KMA13-17	Red mottled
RM2	KMA13-20-3	KMA13-20	Red mottled
RM3	KMA13-20-14	KMA13-20	Red mottled
RM5	KMA13-24-5	KMA13-24	Red mottled
RM6	KMA13-24-11	KMA13-24	Red mottled
RM7	KMA13-24-16	KMA13-24	Red mottled
RM8	KMA13-24-17	KMA13-24	Red mottled
RM9	KMA13-22-25	KMA13-22	Red mottled
RM10	KMA13-27-25	KMA13-27	Red mottled
RM11	KMA13-28-3	KMA13-28	Red mottled
RM12	KMA13-28-13	KMA13-28	Red mottled
RM13	KMA13-29-21	KMA13-29	Red mottled
RM14	KMA13-29-24	KMA13-29	Red mottled
RM15	KMA13-32-24	KMA13-32	Red mottled
RM16	KMA13-32-28	KMA13-32	Red mottled
RM17	KMA13-17-17	KMA13-17	Red mottled
BRB191*	BRB191^{A}	N/A	Red mottled
	Red kidney lines		
RK1	KMA13-17-25	KMA13-17	Red kidney

RK2	KMA13-19-12	KMA13-19	Red kidney
RK3	KMA13-19-16	KMA13-19	Red kidney
RK4	KMA13-20-3	KMA13-20	Red kidney
RK5	KMA13-21-11	KMA13-21	Red kidney
RK6	KMA13-25-3	KMA13-25	Red kidney
RK7	KMA13-25-20	KMA13-25	Red kidney
RK8	KMA13-26-32	KMA13-26	Red kidney
RK9	KMA13-27-31	KMA13-27	Red kidney
RK10	KMA13-28-2	KMA13-28	Red kidney
RK11	KMA13-29-28	KMA13-29	Red kidney
RK12	KMA13-29-30	KMA13-29	Red kidney
RK13	KMA13-30-22	KMA13-30	Red kidney
AND1062*	AND1062^{A}	N/A	Red kidney
Mex54*	Mex54^{M}	N/A	Cream beige
	Small red		
SR1	KMA13-22-27	KMA13-22	Small red
SR2	KMA13-22-29	KMA13-22	Small red
SR3	KMA13-23-14	KMA13-23	Small red
SR4	KMA13-23-21	KMA13-23	Small red
SR5	KMA13-25-9	KMA13-25	Small red
SR6	KMA13-28-13	KMA13-28	Small red
SR7	KMA13-30-2	KMA13-30	Small red
SR8	KMA13-30-14	KMA13-30	Small red
SR9	KMA13-30-16	KMA13-30	Small red
SR10	KMA13-31-1	KMA13-31	Small red
SR11	KMA13-30-30	KMA13-30	Small red
SR12	KMA13-31-3	KMA13-31	Small red
SR13	KMA13-31-4	KMA13-31	Small red
SR14	KMA13-31-5	KMA13-31	Small red
SR15	KMA13-31-6	KMA13-31	Small red
SR16	KMA13-31-8	KMA13-31	Small red
SR17	KMA13-31-9	KMA13-31	Small red
SR18	KMA13-32-26	KMA13-32	Small red
SR19	KMA13-32-28	KMA13-32	Small red
KATB9*	KATB9^{M}	N/A	Small red
RWR719*	RWR719^{M}	N/A	Small red
GLP585*	GLP585^{M}	N/A	Small red
G10909*	G10909^{M}	N/A	Small red
G2333*	G2333^{M}	N/A	Small red
	Mixed color lines		
MC1	KMA13-21-23	KMA13-21	Tan red
MC2	KMA13-22-16	KMA13-22	Tan red
MC3	KMA13-22-321	KMA13-22	Tan red
MC4	KMA13-23-9	KMA13-23	Tan red
MC5	KMA13-23-20	KMA13-23	Tan red
MC6	KMA13-24-10	KMA13-24	Tan red
MC7	KMA13-25-1	KMA13-25	Tan red
MC8	KMA13-27-13	KMA13-27	Tan red
MC9	KMA13-27-14	KMA13-27	Tan red
MC10	KMA13-27-27	KMA13-27	Tan red

MC11	KMA13-28-5	KMA13-28	Tan red
MC12	KMA13-28-13	KMA13-28	Tan red
MC13	KMA13-29-21	KMA13-29	Tan red
MC14	KMA13-31-61	KMA13-31	Tan brown
MC15	KMA13-22-322	KMA13-22	Tan brown
MC16	KMA13-29-19	KMA13-29	Tan brown
MC17	KMA13-30-7	KMA13-30	Tan brown
MC18	KMA13-31-62	KMA13-31	Tan brown
MC19	KMA13-32-22	KMA13-32	Tan brown
MC20	KMA13-32-24	KMA13-32	Tan brown
MC21	KMA13-22-23	KMA13-22	Black
MC22	KMA13-23-10	KMA13-23	Black
MC23	KMA13-23-11	KMA13-23	Black
MC24	KMA13-25-4	KMA13-25	Black
MC25	KMA13-27-101	KMA13-27	Black
MC26	KMA13-27-102	KMA13-27	Black
MC27	KMA13-27-12	KMA13-27	Black
MC28	KMA13-28-21	KMA13-28	Black
MC29	KMA13-28-22	KMA13-28	Black
MC30	KMA13-28-29	KMA13-28	Black
MC31	KMA13-27-1	KMA13-27	Green
MC32	KMA13-21-20	KMA13-21	Yellow
KATB1*	KATB1^{M}	N/A	Green

[1]Pedigrees that produced these populations are presented in Table 3.4 (chapter 3); M: Mesoamerican gene pool; A: Andean gene pool; MA denotes marker-assisted *****: commercial checks or donor parents

4.2.3. Experimental design and crop management

A simple lattice experimental design with four replicates was used for each market class depending on the number of tested lines (4 x 4 lattice design used for red kidney, red mottled and pinto beans; a 5 x 5 lattice for small reds and a 6 x 6 lattice for mixed colors). A plot consisted of three 4m rows. Seed rate was 10 seeds m^{-1} spaced by 0.2 m within rows and 0.5 m between rows. Two guard rows were erected to avoid competition and interference between genotypes (Goncalves-Vidigal *et al.*, 2008). All the field experiments were planted in October 2017 during the short rain season. Diammonium phosphate (DAP) at a rate of 80 kg ha^{-1} was applied at planting. Weeding at all sites were carried out three times: two weeks after seedling emergence, before flowering and after podding. The pesticide Confidor (200 g l^{-1} Imidacloprid) was used to control whiteflies and leafminer at all the sites.

Data collection

Data were collected on seedling emergence rate, plant vigor, days to flowering, growth habit, days to maturity, number of pods per plant, number of seeds per pod, 100-seed mass, grain yield, harvest index and the field disease score using the standard system for the evaluation of bean germplasm (Schoonhoven and Pastor-Corrales, 1987):

(1) Seedling emergence rate was the total number of plants emerged over the total number of grains sown (expressed in percentage);
(2) Plant vigor was recorded when plants reached their maximum development at R5 stage using the 1-9 CIAT scale, where 1 is excellent, 3 good, 5 intermediate, 7 is poor, and 9 is very poor vigor;
(3) Days to flowering were the duration from the day of seedling emergence to the day when at least 50% of flowers were opened;
(4) Flower color was determined by visual observation in the field during the flowering stage;
(5) Growth habit was determined at R6 and R9 growth stages. Plants were classified into four types: I (determinate), II (indeterminate, upright), III (indeterminate, prostrate) and IV (climbing);
(6) Days to maturity were the duration from seedling emergence to the initiation of developmental stage R9 when 75% of the plants have reached physiological maturity. Liebenberg (2002) scale was used to classify the genotypes: 85-94 (early maturity); 95-104 (medium maturity) and 105-115 (late maturity);
(7) Number of pods per plant was obtained by the total count of pods produced per plant in each plot. Ten randomly selected plants were sampled per replicate;
(8) Number of seeds per pod was expressed in numbers, obtained by the total count of seeds from ten randomly selected pods per plot;
(9) 100-seed mass expressed in grams, was obtained by weighing a random sample of 100 seeds from each plot;
(10) Seed yield is the weight of seeds from the middle row of each plot dried to 13% moisture content, expressed in kg ha^{-1};
(11) Diseases were scored using a 1 to 9 CIAT scale where 1-3 is resistant, 4-6 intermediate resistant and 7-9 susceptible (Schoonhoven and Pastor-Corrales, 1987);

(12) The harvest index (HI) was obtained by dividing seed yield by the total plot biomass from each plot and expressing it as a percentage.

4.2.4. Data analysis

Statistical analysis was performed using GenStat 17th edition (GenStat, 2016) and Statistix 8.0 version (USDA and NRCS, 2007). Combined analysis of variance (ANOVA) was conducted to determine the magnitude of variation associated with each source (environment, genotype and their interaction) based on a generalized linear model procedure. Fisher's least significant difference (LSD) test was used for separation of means at 5% probability level. The linear additive model of ANOVA used was as follows:

$$y_{ij} = \mu + G_i + E_j + GE_{ij} + \varepsilon_{ij} \qquad (1)$$

Where y_{ij} is the variation associated with the i^{th} genotype and j^{th} environment; μ is the total mean; G_i and E_j are the effects of the i^{th} genotype and j^{th} environment, respectively; GE_{ij} is the effect of G x E interaction and ε_{ij} is the error (residual) effect of genotype i in environment j .

ANOVA is based on a linear additive model in which the G x E interaction is a source of variation, but its intrinsic effects are not analyzed. The additive main effect and multiplicative interaction (AMMI) model was, therefore, necessary to separate the additive variance from the G x E interaction (Gauch and Zobel, 1997; Gauch *et al.*, 2008). The Interaction Principal Component Analysis (IPCA) was used to explain the residual matrix as well as the extraction of the new set of coordinate axis which accounts more effectively for the interaction patterns. In fact, AMMI uses ANOVA to test the main effects of genotypes and environments, and PCA to analyze the residual multiplicative interaction between genotypes and environments to determine the sum of squares of the G × E interaction, with a minimum number of degrees of freedom (Zobel *et al.*, 1988). The AMMI model used was:

$$y_{ger} = \mu + \alpha_g + \beta_e + \Sigma\lambda_n y_{gn} \delta_{en} + \rho_{ge} + \varepsilon_{ger} \qquad (2)$$

Where Y_{ger} is the yield of genotype g in the environment e for replicate r ; μ is the grand mean; αg is the genotype mean deviations; β_e is the environment mean deviation; n is the number of PCA axes retained in the model, λ_n is singular value for PCA axis n; y_{gn} is the Genotype eigenvector values for PCA axis n ; δ_{en} is the environment eigenvector values for PCA axis n ; ρ_{ge} represents the residuals and ε_{ger} is for error.

AMMI analysis was also used to determine the stability of the genotypes across locations using the PCA scores (IPCA1 and IPCA2). The IPCA score near zero reveals more stable genotypes, while large values indicate more responsive and less stable genotypes. AMMI's stability value for the grain yield was estimated as shown as follows (Purchase, 1997):

$$\text{ASV} = \sqrt{\left[\frac{\text{SS IPCA 1}}{\text{SS IPCA 2}}(\text{IPCA 1 Score})\right]^2 + (\text{IPCA 2 Score})^2} \quad (3)$$

Where ASV is the AMMI stability value, SS IPCA 1 and SS IPCA 2 are the sum of squares of IPCA 1 and 2, respectively and IPCA is the interaction principal component analysis. Thus, lowest ASV indicates a wide adaptation of specific genotypes for certain environments and vice-versa.

AMMI and GGE biplots were subsequently constructed to determine adaptation and stability of genotypes across test environment. From this analysis, genotypes located near the biplot origin were considered as widely adapted, while genotypes located far were specifically adapted. All the genotypes with positive IPCA1 scores responded positively to the environment having positive IPCA1 scores, and were, therefore, adapted to that particular environment (Samonte *et al.,* 2005; Assefa *et al.,* 2017).

4.3. RESULTS

4.3.1. Agronomic performance across environments

Mean squares for seed yield and seed yield components of pinto, red kidney, red mottled, small red and mixed color $F_{1.7}$ bean lines are summarized on Appendices 18, 19, 20, 21 and 22, respectively.

4.3.1.1. Seedling emergence rate, growth habit and flower color

Data on seedling emergence rate, growth habit and flower color of pinto bean lines grown at Kabete, Mwea and Tigoni are presented in Table 4.2. There were significant differences in their seedling emergence rate across sites (*P<0.001*) but no significant differences were detected among genotypes and the interaction between the sites and the genotypes. The seedling emergence rate was higher in low altitude (Mwea) (79.1%) compared to medium (Kabete) (71.3%) and high altitudes (Tigoni) (52.8%). All the 13 pinto lines possessed white flowers and were of Type III growth habit (Figure 4.1).

Figure 4.1. Pinto lines showing Type III growth habit

The seedling emergence rate of the red mottled advanced lines varied significantly with sites (*P<0.001*), genotypes (*P<0.05*), and the interaction between genotypes and sites (*P<0.001*). Among sites, the highest seedling emergence rate was recorded at the medium altitude site

(72.9%) and the lowest at the high altitude site (44%) suggesting that soil and ambient temperatures influenced seed germination and emergence. Two advanced red mottled lines (KMA13-24-17 and KMA13-29-24) had the highest seedling emergence rate at Kabete. These two lines had a seedling emergence rate of 83.7% which was the highest among the red mottled lines and significantly better than the check variety BRB191. Table 4.3 shows also that most of the red mottled advanced lines had white colored flowers, except the lines KMA13-22-25, KMA13-27-25 and KMA13-28-03 which had purple colored flowers. Their growth habit ranged from determinate growth (Type I) to climbing growth habit (Type IV).

There were highly significant differences ($P<0.001$) for the seedling emergence rate among red kidney genotypes across sites. Moreover, a significant interaction between sites and genotypes was detected. In general, the average seedling emergence rate was higher in the medium altitude (Kabete) compared to the other two sites. KMA13-25-20 and KMA13-27-31 had the highest seedling emergence rate (85%) at medium altitude site (Kabete). In contrast, KMA13-26-32 (33.7%) had the lowest seedling emergence rate which was recorded at the high altitude site (Tigoni). The red kidney lines had white flowers, except the lines KMA13-26-32 and KMA13-30-22 which possessed purple colored flowers. All the lines had indeterminate growth habit ranging from indeterminate bush, erect stem and branches (Type II) to indeterminate climbing habit with weak, long and twisted stem and branches (Type IV). Figure 4.2 shows the red kidney market class experiment to illustrating indeterminate growth habits.

Figure 4.2. Red kidney lines showing Type II to Type IV growth habits

There were highly significant location differences (*P<0.001*) in seedling emergence rate among the advanced small red lines as well as a significant site x genotype interaction for seedling emergence rate. Genotype effects were not significant. Seedling emergence rate varied from 38.7% to 93.7%. The study lines had the highest mean seedling emergence rate at Kabete (77.6%) and the lowest at Tigoni (58.9%). Among the study lines, KMA13-22-27 had the highest seedling emergence rate (93.7% at Kabete) compared to all other lines and checks. KMA13-28-13 (38.7%) had the lowest seedling emergence rate, which was recorded at Tigoni. Most of the advanced small red lines had white flowers and a growth habit ranging from determinate growth habit (Type I) to indeterminate climbing growth habit (Type IV) with Types III and IV being the most predominant (Table 4.5). Figure 4.3 illustrates the growth habits found within advanced small red bean lines.

Figure 4.3. Growth habit within small red market class

Seedling emergence rate of the mixed color bean lines differed significantly (*P<0.001*) among the test sites. The highest seedling emergence rate was recorded in the high altitude Tigoni site (81.5%), which was significantly higher to that observed at the medium altitude site at Kabete (69.7%) and low altitude site at Mwea (58.9%)(Table 4.6). However, the differences among the study genotypes were not significant. Most of mixed color advanced lines had purple flowers. Their growth habit ranged from determinate growth habit (Type I) to indeterminate climbing growth habit (Type IV).

Table 4.2. Seedling emergence rate, growth habit and flower color of pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Seedling emergence rate (%)				Growth habit	Flower color
Site	Kabete	Mwea	Tigoni	Mean		
KMA13-21-10	80.0	68.7	55.0	67.9	III	White
KMA13-21-19	87.5	70.0	53.7	70.4	III	White
KMA13-22-03	70.0	75.0	62.5	69.2	III	White
KMA13-22-07	67.5	47.5	46.2	53.7	III	White
KMA13-22-21	80.0	75.0	52.5	69.2	III	White
KMA13-22-30	77.5	80.0	43.7	67.1	III	White
KMA13-22-33	82.5	70.0	45.0	65.8	III	White
KMA13-23-13	80.0	77.5	42.5	66.7	III	White
KMA13-23-18	86.2	66.2	58.7	70.4	III	White
KMA13-23-22	72.5	78.7	47.5	66.2	III	White
KMA13-24-06	82.5	83.7	65.0	77.1	III	White
KMA13-24-07	78.7	61.2	60.0	66.7	III	White
GLP92	83.7	73.7	53.7	70.4	III	White
Mean	79.1	71.3	52.8	67.7		
CV (%)	20.4					
$LSD_{0.05}$:	Line=10.9, Site=5.2, Line x site=18.8					

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.3. Seedling emergence rate, growth habit and flower color of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Seedling emergence rate (%)				Growth habit	Flower color
Site	Kabete	Mwea	Tigoni	Mean		
KMA13-17-17	75.0	68.7	66.2	70.0	II	White
KMA13-17-25	80.0	65.0	50.0	65.0	I	White
KMA13-20-03	62.5	58.7	33.7	51.7	III	White
KMA13-20-14	73.7	52.5	35.0	53.7	II	White
KMA13-22-25	73.7	67.5	28.7	56.7	III	Purple
KMA13-24-05	67.5	58.7	40.0	55.4	II	White
KMA13-24-11	71.2	55.0	47.5	57.9	III	White
KMA13-24-16	81.2	60.0	41.2	60.8	IV	White
KMA13-24-17	83.7	53.7	31.2	56.2	IV	White
KMA13-27-25	80.0	57.5	35.0	57.5	IV	Purple
KMA13-28-03	76.2	81.2	50.0	69.2	IV	Purple
KMA13-28-13	53.7	77.5	48.7	60.0	II	White
KMA13-29-21	-	62.5	55.0	60.0	II	White
KMA13-29-24	83.7	55.0	43.7	60.8	IV	White
KMA13-32-24	73.7	66.2	43.7	61.2	IV	White
KMA13-32-28	72.5	76.2	36.2	61.7	III	White
BRB 191	58.7	67.5	67.5	64.6	I	White
Mean	72.9	63.7	44.0	60.1		
CV (%)	22.1					
$LSD_{0.05}$:	Line=10.7, Site=4.6, Line x site=18.6					

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.4. Seedling emergence rate, growth habit and flower color of red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Seedling emergence rate (%)				Growth habit	Flower color
Site	Kabete	Mwea	Tigoni	Mean		
KMA13-17-25	80.0	66.2	47.5	64.6	II	White
KMA13-19-12	56.2	77.5	57.5	63.7	II	White
KMA13-19-16	47.5	72.5	40.0	53.3	II	White
KMA13-20-03	82.5	72.5	46.2	67.1	II	White
KMA13-21-11	56.2	63.7	36.2	52.1	II	White
KMA13-25-03	25.0	53.7	41.2	40.0	II	White
KMA13-25-20	85.0	62.5	36.2	61.2	II	White
KMA13-26-32	75.0	62.5	33.7	57.1	III	Purple
KMA13-27-31	85.0	55.0	65.0	68.3	III	White
KMA13-28-02	83.7	72.5	51.2	69.2	II	White
KMA13-29-28	68.7	56.2	35.0	53.3	II	White
KMA13-29-30	73.7	62.5	50.0	62.1	II	White
KMA13-30-22	66.2	50.0	50.0	55.4	III	Purple
AND 1062	81.2	56.2	48.7	62.1	I	White
Mex54	72.5	66.2	48.7	62.5	IV	Purple
Mean	69.2	63.3	45.8	59.5		
CV (%)	23.9					
$LSD_{0.05}$	Line=10.1, Site=4.8, Line x site=17.4					

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.5. Seedling emergence rate, growth habit and flower color of small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Seedling emergence rate (%)				Growth habit	Flower color
Site	Kabete	Mwea	Tigoni	Mean		
KMA13-22-27	93.7	62.5	51.2	69.2	IV	White
KMA13-22-29	78.7	85.0	50.0	71.2	I	White
KMA13-23-14	68.7	68.7	45.0	60.8	IV	White
KMA13-23-21	75.0	73.7	52.5	67.1	IV	Purple
KMA13-25-09	83.7	66.2	42.5	64.2	IV	White
KMA13-28-13	86.2	73.7	38.7	66.2	IV	White
KMA13-30-02	78.7	61.2	67.5	69.2	III	White
KMA13-30-14	71.2	75.0	56.2	67.5	III	White
KMA13-30-16	83.7	71.2	61.2	72.1	IV	White
KMA13-30-30	77.5	53.7	68.7	66.7	III	White
KMA13-31-01	82.5	70.0	43.7	65.4	III	White
KMA13-31-03	77.5	81.2	71.2	76.7	III	White
KMA13-31-04	86.2	72.5	67.5	75.4	III	White
KMA13-31-05	71.2	67.5	42.5	60.4	III	White
KMA13-31-06	80.0	57.5	51.2	62.9	III	White
KMA13-31-08	78.7	68.7	62.5	70.0	III	White
KMA13-31-09	76.2	70.0	68.7	71.7	II	White
KMA13-32-26	76.2	58.7	76.2	70.4	I	Purple
KMA13-32-28	81.2	52.5	72.5	68.7	III	Purple
G10909	76.2	81.2	66.2	74.6	IV	White
G2333	67.5	38.7	71.2	59.2	IV	White
GLP585	61.2	53.7	65.0	60.0	I	White
KATB9	81.2	48.7	55.0	61.7	I	Purple
RWR719	70.0	61.2	66.2	65.8	II	Purple
Mean	77.6	65.6	58.9	67.4		
CV (%)	21.4					
$LSD_{0.05}$	Line=11.6, Site=4.1, Line x site=20.1					

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.6. Seedling emergence rate, growth habit and flower color of mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Seedling emergence rate (%)				Growth habit	Flower color
Site	Kabete	Mwea	Tigoni	Mean		
KMA13-21-20	72.5	62.5	71.2	68.7	IV	White
KMA13-21-23	60.0	65.0	86.2	70.4	IV	White
KMA13-22-16	63.7	56.2	83.7	67.9	III	Purple
KMA13-22-23	63.7	47.5	70.0	60.4	III	Purple
KMA13-22-321	48.7	68.7	85.0	67.5	III	Purple
KMA13-22-322	81.2	45.0	83.7	70.0	III	White
KMA13-23-09	57.5	47.5	78.7	61.2	IV	Purple
KMA13-23-10	67.5	58.7	87.5	71.2	III	Purple
KMA13-23-11	68.7	53.7	85.0	69.2	II	Purple
KMA13-23-20	72.5	56.2	58.7	62.5	IV	Purple
KMA13-24-10	66.2	52.5	68.7	62.5	III	White
KMA13-25-01	60.0	41.2	80.0	60.4	III	White
KMA13-25-04	73.7	55.0	82.5	70.4	IV	Purple
KMA13-27-01	78.7	70.0	75.0	74.6	I	Purple
KMA13-27-101	65.0	62.5	75.0	67.5	III	Purple
KMA13-27-102	58.7	53.7	81.2	64.6	III	Purple
KMA13-27-12	65.0	72.5	80.0	72.5	II	Purple
KMA13-27-13	71.2	65.0	82.5	72.9	III	Purple
KMA13-27-14	71.2	80.0	68.7	73.3	III	Purple
KMA13-27-27	87.5	67.5	93.7	82.9	IV	Purple
KMA13-28-05	68.7	53.7	92.5	71.7	IV	Purple
KMA13-28-13	78.7	60.0	82.5	73.7	IV	Purple
KMA13-28-21	68.7	57.5	85.0	70.4	III	Purple
KMA13-28-22	76.2	57.5	96.2	76.7	IV	Purple
KMA13-28-29	61.2	70.0	90.0	73.7	III	Purple
KMA13-29-19	70.0	71.2	80.0	73.7	IV	White
KMA13-29-21	82.5	62.5	88.7	77.9	III	White
KMA13-30-07	70.0	62.5	87.5	73.3	IV	Purple
KMA13-31-61	76.2	46.2	90.0	70.8	IV	White
KMA13-31-62	83.7	65.0	71.2	73.3	III	Purple
KMA13-32-22	66.2	48.7	86.2	67.1	III	Purple
KMA13-32-24	76.2	45.0	77.5	66.2	III	Purple
KATB1	67.5	63.7	85.0	72.1	I	Purple
Mex54	72.5	66.2	48.7	62.5	IV	Purple
Mean	69.7	58.9	81.5	70.1		
CV (%)	21.5					
$LSD_{0.05}$	Line=12.1, Site=3.6, Line x site=20.9					

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

4.3.1.2. Plant vigor

There were significant site (*P<0.001*) and genotypic (*P<0.05*) differences for plant vigor among the pinto lines and checks (Table 4.7). Crops grown at Tigoni showed much better vigor (2.8) compared to Kabete (4.7) and Mwea (5.5). Among test lines, KMA13-23-13 was the most vigorous (3.8) but was not significantly different from the commercial check GLP92.

Highly significant location and genotypic differences (*P<0.001*) were detected among advanced red mottled lines for the plant vigor. Crops grown at Tigoni in the high altitude site were the most vigorous (2.7) compared to those grown at Kabete (4.7) and Mwea (4.9) in the medium and low altitude sites, respectively. The advanced line KMA13-17-17 was the most vigorous grown at Tigoni (1.0). KMA13-24-17 had the poorest vigor when planted in the low altitude site (6.2) (Table 4.8).

There were significant site and genotypic differences (*P<0.001*) among the advanced red kidney lines for plant vigor due to genotypes. A highly significant interaction between the genotypes and the sites (*P<0.01*) for plant vigor was detected. Among sites, better plant vigor was recorded on lines grown at Tigoni in higher altitude (1.8) compared to medium (3.7) and low altitudes (4.2). KMA13-21-11, KMA13-25-20, and KMA13-26-32 were the most vigorous among the advanced lines (2.7). However, there were not significantly different from the donor parent AND1062 (Table 4.9).

There were significant site (*P<0.001*) and genotypic (*P<0.01*) differences in plant vigor among advanced small red lines. However, the genotype x site interaction was not significant. The study lines grew vigorously at Tigoni in high altitude (2.4) compared to Mwea (4.4) and Kabete (4.6) in low and medium altitudes, respectively. The line KMA13-23-14 was, in general, the most vigorous regardless of the sites (3.3) and compared to all the lines and checks. In contrast, KMA13-31-09 was the least vigorous among lines and check varieties (4.7). It was statistically equal to the check variety RWR719. KMA13-25-20 and KMA13-26-32 were the most vigorous among small red lines (Table 4.10). The two lines had a score of 1.0 when grown at high altitude (Tigoni). KMA13-30-22 (5.7) had the poorest performance. It performed poorly at low altitude (Mwea).

Results showed also that there were highly significant differences among lines for the plant vigor due to genotypes, sites and the interactions between genotypes and sites (*P<0.001*) among mixed color lines. The test lines were most vigorous at high altitude (2.4) but less vigorous at medium (4.2) and low altitudes (4.6). KMA13-28-13 had the best plant vigor among the lines when grown at Tigoni (1.5) but was less vigorous than the check variety Mex54 (1.0) (Table 4.11).

Table 4.7. Plant vigor of pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	4.2	4.5	3.2	4.0
KMA13-21-19	4.2	6.5	3.0	4.6
KMA13-22-03	4.2	5.7	2.0	4.0
KMA13-22-07	5.2	6.2	3.2	4.9
KMA13-22-21	4.0	5.7	3.2	4.3
KMA13-22-30	4.7	5.5	3.2	4.5
KMA13-22-33	4.7	5.7	2.7	4.4
KMA13-23-13	4.7	4.2	2.5	3.8
KMA13-23-18	4.7	5.5	3.0	4.4
KMA13-23-22	5.0	5.2	3.2	4.5
KMA13-24-06	5.0	6.0	2.7	4.6
KMA13-24-07	5.5	5.7	2.5	4.6
GLP92	4.2	5.0	2.2	3.8
Mean	4.7	5.5	2.8	4.3
CV (%)	20.2			
$LSD_{0.05}$: Line=0.7, Site=0.3, Line x site=1.2				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.8. Plant vigor of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	3.7	4.2	1.0	3.0
KMA13-17-25	3.7	5.0	3.5	4.1
KMA13-20-14	4.7	6.2	3.0	4.7
KMA13-20-3	4.2	5.7	3.5	4.5
KMA13-22-25	5.0	3.5	2.0	3.5
KMA13-24-11	5.5	5.5	2.5	4.5
KMA13-24-16	5.2	5.5	3.0	4.6
KMA13-24-17	4.7	6.2	3.5	4.8
KMA13-24-5	5.5	5.2	3.2	4.7
KMA13-27-25	4.7	5.0	3.0	4.2
KMA13-28-13	4.7	4.5	3.2	4.2
KMA13-28-3	5.2	4.7	2.5	4.2
KMA13-29-21	-	3.7	1.7	2.9
KMA13-29-24	5.0	5.7	2.7	4.5
KMA13-32-24	4.2	4.7	2.2	3.7
KMA13-32-28	4.5	3.2	2.7	3.5
BRB 191	4.2	5.0	2.0	3.7
Mean	4.7	4.9	2.7	4.1
CV (%)	23.7			
$LSD_{0.05}$: Line=0.8, Site=0.3, Line x site=1.4				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.9. Plant vigor of red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	4.0	4.7	2.0	3.6
KMA13-19-12	5.0	3.0	3.0	3.7
KMA13-19-16	4.2	5.0	2.5	3.9
KMA13-20-03	3.7	4.2	1.5	3.2
KMA13-21-11	3.2	3.5	1.5	2.7
KMA13-25-03	4.2	4.2	3.0	3.8
KMA13-25-20	3.5	3.5	1.0	2.7
KMA13-26-32	4.0	3.2	1.0	2.7
KMA13-27-31	4.0	5.0	1.5	3.5
KMA13-28-02	2.7	4.0	1.7	2.8
KMA13-29-28	3.5	4.2	2.2	3.3
KMA13-29-30	3.2	4.0	1.5	2.9
KMA13-30-22	4.2	5.7	2.7	4.2
AND 1062	2.7	4.2	1.2	2.7
MEX54	3.7	4.2	1.0	3.0
Mean	3.7	4.2	1.8	3.3
CV (%)	23.8			
$LSD_{0.05}$: Line=0.6, Site=0.3, Line x site=1.2				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.10. Plant vigor of small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	4.5	4.2	2.7	3.8
KMA13-22-29	5.0	4.5	1.7	3.7
KMA13-23-14	4.2	3.5	2.2	3.3
KMA13-23-21	5.2	3.7	2.0	3.7
KMA13-25-09	4.7	4.2	1.2	3.4
KMA13-28-13	4.0	3.7	3.0	3.6
KMA13-30-02	4.2	5.0	2.2	3.8
KMA13-30-14	4.5	4.0	2.2	3.6
KMA13-30-16	4.2	3.7	2.2	3.4
KMA13-30-30	4.2	4.2	2.5	3.7
KMA13-31-01	4.7	4.2	2.2	3.7
KMA13-31-03	5.0	4.7	2.7	4.1
KMA13-31-04	4.2	4.2	2.2	3.6
KMA13-31-05	5.0	3.7	2.5	3.7
KMA13-31-06	4.5	4.2	2.2	3.7
KMA13-31-08	4.2	4.0	2.7	3.7
KMA13-31-09	5.5	6.0	2.5	4.7
KMA13-32-26	3.7	5.0	2.0	3.6
KMA13-32-28	4.0	4.0	2.5	3.5
G10909	4.5	4.2	2.3	3.7
G2333	4.7	4.3	2.8	3.9
GLP585	5.7	5.0	2.5	4.4
KATB9	4.5	5.3	2.8	4.2
RWR719	6.0	4.8	3.5	4.7
Mean	4.6	4.4	2.4	3.8
CV (%)	23.4			
$LSD_{0.05}$: Line=0.7, Site=0.2, Line x site=1.2				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.11. Plant vigor of mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	4.7	4.2	2.2	3.7
KMA13-21-23	5.0	3.2	2.2	3.5
KMA13-22-16	4.2	4.5	2.0	3.6
KMA13-22-23	4.2	4.0	2.5	3.6
KMA13-22-321	5.7	4.5	2.0	4.1
KMA13-22-322	4.5	6.0	3.2	4.6
KMA13-23-09	5.0	3.7	3.2	4.0
KMA13-23-10	5.0	4.5	2.5	4.0
KMA13-23-11	4.2	5.5	1.7	3.8
KMA13-23-20	4.0	5.0	3.0	4.0
KMA13-24-10	4.0	5.0	3.2	4.1
KMA13-25-01	4.0	5.7	3.0	4.2
KMA13-25-04	3.5	4.2	2.2	3.3
KMA13-27-01	3.0	2.5	1.7	2.4
KMA13-27-101	4.2	4.5	2.5	3.7
KMA13-27-102	3.0	4.2	3.0	3.4
KMA13-27-12	4.5	5.0	2.5	4.0
KMA13-27-13	4.0	3.7	2.2	3.3
KMA13-27-14	4.5	4.7	2.0	3.7
KMA13-27-27	4.0	3.0	1.7	2.9
KMA13-28-05	4.0	5.0	2.0	3.7
KMA13-28-13	3.5	4.2	1.5	3.1
KMA13-28-21	4.7	5.2	2.7	4.2
KMA13-28-22	4.0	6.0	2.2	4.1
KMA13-28-29	5.2	4.2	2.2	3.9
KMA13-29-19	3.7	4.0	2.0	3.2
KMA13-29-21	4.0	4.7	3.0	3.9
KMA13-30-07	4.2	4.5	1.7	3.5
KMA13-31-61	4.2	4.7	3.2	4.1
KMA13-31-62	4.0	4.0	1.7	3.2
KMA13-32-22	4.0	4.2	2.7	3.7
KMA13-32-24	4.7	5.7	2.7	4.4
KATB1	3.2	2.5	1.5	2.4
Mex54	3.7	4.2	1.0	3.0
Mean	4.2	4.5	2.4	3.7
CV (%)	21.5			
$LSD_{0.05}$: Line=0.6, Site=0.2, Line x site=1.1				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

4.3.1.3. Duration to flowering and maturity

There were highly significant site and genotypic differences (*P<0.001*) for days to flowering for pinto lines. The interaction between genotypes and sites was also highly significant (*P<0.001*). In general, study genotypes flowered earliest at Mwea (38.7 days) and latest at Tigoni (47.3 days). This indicated that warmer conditions may have hasted flowering in all lines. Genotypes KMA13-22-33 and KMA13-24-06 flowered the earliest when grown at low altitude (Mwea). These lines flowered on the 37th day after planting. KMA13-22-03 and KMA13-22-07 took longest to flower (48.5 days) when grown in the high altitude (Tigoni). Results showed highly significant site and location differences (*P<0.001*) for duration to maturity. The interaction between sites and genotypes also was highly significant. In general, study genotypes matured earlier grown at Mwea (87.5 days) compared to the other two sites (95.9 days at Kabete and 105.6 days at Tigoni). KMA13-21-19 grown at Mwea was the first to reach the physiological maturity (83 days). KMA13-22-03 took longest to mature when planted at Tigoni (108 days) (Table 4.12).

Table 4.13 shows that there were highly significant differences for the duration to flowering among the advanced red mottled lines due to genotypic and site effects. The interaction between the genotypes and the sites was highly significant (*P<0.001*). Advanced red mottled lines flowered earlier at Mwea (43.2 days) compared the other sites where the flowering occurred on the 44th day at Kabete, and on the 51st day after sowing at Tigoni. KMA13-28-13 was the earliest to flower when grown at Mwea (37 days) while KMA13-28-03 was the last to flower (54.5 days). Results showed that concerning the days to physiological maturity, there were also highly significant site and genotypic differences in duration to maturity. The interaction between sites and genotypes was highly significant (*P<0.001*). The test lines matured faster at low altitude Mwea site (95 days) compared to the medium altitude at Kabete (98 days) and the high altitude site at Tigoni (110.8 days). The earliest maturing red mottled line was KMA13-20-14, which matured in 90.5 days. KMA13-17-17 matured latest when grown at Mwea (110.0 days) and Tigoni (114 days).

Days to flowering of the advanced red kidney lines varied highly significantly among sites and genotypes. The interaction between genotypes and sites also significantly influenced duration to flowering (*P<0.001*). KMA13-25-03 and KMA13-25-20 were the earliest to flower (39 days)

when grown at Mwea, while KMA13-20-03, which flowered in 53 days, was the last to flower among test lines. However, it flowered slightly earlier compared to the check variety Mex54 (53.5 days) when they were grown at high altitude. There were significant site (*P<0.001*) and genotypic differences (*P<0.01*) for duration to maturity among red kidney lines. The interaction between the genotypes and sites also was significant (*P<0.05*). KMA13-21-11, KMA13-25-03 and KMA13-30-22 lines were the earliest to mature (85.5 days) among the test lines. They matured earlier compared with check varieties at Mwea. Lines KMA13-17-25 and KMA13-19-16 were the latest to mature (109.5 days) compared to all advanced red kidney lines and check varieties at Tigoni (Table 4.14).

There were significant site and genotypic differences (*P<0.001*) among the small red lines for days to flowering and days to maturity. The interaction between sites and genotypes also was significant. Duration to flowering day was shorter at Mwea (39.8 days) than it was at Kabete (43.1 days) and Tigoni (49.9 days). The trend was the same for the days to maturity with 89.4, 95.2 and 106.2 days at Mwea, Kabete and Tigoni (Table 4.15). Among the small red lines, KMA13-32-26 was the earliest to flower (39.2 days) regardless of the site. It was also the earliest to mature compared to all lines and all the check varieties (88.3 days).

There were highly significant differences among the advanced mixed color lines for the days to flowering and the days to maturity due to genotypic and site effects, and the interactions between the genotypes and the sites (*P<0.001*). The line KMA13-27-01 was the earliest to flower (39 days) and to mature (91 days) among the crosses regardless to the site where it was grown. It was however late to flower and to mature when compared to the commercial check KATB1 which flowered in 38 days and matured in 88 days on average (Table 4.16).

Table 4.12. Duration to flowering and maturity among pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Days to flowering				Days to maturity			
Site	**Kabete**	**Mwea**	**Tigoni**	**Mean**	**Kabete**	**Mwea**	**Tigoni**	**Mean**
KMA13-21-10	40.0	40.5	48.0	42.8	95.5	87.0	107.0	96.5
KMA13-21-19	39.0	39.0	46.5	41.5	96.0	83.0	107.0	95.3
KMA13-22-03	42.0	40.0	48.5	43.5	95.5	89.5	108.0	97.7
KMA13-22-07	41.5	39.0	48.5	43.0	94.5	86.0	105.0	95.2
KMA13-22-21	41.5	38.0	46.5	42.0	96.0	90.5	106.5	97.7
KMA13-22-30	41.5	38.5	45.5	41.8	95.5	88.0	104.0	95.8
KMA13-22-33	42.0	37.0	47.0	42.0	96.0	88.0	104.0	96.0
KMA13-23-13	41.0	40.0	47.5	42.8	94.5	85.5	104.0	94.7
KMA13-23-18	41.5	39.5	47.5	42.8	96.0	90.5	106.0	97.5
KMA13-23-22	40.5	39.5	48.0	42.7	97.5	85.5	105.0	96.0
KMA13-24-06	41.5	37.0	47.5	42.0	99.0	88.0	104.5	97.2
KMA13-24-07	41.0	37.0	46.0	41.3	94.5	84.5	105.0	94.7
GLP92	41.5	38.5	47.5	42.5	96.5	92.0	107.0	98.5
Mean	41.1	38.7	47.3	42.4	95.9	87.5	105.6	96.4
CV (%)	2.6				2.1			
$LSD_{0.05}$:	Line=0.7, Site=0.4, Line x site=1.3				Line=1.2, Site=0.6, Line x site=2.1			

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.13. Duration to flowering and maturity among red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Days to flowering				Days to maturity			
Site	**Kabete**	**Mwea**	**Tigoni**	**Mean**	**Kabete**	**Mwea**	**Tigoni**	**Mean**
KMA13-17-17	45.5	52.0	54.0	50.5	103.5	110.0	114.5	109.3
KMA13-17-25	42.0	43.0	49.5	44.8	95.5	92.5	110.5	99.5
KMA13-20-03	44.0	41.0	51.5	45.5	95.5	92.5	113.5	100.5
KMA13-20-14	45.0	41.0	54.0	46.7	97.0	90.5	116.5	101.3
KMA13-22-25	46.5	40.5	51.5	46.2	100.0	92.0	108.5	100.2
KMA13-24-05	43.5	47.5	49.0	46.7	101.0	91.5	110.0	100.8
KMA13-24-11	43.5	45.0	50.0	46.2	97.0	96.5	108.5	100.7
KMA13-24-16	44.5	46.0	51.0	47.2	97.5	93.0	110.0	100.2
KMA13-24-17	44.0	40.5	52.5	45.7	97.0	94.0	111.5	100.8
KMA13-27-25	47.0	48.0	54.0	49.7	100.5	97.5	114.0	104.0
KMA13-28-03	47.5	47.5	54.5	49.8	102.0	103.0	113.5	106.2
KMA13-28-13	43.0	37.0	50.0	43.3	94.0	93.0	105.0	97.3
KMA13-29-21	-	41.0	51.0	44.3	-	91.0	113.0	98.3
KMA13-29-24	44.0	40.0	50.0	44.7	95.5	92.5	108.0	98.7
KMA13-32-24	44.0	40.5	51.5	45.3	98.5	97.0	107.5	101.0
KMA13-32-28	42.5	40.5	51.5	44.8	100.0	94.5	111.5	102.0
BRB 191	44.0	44.0	50.0	46.0	95.5	94.5	109.0	99.7
Mean	44.4	43.2	51.5	46.4	98.1	95.0	110.8	101.3
CV (%)	3.5				2.3			
$LSD_{0.05}$:	Line=1.3, Site=0.6, Line x site=2.2				Line=1.9, Site=0.8, Line x site=3.3			

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.14. Duration to flowering and maturity among red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Days to flowering				Days to maturity			
Site	**Kabete**	**Mwea**	**Tigoni**	**Mean**	**Kabete**	**Mwea**	**Tigoni**	**Mean**
KMA13-17-25	44.0	44.0	52.0	46.7	98.0	93.0	109.5	100.2
KMA13-19-12	43.5	43.5	50.5	45.8	98.5	93.0	109.0	100.2
KMA13-19-16	43.0	40.0	51.0	44.7	95.5	91.0	109.5	98.7
KMA13-20-03	44.0	46.5	53.0	47.8	96.5	96.0	108.5	100.3
KMA13-21-11	43.5	40.5	49.5	44.5	98.5	87.5	106.0	97.3
KMA13-25-03	44.0	39.0	52.0	45.0	98.0	87.5	108.0	97.8
KMA13-25-20	43.5	39.0	51.0	44.5	98.5	88.5	105.5	97.5
KMA13-26-32	44.0	42.5	50.0	45.5	96.0	91.5	106.0	97.8
KMA13-27-31	44.0	41.0	50.5	45.2	97.0	89.5	107.0	97.8
KMA13-28-02	44.0	40.5	49.5	44.7	96.5	91.5	105.5	97.8
KMA13-29-28	44.5	39.5	51.0	45.0	99.5	91.5	106.0	99.0
KMA13-29-30	44.0	43.5	50.5	46.0	98.0	91.5	106.5	98.7
KMA13-30-22	43.0	41.0	48.5	44.2	93.5	87.5	107.5	96.2
AND 1062	43.5	40.5	50.0	44.7	95.0	90.0	106.0	97.0
MEX54	43.0	39.5	53.5	45.3	96.5	91.5	108.5	98.8
Mean	43.7	41.4	50.8	45.3	97.0	90.7	107.3	98.4
CV (%)	3.2				2.8			
$LSD_{0.05}$	Line=1.1, Site=0.5, Line x site=2.0				Line=2.0, Site=0.6, Line x site=3.1			

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.15. Duration to flowering and maturity among small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Lines	Days to flowering				Days to maturity			
Sites	**Kabete**	**Mwea**	**Tigoni**	**Mean**	**Kabete**	**Mwea**	**Tigoni**	**Mean**
KMA13-22-27	43.5	39.5	51.0	44.7	95.5	90.0	112.0	99.2
KMA13-22-29	45.5	41.0	52.5	46.3	94.5	85.0	103.0	94.2
KMA13-23-14	43.5	39.5	50.0	44.3	98.0	85.5	108.5	97.3
KMA13-23-21	47.0	43.5	53.0	47.8	102.5	90.0	113.5	102.0
KMA13-25-09	44.5	40.5	52.0	45.7	100.0	91.5	109.0	100.2
KMA13-28-13	44.0	39.5	52.5	45.3	94.0	92.5	106.5	97.7
KMA13-30-02	40.0	38.0	48.0	42.0	94.0	88.0	108.5	96.8
KMA13-30-14	42.5	39.5	51.0	44.3	97.0	91.0	110.0	99.3
KMA13-30-16	44.0	40.0	50.0	44.7	99.0	89.5	108.0	98.8
KMA13-30-30	43.0	39.5	50.5	44.3	95.0	91.0	101.0	95.7
KMA13-31-01	42.5	40.0	50.0	44.2	93.0	87.0	101.0	93.7
KMA13-31-03	43.5	40.0	49.5	44.3	93.0	89.0	100.0	94.0
KMA13-31-04	42.5	40.0	49.5	44.0	90.0	87.0	106.5	94.5
KMA13-31-05	42.5	39.5	49.5	43.8	94.0	92.0	105.0	97.0
KMA13-31-06	42.5	40.0	50.0	44.2	93.5	87.5	101.0	94.0
KMA13-31-08	43.5	39.5	50.0	44.3	94.0	91.0	107.0	97.3
KMA13-31-09	44.5	40.5	49.0	44.7	95.5	89.0	100.0	94.8
KMA13-32-26	38.0	36.7	43.0	39.2	83.5	85.0	96.5	88.3
KMA13-32-28	38.0	37.0	44.0	39.7	95.5	91.0	109.5	98.7
G10909	44.0	40.0	51.0	45.0	97.5	91.0	109.0	99.2
G2333	44.0	41.0	51.2	45.4	99.5	91.0	109.5	100.0
GLP585	45.5	40.5	51.5	45.8	97.0	89.5	107.0	97.8
KATB9	40.5	39.5	47.0	42.3	91.5	89.0	103.5	94.7
RWR719	45.0	40.5	52.5	46.0	98.5	92.5	113.0	101.3
Mean	43.1	39.8	49.9	44.3	95.2	89.4	106.2	96.9
CV (%)	2.7				3.0			
$LSD_{0.05}$	Line=1.0, Site=0.3, Line x site=1.7				Line=2.3, Site=0.8, Line x site=4.0			

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

Table 4.16. Duration to flowering and maturity among mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Days to flowering				Days to maturity			
Site	**Kabete**	**Mwea**	**Tigoni**	**Mean**	**Kabete**	**Mwea**	**Tigoni**	**Mean**
KMA13-21-20	43.5	40.5	51.0	45.0	99.0	92.0	109.0	100.0
KMA13-21-23	43.0	40.0	51.0	44.7	97.0	90.0	114.0	100.3
KMA13-22-16	46.5	40.5	52.0	46.3	100.5	87.5	113.0	100.3
KMA13-22-23	44.0	45.5	52.0	47.2	94.5	93.5	113.0	100.3
KMA13-22-321	45.0	43.5	52.0	46.8	98.5	93.0	115.0	102.2
KMA13-22-322	44.0	45.5	51.0	46.8	99.5	98.0	112.0	103.2
KMA13-23-09	45.0	41.0	52.0	46.0	99.5	94.5	114.0	102.7
KMA13-23-10	43.5	39.5	48.0	43.7	97.0	91.0	113.0	100.3
KMA13-23-11	45.0	40.0	48.0	44.3	96.5	92.5	113.0	100.7
KMA13-23-20	45.5	40.5	51.0	45.7	98.0	98.0	112.0	102.7
KMA13-24-10	43.5	41.0	56.0	46.8	96.0	91.5	97.0	94.8
KMA13-25-01	43.5	41.0	54.0	46.2	94.0	91.0	110.0	98.3
KMA13-25-04	42.5	40.0	49.0	43.8	95.0	92.5	114.0	100.5
KMA13-27-01	37.0	35.0	46.0	39.3	78.5	88.0	107.0	91.2
KMA13-27-101	45.0	41.0	52.0	46.0	98.5	90.0	112.0	100.2
KMA13-27-102	45.0	41.0	55.0	47.0	97.0	92.0	112.0	100.3
KMA13-27-12	48.0	46.5	52.0	48.8	98.5	98.0	110.0	102.2
KMA13-27-13	42.0	40.5	51.0	44.5	94.5	88.0	109.0	97.2
KMA13-27-14	44.0	39.5	50.0	44.5	96.0	92.0	111.0	99.7
KMA13-27-27	44.0	39.5	54.0	45.8	98.0	90.0	112.0	100.0
KMA13-28-05	43.5	39.5	54.0	45.7	94.0	93.5	112.0	99.8
KMA13-28-13	44.5	44.0	55.0	47.8	94.5	91.5	111.0	99.0
KMA13-28-21	47.0	43.5	52.0	47.5	101.0	89.0	116.0	102.0
KMA13-28-22	44.0	44.0	52.0	46.7	99.5	106.5	116.0	107.3
KMA13-28-29	46.0	39.5	52.0	45.8	100.0	90.5	116.0	102.2
KMA13-29-19	42.5	40.0	48.0	43.5	93.0	89.5	110.0	97.5
KMA13-29-21	43.0	39.5	49.0	43.8	94.0	91.5	112.0	99.2
KMA13-30-07	45.0	40.5	48.0	44.5	99.5	94.0	110.0	101.2
KMA13-31-61	44.0	43.0	52.0	46.3	93.0	89.5	108.0	96.8
KMA13-31-62	44.5	46.5	44.0	45.0	94.5	90.0	104.0	96.2
KMA13-32-22	44.0	46.0	54.0	48.0	95.0	85.0	113.0	97.7
KMA13-32-24	44.0	47.0	53.0	48.0	98.5	87.0	110.0	98.5
KATB1	36.5	35.0	43.0	38.2	82.0	88.0	94.0	88.0
MEX54	43.0	39.5	53.5	45.3	96.5	91.5	108.5	98.8
Mean	43.9	41.5	51.0	45.5	95.9	91.8	110.8	99.5
CV (%)	2.9				1.8			
$LSD_{0.05}$	Line=1.1, Site=0.3, Line x site=1.8				Line=1.5, Site=0.4, Line x site=2.5			

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05.

4.3.1.4. Reaction of the advanced lines to diseases under field conditions

There were no significant differences in the reaction of study genotypes to infection by diseases in the field (Tables 4.17, 4.18, 4.19, 4.20 and 4.21). This was probably due to the prevailing relatively dry conditions which were not conducive to pathogen development. This indicated the need for artificial inoculation with target pathogens under controlled conditions to validate the multiple disease resistance for which these materials were previously selected.

Table 4.17. Reaction to diseases of pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	ALS			ANTH			CBB			RR			BCMV		
Site	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**
KMA13-21-10	2.0	1.0	3.0	4.2	3.3	2.9	5.5	2.1	4.2	2.2	1.0	3.3	1.0	1.0	1.0
KMA13-21-19	2.0	2.0	2.0	3.0	2.6	2.0	2.0	1.0	3.0	3.0	1.0	4.0	2.0	1.0	3.3
KMA13-22-03	2.0	3.1	2.2	2.8	1.4	4.1	2.9	1.0	2.5	3.0	1.0	3.0	1.0	1.0	3.3
KMA13-22-07	1.0	1.0	2.0	4.0	1.0	2.0	1.0	1.0	3.0	3.0	1.0	3.4	1.6	1.0	2.9
KMA13-22-21	1.4	1.0	1.0	1.0	1.0	2.0	4.4	2.0	3.2	2.0	1.0	3.0	1.0	1.0	3.0
KMA13-22-30	1.0	2.0	2.6	2.0	1.0	2.0	3.1	2.5	1.0	3.0	1.0	3.0	2.2	1.0	3.0
KMA13-22-33	3.2	3.0	1.1	2.0	3.0	1.2	3.0	3.0	2.5	2.7	1.0	3.0	2.2	1.0	1.0
KMA13-23-13	1.0	1.0	1.0	1.9	2.2	1.0	2.0	3.0	3.0	3.0	1.0	3.0	2.0	1.0	2.1
KMA13-23-18	1.0	2.0	3.0	1.0	2.0	1.0	2.0	2.8	1.0	2.5	1.0	1.0	2.0	1.0	2.0
KMA13-23-22	1.2	2.2	2.0	1.0	2.5	3.2	2.0	2.0	2.0	2.1	1.0	3.0	2.0	1.0	4.7
KMA13-24-06	2.0	1.0	2.0	4.1	1.6	1.5	2.0	2.0	3.3	3.0	1.0	2.8	2.0	1.0	3.0
KMA13-24-07	2.0	1.0	2.4	3.0	1.0	1.0	1.5	1.0	1.0	3.0	1.0	3.0	2.0	1.0	1.0
GLP92	1.8	1.0	2.1	2.0	3.0	1.0	2.0	1.4	2.0	3.0	1.0	2.0	2.0	1.0	3.0
Mean	1.7	1.6	2.0	2.5	2.0	1.9	2.6	1.9	2.4	2.7	1.0	2.9	1.8	1.0	2.6
CV (%)	18.4			27.1			22.2			30.5			22.6		
$LSD_{0.05}$: Line(L)	0.7			1.0			1.0			0.6			0.9		
$LSD_{0.05}$: Site(S)	0.3			0.3			0.5			0.3			0.1		
$LSD_{0.05}$: LxS	1.2			1.6			1.1			0.8			1.0		

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05; ALS=angular leaf spot; ANTH=anthracnose; CBB=common bacterial blight; RR=root rot; BCMV=bean common mosaic virus

Table 4.18. Reaction to diseases of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	ALS			ANTH			CBB			RR			BCMV		
Site	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**
KMA13-17-17	1.0	1.0	2.0	1.0	1.0	2.2	2.0	1.0	2.0	5.0	2.0	4.4	1.0	1.0	1.2
KMA13-17-25	1.0	2.1	3.0	1.0	1.0	1.5	2.0	1.0	4.4	1.0	1.0	3.0	2.0	1.0	1.0
KMA13-20-03	2.0	2.0	2.0	1.0	1.0	1.0	3.4	1.0	3.0	1.0	1.0	3.0	2.0	1.0	1.0
KMA13-20-14	1.0	2.0	1.0	3.0	1.0	3.0	1.9	3.0	3.0	3.4	1.4	2.0	2.0	1.0	3.0
KMA13-22-25	1.0	1.5	1.0	2.0	1.0	2.0	3.0	1.0	3.5	3.0	1.0	3.0	1.0	1.0	2.4
KMA13-24-05	1.0	1.0	1.0	4.1	1.0	1.0	3.0	2.0	3.0	1.0	1.0	3.5	1.2	1.0	1.0
KMA13-24-11	1.8	1.0	3.2	2.0	1.0	1.0	3.0	2.4	4.0	4.2	2.0	3.0	1.0	1.0	1.0
KMA13-24-16	1.0	1.0	1.0	2.0	1.0	1.7	4.8	3.0	4.0	2.0	1.0	3.0	2.0	1.0	1.0
KMA13-24-17	1.0	1.0	1.0	2.7	1.0	2.0	3.9	1.1	1.9	1.0	2.2	3.3	1.7	1.0	1.1
KMA13-27-25	2.4	1.0	1.8	2.0	1.0	2.0	3.0	1.0	2.8	3.5	1.0	3.0	1.0	1.0	1.0
KMA13-28-03	3.1	1.0	1.0	1.0	1.0	1.0	3.4	3.0	2.0	2.0	1.0	2.8	1.0	1.0	1.0
KMA13-28-13	1.0	3.0	1.0	1.0	1.0	1.0	2.0	1.0	2.0	4.0	1.1	3.3	1.0	1.0	1.0
KMA13-29-21	1.0	3.0	1.0	2.3	1.0	2.0	1.0	1.0	2.5	4.0	1.0	3.1	2.0	1.0	2.0
KMA13-29-24	1.0	1.0	1.0	2.8	1.0	1.2	2.0	1.9	3.0	3.1	1.0	3.0	1.8	1.0	1.0
KMA13-32-24	1.0	1.0	1.0	1.2	1.0	1.0	3.0	1.0	3.0	1.0	1.0	3.0	2.0	1.0	1.0
KMA13-32-28	1.0	2.0	1.0	1.0	1.0	1.0	1.5	2.8	3.0	3.3	1.0	3.0	1.0	1.0	1.0
BRB 191	2.2	1.0	1.0	2.0	1.0	2.5	3.0	1.0	3.0	3.0	1.0	3.0	1.0	1.0	1.0
Mean	1.4	1.5	1.4	1.9	1.0	1.6	2.7	1.7	2.9	2.7	1.2	3.1	1.4	1.0	1.3
CV (%)	16.4			23.1			33.0			25.7			13.2		
$LSD_{0.05}$: Line(L)	0.9			0.7			1.1			1.5			0.8		
$LSD_{0.05}$: Site(S)	0.4			0.3			0.2			0.6			0.1		
$LSD_{0.05}$: LxS	1.1			0.9			1.4			2.2			0.9		

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05; ALS=angular leaf spot; ANTH=anthracnose; CBB=common bacterial blight; RR=root rot; BCMV=bean common mosaic virus

Table 4.19. Reaction to diseases of red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	ALS			ANTH			CBB			RR			BCMV		
Site	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**
KMA13-17-25	3.1	1.0	2.1	2.5	1.0	3.0	1.0	1.0	1.1	2.1	1.0	1.6	2.1	1.0	1.9
KMA13-19-12	1.1	1.0	1.0	2.0	1.1	2.4	2.2	1.0	1.4	1.1	1.0	1.0	1.1	1.0	1.0
KMA13-19-16	1.9	1.0	1.1	2.0	1.0	2.4	1.7	1.5	1.0	3.0	1.0	2.0	1.0	1.0	1.0
KMA13-20-03	1.0	1.0	1.0	2.1	1.4	2.0	1.3	1.0	1.0	1.0	1.0	2.0	1.0	1.0	1.2
KMA13-21-11	1.0	1.0	1.8	2.0	1.2	2.8	1.0	1.0	1.0	5.1	1.0	2.0	1.3	1.0	1.1
KMA13-25-03	2.5	1.0	1.8	2.0	1.1	2.0	1.0	1.1	2.0	2.8	1.0	1.4	1.7	1.0	2.0
KMA13-25-20	3.2	1.0	2.0	1.5	1.0	2.0	3.3	1.0	2.0	1.0	1.0	2.0	1.0	1.0	1.5
KMA13-26-32	3.0	1.0	1.0	2.2	1.0	2.4	3.0	1.5	2.2	1.9	1.0	1.0	1.2	1.0	1.0
KMA13-27-31	2.2	1.0	2.0	2.3	1.8	2.8	2.8	1.4	1.0	3.2	1.0	1.8	1.1	1.0	1.0
KMA13-28-02	2.0	1.0	1.0	2.8	1.0	3.2	2.0	1.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0
KMA13-29-28	1.0	1.0	1.5	2.4	1.0	2.0	2.0	1.1	1.0	3.0	1.0	1.2	1.0	1.0	1.2
KMA13-29-30	1.0	1.0	1.0	2.0	2.1	2.0	1.2	1.0	1.8	1.3	1.0	1.0	1.1	1.0	1.6
KMA13-30-22	1.3	1.0	1.0	2.0	1.0	1.0	2.1	1.0	1.0	2.8	1.0	1.3	1.1	1.0	1.0
AND 1062	3.0	1.0	1.1	2.0	1.0	2.2	2.0	1.3	1.1	3.1	1.0	1.3	1.4	1.0	2.2
MEX54	3.2	1.0	2.0	2.0	1.0	2.0	1.0	1.1	1.9	2.0	1.0	1.5	1.0	1.0	1.4
Mean	2.0	1.0	1.4	2.1	1.2	2.3	1.8			2.4	1.0	1.5	1.2	1.0	1.3
CV (%)	23.2			31.0			28.7			11.0			12.1		
$LSD_{0.05}$: Line(L)	1.1			1.2			0.9			1.0			0.7		
$LSD_{0.05}$: Site(S)	0.1			0.7			0.1			0.3			0.1		
$LSD_{0.05}$: LxS	1.1			1.6			1.0			1.1			0.7		

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05; ALS=angular leaf spot; ANTH=anthracnose; CBB=common bacterial blight; RR=root rot; BCMV=bean common mosaic virus

Table 4.20. Reaction to diseases of small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	ALS			ANTH			CBB			RR			BCMV		
Site	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**
KMA13-22-27	1.9	1.0	1.2	2.3	1.0	2.2	5.5	1.0	2.0	1.0	1.0	3.0	1.0	1.0	1.2
KMA13-22-29	2.1	1.3	1.5	1.0	1.0	1.5	2.0	1.0	4.4	1.0	1.0	3.0	1.3	1.0	1.1
KMA13-23-14	1.0	1.0	2.0	1.0	1.0	1.0	2.9	1.0	3.0	3.4	1.0	2.0	1.7	1.0	2.0
KMA13-23-21	2.0	1.0	3.0	2.0	1.0	3.0	1.0	1.0	3.0	3.0	1.0	3.0	1.0	1.0	1.5
KMA13-25-09	1.0	1.0	1.3	1.4	1.0	2.0	4.4	1.3	3.5	1.0	1.0	3.5	1.2	1.0	1.0
KMA13-28-13	2.0	1.0	1.5	1.8	1.0	1.0	3.1	1.0	3.0	4.2	1.0	3.0	1.1	1.0	1.0
KMA13-30-02	2.0	1.1	3.5	2.0	1.0	1.0	3.0	1.1	4.0	2.0	1.0	3.0	1.0	1.0	1.0
KMA13-30-14	2.0	1.0	2.0	2.0	1.0	1.7	2.0	1.0	4.0	1.0	1.0	3.3	1.0	1.0	1.2
KMA13-30-16	2.2	1.0	2.4	1.2	1.0	2.0	2.0	1.0	1.9	3.5	1.0	3.0	1.1	1.0	1.6
KMA13-30-30	2.0	1.1	2.0	1.0	1.0	2.0	2.0	1.1	2.8	2.0	1.0	2.8	1.1	1.0	1.0
KMA13-31-01	2.0	1.0	2.0	2.1	1.0	1.0	2.0	1.0	2.0	4.0	1.0	3.3	1.4	1.0	2.2
KMA13-31-03	2.0	1.0	1.0	1.0	1.0	1.0	1.5	1.0	2.0	4.0	1.0	3.1	1.0	1.0	1.4
KMA13-31-04	1.0	1.0	1.0	3.1	1.0	2.0	2.0	1.0	2.5	3.1	1.0	3.0	1.0	1.0	1.0
KMA13-31-05	1.9	1.5	2.0	1.0	1.0	1.2	2.5	1.5	3.0	1.0	1.0	3.0	1.3	1.0	1.0
KMA13-31-06	2.0	1.0	1.0	1.3	1.0	1.0	2.0	1.0	3.0	3.3	1.0	3.0	1.7	1.0	1.0
KMA13-31-08	2.0	1.0	2.0	2.0	1.0	1.0	2.9	1.0	3.0	3.0	1.0	3.0	1.0	1.0	1.2
KMA13-31-09	1.7	1.3	2.0	2.0	1.0	2.5	1.0	1.3	3.0	1.0	1.0	3.5	1.2	1.0	1.6
KMA13-32-26	1.0	1.0	2.0	2.0	1.0	1.0	4.4	1.6	3.0	1.0	1.0	3.0	1.1	1.0	1.0
KMA13-32-28	1.5	1.2	1.0	1.0	1.0	1.3	3.1	1.2	2.0	3.4	1.0	3.0	1.0	1.0	2.2
G10909	2.0	1.3	2.0	1.3	1.0	2.0	3.0	1.3	2.0	3.0	1.0	3.3	1.0	1.0	1.4
G2333	1.8	1.0	1.0	1.3	1.0	2.0	2.0	1.0	2.0	1.0	1.0	3.0	1.1	1.0	2.0
GLP585	2.1	1.0	2.0	2.1	1.0	2.0	2.0	1.0	2.0	4.2	1.0	2.8	1.1	1.0	1.5
KATB9	2.0	1.6	2.0	2.0	1.0	1.0	2.0	1.0	1.5	2.0	1.0	3.3	1.4	1.0	1.0
RWR719	2.0	1.1	2.1	2.0	1.0	2.2	2.0	1.1	2.0	1.0	1.0	3.1	1.0	1.0	1.0
Mean	1.8	1.1	1.8	1.6	1.0	1.5	2.5	1.1	2.7	2.4	1.0		1.2	1.0	1.3
CV (%)	42.0			33.3			21.7			38.1			13.4		
$LSD_{0.05}$: Line(L)	1.0			1.1			0.8			1.2			0.7		
$LSD_{0.05}$: Site(S)	0.3			0.5			0.5			1.0			0.5		
$LSD_{0.05}$: LxS	1.1			0.5			1.2			1.6			1.1		

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05; ALS=angular leaf spot; ANTH=anthracnose; CBB=common bacterial blight; RR=root rot; BCMV=bean common mosaic virus

Table 4.21. Reaction to diseases of mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	ALS			ANTH			CBB			RR			BCMV		
Site	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**	**Kabete**	**Mwea**	**Tigoni**
KMA13-21-20	1.1	1.0	1.1	2.5	1.0	3.0	1.0	1.0	1.1	4.2	1.0	3.0	1.1	1.0	1.0
KMA13-21-23	1.1	1.0	1.0	2.0	1.0	2.4	2.2	1.0	1.4	2.0	1.0	3.0	1.0	1.0	1.0
KMA13-22-16	1.9	1.0	1.1	2.0	1.0	2.4	1.7	1.5	1.0	1.0	1.0	3.3	1.0	1.0	1.2
KMA13-22-23	1.0	1.0	1.0	2.1	1.4	2.0	1.3	1.0	1.0	3.5	1.0	3.0	1.1	1.0	1.6
KMA13-22-321	1.0	1.0	1.8	2.0	1.2	2.8	1.0	1.0	1.0	2.0	1.0	2.8	1.1	1.0	1.0
KMA13-22-322	2.5	1.0	1.8	2.0	1.1	2.0	1.0	1.1	2.0	4.0	1.0	3.3	1.4	1.0	2.2
KMA13-23-10	3.2	1.0	2.0	1.5	1.0	2.0	3.3	1.0	2.0	4.0	1.0	3.1	1.0	1.0	1.4
KMA13-23-11	3.0	1.0	1.0	2.2	1.0	2.4	3.0	1.5	2.2	3.1	1.0	3.0	1.0	1.0	1.0
KMA13-23-20	2.2	1.0	2.0	2.3	1.8	2.8	2.8	1.4	1.0	1.0	1.0	3.0	1.3	1.0	1.0
KMA13-23-9	2.0	1.0	1.0	2.8	1.0	3.2	2.0	1.0	1.0	3.3	1.0	3.0	1.7	1.0	1.0
KMA13-24-10	1.0	1.0	1.5	2.4	1.0	2.0	2.0	1.1	1.0	3.0	1.0	3.0	1.0	1.0	1.2
KMA13-25-1	1.0	1.0	1.0	2.0	2.1	2.0	1.2	1.0	1.8	1.0	1.0	3.5	1.2	1.0	1.6
KMA13-25-4	1.3	1.0	1.0	2.0	1.0	1.0	2.1	1.0	1.0	1.0	1.0	3.0	1.1	1.0	1.0
KMA13-27-1	3.0	1.0	2.1	2.0	1.0	2.2	2.0	1.3	1.1	3.4	1.0	3.0	1.0	1.0	2.2
KMA13-27-101	3.2	1.0	2.0	2.0	1.0	2.0	1.0	1.1	1.9	3.0	1.0	3.3	1.0	1.0	1.4
KMA13-27-102	3.1	1.0	2.1	2.2	1.0	2.4	1.0	1.0	1.0	1.0	1.0	3.0	1.1	1.0	2.0
KMA13-27-12	3.1	1.0	1.0	2.3	1.8	2.8	1.0	1.1	2.0	4.2	1.0	2.8	1.1	1.0	1.5
KMA13-27-13	1.9	1.0	1.1	2.8	1.0	3.2	2.2	1.0	1.4	4.2	1.0	3.0	1.1	1.0	1.0
KMA13-27-14	1.0	1.0	1.0	2.4	1.0	2.0	1.7	1.5	1.0	2.0	1.0	3.0	1.0	1.0	1.0
KMA13-27-27	1.0	1.0	1.8	2.0	2.1	2.0	1.3	1.0	1.0	1.0	1.0	3.3	1.0	1.0	1.2
KMA13-28-13	2.5	1.0	1.8	2.0	1.0	2.4	1.0	1.0	1.0	3.5	1.0	3.0	1.1	1.0	1.6
KMA13-28-21	3.2	1.0	2.0	2.1	1.4	2.0	1.0	1.1	2.0	2.0	1.0	2.8	1.1	1.0	1.0
KMA13-28-22	3.0	1.0	1.0	2.0	1.2	2.8	3.3	1.0	2.0	4.0	1.0	3.3	1.4	1.0	2.2
KMA13-28-29	2.2	1.0	2.0	2.0	1.1	2.0	3.0	1.5	2.2	4.0	1.0	3.1	1.0	1.0	1.4
KMA13-28-5	2.0	1.0	1.0	1.5	1.0	2.0	2.8	1.4	1.0	3.1	1.0	3.0	1.0	1.0	1.0
KMA13-29-19	1.0	1.0	1.5	2.2	1.0	2.4	2.0	1.0	1.0	1.0	1.0	3.0	1.3	1.0	1.0
KMA13-29-21	1.0	1.0	1.0	2.3	1.8	2.8	2.0	1.1	1.0	3.3	1.0	3.0	1.7	1.0	1.0
KMA13-30-7	1.3	1.0	1.0	2.8	1.0	3.2	1.2	1.0	1.8	3.0	1.0	3.0	1.0	1.0	1.2
KMA13-31-61	3.0	1.0	1.1	2.4	1.0	2.0	2.1	1.0	1.0	1.0	1.0	3.5	1.2	1.0	1.6
KMA13-31-62	3.2	1.0	2.0	2.0	2.1	2.0	2.0	1.3	1.1	1.0	1.0	3.0	1.1	1.0	1.0
KMA13-32-22	2.5	1.0	1.0	2.0	1.0	1.0	1.0	1.1	1.9	3.4	1.0	3.0	1.0	1.0	2.2
KMA13-32-24	3.2	1.0	1.0	2.0	1.0	2.2	2.8	1.4	1.0	3.0	1.0	3.3	1.0	1.0	1.4
KATB1	3.0	1.0	1.1	2.0	1.0	2.0	2.0	1.0	1.0	1.0	1.0	3.0	1.1	1.0	2.0
MEX54	2.2	1.0	2.0	2.0	1.0	1.0	2.0	1.1	1.0	4.2	1.0	2.8	1.1	1.0	1.5
Mean	2.1	1.0	1.4	2.1	1.2	2.5	1.8	1.1	1.3	2.6	1.0	3.1	1.3	1.0	1.4

CV (%)	26.0	17.7	55.2	25.0	12.1
$LSD_{0.05}$: Line(L)	1.0	0.9	1.0	0.6	0.5
$LSD_{0.05}$: Site(S)	0.6	0.5	0.4	0.2	0.1
$LSD_{0.05}$: LxS	1.4	1.0	1.3	1.1	0.7

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05; ALS=angular leaf spot; ANTH=anthracnose; CBB=common bacterial blight; RR=root rot; BCMV=bean common mosaic virus

4.3.1.5. Number of pods per plant

There were significant site (*P<0.01*) and genotypic (*P<0.001*) differences among the pinto advanced lines for the number of pods per plant. The interaction between the genotypes and sites (*P<0.05*) was significant. The test genotypes had highest number of pods per plant under high altitude conditions at Tigoni (29.1 pods plant^{-1}) and lowest number at low altitude and warmer environment conditions at Mwea (4.6 pods plant^{-1}) (Table 4.22). KMA13-22-21 had the highest number of pods per plant (22.6) compared to all the advanced pinto lines and to the check variety GLP92 across sites.

For the advanced red kidney lines, there were significant sites and genotypic (*P<0.001*) differences for the number of pods developed. A significant interaction between genotypes and sites (*P<0.001*) was detected. The highest average number of pods per plant was recorded at Tigoni (23.9), which was significantly higher to that recorded at Kabete (9.7 pods per plant) and Mwea (6.6 pods per plant) (Table 4.23). KMA13-25-03 with a mean of 18.2 pods plan^{-1} had the highest number of pods per plant among the test lines. It was superior to all the advanced lines and to the check variety AND1062 but was inferior to the other check variety Mex54 which had an average number of 24.7 pods per plant. The variability among advanced lines was also significant across the sites.

There were highly significant location and genotypic differences among the red mottled advanced lines for the number of pods per plant (Table 4.24). The interaction between genotypes and sites was significant (*P<0.001*). Test lines had the highest number of pods plant^{-1} at Tigoni (30.8), which were significantly higher to 10.8 pods plant^{-1} at Kabete and 5.4 pods plant^{-1} at Mwea. KMA13-27-25 had the highest number of pods per plant (23.7) than all other red mottled lines and the check variety. All advanced lines had significantly more pods per plant than the check variety BRB191 (8.9).

There were highly significant site and genotypic differences for the number of pods per plant among the small red lines. Interactions between genotypes and sites were significant (*P<0.001*). Test lines had the highest number of pods per plant (26.2) at Tigoni, which was significantly higher compared to Kabete (8.6) and Mwea (6.8) (Table 4.25). Among test lines, KMA13-23-14 (22.7 pods plant^{-1}) had the highest number of pods per plant. This line produced significantly

more pods than other advanced small red lines and check varieties. RWR719, with an average of 7.9 pods plant^{-1}, had the lowest number of pods per plant.

There were highly significant site and genotypic differences among the mixed color advanced lines for the number of pods per plant (Table 4.26). The interaction between sites and genotypes was significant (*P<0.001*). The test lines produced the highest number of pods per plant (18.7) at Tigoni, followed by Kabete with a mean of 13.7 pods plant^{-1}, and the lowest at Mwea (7.0 pods plant^{-1}). KMA13-28-21 had the highest number of pods per plant (21.5). However, this was lower than the 24.7 pods plant^{-1} for the check variety Mex54.

Table 4.22. Number of pods per plant of advanced pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	12.4	7.5	28.9	16.3
KMA13-21-19	14.6	5.4	24.2	14.7
KMA13-22-03	14.1	3.1	25.8	14.4
KMA13-22-07	12.3	4.1	20.4	12.3
KMA13-22-21	18.1	5.6	44.2	22.6
KMA13-22-30	11.7	3.2	23.8	12.9
KMA13-22-33	12.7	3.2	30.0	15.3
KMA13-23-13	14.2	3.6	32.2	16.7
KMA13-23-18	12.7	4.4	25.3	14.1
KMA13-23-22	14.8	5.1	30.6	16.8
KMA13-24-06	12.9	3.3	33.3	16.5
KMA13-24-07	12.3	2.7	33.7	16.2
GLP92	14.2	9.2	26.0	16.4
Mean	13.6	4.6	29.1	15.8
CV (%)	33.6			
$LSD_{0.05}$: Line=4.3, Site=2.1, Line x site=7.4				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.23. Number of pods per plant of advanced red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	8.0	4.1	18.4	10.2
KMA13-19-12	10.6	6.4	17.5	11.5
KMA13-19-16	11.7	5.6	30.7	16.0
KMA13-20-03	9.2	4.1	18.2	10.5
KMA13-21-11	11.7	5.6	22.7	13.3
KMA13-25-03	13.4	11.0	27.8	18.2
KMA13-25-20	7.9	6.7	20.0	11.5
KMA13-26-32	10.7	5.6	19.2	11.8
KMA13-27-31	6.3	5.9	22.1	11.5
KMA13-28-02	9.0	4.9	25.3	13.0
KMA13-29-28	7.5	5.1	19.6	10.7
KMA13-29-30	9.0	8.3	19.7	12.3
KMA13-30-22	9.8	4.6	29.0	14.5
AND 1062	9.7	6.7	21.5	12.6
MEX54	13.5	14.5	46.2	24.7
Mean	9.7	6.6	23.9	13.4
CV (%)	33.7			
$LSD_{0.05}$: Line=3.7, Site=1.7, Line x site=6.5				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.24. Number of pods per plant of advanced red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	12.0	2.9	28.3	14.4
KMA13-17-25	11.8	2.5	19.1	11.1
KMA13-20-03	13.1	4.3	28.6	15.3
KMA13-20-14	10.7	2.7	29.6	14.3
KMA13-22-25	7.9	4.0	24.0	12.0
KMA13-24-05	13.1	3.8	28.1	15.0
KMA13-24-11	9.0	5.9	26.8	13.9
KMA13-24-16	13.8	4.7	41.8	20.1
KMA13-24-17	13.1	7.1	36.5	18.9
KMA13-27-25	8.7	9.1	53.1	23.7
KMA13-28-03	8.4	5.0	42.3	18.6
KMA13-28-13	16.0	4.8	35.5	18.7
KMA13-29-21	-	8.3	29.4	15.3
KMA13-29-24	8.6	8.9	32.3	16.6
KMA13-32-24	9.7	8.8	34.4	17.6
KMA13-32-28	8.2	5.8	18.6	10.9
BRB 191	9.3	3.0	14.3	8.9
Mean	10.8	5.4	30.8	15.6
CV (%)	37.3			
$LSD_{0.05}$: Line=4.7, Site=2.0, Line x site=8.1				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.25. Number of pods per plant of small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	6.3	4.3	21.9	10.8
KMA13-22-29	9.4	6.0	39.3	18.2
KMA13-23-14	8.6	13.3	46.1	22.7
KMA13-23-21	7.9	7.3	27.2	14.1
KMA13-25-09	10.0	8.0	41.4	19.8
KMA13-28-13	7.6	6.3	20.2	11.4
KMA13-30-02	7.4	6.2	36.2	16.6
KMA13-30-14	7.0	7.8	31.7	15.5
KMA13-30-16	7.1	7.8	25.9	13.6
KMA13-30-30	6.5	5.1	13.2	8.3
KMA13-31-01	10.0	9.0	28.9	16.0
KMA13-31-03	7.1	6.7	26.0	13.3
KMA13-31-04	9.4	6.3	22.2	12.7
KMA13-31-05	4.6	9.6	31.7	15.3
KMA13-31-06	11.3	6.5	26.8	14.9
KMA13-31-08	9.6	7.0	20.0	12.2
KMA13-31-09	8.0	4.8	23.9	12.3
KMA13-32-26	8.6	3.0	14.5	9.8
KMA13-32-28	8.6	11.3	20.2	13.3
RWR719	7.1	2.6	13.9	7.9
G10909	9.3	4.2	17.1	10.2
G2333	11.9	6.7	30.2	16.2
GLP585	7.7	6.0	23.5	12.4
KATB9	15.1	6.5	26.9	16.2
Mean	8.6	6.8	26.2	13.9
CV (%)	44.1			
$LSD_{0.05}$: Line=4.9, Site=1.7, Line x site=8.5				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.26. Number of pods per plant of the mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	13.1	7.0	15.5	10.6
KMA13-21-23	11.3	5.9	12.0	9.0
KMA13-22-16	9.3	7.8	23.0	10.1
KMA13-22-23	13.6	8.3	12.0	11.9
KMA13-22-321	13.0	6.6	16.3	10.5
KMA13-22-322	15.7	8.0	10.0	12.7
KMA13-23-09	19.8	12.0	40.0	18.6
KMA13-23-10	11.8	6.0	17.8	9.9
KMA13-23-11	13.5	4.8	11.0	9.1
KMA13-23-20	21.2	7.3	24.7	15.4
KMA13-24-10	14.2	2.2	12.5	8.2
KMA13-25-01	18.9	6.0	13.2	12.5
KMA13-25-04	18.9	9.1	14.0	14.0
KMA13-27-01	10.4	4.5	9.2	7.6
KMA13-27-101	17.3	10.4	16.0	14.1
KMA13-27-102	12.8	7.7	25.5	11.9
KMA13-27-12	14.8	7.0	17.3	11.6
KMA13-27-13	10.9	4.7	11.5	8.2
KMA13-27-14	13.3	6.4	29.5	12.0
KMA13-27-27	15.6	13.7	25.7	15.9
KMA13-28-05	11.3	14.3	16.0	13.9
KMA13-28-13	15.5	6.8	13.1	11.1
KMA13-28-21	22.7	8.0	43.5	21.5
KMA13-28-22	12.1	2.5	12.4	7.3
KMA13-28-29	19.3	7.5	14.2	13.4
KMA13-29-19	13.1	8.8	25.3	12.5
KMA13-29-21	10.1	6.3	8.4	8.2
KMA13-30-07	8.9	2.9	8.0	6.6
KMA13-31-61	10.1	4.3	9.0	7.4
KMA13-31-62	11.2	8.8	10.0	10.0
KMA13-32-22	10.4	7.5	6.8	9.1
KMA13-32-24	8.9	2.3	9.3	7.1
KATB1	10.5	1.8	9.8	7.9
MEX54	13.5	14.5	46.2	24.7
Mean	13.7	7.0	18.7	11.5
CV (%)	19.8			
$LSD_{0.05}$: Line=2.0, Site=0.6, Line x site=3.4				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

4.3.1.6. Number of seeds per pod

There were significant differences (*P<0.001*) in seeds per pod among the advanced pinto lines grown at Kabete, Mwea and Tigoni for the average number of seeds per pod due to site and genotypic effects. The interaction between sites and the genotypes was also significant (*P<0.01*). Test lines had more seeds per pod at Tigoni (5.8) compared to Kabete (5.3) and Mwea (4.2) (Table 4.27). KMA13-21-10 (5.8) had the highest number of seeds per pod at all sites. This was higher compared to all the advanced lines and the check variety GLP92.

The red kidney advanced lines also showed highly significant differences for the number of seeds per pod (Table 4.28). These differences were attributed to site and genotypic effects. The highest number of seeds per pod was recorded at Tigoni (4.7) compared to Kabete (4.4) and Mwea (4.0). The interaction between the sites and the genotypes was significant (*P<0.001*). KMA13-30-22 had the highest number of seeds per pod (5.2) compared to all other red kidney lines and check varieties.

There were highly significant differences for the number of seeds per pod among the advanced red mottled lines grown at Kabete, Mwea and Tigoni due to the genotypic, site effects and their interactions (*P<0.001*). Among sites, an average of 4.9 seeds per pod was recorded at Tigoni, which was higher than 4.4 seed pod^{-1} at Kabete and 3.9 seeds per pod at Mwea. KMA13-32-24 had the highest number of seeds per pod (5.5). This line had significantly more seeds per pod than other red mottled lines and the check variety, BRB 191. The check variety had the least number of seeds per pod (3.3 seeds per pod) (Table 4.29).

Results showed that there were significant differences for seeds pod^{-1} among the advanced small red lines due to genotypic (*P<0.001*), sites (*P<0.01*) and to the interactions between the genotypes and the sites (*P<0.001*) (Table 4.30). Among sites, the number of seeds obtained from Kabete (5.9) was not significantly different from the average of Mwea (5.8). However, the test lines had more seeds pod^{-1} (6.1) at Tigoni compared to the other two sites. KMA13-32-28 with a mean of 7.6 seeds pod^{-1} and KMA13-25-09 with 7.0 seeds pod^{-1} had the highest number of seeds per pod compared with all the advanced lines and check varieties.

Table 4.31 showed that there were significant differences for the number of seeds per pod among the advanced mixed color lines grown at Kabete, Mwea and Tigoni due to effects of sites,

genotypes and their interactions (*P<0.001*). KMA13-25-04 had produced the highest number of seeds per pod (6.9) regardless of the sites. This was higher compared to all the advanced lines and check varieties. The check variety KATB1 recorded the lowest number of seeds per pod (3.9) compared the advanced lines and the other check variety Mex54.

Table 4.27. Number of seeds per pod of the advanced pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	6.4	5.0	6.0	5.8
KMA13-21-19	4.4	4.1	5.6	4.7
KMA13-22-03	5.9	3.8	4.4	4.7
KMA13-22-07	5.6	3.9	6.4	5.3
KMA13-22-21	5.0	3.9	5.4	4.8
KMA13-22-30	5.9	4.8	6.1	5.6
KMA13-22-33	5.0	3.7	6.4	5.0
KMA13-23-13	5.0	4.4	5.6	5.0
KMA13-23-18	5.5	3.6	6.1	5.1
KMA13-23-22	5.2	4.6	5.2	5.0
KMA13-24-06	5.1	4.4	5.9	5.1
KMA13-24-07	5.7	4.8	6.4	5.7
GLP92	4.4	4.2	5.5	4.7
Mean	5.3	4.2	5.8	5.1
CV (%)	12.7			
$LSD_{0.05}$: Line=0.5, Site=0.2, Line x site=0.9				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.28. Number of seeds per pods of the red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	4.1	3.9	4.5	4.2
KMA13-19-12	3.6	4.2	3.6	3.8
KMA13-19-16	5.1	4.2	5.5	5.0
KMA13-20-03	4.0	3.1	4.9	4.0
KMA13-21-11	3.7	4.5	4.4	4.2
KMA13-25-03	4.0	3.4	4.4	3.9
KMA13-25-20	4.2	4.7	4.7	4.6
KMA13-26-32	4.5	4.4	4.7	4.5
KMA13-27-31	4.7	3.9	4.6	4.4
KMA13-28-02	5.4	3.9	4.4	4.5
KMA13-29-28	4.0	4.0	4.1	4.0
KMA13-29-30	3.4	3.6	4.2	3.7
KMA13-30-22	5.6	3.7	6.2	5.2
AND 1062	5.0	4.2	5.0	4.7
MEX54	4.7	4.7	5.5	5.0
Mean	4.4	4.0	4.7	4.4
CV (%)	12.5			
$LSD_{0.05}$: Line=0.4, Site=0.2, Line x site=0.8				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.29. Number of seeds per pod of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	4.4	3.4	4.1	4.0
KMA13-17-25	4.0	2.8	3.9	3.5
KMA13-20-03	4.4	3.6	6.6	4.9
KMA13-20-14	4.0	3.5	5.3	4.2
KMA13-22-25	3.9	3.8	5.8	4.5
KMA13-24-05	5.1	4.0	5.6	4.9
KMA13-24-11	3.6	4.6	4.1	4.1
KMA13-24-16	4.0	4.9	5.8	4.9
KMA13-24-17	5.5	3.7	4.8	4.7
KMA13-27-25	5.4	4.4	4.0	4.6
KMA13-28-03	4.0	5.5	4.1	4.5
KMA13-28-13	4.3	3.4	5.8	4.5
KMA13-29-21	-	3.1	3.8	3.3
KMA13-29-24	4.1	4.4	3.6	4.1
KMA13-32-24	5.8	4.3	6.6	5.5
KMA13-32-28	4.3	4.3	4.8	4.4
BRB 191	3.1	2.6	4.1	3.3
Mean	4.4	3.9	4.9	4.4
CV (%)	17.1			
$LSD_{0.05}$: Line=0.6, Site=0.3, Line x site=1.0				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.30. Number of seeds per pod of the small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	7.3	6.3	6.5	6.7
KMA13-22-29	4.3	4.4	5.1	4.6
KMA13-23-14	5.8	5.9	5.4	5.7
KMA13-23-21	5.3	4.0	4.8	4.7
KMA13-25-09	7.9	5.5	7.6	7.0
KMA13-28-13	5.1	4.8	6.1	5.4
KMA13-30-02	5.4	5.0	6.6	5.7
KMA13-30-14	6.4	6.2	6.3	6.3
KMA13-30-16	5.6	5.0	4.9	5.2
KMA13-30-30	5.5	7.0	5.6	6.0
KMA13-31-01	5.9	6.3	5.6	5.9
KMA13-31-03	6.1	5.6	6.4	6.0
KMA13-31-04	6.3	5.1	5.8	5.7
KMA13-31-05	6.0	6.6	6.3	6.3
KMA13-31-06	5.9	6.0	6.4	6.1
KMA13-31-08	5.8	5.9	6.9	6.2
KMA13-31-09	7.1	6.3	5.8	6.4
KMA13-32-26	4.0	4.5	4.5	4.3
KMA13-32-28	7.3	7.6	8.0	7.6
RWR719	6.1	5.6	6.9	6.2
G10909	6.6	6.9	7.0	6.8
G2333	6.0	6.3	7.0	6.4
GLP585	5.8	6.5	7.4	6.5
KATB9	5.1	5.3	4.6	5.0
Mean	5.9	5.8	6.1	6.0
CV (%)	12.0			
$LSD_{0.05}$: Line=0.6, Site=0.2, Line x site=1.0				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.31. Number of seeds per pod of the advanced mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	6.1	5.5	5.3	5.8
KMA13-21-23	5.3	5.9	5.5	5.6
KMA13-22-16	5.6	4.6	4.5	5.1
KMA13-22-23	5.3	5.8	3.8	5.2
KMA13-22-321	4.9	5.4	5.3	5.1
KMA13-22-322	4.6	5.7	5.8	5.1
KMA13-23-09	4.8	5.5	5.8	5.2
KMA13-23-10	5.4	5.1	5.8	5.3
KMA13-23-11	5.5	5.3	5.7	5.5
KMA13-23-20	4.8	4.0	4.8	4.4
KMA13-24-10	5.0	3.8	4.6	4.5
KMA13-25-01	4.5	4.5	4.5	4.5
KMA13-25-04	6.3	7.5	7.0	6.9
KMA13-27-01	4.6	5.1	3.8	4.8
KMA13-27-101	5.6	5.8	5.8	5.7
KMA13-27-102	6.4	4.5	5.3	5.4
KMA13-27-12	6.5	3.3	5.5	4.5
KMA13-27-13	5.1	4.3	4.8	4.7
KMA13-27-14	3.9	4.3	4.5	4.1
KMA13-27-27	6.1	4.4	6.0	5.3
KMA13-28-05	4.9	5.7	6.1	5.6
KMA13-28-13	6.3	5.6	6.2	6.0
KMA13-28-21	6.1	5.0	5.0	5.6
KMA13-28-22	4.8	4.8	5.0	4.9
KMA13-28-29	5.8	5.1	5.5	5.5
KMA13-29-19	4.1	4.6	4.5	4.4
KMA13-29-21	5.1	4.1	6.0	4.8
KMA13-30-07	4.3	4.4	4.0	4.3
KMA13-31-61	6.1	5.4	5.8	5.8
KMA13-31-62	4.5	5.3	4.0	4.6
KMA13-32-22	5.8	5.3	3.8	5.3
KMA13-32-24	4.9	2.8	6.0	4.4
KATB1	4.6	2.8	3.5	3.9
MEX54	4.7	4.7	5.5	5.0
Mean	5.2	4.8	5.0	5.0
CV (%)	10.4			
$LSD_{0.05}$: Line=0.4, Site=0.1, Line x site=0.7				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

4.3.1.7. 100-seed mass

There were significant differences for the 100-seed mass among the advanced pinto bean lines due to the site and genotypic effects (*P<0.001*), and their interaction (*P<0.01*). Seeds were larger in the highland site at Tigoni (31.4 g 100 seeds^{-1}) while the lowest values were recorded at Kabete at medium altitude (24.4 g 100 seeds^{-1}) (Table 4.32). KMA13-21-19 had the highest seed size among the advanced lines (28.9 g 100 seeds^{-1}). However, this was lower compared to the check variety GLP92 (30.9 g 100 seeds^{-1}).

For the red kidney market class, there were highly significant differences among the advanced lines for the 100-seed mass due to effects of site, genotype and to their interaction (*P<0.001*). Among sites, seeds were larger at Tigoni (46.7 g 100 seeds^{-1}) compared to the other two sites (41.6 g at Kabete and 39.8 g at Mwea). Lines KMA13-17-25 (47.1 g 100 seeds^{-1}), KMA13-21-11 (47.6 g 100 seeds^{-1}) and KMA13-29-30 (47.0 g 100 seeds^{-1}) had the highest 100-seed mass averages compared to all the other red kidney lines and commercial checks (Table 4.33).

Results in Table 4.34 show highly significant differences among the red mottled lines for the 100-seed mass due to effects of genotypes, sites and their interactions (*P<0.001*). Among test sites, the largest seeds were obtained at Tigoni (43.9 g 100 seeds^{-1}). The smallest seed size was recorded at Mwea (34.0 g 100-seed mass). Among lines, KMA13-32-24 had the largest seeds (50.8 g 100 seeds^{-1}) but which were not significantly different from the check variety BRB191 (50.4 g 100 seeds^{-1}). The variability for the 100-seed mass among the red mottled lines was very high. It varied from 27.8 g for KMA13-24-17 to 50.8 g for KMA13-32-24.

There were highly significant differences among the small red lines (Table 4.35) for the 100-seed mass, which was attributed to genotypic and site effects and their interactions (*P<0.001*). The seed size varied from small (<25 g 100 seeds^{-1}) to medium (25-40 g 100 seeds^{-1}). Among sites, the test lines had largest seeds at Tigoni (28.8 g 100 seeds^{-1}) compared to Kabete (25.8 g 100 seeds^{-1}) and Mwea (24.5 g 100 seeds^{-1}). KMA13-23-21 had the largest seed seeds (39.0 g 100 seeds^{-1}), which were larger than all the advanced lines and check varieties for this market class. In contrast, KMA13-31-04 had the smallest seeds (21.5 g 100 seeds^{-1}). Seeds of this line were smaller than that of all the advanced lines and check varieties.

There were significant differences (*P<0.001*) in 100-seed mass among the mixed colour lines (Table 4.36) due to the genotypes, sites and the interaction between genotypes and sites. Among sites, Tigoni produced beans with larger seeds (37.7 g 100 seeds^{-1}), compared to the other two sites which had average means of 33.2 and 29.1 g 100 seeds^{-1} for Kabete and Mwea, respectively. KMA13-27-01 had the highest 100-seed mass (38.1 g 100 seeds^{-1}), which was higher than all the mixed color lines and checks.

Table 4.32. 100-seed mass (in g) of the advanced pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	23.0	25.0	32.2	26.8
KMA13-21-19	25.0	30.4	31.3	28.9
KMA13-22-03	25.7	24.6	31.1	27.2
KMA13-22-07	21.5	22.8	29.6	24.6
KMA13-22-21	26.0	25.2	31.7	27.6
KMA13-22-30	23.3	28.2	31.2	27.6
KMA13-22-33	25.6	24.8	29.9	26.8
KMA13-23-13	24.1	25.5	30.8	26.8
KMA13-23-18	24.3	23.7	31.3	26.4
KMA13-23-22	22.3	25.8	31.1	26.4
KMA13-24-06	24.3	22.6	31.3	26.1
KMA13-24-07	21.4	23.6	31.9	25.7
GLP92	30.9	27.4	34.2	30.9
Mean	24.4	25.4	31.4	27.1
CV (%)	7.9			
$LSD_{0.05}$: Line=1.7, Site=0.8, Line x site=3.0				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.33. 100-seed mass (in g) of red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	47.3	42.0	52.1	47.1
KMA13-19-12	37.2	40.9	40.0	39.4
KMA13-19-16	34.3	32.6	30.8	32.6
KMA13-20-03	32.9	38.6	53.1	41.6
KMA13-21-11	49.7	42.1	51.1	47.6
KMA13-25-03	36.0	39.8	41.7	39.8
KMA13-25-20	44.8	41.5	46.8	44.4
KMA13-26-32	39.6	38.0	47.7	41.8
KMA13-27-31	45.7	41.3	51.9	46.3
KMA13-28-02	46.8	42.8	50.0	46.5
KMA13-29-28	45.0	41.9	50.8	45.9
KMA13-29-30	46.7	42.5	51.9	47.0
KMA13-30-22	36.6	34.0	43.8	38.1
AND 1062	46.2	40.3	51.6	46.0
Mex54	32.2	38.6	36.1	35.6
Mean	41.6	39.8	46.6	42.7
CV (%)	7.5			
$LSD_{0.05}$: Line=2.6, Site=1.2, Line x site=4.5				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.34. 100-seed mass (in g) of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	54.0	44.9	50.9	49.9
KMA13-17-25	47.0	38.2	51.6	45.6
KMA13-20-03	33.6	32.5	43.9	36.6
KMA13-20-14	35.1	27.2	46.1	36.1
KMA13-22-25	39.7	31.2	38.4	36.4
KMA13-24-05	33.4	26.6	34.9	31.6
KMA13-24-11	26.4	30.7	37.5	31.5
KMA13-24-16	28.3	27.7	33.3	29.7
KMA13-24-17	28.3	23.3	31.8	27.8
KMA13-27-25	30.9	33.3	34.9	33.0
KMA13-28-03	33.2	28.7	34.9	32.3
KMA13-28-13	29.4	29.4	36.0	31.6
KMA13-29-21	-	40.0	55.8	45.2
KMA13-29-24	37.7	35.1	41.1	38.0
KMA13-32-24	41.3	45.6	65.6	50.8
KMA13-32-28	52.1	46.5	50.9	49.8
BRB191	47.6	38.0	65.5	50.4
Mean	37.4	34.0	43.9	38.4
CV (%)	14.6			
$LSD_{0.05}$: Line=4.5, Site=1.9, Line x site=7.8				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.35. 100-seed mass (in g) of advanced small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	24.5	21.7	30.0	25.4
KMA13-22-29	26.6	21.5	28.7	25.6
KMA13-23-14	25.9	25.0	32.4	27.7
KMA13-23-21	40.8	36.5	39.6	39.0
KMA13-25-09	27.8	26.7	27.6	27.3
KMA13-28-13	24.2	22.7	28.9	25.3
KMA13-30-02	20.4	23.9	27.8	24.0
KMA13-30-14	30.0	28.8	29.5	29.4
KMA13-30-16	31.9	36.3	35.5	34.5
KMA13-30-30	26.5	25.0	29.7	27.0
KMA13-31-01	22.3	24.8	24.6	23.9
KMA13-31-03	23.6	20.8	24.6	23.0
KMA13-31-04	19.1	18.7	26.8	21.5
KMA13-31-05	25.6	24.5	26.3	25.4
KMA13-31-06	21.5	22.6	25.0	23.0
KMA13-31-08	22.2	21.7	24.5	22.8
KMA13-31-09	25.6	20.1	24.6	23.4
KMA13-32-26	34.5	28.3	40.3	35.6
KMA13-32-28	26.7	24.7	30.7	27.4
RWR719	21.4	22.1	21.9	21.8
G10909	24.3	22.2	28.4	25.0
G2333	24.4	22.5	27.2	24.7
GLP585	25.4	24.4	28.5	26.1
KATB9	24.9	23.9	28.4	25.7
Mean	25.8	24.5	28.8	26.4
CV (%)	9.3			
$LSD_{0.05}$: Line=2.0, Site=0.7, Line x site=3.4				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.36. 100-seed mass (in g) of the advanced mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	37.5	31.9	38.1	35.1
KMA13-21-23	30.0	26.5	36.1	29.1
KMA13-22-16	41.5	24.6	35.0	33.3
KMA13-22-23	28.4	27.7	39.9	29.8
KMA13-22-321	34.0	27.3	34.6	31.1
KMA13-22-322	31.4	34.6	33.7	32.6
KMA13-23-09	35.2	31.7	40.2	34.2
KMA13-23-10	34.1	29.0	39.4	32.4
KMA13-23-11	33.6	24.4	29.0	29.0
KMA13-23-20	36.8	32.6	42.0	35.5
KMA13-24-10	31.5	25.4	33.1	30.0
KMA13-25-01	27.8	29.7	33.0	29.1
KMA13-25-04	28.4	25.0	28.0	27.1
KMA13-27-01	36.2	36.7	51.0	38.1
KMA13-27-101	25.6	26.9	33.8	27.1
KMA13-27-102	24.0	24.4	23.0	24.1
KMA13-27-12	32.3	24.0	29.6	29.5
KMA13-27-13	30.8	24.2	35.4	28.4
KMA13-27-14	34.1	40.7	40.4	37.7
KMA13-27-27	37.5	35.9	39.0	37.0
KMA13-28-05	30.2	29.9	33.0	30.0
KMA13-28-13	29.5	22.1	34.5	28.7
KMA13-28-21	34.4	28.2	37.0	33.0
KMA13-28-22	37.2	21.4	35.4	31.3
KMA13-28-29	26.7	21.2	30.2	26.0
KMA13-29-19	27.9	32.4	35.6	30.7
KMA13-29-21	33.9	30.5	42.6	33.3
KMA13-30-07	41.0	31.3	38.5	36.2
KMA13-31-61	29.5	24.2	29.6	27.1
KMA13-31-62	38.7	34.0	40.1	36.8
KMA13-32-22	38.1	28.0	50.1	36.9
KMA13-32-24	36.3	29.6	37.2	34.5
KATB1	37.8	32.5	44.0	37.1
Mex54	32.2	38.6	36.1	35.6
Mean	33.2	29.1	37.7	32.1
CV (%)	6.2			
$LSD_{0.05}$: Line=1.6, Site=0.5, Line x site=2.8				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

4.3.1.8. Harvest index

There were significant differences among the pinto advanced lines for the harvest index due to genotype (*P<0.05*) and the site (*P<0.001*) effects. The interaction between the site and the genotype on the harvest index was not significant. Among sites, Tigoni recorded the highest bean harvest index (59.1%) while the lowest harvest index was obtained at Mwea (25.7% in average). Among lines, KMA13-21-10 recorded the highest harvest index (52.1%). This line had a higher harvest index than all the other test lines and the check variety. KMA13-22-07 and KMA13-22-33 with a mean value of 41.8% had the lowest harvest index among lines and compared to the check variety GLP92 (Table 4.37).

Analysis of variance for the red kidney lines revealed highly significant differences among the advanced lines for the harvest index due to genotypes, sites and the interactions between the genotypes and sites (*P<0.001*) (Table 4.38). Crops grown at Tigoni recorded the highest harvest index (55.1%) compared to Kabete and Mwea with means of 43.4% and 18.8%, respectively. The line KMA13-30-22 had the highest harvest index (51.4%), compared with other red kidney lines and checks.

Significant differences for harvest index due to genotypes (*P<0.05*), sites (*P<0.001*) and the interactions between the genotypes and the sites (*P<0.05*) were detected among the advanced red mottled lines. The best harvest index among sites was recorded at Tigoni (48.1%) compared to Kabete (33.7%) and Mwea (23.8%)(Table 4.39). Among advanced lines, KMA13-32-28 (43.4%) and KMA13-20-14 (43.0%) had the highest values for the harvest index. However, all the advanced red mottled lines were inferior to the check variety BRB191 (49.9%) for harvest index.

There were highly significant differences among advanced small red lines for the harvest index due to genotypes, sites and to the interactions between genotypes and sites (*P<0.001*) (Table 4.40). Among the test sites, Tigoni recorded the highest mean harvest index (60.4%) compared to Kabete (41.3%) and Mwea (38.4%). KMA13-31-04 had the highest mean for the harvest index (60.5%) among the test lines. However, the harvest index of KMA13-31-04 was inferior to that of the check variety KATB9 (66.4%).

Table 4.41 shows that there were significant genotypic and sites differences (*P<0.001*) for the harvest index among the advanced mixed color lines. The interaction between genotypes and

sites was also significant. Harvest index was highest when the test lines were grown at Tigoni (61.3%). Mean harvest index was 44.8% at Kabete and 27.4% at Mwea. Among lines, KMA13-32-22 (55.6%) and KMA13-27-10/1(55.3%) had the highest harvest index. Harvest index of these lines was higher compared to all the advanced lines and check varieties.

Table 4.37. Harvest index (in %) of advanced pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	61.1	29.6	65.5	52.1
KMA13-21-19	54.5	28.2	54.4	45.7
KMA13-22-03	54.6	25.7	67.0	49.1
KMA13-22-07	50.8	22.0	52.7	41.8
KMA13-22-21	58.1	29.8	66.3	51.4
KMA13-22-30	50.1	24.5	72.1	48.9
KMA13-22-33	54.5	23.6	47.4	41.8
KMA13-23-13	66.6	25.0	57.7	49.8
KMA13-23-18	51.3	23.1	60.1	44.8
KMA13-23-22	60.7	21.3	51.7	44.6
KMA13-24-06	52.8	27.3	50.7	43.6
KMA13-24-07	53.6	26.3	57.1	45.7
GLP92	50.5	27.8	65.8	48.1
Mean	55.3	25.7	59.1	46.7
CV (%)	18.0			
$LSD_{0.05}$: Line=6.8, Site=3.3, Line x site=11.8				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.38. Harvest index (in %) of red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	46.0	18.3	52.2	38.8
KMA13-19-12	42.9	6.3	53.0	34.1
KMA13-19-16	47.7	23.5	58.6	43.2
KMA13-20-03	39.3	16.2	50.9	35.5
KMA13-21-11	48.1	18.7	44.9	37.3
KMA13-25-03	13.5	15.5	59.0	32.5
KMA13-25-20	45.4	14.3	54.2	38.0
KMA13-26-32	48.4	27.4	55.5	43.8
KMA13-27-31	56.1	12.4	61.2	43.2
KMA13-28-02	42.9	15.8	59.0	39.2
KMA13-29-28	25.5	16.0	45.8	29.1
KMA13-29-30	33.8	18.2	46.4	32.8
KMA13-30-22	60.7	25.4	68.2	51.4
MEX54	44.9	26.9	67.0	46.3
AND 1062	41.3	26.8	50.7	39.6
Mean	43.4	18.8	55.1	39.1
CV (%)	12.5			
$LSD_{0.05}$: Line=4.0, Site=1.8, Line x site=6.9				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.39. Harvest index (in %) of red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	28.3	9.2	35.0	24.2
KMA13-17-25	42.2	22.4	47.1	37.2
KMA13-20-03	34.6	27.8	62.2	41.5
KMA13-20-14	30.7	50.3	47.9	43.0
KMA13-22-25	34.3	7.1	36.1	25.8
KMA13-24-05	33.2	17.2	46.5	32.3
KMA13-24-11	25.0	19.9	42.1	29.0
KMA13-24-16	38.5	17.6	36.1	30.8
KMA13-24-17	36.4	30.3	45.2	37.3
KMA13-27-25	24.1	9.9	34.6	22.9
KMA13-28-03	26.5	8.5	58.5	31.2
KMA13-28-13	33.9	31.5	51.8	39.1
KMA13-29-21	-	24.4	63.4	37.4
KMA13-29-24	38.4	14.1	68.4	40.3
KMA13-32-24	47.2	9.4	41.3	32.6
KMA13-32-28	36.1	28.5	65.5	43.4
BRB 191	29.4	77.0	43.2	49.9
Mean	33.7	23.8	48.1	35.1
CV (%)	57.1			
$LSD_{0.05}$: Line=16.1, Site=7.0, Line x site=27.9				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.40. Harvest index (in %) of small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	42.9	18.8	64.9	42.2
KMA13-22-29	49.9	41.7	55.5	49.1
KMA13-23-14	40.6	34.5	71.6	48.9
KMA13-23-21	23.8	26.2	38.2	29.4
KMA13-25-09	33.0	22.8	56.4	37.4
KMA13-28-13	51.6	23.1	45.4	40.1
KMA13-30-02	37.3	59.6	53.8	50.2
KMA13-30-14	41.6	10.8	77.4	43.3
KMA13-30-16	39.3	30.5	65.0	44.9
KMA13-30-30	33.8	49.7	50.4	44.6
KMA13-31-01	41.2	36.5	53.8	43.8
KMA13-31-03	38.5	61.5	54.5	51.5
KMA13-31-04	49.7	68.0	63.8	60.5
KMA13-31-05	43.1	73.2	59.4	58.6
KMA13-31-06	46.0	66.9	64.6	59.2
KMA13-31-08	45.9	35.3	66.5	49.2
KMA13-31-09	45.3	32.4	51.2	43.0
KMA13-32-26	35.4	52.2	54.1	46.2
KMA13-32-28	41.4	35.5	82.6	53.2
RWR719	19.9	13.4	54.2	29.1
G10909	44.9	20.5	72.8	46.1
G2333	47.7	20.2	64.4	44.1
GLP585	31.7	23.0	69.7	41.4
KATB9	67.0	72.1	60.2	66.4
Mean	41.3	38.4	60.4	46.8
CV (%)	22.7			
$LSD_{0.05}$: Line=8.5, Site=3.0, Line x site=14.7				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.41. Harvest index (in %) of advanced mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	53.7	22.0	67.0	41.1
KMA13-21-23	47.4	21.3	52.8	36.4
KMA13-22-16	24.6	28.7	54.5	29.7
KMA13-22-23	49.0	8.5	76.0	41.3
KMA13-22-321	38.3	12.6	40.3	27.1
KMA13-22-322	34.4	17.4	61.8	33.5
KMA13-23-09	36.4	20.8	45.3	30.5
KMA13-23-10	44.9	17.9	56.1	34.1
KMA13-23-11	42.5	15.8	35.8	31.4
KMA13-23-20	51.7	43.4	50.4	47.8
KMA13-24-10	53.2	27.3	48.0	39.9
KMA13-25-01	49.4	35.5	69.4	48.3
KMA13-25-04	52.0	29.2	57.2	46.1
KMA13-27-01	53.4	33.9	65.2	46.1
KMA13-27-101	37.1	72.7	58.6	55.3
KMA13-27-102	42.2	36.9	56.1	41.4
KMA13-27-12	37.7	10.1	63.2	33.4
KMA13-27-13	39.7	12.8	61.0	30.1
KMA13-27-14	34.1	17.9	57.6	29.5
KMA13-27-27	50.3	19.3	76.6	39.5
KMA13-28-05	49.9	46.0	60.1	52.0
KMA13-28-13	55.8	37.2	55.0	49.3
KMA13-28-21	56.9	33.2	75.6	52.8
KMA13-28-22	51.2	42.5	55.9	49.9
KMA13-28-29	33.2	16.2	37.0	24.7
KMA13-29-19	49.8	16.3	73.9	37.6
KMA13-29-21	43.7	36.1	58.9	42.0
KMA13-30-07	31.3	16.0	37.0	28.1
KMA13-31-61	51.3	27.7	58.4	41.6
KMA13-31-62	40.7	32.2	45.1	36.5
KMA13-32-22	44.3	61.7	88.4	55.6
KMA13-32-24	38.4	6.8	49.9	31.0
KATB1	60.7	15.7	54.9	47.0
MEX54	44.9	26.9	67.0	46.3
Mean	44.8	27.4	61.3	39.1
CV (%)	13.9			
$LSD_{0.05}$: Line=4.8, Site=1.4, Line x site=8.3				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

4.3.1.9. Seed yield

There were significant differences for seed yield among the advanced pinto lines due to the site (*P<0.001*), genotype (*P<0.01*) and to the interaction between the genotype and the site (*P<0.01*). There was a great variability in seed yield across sites. The best yields were recorded at Tigoni (4,346.9 kg ha^{-1}) while the lowest yields were obtained on crops grown at Mwea (585.6 kg ha^{-1}) (Table 4.42). Lines KMA13-22-21 (2,747.6 kg ha^{-1}) and KMA13-22-30 (2,725.9 kg ha^{-1}) were the best yielding among advanced lines across sites. However, their yields were not significantly different from that of the check variety GLP92 (2,543.1 kg ha^{-1}). All other advanced lines were either equal or inferior to the check variety.

Table 4.43 shows that there were highly significant differences for the seed yield among advanced red kidney lines grown at Kabete, Mwea and Tigoni due to the genotypes, sites and the interactions between the genotypes and sites (*P<0.001*). Among sites, the highest seed yields were recorded at Tigoni in the high altitude conditions (4,641.8 kg ha^{-1}). The lowest yields were obtained at low altitude Mwea site. The mean yield at Mwea was 954.1 kg ha^{-1}. KMA13-30-22 (3,225.8 kg ha^{-1}) was the best yielding line. However, the yield of this line was not significantly different from best check variety Mex54 (3,722.4 kg ha^{-1}). Other high yielding lines were KMA13-21-11 (2,447.5 kg ha^{-1}), KMA13-26-32 (2,369.8 kg ha^{-1}) but which were not statistically different from the other check variety AND 1062 (2,265.5 kg ha^{-1}). All other advanced lines were either equal or inferior to check varieties.

There were highly significant differences for the seed yield among the advanced red mottled lines due to the genotypes, sites and to the interactions between the genotypes and sites (*P<0.001*). Among sites, crops grown at Tigoni gave the highest seed yield (4,623.2 kg ha^{-1}), which was significantly higher than 1,254.3 kg ha^{-1} at Kabete, and 550.9 kg ha^{-1} at Mwea. Among advanced lines, KMA13-29-21 had the highest seed yield (3,269.7 kg ha^{-1}). KMA13-24-11 had the lowest seed yield (1,324.1 kg ha^{-1}) and was the only advanced line inferior to the check variety BRB191 (1,351.6 kg ha^{-1}). However, the yield difference between KMA13-24-11 and check variety was not statistically significant. All other fifteen red mottled lines were superior to that check variety (Table 4.44).

Results on small red lines revealed highly significant differences for the seed yield among advanced lines grown at Kabete, Mwea and Tigoni due to the genotypes, sites and to the

interactions between genotypes and sites (*P<0.001*) (Table 4.45). Among sites, Tigoni produced the highest seed yield (3,808.6 kg ha^{-1}), which was significantly higher than the grain yield at Kabete (1,100.1 kg ha^{-1}) and Mwea (1,051.1 kg ha^{-1}). Differences in seed yield for Kabete and Mwea were not significant. KMA13-25-09 (3,385.2 kg ha^{-1}) and KMA13-23-14 (3,021.6 kg ha^{-1}) were the best yielding lines and were superior to all the other lines and to all the check varieties. All the other lines were either statistically equal or inferior to the best check variety G2333 (2,900.7 kg ha^{-1}).

For the mixed color market class, there were highly significant differences for the seed yield among test lines due to the genotypes, sites and to the interaction between the genotypes and sites (*P<0.001*). The highest yields were recorded at Tigoni (2,687.9 kg ha^{-1}), higher compared to Kabete (1,797.6 kg ha^{-1}) and Mwea (791.2 kg ha^{-1}). Among advanced lines, KMA13-28-21 (3,010.0 kg ha^{-1}) was the best yielding. The other higher yielding lines were KMA13-27-27 (2,823.7 kg ha^{-1}) and KMA13-27-12 (2,012.4 kg ha^{-1}) but all were inferior to the best check variety Mex54 (3,722.4 kg ha^{-1}) (Table 4.46).

Table 4.42. Seed yield (in kg ha^{-1}) of pinto advanced $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-10	1,416.6	981.6	4,456.3	2,284.8
KMA13-21-19	1,181.7	891.0	2,481.2	1,518.0
KMA13-22-03	1,428.4	297.0	3,413.8	1,713.1
KMA13-22-07	1,160.0	450.8	3,274.7	1,628.5
KMA13-22-21	1,814.0	608.8	5,819.9	2,747.6
KMA13-22-30	1,307.1	434.8	6,435.7	2,725.9
KMA13-22-33	1,423.1	453.1	3,450.6	1,775.6
KMA13-23-13	1,449.7	514.5	4,129.1	2,031.1
KMA13-23-18	1,504.5	513.5	3,723.8	1,913.9
KMA13-23-22	1,261.0	592.8	5,225.8	2,359.9
KMA13-24-06	1,223.9	528.1	4,282.8	2,011.6
KMA13-24-07	1,005.6	370.3	5,031.3	2,135.8
GLP92	1,868.3	976.3	4,784.6	2,543.1
Mean	1,388.0	585.6	4,346.9	2,106.8
CV (%)	42.4			
$LSD_{0.05}$: Line=722.2, Site=346.9, Line x site=1,251.0				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.43. Seed yield (in kg ha^{-1}) of advanced red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-17-25	1,403.3	794.8	4,144.2	2,114.1
KMA13-19-12	1,020.5	477.3	3,111.9	1,536.6
KMA13-19-16	1,248.0	903.0	4,616.4	2,255.8
KMA13-20-03	806.4	700.2	4,343.1	1,949.9
KMA13-21-11	2,303.2	750.0	4,289.3	2,447.5
KMA13-25-03	762.0	1,079.0	3,826.7	2,114.7
KMA13-25-20	1,120.3	884.6	4,513.8	2,172.9
KMA13-26-32	1,350.1	1,156.0	4,603.1	2,369.8
KMA13-27-31	1,119.9	1,113.7	4,173.1	2,135.6
KMA13-28-02	1,192.5	882.7	4,877.9	2,317.7
KMA13-29-28	727.1	689.8	3,947.7	1,788.2
KMA13-29-30	1,225.9	703.3	4,208.4	2,045.9
KMA13-30-22	1,595.3	942.1	7,139.9	3,225.8
AND 1062	1,428.9	762.7	4,604.9	2,265.5
MEX54	1,468.8	2,472.7	7,225.8	3,722.4
Mean	1,268.4	954.1	4,641.8	2,299.5
CV (%)	28.9			
$LSD_{0.05}$: Line=543.2, Site=251.5, Line x site=940.9				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.44. Seed yield (in kg ha^{-1}) of advanced red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Lines	Kabete	Mwea	Tigoni	Mean
KMA13-17-17	1,968.3	341.9	5,264.2	2,524.8
KMA13-17-25	1,583.7	256.6	4,274.2	2,038.2
KMA13-20-03	1,238.6	649.8	3,443.6	1,777.3
KMA13-20-14	1,037.8	151.3	4,416.9	1,868.7
KMA13-22-25	1,191.7	292.1	3,429.0	1,637.6
KMA13-24-05	1,551.3	487.5	5,937.6	2,658.8
KMA13-24-11	687.0	593.9	2,691.5	1,324.1
KMA13-24-16	1,493.8	350.5	4,636.7	2,160.3
KMA13-24-17	1,082.1	608.9	6,122.9	2,604.6
KMA13-27-25	645.0	991.4	5,297.0	2,311.1
KMA13-28-03	872.4	491.8	5,739.1	2,367.7
KMA13-28-13	1,228.7	245.8	3,398.6	1,624.4
KMA13-29-21	-	939.4	7,930.5	3,269.7
KMA13-29-24	1,288.0	791.8	5,838.7	2,639.5
KMA13-32-24	1,599.7	671.2	4,123.1	2,131.3
KMA13-32-28	1,422.7	1,236.9	5,092.3	2,584.0
BRB 191	1,178.1	263.9	2,612.8	1,351.6
Mean	1,254.3	550.9	4,623.2	2,135.7
CV (%)	34.4			
$LSD_{0.05}$: Line=583.8, Site=252.8, Line x site=1,011.3				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.45. Seed yield (in kg ha^{-1}) of the small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-22-27	701.6	399.3	5,095.6	2,065.5
KMA13-22-29	783.6	648.2	2,960.2	1,464.0
KMA13-23-14	1,202.8	1,779.1	6,083.0	3,021.6
KMA13-23-21	1,090.3	1,440.5	3,357.6	1,962.8
KMA13-25-09	1,362.3	1,983.5	6,809.8	3,385.2
KMA13-28-13	862.9	515.3	2,636.5	1,338.2
KMA13-30-02	850.7	705.6	3,506.3	1,687.5
KMA13-30-14	1,364.4	905.1	6,090.4	2,786.6
KMA13-30-16	1,553.2	2,267.3	4,198.8	2,673.1
KMA13-30-30	848.9	603.8	1,579.1	1,010.6
KMA13-31-01	961.4	1,496.7	3,975.0	2,144.4
KMA13-31-03	943.0	708.9	2,150.7	1,267.6
KMA13-31-04	906.2	1,354.2	3,678.6	1,979.7
KMA13-31-05	1,091.9	1,525.1	4,320.1	2,312.4
KMA13-31-06	1,100.4	1,205.7	4,340.1	2,215.4
KMA13-31-08	1,049.7	805.9	2,278.7	1,378.1
KMA13-31-09	1,124.5	477.0	2,175.5	1,259.0
KMA13-32-26	660.8	518.4	2,199.9	1,248.0
KMA13-32-28	1,048.8	1,702.1	4,606.9	2,452.6
RWR719	700.5	505.3	2,192.6	1,132.8
G10909	1,744.3	597.1	4,186.7	2,176.0
G2333	1,938.6	1,356.3	5,407.4	2,900.7
GLP585	1,079.3	858.7	4,676.0	2,204.7
KATB9	1,431.3	601.4	2,901.9	1,644.9
Mean	1,100.1	1,051.1	3,808.6	1,993.2
CV (%)	39.8			
$LSD_{0.05}$: Line=632.7, Site=223.7, Line x site=1,095.9				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

Table 4.46. Seed yield (in kg ha^{-1}) for the advanced mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Line	Kabete	Mwea	Tigoni	Mean
KMA13-21-20	2,610.4	1,027.0	3,348.4	1,988.7
KMA13-21-23	1,297.1	729.8	1,760.8	1,096.5
KMA13-22-16	1,125.3	766.9	2,580.4	1,127.7
KMA13-22-23	1,268.4	611.3	3,646.5	1,420.4
KMA13-22-321	1,912.3	735.9	2,186.2	1,419.9
KMA13-22-322	1,451.3	928.1	2,481.4	1,449.0
KMA13-23-09	1,975.7	1,356.3	2,432.4	1,751.1
KMA13-23-10	1,579.9	912.5	2,405.8	1,375.0
KMA13-23-11	1,990.0	287.5	1,720.0	1,332.5
KMA13-23-20	2,265.3	895.0	2,889.7	1,725.6
KMA13-24-10	1,912.3	450.0	1,948.1	1,436.8
KMA13-25-01	2,077.1	1,087.5	2,141.3	1,803.5
KMA13-25-04	1,965.2	784.5	2,009.4	1,586.4
KMA13-27-01	1,350.5	415.8	1,263.8	925.4
KMA13-27-101	1,404.8	640.3	2,068.8	1,138.8
KMA13-27-102	2,142.3	871.4	2,173.4	1,580.9
KMA13-27-12	2,491.1	481.3	3,159.9	2,012.4
KMA13-27-13	1,205.1	444.4	2,447.7	1,005.1
KMA13-27-14	1,385.0	837.8	2,964.8	1,317.3
KMA13-27-27	1,910.4	1,104.0	5,521.0	2,823.7
KMA13-28-05	2,045.8	1,811.9	1,982.7	1,946.8
KMA13-28-13	2,467.0	838.5	2,301.4	1,869.0
KMA13-28-21	3,085.9	657.1	7,412.0	3,010.0
KMA13-28-22	2,302.0	247.9	2,121.0	1,556.9
KMA13-28-29	2,202.1	613.5	2,000.4	1,605.3
KMA13-29-19	1,483.2	902.4	2,966.7	1,389.9
KMA13-29-21	1,250.7	710.4	2,110.4	1,106.1
KMA13-30-07	1,663.5	518.0	1,894.0	1,358.5
KMA13-31-61	1,782.9	491.3	1,977.8	1,230.5
KMA13-31-62	1,434.8	1,626.2	2,906.1	1,989.0
KMA13-32-22	1,305.8	507.2	1,407.7	1,092.2
KMA13-32-24	1,430.5	52.5	2,184.1	1,144.4
KATB1	1,547.5	136.6	1,748.3	1,173.1
MEX54	1,468.8	2,472.7	7,225.8	3,722.4
Mean	1,797.6	791.2	2,687.9	1,599.3
CV (%)	18.7			
$LSD_{0.05}$: Line=255.3, Site=77.0, Line x site=442.3				

CV=coefficient of variation; LSD=least significant difference at P-value threshold of 0.05

4.3.1.10. Correlations among seed yield and yield components

Correlation analysis for pinto bean lines showed that the seed yield was highly and positively correlated to days to flowering (r=0.79***), days to maturity (r=0.65***); number of pods per plant (r=0.91***), number of seeds per pod (r=0.58***), 100-seed mass (r=0.69***) and the harvest index (r=0.64***). It was, however, negatively correlated with the seedling emergence rate (r=-0.52***) and to the plant vigor score (r=-0.68***). This would imply that the higher the number of pods per plant and the higher the number of seeds per pod, the higher the yield was. Better yielding lines were late to reach the 50% flowering stage as they contained a large number of flowers which appeared progressively. This had also an impact on the duration to maturity which was longer compared to plant developing fewer flowers and fewer pods. As the plant vigor score varied from 1 to 9 (Schoonhoven and Pastor-Corrales, 1987) with 1 being the best score, and 9 the worst, the more a plant was vigorous, the more it could carry more flowers and more pods and consequently, higher yield. Generally, the yield is positively correlated with seedling emergence rate because of better stands. But this may be lost if yield ha^{-1} is extrapolated from single plant yield, which essentially standardizes it. The negative correlation recorded in this study could, therefore, be largely due to extrapolation. If the yield per m^2 (or per plot) was considered in extrapolation regardless of the number of plants, the relationship may change (Table 4.47).

Correlation analysis for the red kidney lines showed significant and positive correlations between the seed yield and the days to flowering (r=0.77***), days to maturity (r= 0.78***), growth habit (r=0.19*), the number of pods per plant (r=0.90***), the number of seeds per pod (r=0.44***), 100-seed mass (r=0.38***) and the harvest index (0.71***). The results indicated that the number of pods per plant was strongly correlated with seed yield for the red kidney advanced lines. However, there were significant but negative correlations between the seed yield and the seedling emergence rate (r=-0.48***) and the plant vigor score (r=-0.66***). The negative correlation between yield and seedling emergence rate was largely due to extrapolation. The negative correlation between the plant vigor and grain yield suggests that the more vigorous a plant was (smaller score for plant vigor on the 1-9 CIAT scale), the better the yield would be (Table 4.48).

Table 4.49 shows that among the red mottled lines, seed yield was significantly and positively correlated with the days to flowering (r=0.68***), days to maturity (r= 0.79***), number of pods per plant (r=0.83***), number of seeds per pod (r=0.29***), 100-seed mass (r=0.35***) and the harvest index (r= 0.43***). The most important among them was the number of pods per plant. However, the seedling emergence rate (r=-0.52***) and the plant vigor (r=-0.63***) were significantly but negatively correlated to the seed yield. Results suggested that seed yield was higher in more vigorous plants. The negative correlation between yield and seedling emergence rate was largely due to extrapolation as single plant yield was used to estimate the yield ha^{-1}.

In the small red market class, seed yield was significantly and positively correlated with days to flowering (r=0.66***), days to maturity (r=0.74***), the growth habit (r=0.33***), number of pods per plant (r=0.85***), number of seeds per pod (r=0.26***), the 100-seed mass (r=0.39***) and the harvest index (r=0.47***) (Table 4.5). However, seed yield was significantly and negatively correlated with the seedling emergence rate (r=-0.40***) and the plant vigor (r=-0.66***).

Similar results were obtained for the mixed color lines. The results showed that seed yield was significantly and positively correlated with days to flowering (r=0.57***); days to maturity (r=0.61***); number of pods per plant (r=0.77***); number of seeds per pod (r=0.19***), 100-seed mass (r=0.39***) and the harvest index (r=0.62***) (Table 4.51). However, unlike other market classes, seed yield was positively associated with seedling emergence rate (r=0.28***). From these results, it can be concluded that high yielding lines had more pods per plant, took longer to flower and to mature, had larger seeds and a higher harvest index and consequently, higher the seed yield. The association between seed yield and plant vigor in mixed color lines was negative but not significant.

Looking at the correlation between growth habit and yield and yield components such as pods per plant, it has been observed heterogeneity among market classes. There were negative but no significant correlations between the growth habit and the seed yield ($r=-0.05^{ns}$) and between the growth habit and the number of pods per plant ($r=-0.06^{ns}$) for the pinto bean lines. However, the trend was different for other market classes for which the growth habit was positively correlated with the seed yield and the number of pods per plant. The correlation was stronger between the growth habit and the seed yield (r=0.33***) and between the growth habit and the number of

pods per plant (r=0.17**) on small red bean lines. The growth habit was positively but not significantly correlated with the seed yield (r= 0.04^{ns}) for the red mottled market class. However, the correlation between the growth habit and the number of pods on red mottled was positive and significant (r=0.14*). The trend was the same on red kidney lines for which the correlations were significant and positive between the growth habit and the seed yield (r=0.20*) and between the growth habit and the number of pods per plant (r=0.24**). This study reflected the general assumption that yield increases with growth habit such that type IVs (climbers) are the best yielding.

Table 4.47. Pearson's correlation coefficients among seed yield and yield components of pinto $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Parameters	SER	DTF	DTM	GH	PP	SP	VIG	100SW	HI
DTF	-0.48***								
DTM	-0.56***	0.68***							
GH	0.15^{ns}	-0.08^{ns}	0.00^{ns}						
PP	-0.46***	0.81***	0.56***	-0.06^{ns}					
SP	-0.24**	0.52***	0.19*	-0.00^{ns}	0.58***				
VIG	0.21**	-0.76***	-0.52***	-0.10^{ns}	-0.69***	-0.49***			
100SW	-0.41***	0.69***	0.74***	-0.05^{ns}	0.64***	0.26**	-0.57***		
HI	-0.16*	0.59***	0.13^{ns}	-0.16^{ns}	0.68***	0.61***	-0.58***	0.27**	
SY	-0.52***	0.79***	0.65***	-0.05^{ns}	0.91***	0.58***	-0.68***	0.69***	0.64***

Abbreviations: SER, seedling emergence rate (in %); DTF, days to flowering; DTM, days to maturity; GH, growth habit; PP, number of pods per plant; SP, number of seeds per plant; VIG, plant vigor; 100SW,100-seed mass (in g); HI, harvest index (in %) and SY, seed yield (in kg ha^{-1}). *, **, ***Significant at P = 0.05, 0.01, or 0.001, respectively.

Table 4.48. Pearson's correlation coefficients among seed yields and seed components for red kidney $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Parameters	SER	DTF	DTM	GH	VIG	PP	SP	100SW	HI
DTF	-0.39***								
DTM	-0.31***	0.90***							
GH	0.10^{ns}	0.01^{ns}	0.09^{ns}						
VIG	0.21**	-0.69***	-0.70***	-0.04^{ns}					
PP	-0.43***	0.68***	0.70***	0.24**	-0.59***				
SP	-0.18*	0.16*	0.25**	0.16*	-0.29**	0.45***			
100SW	-0.07^{ns}	0.41***	0.43***	-0.05^{ns}	-0.51***	0.19*	-0.02^{ns}		
HI	-0.23**	0.64***	0.73***	0.08^{ns}	-0.50***	0.68***	0.49***	0.25***	
SY	-0.48***	0.77***	0.78***	0.20*	-0.66***	0.90***	0.44***	0.38***	0.71***

Abbreviations: SER, seedling emergence rate (in %); DTF, days to flowering; DTM, days to maturity; GH, growth habit; PP, number of pods per plant; SP, number of seeds per plant; VIG, plant vigor; 100SW,100-seed mass (in g); HI, harvest index (in %) and SY, seed yield (in kg ha^{-1}). *, **, ***Significant at P = 0.05, 0.01, or 0.001, respectively.

Table 4.49. Pearson's correlation coefficients among seed yield and yield components for the advanced red mottled $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Parameters	SER	DTF	DTM	GH	VIG	PP	SP	100SW	HI
DTF	-0.47***								
DTM	-0.41***	0.84***							
GH	0.02^{ns}	0.00^{ns}	-0.02^{ns}						
VIG	0.12^{ns}	-0.48***	-0.58***	0.06^{ns}					
PP	-0.52***	0.64***	0.69***	0.14*	-0.57***				
SP	-0.28***	0.29***	0.28***	0.37***	-0.22**	0.38***			
100SW	0.03^{ns}	0.23**	0.37***	-0.22**	-0.15*	0.19**	0.05^{ns}		
HI	-0.27***	0.23**	0.25***	-0.13^{ns}	-0.15*	0.30***	0.05^{ns}	0.15*	
SY	-0.52***	0.68***	0.79***	0.04^{ns}	-0.63***	0.83***	0.29***	0.35***	0.43***

Abbreviations: SER, seedling emergence rate (in %); DTF, days to flowering; DTM, days to maturity; GH, growth habit; PP, number of pods per plant; SP, number of seeds per plant; VIG, plant vigor; 100SW,100-seed mass (in g); HI, harvest index (in %) and SY, seed yield (in kg ha^{-1}). *, **, ***Significant at P = 0.05, 0.01, or 0.001, respectively.

Table 4.50. Pearson's correlation coefficients among seed yield and yield components for the advanced small red $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Parameters	SER	DTF	DTM	GH	VIG	PP	SP	100SW	HI
DTF	-0.30***								
DTM	-0.29***	0.86***							
GH	-0.07^{ns}	-0.07***	0.29***						
VIG	0.22***	-0.51***	-0.52***	-0.25***					
PP	-0.41***	0.67***	0.70***	0.17**	-0.66***				
SP	-0.05ns	0.14*	0.29***	0.37***	-0.11^{ns}	0.13*			
100SW	-0.09ns	0.29***	0.37***	0.10^{ns}	-0.36***	0.31***	-0.18**		
HI	-0.16**	0.37***	0.39***	-0.10^{ns}	-0.32***	0.44***	0.09^{ns}	0.04^{ns}	
SY	-0.40***	0.66***	0.74***	0.33***	-0.66***	0.85***	0.26***	0.39***	0.47***

Abbreviations: SER, seedling emergence rate (in %); DTF, days to flowering; DTM, days to maturity; GH, growth habit; PP, number of pods per plant; SP, number of seeds per plant; VIG, plant vigor; 100SW,100-seed mass (in g); HI, harvest index (in %) and SY, seed yield (in kg ha^{-1}). *, **, ***Significant at P = 0.05, 0.01, or 0.001, respectively.

Table 4.51. Pearson's correlation coefficients among seed yield and yield components of mixed color $F_{1.7}$ bean lines grown at Kabete, Mwea and Tigoni during the 2017 short rain season

Parameters	SER	DTF	DTM	VIG	PP	SP	100SW	HI
DTF	0.31***							
DTM	0.40***	0.82***						
VIG	-0.32***	0.23***	0.14**					
PP	0.16**	0.45***	0.49***	-0.00^{ns}				
SP	0.04^{ns}	0.18***	0.18***	0.00^{ns}	0.20***			
100SW	0.28***	0.28***	0.37***	-0.08^{ns}	0.22***	-0.20***		
HI	0.33***	0.51***	0.53***	-0.01^{ns}	0.45***	0.08^{ns}	0.40***	
SY	0.28***	0.57***	0.61***	-0.05^{ns}	0.77***	0.19***	0.39***	0.62***

Abbreviations: SER, seedling emergence rate (in %); DTF, days to flowering; DTM, days to maturity; GH, growth habit; PP, number of pods per plant; SP, number of seeds per plant; VIG, plant vigor; 100SW,100-seed mass (in g); HI, harvest index (in %) and SY, seed yield (in kg ha^{-1}). *, **, ***Significant at P = 0.05, 0.01, or 0.001, respectively.

4.3.2. Genotype-environment interactions and yield stability

4.3.2.1. ANOVA of Main effects and Multiplicative Interaction (AMMI)

Analysis of the main effects and multiplicative interaction (AMMI) for the pinto bean lines showed that the effects on seed yield of genotypes (G) (*P<0.01*), environments (E) (*P<0.001*) and the interactions between genotypes and environments (G x E) (*P<0.01*) were significant (Table 4.52). Treatments (G, E, and G x E) contributed up to 83.7% to the total variability of seed yield with the environment making the highest contribution to the observed variation (86.4%). The variability due to genotypes and interaction between genotypes and environments were 5.0% and 8.6%, respectively. Genotype contributed 96.2% of the variability (IPCA1) in the interaction between genotype and environment (G x E) among the pinto bean lines.

Among the red kidney lines, the effects on seed yield due to genotypes, environments and to the interaction between genotypes and environments were highly significant (*P<0.001*). Treatments (G, E, and G x E) were responsible for up to 90.8% of the seed yield variability. When partitioning the treatment variability, the environment contributed most to the variance (84.8%), followed by the genotype (8.5%) and the G x E interaction (6.7%). IPCA1 contributed the most to the G x E effects covering up to 79.7% of the variability, suggesting a high contribution of the genotypes in the interaction (Table 4.53).

The effects on seed yield due to genotypes, environments and the interactions between genotypes and environments on red mottled lines were also highly significant (*P<0.001*). The contribution due to treatments (G, E and G x E) was high and accounted for 91.3% of the total variation. The partition of the treatments variability showed that most of the variability for seed yield was due to environments (82.3%). The contributions of genotypes and the interaction between genotypes and environments were 9.1% and 8.6%, respectively. IPCA1 contributed the most to the G x E effects on seed yield (84.5%) revealing an important role of genotypes in the interaction (Table 4.54).

Table 4.55 shows that the effects of the genotypes, environments and the interactions between genotypes and the environments on the small red lines seed yields were highly significant (*P<0.001*). Treatments contribution to the total variability was 91.1% from which 68.0% was contributed by the environments while 17.6% and 14.4% of treatment variability were contributed by the genotypes and the interactions between genotypes and environments. IPCA1 accounted for 88.9% of the G x E effects for seed yield.

The effects of genotypes, environments and their interaction significantly influenced the grain yield of the mixed color lines (*P<0.001*). They accounted for 93.2% of the total variability. By partitioning that treatment variability, it was found that the highest contribution was from the environment (49.5%) which was followed by the interaction between genotypes and environments (26.7%). The least contribution was from the genotypes (23.7%). This high contribution of variability due to the interaction between genotypes and environments suggests that tested lines were not stable and thus responded differently across locations. Genotypes should, therefore, be selected and recommended to specific environments. IPCA1 contributed the most to the G x E effects on seed yield (82.9%)(Table 4.56).

Table 4.52. Summary of ANOVA for Additive Main effects and Multiplicative Interaction (AMMI) for seed yield (kg ha^{-1}) of advanced pinto bean lines grown at three locations during the 2017 short rain season.

Source of variation	df	MS	% CTV	% CGxE
Total	155	3642323		
Treatments (G,E,GxE)	38	12429868***	83.7	
Genotypes (G**)**	12	1972916**	5.0	
Environments (E)	2	204067922***	86.4	
Interactions (GxE)	24	1688507**	8.6	
IPCA1	13	2998943***	6.9	96.2
IPCA2	11	139810^{ns}	0.3	3.8
Replications	9	578563^{ns}	0.9	
Error	108	805722		

Legend: : ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively; d.f. = degree of freedom; IPCA1 and IPCA2 = interaction principal component one and two, respectively; MS = mean squares; % CTV = percent of contribution to the total variation; % CGxE = percent of the contribution to the G x E interaction.

Table 4.53. Summary of ANOVA for Additive Main effects and Multiplicative Interaction (AMMI) for seed yield (kg ha^{-1}) of advanced red kidney bean lines grown at three locations during the 2017 short rain season.

Source of variation	df	MS	% CTV	% CGxE
Total	179	3666741		
Treatments (G,E,GxE)	44	13545634***	90.8	
Genotypes (G)	14	3637379***	8.5	
Environments (E)	2	252676724***	84.8	
Interactions (GxE)	28	1418969***	6.7	
IPCA1	15	2111182***	4.8	79.7
IPCA2	13	620262^{ns}	1.2	20.3
Replications	9	680006^{ns}	0.9	
Error	124	437248		

Legend: : ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively; d.f. = degree of freedom; IPCA1 and IPCA2 = interaction principal component one and two, respectively; MS = mean squares; % CTV = percent of contribution to the total variation; % CGxE = percent of the contribution to the G x E interaction

Table 4.54. Summary ANOVA for Additive Main effects and Multiplicative Interaction (AMMI) for seed yield (kg ha^{-1}) of advanced red mottled bean lines grown at three locations during the 2017 short rain season.

Source of variation	df	MS	% CTV	% CGxE
Total	203	4322943		
Treatments (G,E,GxE)	50	16018795***	91.3	
Genotypes (G)	16	4554833***	9.1	
Environments (E)	2	329566654***	82.3	
Interactions (GxE)	31	2223519***	8.6	
IPCA1	17	3426531***	6.6	84.5
IPCA2	15	711872^{ns}	1.2	15.5
Replications	9	865981^{ns}	0.9	
Error	139	495136		

Legend: : ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively; d.f. = degree of freedom; IPCA1 and IPCA2 = interaction principal component one and two, respectively; MS = mean squares; % CTV = percent of contribution to the total variation; % CGxE = percent of the contribution to the G x E interaction

Table 4.55. Summary of ANOVA for Additive Main effects and Multiplicative Interaction (AMMI) for seed yield (kg ha^{-1}) of advanced small red bean lines grown at three locations during the 2017 short rain season.

Source of variation	df	MS	% CTV	%CGxE
Total	287	3097461		
Treatments (G,E,GxE)	71	10002229***	79.9	
Genotypes (G)	23	5438645***	17.6	
Environments (E)	2	241460323***	68.0	
Interactions (GxE)	46	2220626***	14.4	
IPCA1	24	3785111***	10.2	88.9
IPCA2	22	513916^{ns}	1.3	11.1
Replications	9	10229384^{ns}	10.3	
Error	205	423163		

Legend: : ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively; d.f. = degree of freedom; IPCA1 and IPCA2 = interaction principal component one and two, respectively; MS = mean squares; % CTV = percent of contribution to the total variation; % CGxE = percent of the contribution to the G x E interaction

Table 4.56. Summary of ANOVA for Additive Main effects and Multiplicative Interaction (AMMI) for seed yield (kg ha^{-1}) of advanced mixed color bean lines grown at three locations during the 2017 short rain season.

Source of variation	df	MS	% CTV	% CGxE
Total	395	1194115		
Treatments (G,E,GxE)	98	4486728***	93.2	
Genotypes (G)	32	3260277***	23.7	
Environments (E)	2	108945864***	49.5	
Interactions (GxE)	64	1835605***	26.7	
IPCA1	33	2952261***	20.6	82.9
IPCA2	31	646908***	4.2	17.1
Replications	9	383306^{ns}	0.7	
Error	288	99050		

Legend: : ^{ns}, *, ** and *** = no significant, significant, highly significant and very highly significant at P-value tresholds of P>0.05, <0.05, <0.01 and <0.001, respectively; d.f. = degree of freedom; IPCA1 and IPCA2 = interaction principal component one and two, respectively; MS = mean squares; % CTV = percent of contribution to the total variation; % CGxE = percent of the contribution to the G x E interaction

4.3.2.2. Stability analysis

This section presents results generated by the AMMI analysis. As stated in the method section, this model combines the additive effects of the analysis of variance with the multiplicative effects of the principal components analysis of the genotype by environment interaction. This allowed to clearly separating main and interaction effects and, thus providing a meaningful interpretation of data for genotype stability. Results have been presented and interpreted separately for each market class to avoid confusion from readers. Means of seed yield were presented and ranked to determine the most productive genotypes across environments. AMMI stability values are also provided to determine genotypes with wider adaptation and those adapted to specific environments. In this section, the focus is on environments rather than sites. Sites represent environments. It is assumed that these sites are representatives of mega-environments. We are, therefore, trying to identify genotypes adapted to specific environments and those with wide adaptation in more than one environment.

4.3.2.2.1. Pinto lines

The AMMI model showed that the highest seed yields of pinto bean lines across sites were recorded at Tigoni in the high altitude (4,347 kg ha^{-1}), followed by Kabete in medium altitude (1,388 kg ha^{-1}) whereas the lowest yields were from Mwea located in the low altitude (585.6 kg ha^{-1}) (Table 4.57). Across sites, the genotypes KMA13-22-21 (P5) and KMA13-22-30 (P6) were

the best yielding with 2,748 kg ha^{-1} and 2,726 kg ha^{-1}, respectively, but not significantly different from the check variety GLP92 (P13) which yielded 2,543 kg ha^{-1}. All the other lines were either statistically equal or inferior to the check variety.

The AMMI stability value (ASV) of pinto bean lines showed that the check variety GLP92 (P13) was the most stable across sites (ASV=3.5). Among advanced lines, KMA13-24-6 (P11) and KMA13-21-10 (P1) were the most stable genotypes across sites with ASV of 15.6 and 45.8, respectively. KMA13-22-30 (P6) was the least stable across sites (ASV=816.7). The first four AMMI selections per environment were KMA13-21-10 (P1), GLP92 (P13), KMA13-21-19 (P2) and KMA13-22-21 (P5) for low altitudes; GLP92 (P13), KMA13-22-21 (P5), KMA13-23-18 (P9) and KMA13-23-13 (P8) for medium altitudes and KMA13-22-30 (P6), KMA13-22-21 (P5), KMA13-23-22 (P10) and KMA13-24-7 (P12) for the high altitude (Table 4.57).

Table 4.57. Seed yield (kg ha^{-1}), ranking (in parenthesis), IPCA scores and AMMI stability values (ASV) of advanced pinto lines grown at three locations during the 2017 short rain season.

Code	Genotype	Environments			Genotype Mean	IPCAg[1] score	IPCAg[2] score	ASV
		Kabete	Mwea	Tigoni				
P1	KMA13-21-10	1,417	982	4,456	2,285 (5)	1.8	10.2	45.8
P2	KMA13-21-19	1,182	891	2,481	1,518 (13)	28.3	11.0	717.7
P3	KMA13-22-3	1,428	297	3,414	1,713 (11)	11.6	-10.8	293.5
P4	KMA13-22-7	1,160	451	3,275	1,629 (12)	13.1	1.0	331.1
P5	KMA13-22-21	1,814	609	5,820	2,748 (1)	-18.5	-9.1	469.1
P6	KMA13-22-30	1,307	435	6,436	2,726 (2)	-32.2	2.1	816.7
P7	KMA13-22-33	1,423	453	3,451	1,776 (10)	12.2	-6.3	310.5
P8	KMA13-23-13	1,450	514	4,129	2,031 (7)	3.0	-4.2	76.5
P9	KMA13-23-18	1,504	513	3,724	1,914 (9)	9.3	-6.5	235.4
P10	KMA13-23-22	1,261	593	5,226	2,360 (4)	-13.6	5.5	344.9
P11	KMA13-24-6	1,224	528	4,283	2,012 (8)	-0.6	3.1	15.6
P12	KMA13-24-7	1,006	370	5,031	2,136 (6)	-14.2	6.5	360.7
P13	GLP92	1,868	976	4,785	2,543 (3)	-0.1	-2.5	3.5
E Mean		1,388 (2)	586 (3)	4,347 (1)	2,107			
IPCAe[1]		20.6	-18.1	-45.5				
IPCAe[2]		25.0	17.0	1.1				
ASV		521.7	633.6	1,154.7				
$LSD_{0.05}$					722.2			

Legend: IPCA 1 and IPCA 2 = interaction principal component one and two, respectively; ASV= AMMI Stability value; e=E=environment; g=genotype; LSD=least significant difference at 5% P-value threshold.

4.3.2.2.2. Red kidney lines

For the red kidney lines (Table 4.58), the highest seed yields across sites were recorded at Tigoni (4,642 kg ha^{-1}), much higher than Kabete (1,238 kg ha^{-1}) and Mwea (954 kg ha^{-1}). Mex54 (RK15) with a mean of 3,722 kg ha^{-1} out-yielded all the advanced lines and the other check variety AND1062 (RK14) which yielded 2,266 kg ha^{-1}. The best genotype among the advanced red kidney lines was KMA13-30-22 (RK13) with a seed yield of 3,226 kg ha^{-1} which was higher than all test lines and one of the check varieties, AND1062. It was not however significantly different from the best check variety (Mex54). Most of the red kidney lines were bush lines (Type I and II). This could explain why the cultivar Mex54 which has Type III growth habit (i.e semi-climber) had a significantly higher yield than most of the red kidney lines. It is known that climbers yield more than bush, and ideally should not be compared. That conclusion has been supported by findings from this study.

KMA13-19-16 (RK3), KMA13-25-20 (RK7), KMA13-20-3 (RK4) and AND1062 (RK14) were the most stable genotypes across sites with ASV of 1.5, 1.8, 5.6 and 9.5, respectively. The high yielding genotypes KMA13-30-22 (RK13) and Mex54 (RK15) were also the least stable across sites. The first four AMMI selections per environment were KMA13-21-11 (RK5), KMA13-30-22 (RK13), Mex54 (RK15), and AND1062 (RK14) for medium altitude areas such as Kabete; Mex54 (RK15), KMA13-26-32 (RK8), KMA13-27-31 (RK9), KMA13-25-3 (RK6) for low altitude agro-ecological zones such as Mwea, and Mex54 (RK15), KMA13-30-22 (RK13), KMA13-28-2 (RK10), and KMA13-19-16 (RK3) for high altitude zones such as Tigoni.

Table 4.58. Seed yield (kg ha^{-1}), ranking (in parenthesis), IPCA scores and AMMI stability values (ASV) of advanced red kidney lines grown at three locations during the 2017 short rain season.

Code	Genotype	Environments			Genotype Mean	IPCAg[1] score	IPCAg[2] score	ASV
		Kabete	Mwea	Tigoni				
RK1	KMA13-17-25	1,403	795	4,144	2,114 (10)	8.5	3.5	33.5
RK2	KMA13-19-12	1,020	477	3,112	1,537 (15)	18.5	-1	72.7
RK3	KMA13-19-16	1,248	903	4,616	2,256 (7)	0.3	1.1	1.5
RK4	KMA13-20-3	806	700	4,343	1,950 (12)	-1.2	-3	5.6
RK5	KMA13-21-11	2,303	750	4,289	2,448 (3)	15.5	19.4	64
RK6	KMA13-25-3	553	1,079	3,827	1,819 (13)	5.6	-17.4	28.1
RK7	KMA13-25-20	1,120	885	4,514	2,173 (8)	0.4	-1	1.8
RK8	KMA13-26-32	1,350	1,156	4,603	2,370 (4)	2.7	-2.6	10.8
RK9	KMA13-27-31	1,120	1,114	4,173	2,136 (9)	6.5	-7.4	26.7
RK10	KMA13-28-2	1,193	883	4,878	2,318 (5)	-4.3	1.9	17.1
RK11	KMA13-29-28	727	690	3,948	1,788 (14)	3.9	-6	16.3
RK12	KMA13-29-30	1,226	703	4,208	2,046 (11)	5.2	2.9	20.8
RK13	KMA13-30-22	1,595	942	7,140	3,226 (2)	-33.8	18	133.9
RK14	AND1062	1,429	763	4,605	2,266 (6)	1.7	6.8	9.5
RK15	MEX54	1,469	2,473	7,226	3,722 (1)	-29.5	-15.3	116.8
E Mean		1,238 (2)	954 (3)	4,642 (1)	2,278			
IPCAe[1]		29.5	12.7	-42.2				
IPCAe[2]		22.5	-29.4	6.9				
ASV		22.5	29.4	6.9				
$LSD_{0.05}$					543.2			

Legend: IPCA 1 and IPCA 2 = interaction principal component one and two, respectively; ASV= AMMI Stability value; e=E=environment; g=genotype; LSD=least significant difference at 5% P-value threshold.

4.3.2.2.3. Red mottled lines

Across environments, the highest yields for the red mottled lines were recorded from Tigoni (4,703 kg ha^{-1}), followed by Kabete (1,358 kg ha^{-1}) whereas the lowest means were from Mwea (551 kg ha^{-1}). KMA13-29-21 (RM13) with a mean seed yield of 3,860 kg ha^{-1} out-yielded all the advanced red mottled lines and the check variety BRB191 (RM4) which recorded a mean yield of 1,352 kg ha^{-1} (Table 4.59). Among the red mottled advanced lines, only KMA13-24-11 (RM6) yielded lower than the check variety but the difference was not significant (1,324.0 kg ha^{-1}) (Table 4.59).

KMA13-20-14 (RM3) and KMA13-24-16 (RM7) were the most stable genotypes across environments with ASV scores of 5.8 and 6.0, respectively. However, the best yielding line, KMA13-29-21 (RM13), was also the least stable across environments. The first four AMMI selections per environment were KMA13-24-11 (RM16), KMA13-27-25 (RM10), KMA13-29-

21 (RM13) and KMA13-29-24 (RM14) for the low altitudes agro-ecological zones; KMA13-29-21 (RM13), KMA13-17-17 (RM17), KMA13-32-24 (RM15), KMA13-17-25 (RM1) for the medium altitudes and KMA13-29-21 (RM13), KMA13-24-17 (RM8), KMA13-24-5 (RM5) and KMA13-29-24 (RM14) for the high altitudes (Table 4.59).

Table 4.59. Seed yield (kg ha^{-1}), ranking (in parenthesis), IPCA scores and AMMI stability values (ASV) of advanced red mottled bean lines grown at three locations during the 2017 short rain season.

Code	Genotype	Environments			Genotype Mean	IPCAg[1] Score	IPCAg[2] score	ASV
		Kabete	Mwea	Tigoni				
RM1	KMA13-17-25	1,584	257	4,274	2,038 (11)	4.8	9.6	27.8
RM2	KMA13-20-3	1,239	650	3,444	1,777 (13)	16.6	-2.0	90.8
RM3	KMA13-20-14	1,038	151	4,417	1,869 (12)	-1.0	1.3	5.8
RM4	BRB191	1,178	264	2,613	1,352 (16)	24.4	4.5	133.1
RM5	KMA13-24-5	1,551	487	5,938	2,659 (2)	-15.6	2.8	85.3
RM6	KMA13-24-11	687	594	2,691	1,324 (17)	23.0	-10.0	125.6
RM7	KMA13-24-16	1,494	350	4,637	2,160 (9)	0.2	5.9	6.0
RM8	KMA13-24-17	1,082	609	6,123	2,605 (4)	-19.9	-8.0	108.8
RM9	KMA13-22-25	1,192	292	3,429	1,638 (14)	13.9	3.1	76.0
RM10	KMA13-27-25	645	991	5,297	2,311 (8)	-8.7	-21.2	51.9
RM11	KMA13-28-3	872	492	5,739	2,368 (7)	-16.9	-9.3	92.7
RM12	KMA13-28-13	1,229	246	3,399	1,624 (15)	14.2	4.6	77.6
RM13	KMA13-29-21	3,012	939	7,630	3,860 (1)	-26.1	19.4	144.0
RM14	KMA13-29-24	1,288	792	5,839	2,640 (3)	-13.6	-6.9	74.5
RM15	KMA13-32-24	1,600	671	4,123	2,131 (10)	9.9	3.2	54.3
RM16	KMA13-32-28	1,423	1,237	5,092	2,584 (5)	0.3	-10.9	11.0
RM17	KMA13-17-17	1,968	342	5,264	2,525 (6)	-5.4	13.8	32.6
E Mean		1,358 (3)	551 (2)	4,703 (1)	2,204			
IPCAe[1]		22.1	28.2	-50.3				
IPCAe[2]		29.7	27.3	-2.3				
ASV		124.2	156.2	274.4				
$LSD_{0.05}$					583.8			

Legend: IPCA 1 and IPCA 2 = interaction principal component one and two, respectively; ASV= AMMI Stability value; e=E=environment; g=genotype; LSD=least significant difference at 5% P-value threshold.

4.3.2.2.4. Small red lines

Table 4.60 shows that the best yields across sites for the small red lines were recorded at Tigoni (3,809 kg ha^{-1}) followed by Kabete (1,100 kg ha^{-1}). Mwea was the least productive site (1,025 kg ha^{-1}). However, yield differences between the Kabete and Mwea sites were not significant. Among lines, KMA13-25-9 (SR5) with a yield of 3,385 kg ha^{-1}, and KMA13-23-14 (SR3) with a yield of 3,022 kg ha^{-1} were the best yielding genotypes. These two lines had higher grain yield compared to all the other lines and the five check varieties. Their yield advantage compared with

the best check was 10.4%. All other lines had grain yield that was either statistically equal to or lower than the check varieties. The best check variety was G2333 (a climber, also known as Umubano) with a mean yield of 2,901 kg ha^{-1}. The least productive line was KMA13-32-26) (SR18) (1,005 kg ha^{-1}). It had a lower grain yield than all the other lines and all the check varieties.

KMA13-30-2 (SR7) was the most stable line across environments (ASV score of 1.2). Other stable genotypes were KMA13-31-6 (SR15), KMA13-22-29 (SR2), KMA13-31-5 (SR14) and KMA13-31-4 (SR13) with ASV scores of 6.0, 6.2, 9.0 and 9.6, respectively. However, the best yielding line KMA13-25-9 (SR5) was also the least stable line across sites. The first four AMMI selections per environment were G2333, G10909, KMA13-30-16 (SR9), KATB9 for medium altitudes; KMA13-30-16 (SR9), KMA13-25-9 (SR5), KMA13-23-14 (SR3), KMA13-32-28 (SR19) for low altitudes, and KMA13-25-9 (SR5), KMA13-30-14 (SR8), KMA13-23-14 (SR3) and G2333 for high altitude zones.

Table 4.60. Seed yield (kg ha^{-1}), ranking (in parenthesis), IPCA scores and AMMI stability values (ASV) of advanced small red lines grown at three locations during the 2017 short rain season.

Code	Genotype	Environments			Genotype Mean	IPCAg[1] Score	IPCAg[2] score	ASV
		Kabete	Mwea	Tigoni				
SR1	KMA13-22-27	702	399	5,096	2,066 (12)	-20.9	7.6	23.2
SR2	KMA13-22-29	784	648	2,960	1,464 (17)	6.0	0.0	6.2
SR3	KMA13-23-14	1,203	1,779	6,083	3,022 (2)	-22.4	-7.4	24.6
SR4	KMA13-23-21	1,090	1,440	3,358	1,963 (14)	7.2	-8.6	11.5
SR5	KMA13-25-9	1,362	1,984	6,810	3,385 (1)	-28.9	-7.1	31.0
SR6	KMA13-28-13	863	515	2,636	1,338 (19)	9.7	3.0	10.6
SR7	KMA13-30-2	851	706	3,506	1,688 (15)	0.3	1.2	1.2
SR8	KMA13-30-14	1,364	905	6,090	2,787 (4)	-25.6	11.1	29.0
SR9	KMA13-30-16	1,553	2,267	4,199	2,673 (5)	4.6	-14.5	15.2
SR10	KMA13-31-1	961	1,497	3,975	2,144 (11)	-0.6	-10.5	10.5
SR11	KMA13-30-30	849	604	1,579	1,011 (23)	22.5	-0.9	23.5
SR12	KMA13-31-3	943	709	2,151	1,268 (20)	16.9	-0.2	17.7
SR13	KMA13-31-4	906	1,354	3,679	1,980 (13)	1.8	-9.4	9.6
SR14	KMA13-31-5	1,092	1,525	4,320	2,312 (7)	-3.7	-8.2	9.0
SR15	KMA13-31-6	1,100	1,206	4,340	2,215 (8)	-5.4	-2.2	6.0
SR16	KMA13-31-8	1,050	806	2,279	1,378 (18)	16.6	0.0	17.4
SR17	KMA13-31-9	1,125	477	2,176	1,259 (21)	16.7	7.0	18.9
SR18	KMA13-32-26	661	155	2,200	1,005 (24)	11.7	5.4	13.4
SR19	KMA13-32-28	1,049	1,702	4,607	2,453 (6)	-6.5	-11.5	13.4
SR20	KATB9	1,431	601	2,902	1,645 (16)	10.9	11.2	16.0
SR21	RWR719	701	505	2,193	1,133 (22)	13.7	-0.3	14.4
SR22	GLP585	1,079	859	4,676	2,205 (9)	-11.2	4.5	12.5
SR23	G10909	1,744	597	4,187	2,176 (10)	-2.1	18.9	19.1
SR24	G2333	1,939	1,356	5,407	2,901 (3)	-11.4	10.8	16.1
E Mean		1,100 (2)	1,025 (3)	3,809 (1)	1,978			
IPCAe[1]		33.0	23.0	-56.1				
IPCAe[2]		27.1	-30.6	3.4				
ASV		43.9	38.9	58.8				
$LSD_{0.05}$					632.7			

Legend: IPCA 1 and IPCA 2 = interaction principal component one and two, respectively; ASV= AMMI Stability value; e=E=environment; g=genotype; LSD=least significant difference at 5% P-value threshold.

4.3.2.2.5. Mixed color lines

The best yields for mixed color lines were obtained from Tigoni (2,550 kg ha^{-1}), followed by Kabete (1,797 kg ha^{-1}). Mwea with a mean grain yield of only 742 kg ha^{-1} was the least productive site. Among test lines, KMA13-28-21 (MC28), a black-seeded line out-yielded all the other lines and the check varieties with a mean seed yield of 3,718 kg ha^{-1}. The other high performing lines included KMA13-27-27 (MC10) with a yield of 2,845 kg ha^{-1}, KMA13-21-20 (MC32) (2,329 kg ha^{-1}), KMA13-27-12 (MC27) (2,044 kg ha^{-1}) and KMA13-23-20 (MC5) (2,017 kg ha^{-1}). The lowest yielding line was KMA13-27-1 (MC31). This line characterized by greyish green seeds had a mean yield of 1,010 kg ha^{-1}, which was lower than the greyish green seeded check variety KATB1 which yielded 1,144 kg ha^{-1}.

The most stable lines across sites were KMA13-23-20 (MC5) (ASV score of 5.7) and KMA13-22-322 (MC15) (ASV score of 8.3). KMA13-27-27 (MC10) (ASV score of 152.2) was the least stable across environments. The first four AMMI selections per environment were KMA13-28-5 (MC11), KMA13-31-62 (MC18), KMA13-23-9 (MC4) and KMA13-27-27 (MC10) for low altitudes; KMA13-28-21 (MC28), KMA13-21-20 (MC32), KMA13-27-12 (MC27), KMA13-28-13 (MC12) for medium altitudes, and KMA13-28-21 (MC28), KMA13-27-27 (MC10), KMA13-22-23 (MC21) and KMA13-21-20 (MC32) for high altitude bean growing environments (Table 4.61).

Table 4.61. Seed yield (kg ha^{-1}), ranking (in parenthesis), IPCA scores and AMMI stability values (ASV) of advanced mixed color lines grown at three locations during the 2017 short rain season.

Code	Genotype	Environments			Genotype Mean	IPCAg[1] Score	IPCAg[2] score	ASV
		Kabete	Mwea	Tigoni				
MC1	KMA13-21-23	1,297	730	1,761	1,263 (29)	6.7	6.2	33.3
MC2	KMA13-22-16	1,125	767	2,580	1,491 (21)	-3.3	11.1	19.4
MC3	KMA13-22-321	1,912	736	2,186	1,611 (17)	4.7	-2.6	22.9
MC4	KMA13-23-9	1,976	1,356	2,432	1,921 (8)	6.4	5.5	31.8
MC5	KMA13-23-20	2,265	895	2,890	2,017 (5)	-0.7	-4.6	5.7
MC6	KMA13-24-10	1,912	450	1,948	1,437 (22)	5.5	-7.1	27.4
MC7	KMA13-25-1	2,077	1,087	2,141	1,769 (12)	8.4	-0.5	40.9
MC8	KMA13-27-13	1,205	444	2,448	1,366 (25)	-3.6	5.1	18.2
MC9	KMA13-27-14	1,385	838	2,965	1,729 (14)	-6.0	8.7	30.5
MC10	KMA13-27-27	1,910	1,104	5,521	2,845 (2)	-31.3	9.2	152.2
MC11	KMA13-28-5	2,046	1,812	1,983	1,947 (7)	15.1	9.8	74.1
MC12	KMA13-28-13	2,467	838	2,301	1,869 (9)	6.6	-9.8	33.7
MC13	KMA13-29-21	1,251	710	2,110	1,357 (27)	2.3	7.4	13.5
MC14	KMA13-31-61	1,783	491	1,978	1,417 (23)	4.8	-4.4	23.7
MC15	KMA13-22-322	1,451	928	2,481	1,620 (16)	0.5	7.9	8.3
MC16	KMA13-29-19	1,483	902	2,967	1,784 (11)	-5.1	8.0	26.2
MC17	KMA13-30-7	1,663	518	1,894	1,358 (26)	5.4	-2.3	26.4
MC18	KMA13-31-62	1,435	1,626	2,906	1,989 (6)	0.4	18.7	18.8
MC19	KMA13-32-22	1,306	507	1,408	1,074 (32)	9.3	2.3	45.2
MC20	KMA13-32-24	1,431	52	2,184	1,222 (30)	-2.2	-4.5	11.8
MC21	KMA13-22-23	1,268	611	3,647	1,842 (10)	-16.0	8.8	78.2
MC22	KMA13-23-10	1,580	912	2,406	1,633 (15)	1.8	5.5	10.5
MC23	KMA13-23-11	1,990	287	1,720	1,332 (28)	7.3	-11.0	37.2
MC24	KMA13-25-4	1,965	784	2,009	1,586 (19)	7.3	-3.1	35.7
MC25	KMA13-27-101	1,405	640	2,069	1,371 (24)	3.0	3.9	15.3
MC26	KMA13-27-102	2,142	871	2,173	1,729 (13)	6.8	-4.4	33.5
MC27	KMA13-27-12	2,491	481	3,160	2,044 (4)	-5.6	-13.4	30.5
MC28	KMA13-28-21	3,086	657	7,412	3,718 (1)	-50.8	-11.9	247
MC29	KMA13-28-22	2,302	248	2,121	1,557 (20)	3.9	-15.7	24.4
MC30	KMA13-28-29	2,202	613	2,000	1,605 (18)	7.3	-9.3	36.8
MC31	KMA13-27-1	1,350	416	1,264	1,010 (33)	10.5	0.0	51.2
MC32	KMA13-21-20	2,610	1,027	3,348	2,329 (3)	-3.5	-7.3	18.5
MC33	KATB1	1,547	137	1,748	1,144 (31)	3.9	-6.0	19.9
E Mean		1,797 (2)	742 (3)	2,550 (1)	1,696			
IPCAe[1]		22.7	34.2	-57.0				
IPCAe[2]		-35.5	31.0	4.5				
ASV		115.9	169.0	276.9				
$LSD_{0.05}$					255.3			

Legend: IPCA 1 and IPCA 2 = interaction principal component one and two, respectively; ASV= AMMI Stability value; e=E=environment; g=genotype; LSD=least significant difference at 5% P-value threshold.

4.3.2.3. Genotype and Genotype x Environment (GGE) Biplots for seed yield

AMMI biplots of genotype and genotype x environment interactions permit visualization of differences in the interaction main effects. For the pinto bean lines, genotypes KMA13-22-30 (P6), GLP92 (P13), KMA13-22-7 (P4) were more widely adapted across environments. KMA13-22-21 (P5), KMA13-22-30 (P6) and GLP92 (P13) were the high yielding lines, reaching approximately 3,000 kg ha^{-1}. Most of the lines did well at Tigoni compared to the other two sites (Figure 4.4a).

Figure 4.5a shows that most of the red kidney lines were widely adapted across sites with optimum conditions occurring in high altitude agro-ecological zones such as Tigoni. Mex54 (RK15) and KMA13-30-22 (RK13) were the better yielding lines reaching seed yields of approximately 3,500 kg ha^{-1}.

The Figure 4.6a shows that Tigoni was the best environment for the red mottled lines, followed by Kabete and Mwea. Most of the lines did well at Tigoni. KMA13-29-21 (RM13) was outstanding and reached the highest yields with approximately 3,500 to 4,000 kg ha^{-1}. KMA13-20-3 (RM2), KMA13-20-14 (RM3), KMA13-29-21 (RM13) were among the most stable lines.

The same trend was observed for the small red lines. Tigoni was the most suitable environment for bean production. Lines KMA13-25-9 (SR5) and KMA13-23-14 (SR3) were outstanding in terms of productivity compared to the checks and other advanced lines. KMA13-30-2 (SR7), RWR719 (SR21) and GLP585 (SR22) were among the most stable lines (Figure 4.7a).

Among mixed color lines, KMA13-28-21 (MC28), a black-seeded line, was the most productive as it yielded approximately 3,500 kg ha^{-1}. Tigoni was the best site for the mixed color lines compared to the other two sites (Figure 4.8a). From the GGE biplots, Tigoni was the most discriminative as it was far from the origin of the biplot graph regardless of the market classes.

Most of the variability was explained by the 2 PCs regardless of the market class (97.6%, 94.5%, 95.9%, 96.9% and 92% for pinto, red kidney, red mottled, small red and mixed color genotypes, respectively). PC1 contributed the most to that variability (92%, 86.4%, 87.4%, 89.4%, 81.8% for pinto, red kidney, red mottled, small red and mixed color bean lines, respectively). Tigoni in high altitude was the best environment for most of the genotypes regardless of the market class. The variability across environments was high for the red mottled genotypes for which there were

three distinct mega-environments; genotypes having performed differently in each site (Figure 4.6b). The variability across environments was lower for the mixed color genotypes for which there is only one mega-environment suggesting that better yielding genotypes in one site were the better in the other two environments (Figure 4.8b). KMA13-22-21 (P5) and GLP92 (P13) performed best at Kabete and Mwea while KMA13-22-30 (P6) was best for Tigoni (Figure 4.4b).

In the red mottled market class, three mega-environments were identified. Mex54 (RK15) was best for low altitude environments such as Mwea while KMA13-21-11 (RK5) and KMA13-30-22 (RK13) did better in medium altitude environments such as Kabete (Figure 4.5b). KMA13-17-17 (RM17) and KMA13-24-5 (RM5) were suited for medium altitude conditions and KMA13-24-17 (RM8) for low altitude (Figure 4.6b).

For the small red, the three test sites represented two mega-environments. Lines yielding better in medium altitude did well in high altitude too. The low altitude condition behaved differently from the medium and high altitude. KMA13-23-14 (SR3) and KMA13-25-9 (SR5) were best for both medium and high altitude conditions while KMA13-30-16 (SR9) was suited to low altitude (Figure 4.7b).

Among mixed color bean lines, KMA13-27-27 (MC10) and KMA13-28-21 (MC28) were the best for Mwea (low altitude) and Tigoni (high altitude) whereas KMA13-21-20 (MC32) and KMA13-27-12 (MC27) won at Kabete in medium altitude (Figure 4.8b).

From the GGE biplots, Tigoni was the most discriminative as it was far from the origin of the biplot graph regardless of the market classes. All genotypes inside the polygon, mainly those located close to the plot origin were less responsive than the vertex genotypes and not the best in any environment.

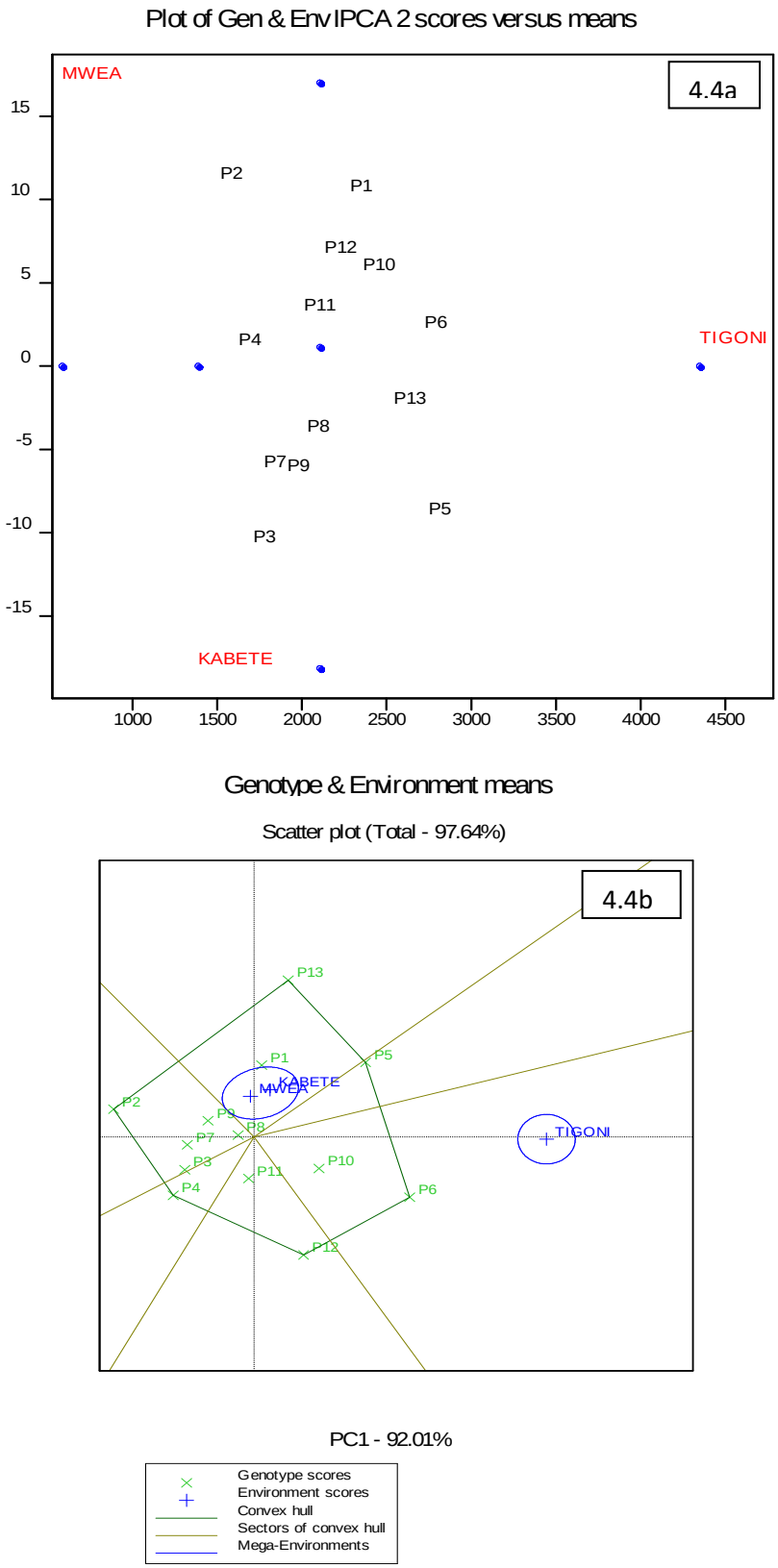


Figure 4.4. AMMI (a) and GGE (b) biplots of the pinto lines for seed yield across three environments

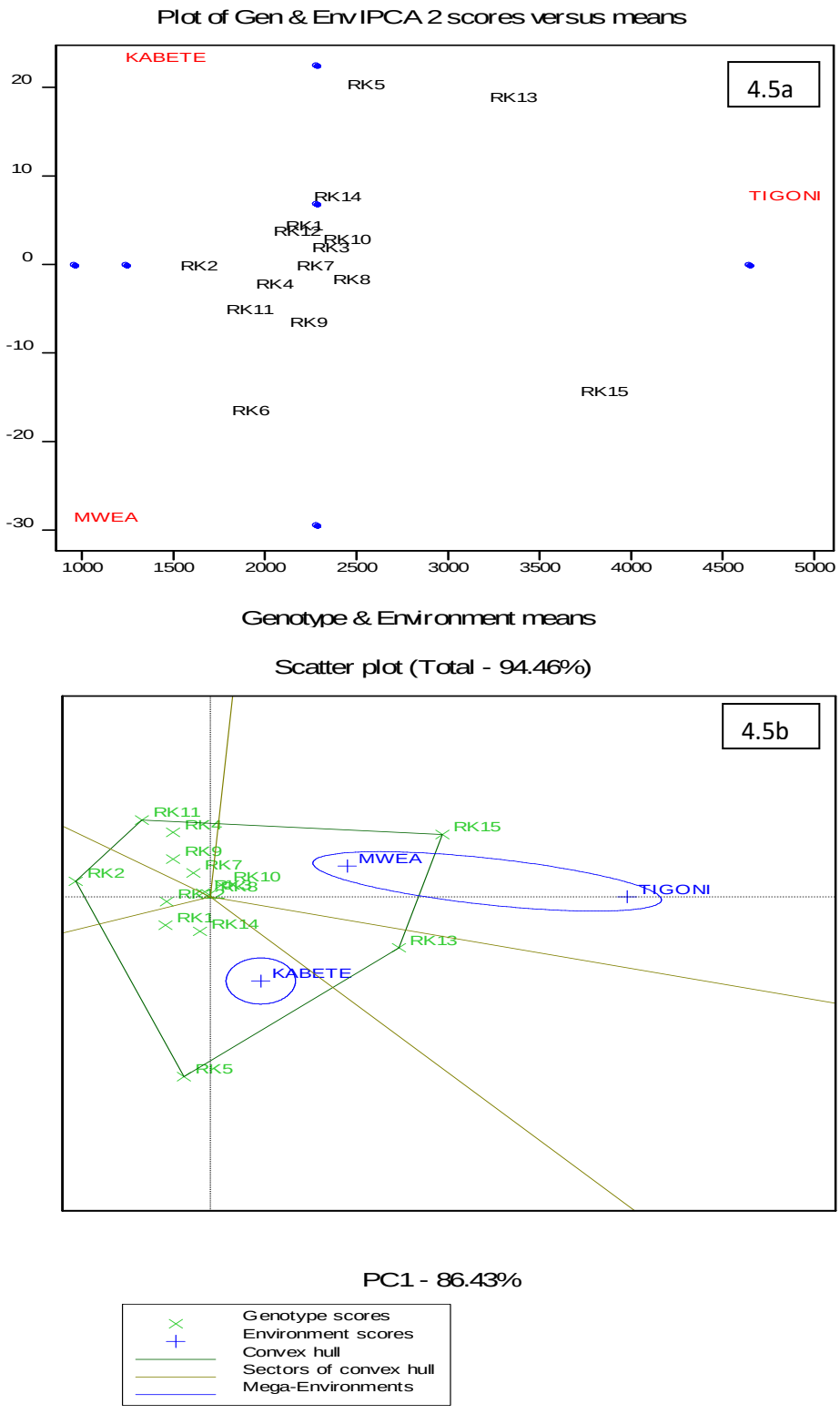


Figure 4.5. AMMI (a) and GGE (b) biplots of the red kidney lines for seed yield across three environments

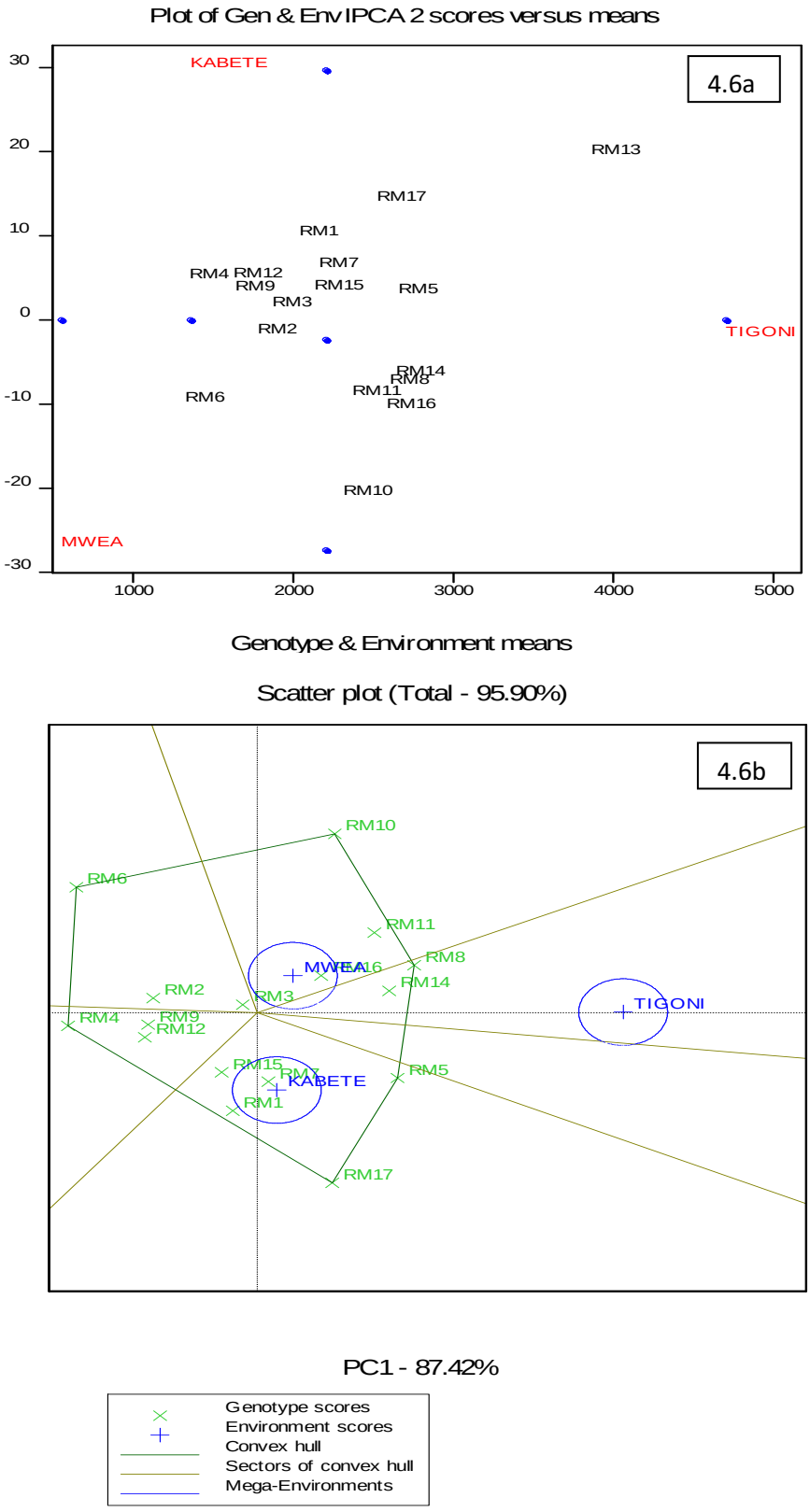
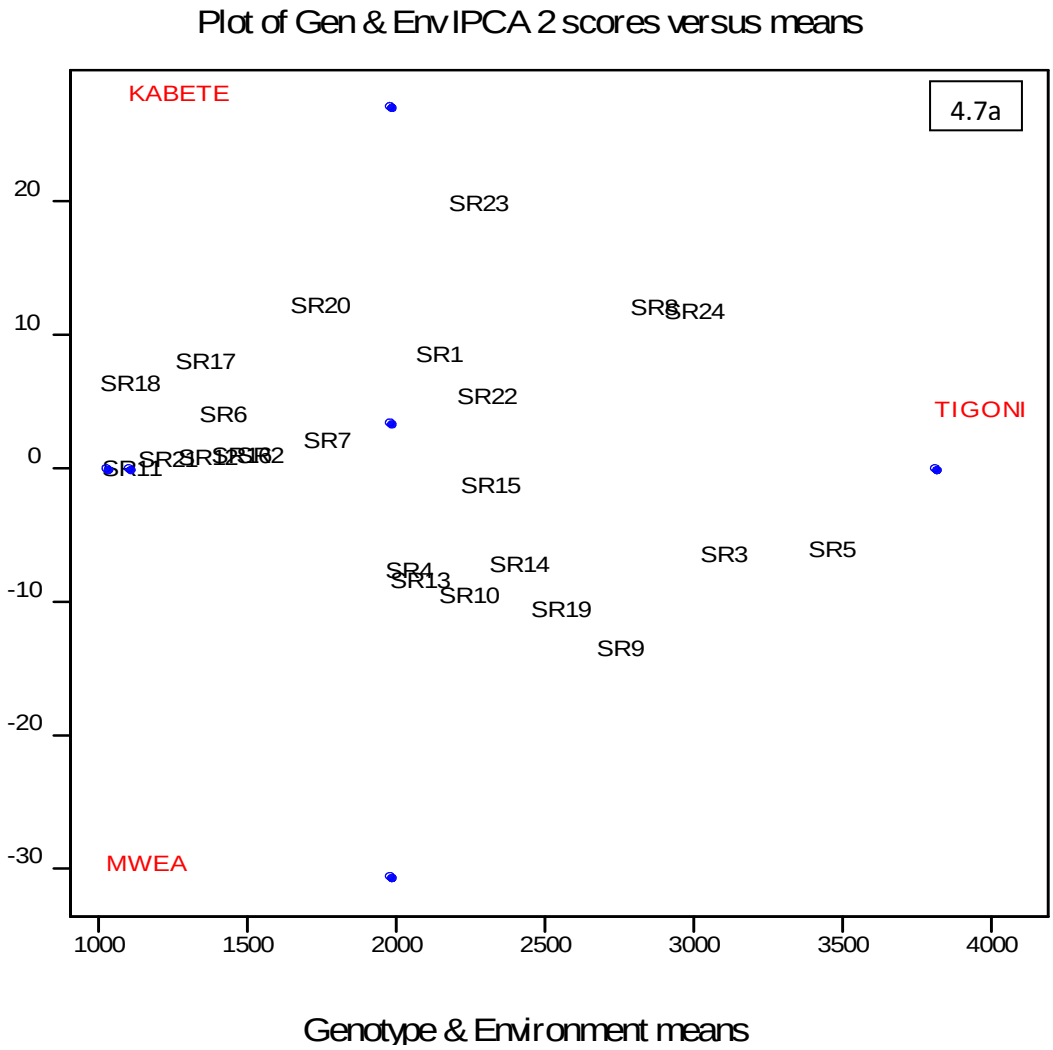


Figure 4.6. AMMI (a) and GGE (b) biplots of the red mottled lines for seed yield across three environments


Plot of Gen & Env IPCA 2 scores versus means
KABETE
4.7a
20
10
0
-10
-20
-30
SR23
SR20
SR8
SR24
SR17
SR1
SR18
SR22
SR6
TIGONI
SR7
SR15
SR3
SR5
SR14
SR4
SR13
SR10
SR19
SR9
MWEA
1000
1500
2000
2500
3000
3500
4000
Genotype & Environment means

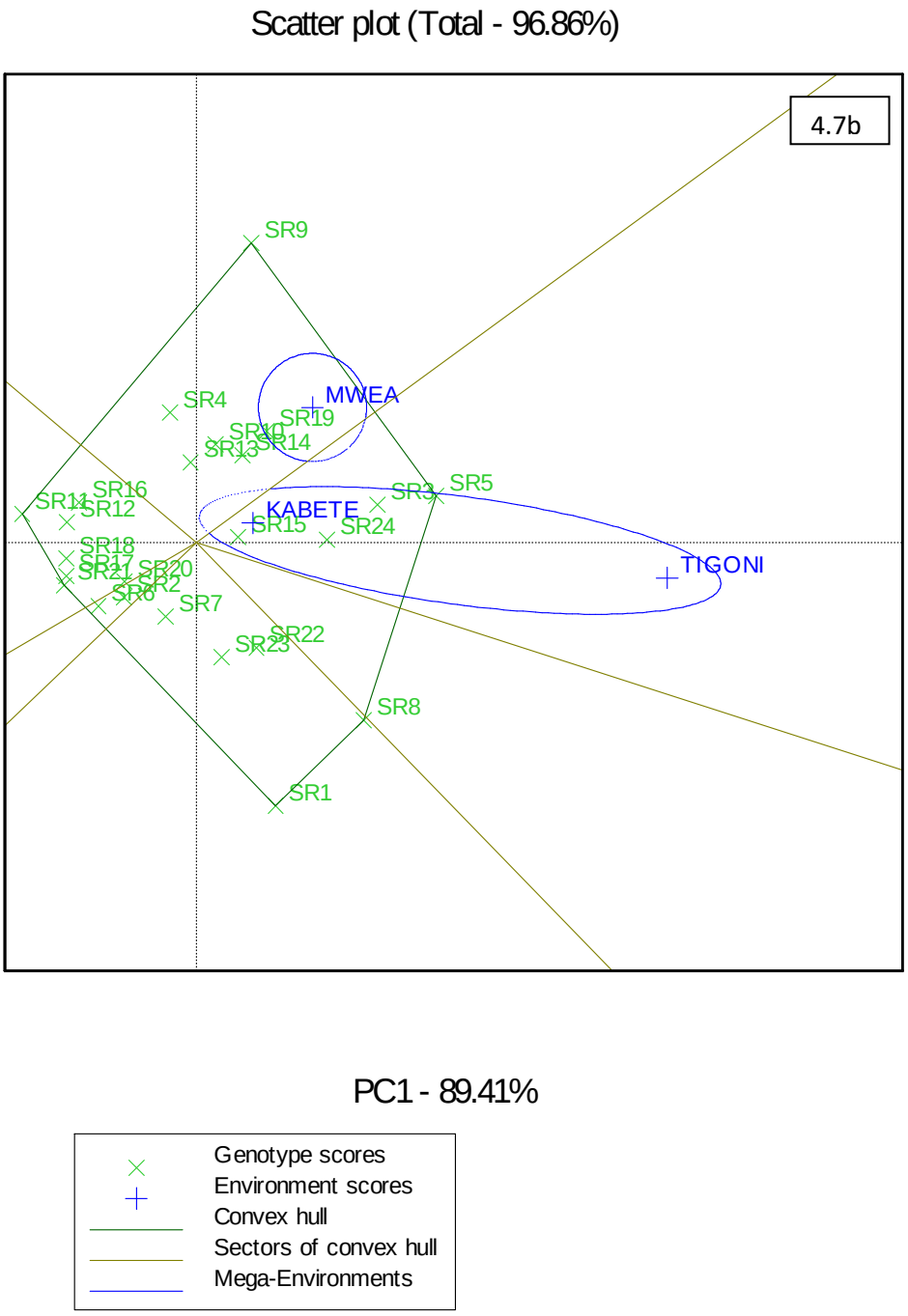
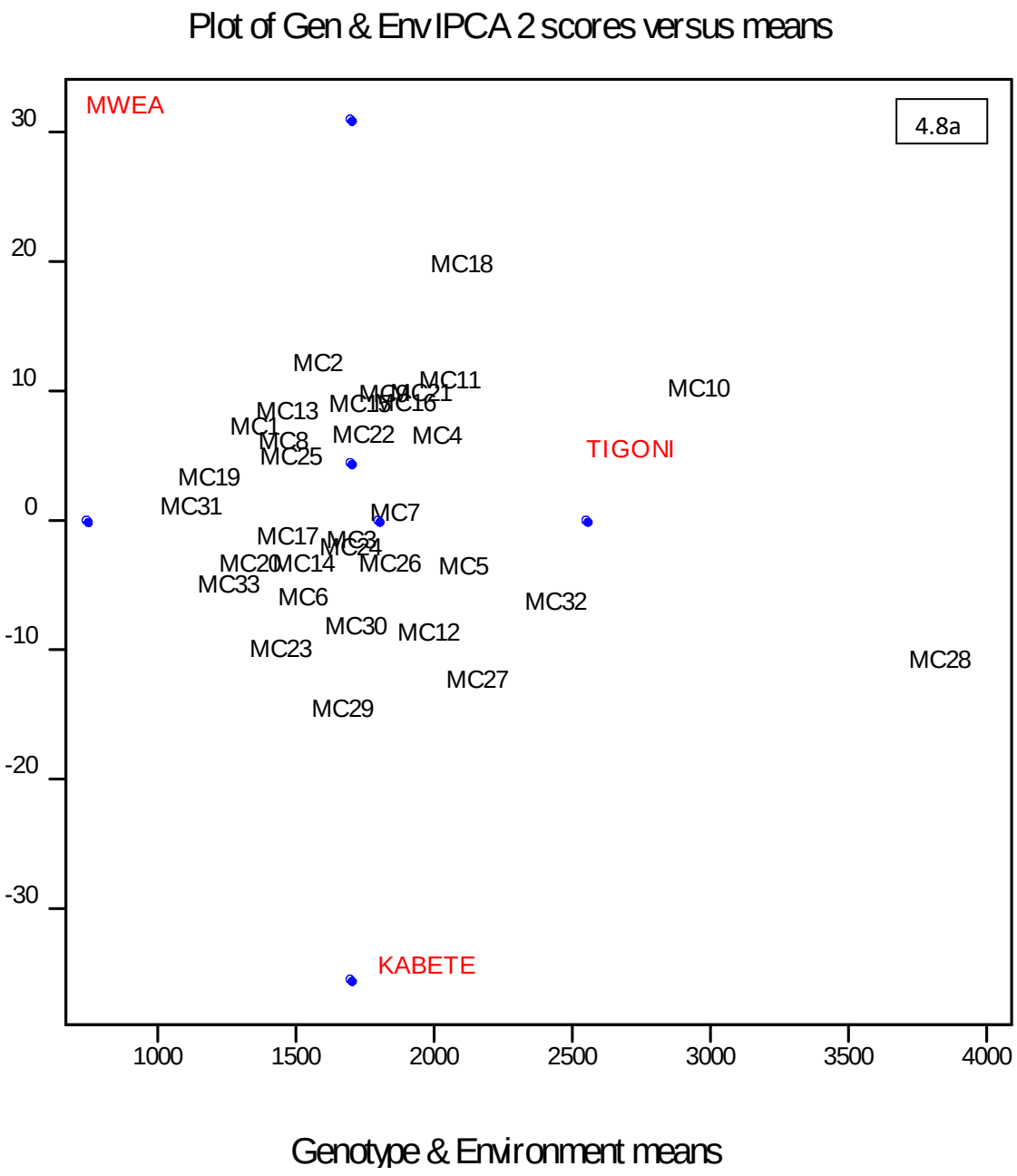


Figure 4.7. AMMI (a) and GGE (b) biplots of the small red lines for seed yield across three environments


Plot of Gen & Env IPCA 2 scores versus means
MWEA
4.8a
30
20
10
0
-10
-20
-30
MC18
MC2
MC11
MC10
MC13
MC1
MC8
MC22
MC4
MC25
TIGONI
MC19
MC31
MC7
MC17
MC24
MC20
MC14
MC26
MC5
MC33
MC6
MC32
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MC28
MC27
MC29
KABETE
1000
1500
2000
2500
3000
3500
4000
Genotype & Environment means

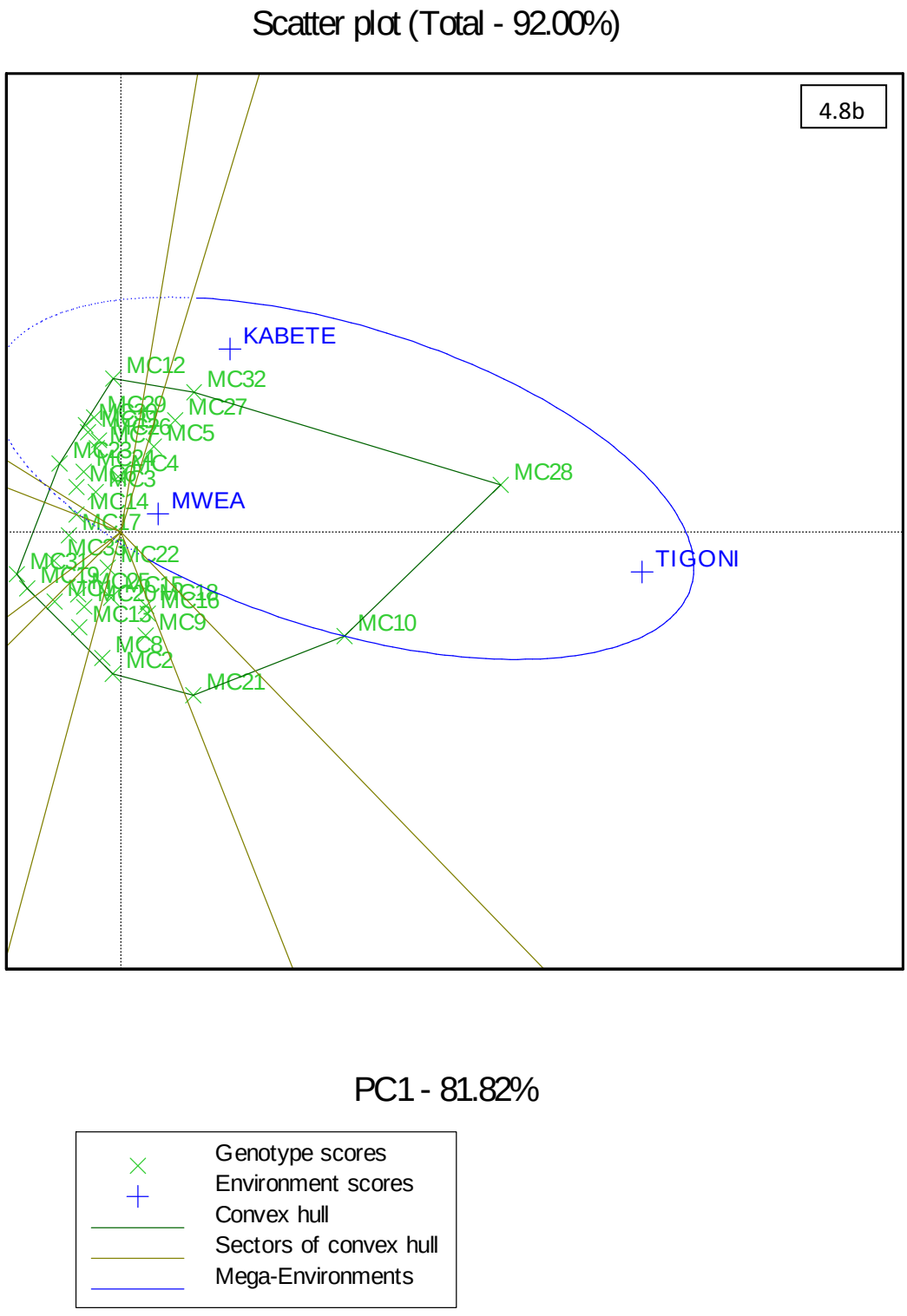

Figure 4.8. AMMI (a) and GGE (b) biplots of the mixed color lines for seed yield across three environments

4.3.2.4. List of recommendations for further testing and release from AMMI model

Recommended lines and their characteristics based on the AMMI model for the genotype-environment interactions are given in Table 4.62.

Table 4.62. Materials recommended for further testing and release as generated based on AMMI analyses

Genotype IDs	Line	Seed color	Growth habit	Seed size	Yield (kg ha^{-1})	Recommended areas
MC10	KMA13-27-27	Tan red	IV	Medium	2,845	Low- & highland
MC11	KMA13-28-5	Tan red	IV	Medium	1,947	Lowland
MC12	KMA13-28-13	Tan red	IV	Medium	1,869	Midland
MC18	KMA13-31-62	Tan brown	III	Medium	1,989	Lowland
MC21	KMA13-22-23	Black	III	Medium	1,842	Highland
MC27	KMA13-27-12	Black	II	Medium	2,044	Midland
MC28	KMA13-28-21	Black	III	Medium	3,718	Mid- & highland
MC32	KMA13-21-20	Yellow	IV	Medium	2,329	Mid- & highland
MC4	KMA13-23-9	Tan red	IV	Medium	1,921	Lowland
P1	KMA13-21-10	Pinto	III	Medium	2,285	Lowland
P10	KMA13-23-22	Pinto	III	Medium	2,360	Highland
P12	KMA13-24-7	Pinto	III	Medium	2,136	Highland
P2	KMA13-21-19	Pinto	III	Medium	1,518	Lowland
P5	KMA13-22-21	Pinto	III	Medium	2,748	Low-, mid-, highland
P6	KMA13-22-30	Pinto	III	Medium	2,726	Highland
P8	KMA13-23-13	Pinto	III	Medium	2,031	Midland
P9	KMA13-23-18	Pinto	III	Medium	1,914	Midland
RK10	KMA13-28-2	Red kidney	II	Large	2,318	Highland
RK13	KMA13-30-22	Red kidney	III	Medium	3,226	Mid- & highland
RK3	KMA13-19-16	Red kidney	II	Medium	2,256	Highland
RK5	KMA13-21-11	Red kidney	II	Large	2,448	Midland
RK6	KMA13-25-3	Red kidney	II	Medium	1,819	Lowland
RK8	KMA13-26-32	Red kidney	III	Large	2,370	Lowland
RK9	KMA13-27-31	Red kidney	III	Large	2,136	Lowland
RM1	KMA13-17-25	Red mottled	I	Large	2,038	Midland
RM10	KMA13-27-25	Red mottled	IV	Medium	2,311	Lowland
RM13	KMA13-29-21	Red mottled	II	Large	3,860	Low-, mid-, highland
RM14	KMA13-29-24	Red mottled	IV	Medium	2,640	Low- & highland
RM15	KMA13-32-24	Red mottled	IV	Large	2,131	Midland
RM16	KMA13-32-28	Red mottled	III	Large	2,584	Lowland
RM17	KMA13-17-17	Red mottled	II	Large	2,525	Midland
RM5	KMA13-24-5	Red mottled	II	Medium	2,659	Highland
RM8	KMA13-24-17	Red mottled	IV	Medium	2,605	Highland
SR19	KMA13-32-28	Small red	III	Medium	2,453	Lowland
SR3	KMA13-23-14	Small red	IV	Medium	3,022	Low- & highland
SR5	KMA13-25-9	Small red	IV	Medium	3,385	Low- & highland
SR8	KMA13-30-14	Small red	III	Medium	2,787	Highland
SR9	KMA13-30-16	Small red	IV	Medium	2,673	Mid- & lowland,

4.4. DISCUSSION

This study aimed at determining yield stability and genotype x environment interactions of elite common bean lines across three agro-ecological conditions (low, medium and high altitudes). This section proceeds to state the extent to which this objective was met. It also explains why the genotypes responded the way they did by providing the science behind the results. Then it compares findings from this study with reports of others and draws some general conclusions.

4.4.1. Agronomic performance of the inter-racial advanced lines across sites

The effects due to interaction between the sites and the genotypes for all the traits and all the market classes were significant ($P<0.05$), implying that the advanced bean lines responded differently to environmental conditions prevailing at test sites. As a result, their ranking varied significantly across the three sites. For all the traits, crops grown at Tigoni in high altitude recorded the highest means statistically superior to the other two sites namely Kabete and Mwea located in medium and low altitudes, respectively. The better performance recorded at Tigoni could be attributed to the relatively cooler conditions offered to crops; which led to slower plant growth and the delayed maturity and, therefore, longer seed filling period which resulted in higher seed yields (Singh *et al.,* 2002). The low yield recorded at Mwea in low altitude could be due to dry spells and erratic rainfall received in that site during the experiment. In fact, the mean monthly temperature was 24.3°C with a total rainfall of approximately 311.4 mm for the period of September 2017 to February 2018. In addition, more than 85% of that rainfall was recorded for October and November flooding the young seedlings. The most critical phases (flowering and podding) experienced a dry period as no rain was recorded in January and February 2018 (0 mm), and thus affecting negatively the grain yield. This was by affecting the flowering, pod filling and the harvest index (Mwale *et al.,* 2008; Beebe *et al.,* 2013; Rao *et al.,* 2013; 2017). In fact, it was demonstrated by several researches that erratic rainfall could result in seed yield decrease of 20% if the stress occurs during the early vegetative growth and could reach up to 50% in the early pod filling (White and Singh, 1991; Blair *et al.*, 2012; Assefa *et al.,* 2017). As most of the lines under study was of indeterminate growth habit, the effects of water stress in low altitude Mwea site were more pronounced compared to dwarf cultivars as reported in Malawi by Chataika (2006) and Mwale *et al.* (2009). Singh *et al.* (1989) demonstrated that humid high altitude conditions are more conducive to indeterminate growth habit cultivars. At Mwea, the

high temperature during the experiment, associated to the erratic rainfall could explain the low yield recorded regardless of the market classes.

The seed yield and seed yield components varied significantly among the genotypes and the market classes. In all the market classes, there were promising genotypes for seed yield compared to the commercial check varieties and donor parents used, apart from the red kidney market class where the best yielding line was not significantly different from the best check variety (Mex54). This was probably an effect of growth habit as Mex54 is a semi-climber while most of test red kidney lines were bush lines (Type I and Type II growth habit). However, 4 of the 15 advanced red kidney lines were superior to the other check variety (AND1062) which is a bush cultivar. The presence of promising lines regardless of the market class and seed size demonstrated the effectiveness of inter-racial crosses to improve the seed yield of common bean. Singh *et al.* (2002) after studying the effects on seed yields of the Andean intra-gene pool and Andean-Middle America inter-gene pool crosses, concluded that the utilization of high yielding genotypes from both gene pools which are diverse and with positive general combining ability could maximize gains from seed yield selection. Welsh *et al.* (1995) and Singh and Urrea (1995) had previously demonstrated the superiority of the inter-racial lines over the intra-racial, suggesting the necessity to explore them as a mean to create useful genetic variations and to broaden the genetic base of commercial cultivars as well as maximizing gains from selections.

The seed yield was high for market classes with higher 100-seed mass compared to the smaller seeds. Lima *et al.* (2005), when assessing the effects of size of seed grown on the growth and yield of common bean, concluded that sowing larger seeds improves the early-season plant growth which is advantageous for crop establishment in stressed environments. This could explain why red kidney and red mottled market classes had higher yields than small red, pinto and mixed color market classes. However, the delay in leaf senescence, higher net assimilation rate, the greater number of pods per plant or the number of seeds per pod allow to small-seeded beans to achieve the same level of yield as the large-seeded counterpart. Singh *et al.* (2002) had even reported up to 40-60% more yield from small-seeded genotypes compared to the large-seeded counterparts. The effects of seed size on yield were much more pronounced among the lines within the same market class than among market classes. This study which had both large and small/medium classes disagrees with the general observation (especially in Colombia/CIAT)

that small-seeded lines yield better than large-seeded types (Singh *et al.,* 2002). Debouck *et al.* (1993) presented evidence that the large-seeded Andean common bean germplasmwas better adapted to cooler, higher elevations than Mesoamerican germplasm.

4.4.2. Correlations between seed yield and yield components

Seed yield was significantly and positively correlated with days to flowering, days to maturity, number of pods per plant, number of seeds per pod, 100-seed mass and harvest index ($P<0.05$). Similar results were found by Lad *et al.* (2017). The most important among those components regardless of the market class was the number of pods per plant (r=0.91*** for pinto, r=0.90*** for red kidney, r=0.83*** for red mottled, r=0.85*** for small red and r=0.77*** for mixed color bean lines). This would imply that the higher the number of pods per plant and the higher the number of seeds per plant, the higher the seed yield was. Similar results were reported by Darkwa *et al.* (2016); Rao *et al.* (2017) and Assefa *et al.* (2017), suggesting that the number of pods per plant could be used by plant breeders as an additional and indirect selection method for seed yield. This study reflected the general assumption that yield increases with growth habit such that Type IVs (climbers) are the best yielding. In fact, this study revealed a positive correlation between growth habit and the number of pods per plant and between growth habit and the seed yield regardless of the market class. However, the trend was opposite for the pinto bean lines for which correlations were negative but not significantly.

Better yielding lines were late to reach the 50% flowering stage as they contained a large number of flowers which appeared progressively. This had also impacted the days to maturity which was longer compared to plant developing fewer flowers and fewer pods (Welsh *et al.,* 1995; Singh *et al.,* 2002; Lad *et al.,* 2017). However, opposite results were found in drought stress environments where higher yield was in negative correlation with the days to maturity (Polania *et al.,* 2016; Gereziher *et al.,* 2017). Except for the small red lines for which the growth habit was significantly correlated to duration to flowering (r=-0.07***) and to maturity (r=0.29***), there were no significant correlations between the growth habit and the duration to flowering and to maturity for all other market classes. This contrasts the general assumption that climbers take longer to flower and mature compared to bush bean lines.

Significant negative correlations were detected between the seed yield and the plant vigor and between the seed yield and the seedling emergence rate within the market classes. As the plant vigor score varied from 1 to 9 (Schoonhoven and Pastor-Corrales, 1987) from which 1 is the best score and 9 the worst, the more a plant was vigorous, the more it could carry more flowers and more pods and consequently, the more the yield was higher. The negative correlation existing between yield and the seedling emergence rate could suggest that most of the lines require much more spacing for optimum growth and yield. This is particularly true for climbers which need much more space than bush bean lines. So the germinated plants have explored space left by seeds which failed to germinate as no gapping was done after planting. Another key reason that could explain this negative correlation between the seed yield and the seedling emergence rate is that the extrapolation to estimate the seed yield ha^{-1} which was done on the basis of single plants. If the yield per m^2 (or per plot) was considered in extrapolation regardless of the number of plants, the relationship may change.

4.4.3. Seed yield stability and genotype-environment interaction (G x E) effects on seed yield

From the AMMI ANOVA, the variability among genotypes across sites was highly significant (*P<0.001*) regardless of the market class. The treatments (G, E, and G x E) contributed the most to the variability for more than 80% regardless of the market class. This showed the diversity of sites and the existence of significant genetic differences among the advanced lines for seed yield (Tamene and Tadesse, 2014; Ashango *et al.,* 2016). By partitioning the treatments contribution for every market class, the environment contributed the most to the variability compared to the genotypes and the interactions among genotypes and environments. The effect of the environment was, therefore, responsible for the largest part of the variability. Similar results were reported on common bean by Mwale *et al.* (2009) in Malawi and Ashango *et al.* (2016) and Tadesse *et al.* (2017; 2018) in Ethiopia. Although the environment is a very broad term and includes many factors (predictable and unpredictable); it was the temperature and the amount and distribution of rainfall that had mainly contributed to observed results. Tigoni in low altitude experienced cooler conditions (15.8°C) with a relatively well-distributed rainfall along the growing season (506 mm). Kabete experienced mean monthly temperatures of 18.2°C and an amount of rainfall of 372 mm. Mwea in low altitude was warmer (24°C) with erratic rainfall as

described previously (311 mm) (Appendix 25). Other key environmental factors (e.g. soil type, nutrients, pH, etc.) were not significantly different among the three sites. Thung and Rao (1999) showed that differences in rainfall pattern and temperature during the reproductive period may be the most important factors contributing to the changes detected in the duration of the reproductive phase and seed yield.

The interaction between the genotype and environment was high for the small reds and the mixed colors (17.6% and 26.7%, respectively) suggesting that tested lines were not stable and thus responded differently across locations. Similar findings were reported by Mwale *et al.* (2009) and Wera *et al.* (2018). Those genotypes should, therefore, be selected and recommended to specific environments. From ASV, the higher yielding lines were also the most unstable across sites. This is supporting results found by Swegarden *et al.* (2016) and Tadesse *et al.* (2017; 2018) showing that the stable lines are not always the better yielding. In fact, Lin *et al.* (1986) demonstrated that a satisfactory Type I stability parameter (i.e., CV) is often linked with reduced yield performance.

4.5. CONCLUSION

The present study aimed to assess the agronomic performance and seed yield stability of 92 advanced inter-racial $F_{1.7}$ lines grouped in 5 market classes across three agro-ecological conditions of central Kenya. Promising genotypes combining high seed yield potential, seed quality and high stability were identified from all the market classes, which were significantly superior to the commercial check varieties and the donor parents. This demonstrated the effectiveness of the inter-racial crosses to improve the seed yield regardless of the market class and the seed size. The environment contributed the most to the variability among lines. The high interaction between the genotypes and the environments for some market classes suggested that the genotypes should be selected and recommended to specific environments. Although the best yielding lines were not the most stable, KMA13-22-21 (P5) a pinto line and KMA13-29-21 (RM13) a red mottled line combined high yield potential and wider adaptation across the three agro-ecological conditions. All others had either specific adaptation or adapted in two of the three locations.

CHAPTER 5: VALIDATION OF MARKER-ASSISTED COMMON BEAN SELECTIONS FOR MULTIPLE DISEASE RESISTANCE

ABSTRACT

The objective of this study was to validate 26 $F_{1.8}$ elite lines selected for resistance to angular leaf spot, anthracnose, root rots, common bacterial blight and bean common virus from inter-racial and inter-gene pool populations in early generations using marker-assisted gamete selection procedure. Pathogens were isolated from diseased plants collected from various areas of central Kenya, multiplied on appropriate media and used to inoculate the tested lines two weeks after seedling emergence by spraying spore suspension on the leaves evenly with a handheld atomizer in a greenhouse at Kabete Field Station, University of Nairobi. For the root rot experiment, millet grains infested by root rot pathogens were mixed with pre-sterilized soil three days before planting. Data on disease incidence and severity were collected at 14^{th}, 21^{st}, 28^{th} days after inoculation using the 1-9 CIAT scale, except the root rot experiments for which data were recorded once at 21^{st} day after seedling emergence. Analysis of variance (ANOVA) and area under disease progression curve (AUDPC) were performed on collected data.

Results showed that five of the 26 elite lines possessed multiple resistance to five pathogens; eight to four pathogens; nine to three pathogens, three to two pathogens and one was resistant to one pathogen. This implied that markers were effective in the identification and transfer of resistance genes to susceptible commercial varieties. However, there were no significant correlations in the reaction of tested genotypes to the seven diseases used in this study, except the significant correlation ($P<0.05$) between the reaction to BCMV and ALS (r=0.3942*). This suggested that resistance genes were located in different chromosomes and assorted independently. The presence of genotypes with multiple disease resistance among tested elite lines confirmed the effectiveness of inter-racial crosses and marker-assisted gamete selection to concurrently improve the resistance to common bean major diseases in Eastern Africa.

Keywords: Gamete selection, resistance genes, elite lines, severity, AUDPC, pathogens

5.1. INTRODUCTION

Common bean (*Phaseolus vulgaris* L.) is the most important legume crop for human consumption worldwide, contributing protein, complex carbohydrates, dietary fiber, isoflavones and micronutrients (iron, phosphorus, zinc) to diets of large millions of people especially in Africa and Latin America (Broughton *et al.,* 2003; Beebe *et al.,* 2013). In addition to its nutritional value, the common bean is also an important source of income for the small-scale and resource-poor farmers of sub-Saharan Africa (Buruchara *et al*., 2011; CGIAR, 2017). Common bean has multiple health benefits. It reduces the risk of chronic diseases such as diabetes, heart disease, and cancer (Mitchell *et al.,* 2009; Mukankusi *et al.,* 2018; Winham *et al.,* 2018). Eastern and Central African countries are the major producers and consumers of common bean in Africa where it contributes up to 25% of total caloric intake and 45% of total dietary protein and, thus, making it the highest level of contribution of protein in the world (Kilimo Trust, 2012; Alladassi *et al.,* 2018). Western Kenya and Rwanda have the highest per capita bean consumption in the region (more than 60 kg per capita per year). Kenya, Tanzania and Uganda are the leading producers in Africa (Beebe *et al.,* 2013; FAO, 2018). However, Kenya has been a net bean importer for last two decades because demand exceeds production (Kimani *et al.,* 2005a).

Despite the importance of common bean in Eastern and Central Africa, its productivity is still among the lowest in the world with an average seed yield of 0.5 t ha^{-1} (FAO, 2018; Alladassi *et al.,* 2018) while potential yields range from 1 to 3 t ha^{-1} for bush genotypes and could be as high as 5 t ha^{-1} for climbers (Kaizzi *et al.,* 2012; Ronner *et al.,* 2017). Many constraints are responsible for poor performance of common bean in the region. Major constraints include drought stress, low soil fertility, plant diseases and pests, poor adaptation of introduced varieties to local conditions, and socio-economic factors such as low and timely access to external inputs (seed of improved varieties and fertilizers) and poor farming practices (Wortmann *et al.,* 1998; Kimani *et al.,* 2005b; Lunze *et al.,* 2011; Beebe *et al.,* 2013; Kimani, 2014; Mukankusi *et al.,* 2015; Olango *et al.,* 2017).

The major diseases constraining common bean productivity in Eastern and Central Africa include angular leaf spot (*Pseudocercospora griseola* (Sacc.) (Wagara *et al.,* 2004; Ddamulira *et al.,* 2014a; Leitich *et al.,* 2016; Olango *et al.,* 2017), anthracnose (*Colletotrichum*

lindemuthianum (Sacc. and Magn.) (Gathuru and Mwangi, 1991; Kiryowa *et al.,* 2016), root rots (*Pythium spp*., *Fusarium spp., Sclerotium rolfsii* and *Rhizoctonia solani*) (Nzungize *et al.,* 2011a; Obala *et al.,* 2012; Buruchara *et al.,* 2015; Paparu *et al.,* 2018; Mukankusi *et al.,* 2018), bean common mosaic and necrotic viruses (BCMV/BCMNV) (Kapil *et al.,* 2011; Mutuku *et al.,* 2016; Mwaipopo *et al.,* 2017), and common bacterial blight (CBB) caused by *Xanthomonas axonopodis* pv. *phaseoli* (Belete and Bastas, 2017; Alladassi *et al.,* 2017; 2018). These diseases cause severe losses to seed yield and quality of common bean ranging from 20% to as high as 80 to 100% (Singh and Schwartz, 2010; Blair *et al.,* 2010; Mahuku *et al.,* 2011; Olango *et al.,* 2017). Wortmann *et al.* (1998) estimated the annual production losses in Eastern Africa caused by angular leaf spot at 281,300 t; anthracnose at 247,400 t; root rot at 179,800 t; common bacterial blight at 145,900 t and bean common mosaic virus at 144,600 t.

Several approaches have been used to control those common bean diseases such as combinations of cultural and the chemical controls but were found to be ineffective to many diseases (Okii *et al.,* 2017). In addition to negative environmental impacts of chemicals, associated costs are not practical for the widespread low-input systems and, therefore, breeding for resistance is the most cost-effective and environmentally friendly approach for resource-poor farmers of Eastern and Central Africa (Odogwu *et al*., 2017) since there is no additional cost. This approach can greatly reduce the need for chemicals hence increasing returns on farmers' investment (Kimani and Mwang'ombe, 2007; Ddamulira *et al.,* 2015). Okii *et al.* (2017) showed that multiple pathogen co-infections on common beans are responsible for complete crop losses in susceptible bean varieties, suggesting that common bean breeding for disease resistance should target multiple pathogens simultaneously by pyramiding resistance genes in a single genotype for a broader and durable resistance. Because several diseases normally occur in a particular production environment, incorporating resistance to a single disease will not result in significant changes (Singh, 1994; Kimani *et al.,* 2005b; Mahuku *et al.,* 2009).

Development of improved dry bean varieties in Eastern and Central Africa faces four key challenges. First, is the occurrence of new races and strains of disease pathogens such as angular leaf spot, anthracnose, root rots, and bean common mosaic viruses (Leitich *et al.,* 2016; Mwaipopo *et al.,* 2017); secondly, identification and deployment of new sources of resistance to

the emerging pathotypes (Ddamulira *et al.*, 2014a; Kijana *et al.*, 2017; Mukankusi *et al.*, 2018); thirdly, broadening the genetic base of existing breeding populations to enhance genetic potential for important agronomic traits (Kimani *et al.*, 2005b; Okii *et al.*, 2014), and finally, improving efficiency of breeding methodology (Kimani *et al.*, 2005b; Ceccarelli, 2015).

These four issues listed above were the main focus of the marker-assisted breeding programme at the University of Nairobi since 2009. In fact, the programme initiated studies to determine whether marker-assisted gamete selection can be effective in pyramiding genes for resistance to bean major diseases in Eastern Africa (mainly angular leaf spot, anthracnose, common bacterial blight, bean common mosaic virus and root rot) and introduce these genes into susceptible, but popular, large- and small-seeded bean varieties (Kimani *et al.*, 2012; Musyimi, 2014; Njuguna, 2014). Sixteen inter-racial and inter-gene pool populations were developed from crosses among Middle American (Mesoamerican) and Andean gene pool cultivars to broaden the genetic base of commercial cultivars and take advantage of attributes of both gene pools. In addition to high yield potential of Middle American cultivars, they are resistant to major diseases of the Andean gene pool counterparts and possess genes for drought resistance while the Andean cultivars are the most preferred in Africa for their seed quality and thus, fetch higher prices in local markets (Welsh *et al.*, 1995; Singh *et al.*, 2002; Sichilima *et al.*, 2016). This, therefore, justified the necessity of inter-racial crosses in developing breeding populations. To shorten and increase the efficiency and precision of the breeding programme, the marker-assisted gamete selection method was followed as a possible improvement of the original phenotypic gamete selection developed by Singh (1994).

This study aimed to validate the presence of multiple disease resistance in $F_{1.8}$ elite lines, selected previously for high seed yield potential and seed quality, using artificial inoculations under greenhouse conditions. This would lead to identification of new genotypes combining high yield potential, seed quality and multiple disease resistance for further testing and release.

5.2. MATERIAL AND METHODS

5.2.1. Study site

This study was carried out in screenhouse conditions at Kabete Field Station of the University of Nairobi, which is located at coordinates 01°15' S (latitude); 036°44' E (longitude) and at an altitude of approximately 1820 m above sea level. The station receives an average rainfall of 1059 mm annually, spread over two seasons. It has mean maximum and minimum temperatures of 22.5°C and 12.3°C, respectively. Soils are well drained, very deep, dark reddish brown, friable clay with acid humic topsoil, humic nitisols. The pH is about 5.0 to 5.4 and a mean sunshine of 6.6 hours per day (Jaetzold *et al.*, 2006).

5.2.2. Plant materials

Plant materials used for the experiments were 26 elite $F_{1.8}$ lines selected for seed yield and seed quality from a multi-site testing conducted during 2017 short rain season in three agro-ecological conditions of central Kenya (low, medium and high altitudes). The major characteristics of these lines are presented in Table 5.1. In addition to these elite lines, 10 parental cultivars used in population development were included as checks. During population development, Mex54 and G10909 were used as sources of resistance to angular leaf spot; G2333 for anthracnose, RWR719 and AND1062 for root rots and BRB191 for bean common mosaic virus. Commercial check varieties included GLP92 (*Mwitemania*), GLP585 (*Wairimu*), KATB9 and KATB1 which are susceptible parents but with high yield potential, market-demanded traits and good adaptation to agro-ecological conditions of Eastern Africa. Major characteristics of these parental genotypes are described in Table 3.1 (Chapter 3).

Table 5.1. Characteristics of 26 elite lines used in the multiple disease resistance validation experiment.

Genotype code	*Line	Seed color	Growth habit	Seed size	§Yield (kg ha^{-1})
MC10	KMA13-27-27	Tan red	IV	Medium	2,845
MC11	KMA13-28-5	Tan red	IV	Medium	1,947
MC12	KMA13-28-13	Tan red	IV	Medium	1,869
MC18	KMA13-31-62	Tan brown	III	Medium	1,989
MC27	KMA13-27-12	Black	II	Medium	2,044
MC28	KMA13-28-21	Black	III	Medium	3,718
MC32	KMA13-21-20	Yellow	IV	Medium	2,329
P01	KMA13-21-10	Pinto	III	Medium	2,285
P05	KMA13-22-21	Pinto	III	Medium	2,748
P06	KMA13-22-30	Pinto	III	Medium	2,726
P08	KMA13-23-13	Pinto	III	Medium	2,031
P10	KMA13-23-22	Pinto	III	Medium	2,360
P12	KMA13-24-7	Pinto	III	Medium	2,136
RK08	KMA13-26-32	Red kidney	III	Large	2,370
RK09	KMA13-27-31	Red kidney	III	Large	2,136
RK10	KMA13-28-2	Red kidney	II	Large	2,318
RK13	KMA13-30-22	Red kidney	III	Medium	3,226
RK5	KMA13-21-11	Red kidney	II	Large	2,448
RM01	KMA13-17-25	Red mottled	I	Large	2,038
RM13	KMA13-29-21	Red mottled	II	Large	3,860
RM14	KMA13-29-24	Red mottled	IV	Medium	2,640
RM17	KMA13-17-17	Red mottled	II	Large	2,525
SR03	KMA13-23-14	Small red	IV	Medium	3,022
SR05	KMA13-25-9	Small red	IV	Medium	3,385
SR08	KMA13-30-14	Small red	III	Medium	2,787
SR19	KMA13-32-28	Small red	III	Medium	2,453

*Pedigrees of these genotypes are given in Table 3.4 (Chapter 3); §Yield data is from the multi-environment evaluation at three locations during the 2017 short rain season.

5.2.3. Methods

5.2.3.1. Pathogen isolation, inoculum preparation and plant inoculation

Common bean parts (leaves, roots, stems or pods) infected by anthracnose, angular leaf spot, root rot, common bacterial blight and bean common mosaic virus were collected from various areas of Kenya including Kabete (Nairobi County), Tigoni and Limuru (Kiambu County), Mwea (Kirinyaga County) and Naivasha (Nakuru County). The collection areas were selected based on previous country-wide survey conducted by Musyimi (2014), Njuguna (2014) and other reports (Omunyin *et al.*, 1995; Wagara *et al.*, 2004; Mwang'ombe *et al.*, 2007) which identified regions with the highest prevalence for each of those pathogens. Diseased plant samples were collected during the 2017 short rain season (from October 2017 to February 2018).

Anthracnose: Leaves infected by the anthracnose (*Collectotrichum lindemuthianum*) were thoroughly washed in sterile water and dried between sterile filter papers. The marginal areas of fresh lesions were cut into 0.5 cm pieces and emerged into 1% sodium hypochlorite for two minutes and rinsed in three changes of sterile distilled water. The surface sterilized tissues were blotted by sterile filter papers and then transferred into potato dextrose agar (PDA) supplemented with 40g L^{-1} streptomycin to suppress bacterial growth. The plates were incubated in darkness at 21 to 25°C (room temperature) for five days after which the fungus was sub-cultured on fresh PDA and incubated for two weeks (Sicard *et al.*, 1997). After incubation, inoculums were separated by scrapping off spores from the surface of fourteen-day-old cultures. The concentration of the inoculum was adjusted to 2×10^6 conidia per ml using a haemocytometer for pathogens (Bigirimana and Hofte, 2001). Twenty one-day-old seedlings were covered with polythene plastic bags to provide a humid environment 12 hours before inoculation. The plants were then inoculated by spraying spore suspension on the leaves evenly with a handheld atomizer. After inoculation, the plants were covered with moistened polythene bags and transferred into the greenhouse.

Angular leaf spot: The *Pseudocercospora griseola* causing the angular leaf spot was isolated from infected leaves by transfer of angular leaf spot lesions on the underside of leaves on V8 agar using an inoculating needle. A small agar block was used to pick the spores by touching the lesions and transferred to the Petri plate with V8 juice medium. After incubation for five days, the pathogen was sub-cultured into new V8 agar by cutting agar bloc containing fungal growth. The plates were then incubated and maintained at 20°C for two weeks (Correa and Saettler, 1987; Olango *et al.*, 2017). Spores for inoculation were obtained by gently scraping the surface of sporulating colonies incubated for 14 days in sterile distilled water. The suspension was then filtered through a triple layer of cheesecloth (Correa and Saettler, 1987). Inoculations were done on both sides of the first and second trifoliolate leaves 21 days after planting (Wagara *et al.*, 1999).

Root rots: Plants were uprooted based on the presence of root rot-like symptoms prevailing on leaves (yellowing), roots and stems. Once the samples were collected, the isolation procedure described by White (1988) as modified by Nzungize *et al.* (2011b) was used to isolate the root rot agents related to the observed symptoms. A selective medium was prepared by mixing corn

meal agar CMA (17 g) and distilled water (1000 ml) before autoclaving at 121°C for 20 min. The antibiotic preparation [Rifamycin (0.03 g/L) and Pimaricin (0.02 g/L)] was then added after heat sterilization when the medium was cooling (around 40°C) to avoid contamination of medium by bacteria. Isolations were accomplished by first washing soil from the plant tissues in a jet-stream of tap water, rinsing twice in sterile distilled water, blotting dry on a new paper towel, and placing infected root pieces (approximately 0.5 to 2 cm long) cut from expanding lesions on the prepared selective medium (CMA). Petri plates with plant samples were observed after incubation for four days at room temperature (20 to 25°C). The root rot mycelia developing from the plant tissues were then transferred on potato dextrose agar (PDA) slants and incubated for 14 days (Nzungize *et al.*, 2011b). *Fusarium*, *Rhizoctonia* and *Pythium* root rots were then multiplied by plating mycelia on autoclaved millet grains (300 g) mixed with 200 ml of water in 1000 ml bottles. After two weeks of incubation under darkness and at 25°C, a pre-sterilized soil was mixed with the infested millet at a ratio of 1:10 v/v in polyphene pots three days before planting (Buruchara *et al.,* 2015). Three weeks after emergence of the seedlings, the surviving plants were uprooted and washed with water to remove soil.

Bean common mosaic virus: Young infected leaves of bean with distinct mosaic symptoms under field condition were collected and ground in a mortar and 0.1 M phosphate buffer (pH = 7.0) was added in 1:1 ratio (w/v). The slurry was squeezed through a muslin cloth. Sap was centrifuged at 3,000 rpm for 5 min. The supernatant thus obtained was used as a standard inoculum (Verma and Gupta, 2010). One primary leaf per plant was inoculated mechanically with a triturate of infected tissue (1 g of tissue per 10 mL of 50 mM sodium phosphate buffer, pH 7) with a small amount of 600 mesh carborundum powder when primary leaves were fully expanded (14 days after seedling emergence) (Strausbaugh *et al.*, 1999).

Common bacterial blight: The pathogen was isolated from leaves, or blighted petioles and stems. Tissue pieces on the margin between diseased and healthy areas were lightly surface disinfested with 70% ETOH and 10% sodium hypochlorite (bleach) followed by a sterile water rinse and plated on Yeast Dextrose Carbonate Agar (YDCA) medium (Claflin *et al.*, 1985; Schaad and Stall, 1988; Ishimaru *et al.,* 2005; Harveson and Schwartz, 2007). The inoculum was then adjusted to approximately 10^6 to 10^7colony-forming units (cfu)/ml. Inoculum spraying on plants was performed 14 days after seedling emergence using a fine mist with an atomizer

(Lelliott and Stead, 1987; Schaad and Stall, 1988; Harveson and Schwartz, 2007). Inoculated plants were covered with plastic bags, and placed into incubators. After four days, plants were then transferred in the greenhouse (25 to 28°C) until symptom development (Harveson and Schwartz, 2007).

5.2.3.2. Experimental design and data collection

The experiments for angular leaf spot (ALS), anthracnose, bean common mosaic virus (BCMV), and common bacterial blight (CBB) were conducted in a greenhouse at Kabete Field Station. Screening for resistance to *Fusarium solani* pv. *phaseoli*, *Rhizoctonia solani*, and *Pythium ultimum* root rots was conducted in an insectproof screenhouse at Kabete Field Station. The experimental design for each trial was a randomized complete block design (RCBD) with four replications. Each plot consisted of four pots each containing four plants making a total of 16 plants for each genotype in a replication.

Pots were filled with pre-sterilized soils mixed with cow manure and sand at a ratio of 3:1:1. As described previously, Kabete'soils used for this experiment are well drained, very deep, dark reddish brown, friable clay with acid humic topsoil, humic nitisols and a pH ranging from 5.0 to 5.4. Diammonium phosphate (DAP) (N 18%: P_2O_5 46%) at a rate of 80 kg ha^{-1} (12.8 g per pot) was applied at planting in each pot. The pots were irrigated to field capacity to ensure moisture-free conditions for the study plants. The root rot experiments relied exclusively on rain for water. Rainfall distribution during the study period was favourable for disease development in the screenhouse.

Data on disease incidence and severity were recorded at the 14^{th}, 21^{st} and 28^{th} days after inoculation for ALS, BCMV, anthracnose and CBB. Data on root rots were taken once, 21 days after seedling emergence. The disease severity was rated using a 1-9 CIAT scale: 1-3 being resistant, 3.1-6 intermediate and 6.1-9 susceptible (Schoonhoven and Pastor-Corrales, 1987; Okii *et al.,* 2017). The disease incidence was the percentage of diseased plants from the total number of plants initially inoculated. It was calculated as follows: Disease incidence= (No. of infected plants / Total no. of plants inoculated) x 100.

5.2.4. Data analysis

Genstat 15th edition software (VSN Int., 2013) was used for analysis of variance and mean separation. Analysis of variance (ANOVA) was used to reveal differences in reaction among genotypes to disease effects. Fisher's protected least significant difference (LSD) was used for mean separation at 1 and 5 percent probability levels. Area under disease progression curve (AUDPC) was performed for each genotype using the midpoint rule method (Campbell and Madden, 1990; Jeger and Viljanen-Rollinson, 2001; Olango *et al.*, 2017) as follows:

$$\text{AUDPC} = \sum_{i=1}^{n-1}\left(\frac{y_i + y_{i+1}}{2}\right)(t_{i+1} - t_i)$$

Where *t* represents the time in days of each observation, *y* is disease severity at observation and, *n* is the number of observations. The AUDPCs were next subjected to ANOVA to compare amounts of disease among different bean lines for each disease pathogen. Highest values corresponded to more susceptible while lowest values corresponded to more resistant varieties.

5.3. RESULTS

5.3.1. Preliminary tests of isolated pathogens on susceptible check varieties

Table 5.2 presents results of the preliminary tests showing reproduction of disease from isolated pathogens on susceptible checks and donor parents. This was to confirm that the disease screening system was effective and appropriate for germplasm evaluation following Koch's postulates. These results were in agreement with those of Musyimi (2014) and Njuguna (2014), confirming AND1062 and RWR719 as sources of resistance to root rot pathogens; BRB191 as a moderate source of resistance to bean common mosaic virus; G10909 and Mex54 for resistance to angular leaf spot and G2333 for the anthracnose. However, none of the donor parents and commercial checks used in population development showed high levels of resistance to common bacterial blight.

Table 5.2. Reaction of commercial checks and donor parents to disease pathogens under greenhouse conditions at Kabete Field Station, University of Nairobi

Genotypes	ALS	ANTH	BCMV	CBB	FRR	PRR	RRR
Donor parents							
AND1062	6.0	8.1	5.2	4.0	4.4	2.3	2.0
BRB191	4.0	7.4	3.3	4.0	6.5	3.0	2.3
G10909	2.0	2.0	6.0	6.7	6.1	6.3	2.6
G2333	1.8	1.8	5.5	6.5	3.9	6.5	2.0
Mex54	2.1	1.5	6.5	7.0	6.1	5.6	2.0
RWR719	5.5	2.0	4.2	4.0	4.2	1.8	2.0
Commercial checks							
GLP585	5.5	5.3	2.9	5.1	2.9	5.7	2.0
GLP92	6.3	2.0	5.0	5.9	6.0	6.1	2.0
KATB1	6.7	8.0	7.0	4.0	3.9	7.1	2.8
KATB9	7.0	7.8	5.7	3.8	6.0	6.9	2.0

ALS=angular leaf spot, ANTH=anthrachnose, BCMV=bean common mosaic virus, CBB=bean bacterial blight, FRR=*Fusarium* root rot, PRR=*Pythium* root rot, and RRR=*Rhizoctonia* root rot

Figure 5.1 presents pictures showing disease symptoms in susceptible varieties during preliminary tests.

a) **Root rot**

b) Common bacterial blight

c) Angular leaf spot

d) Bean common mosaic virus

e) Anthracnose

Figure 5.1. Disease symptoms in susceptible varieties

5.3.2. Mean squares for disease severity and AUDPC of pathogens on test lines

Mean squares for the severity, incidence and severity AUDPC from the analysis of variance are presented in Tables 5.3, 5.4 and 5.5 and were referred to in various sections on individual diseases. Table 5.3 shows that there were no significant differences in the reaction of elite lines and check varieties to the three root rot pathogens ($P>0.05$). However, genotypes reacted differently to angular leaf spot ($P<0.05$), bean common mosaic virus ($P<0.01$), common bean bacterial blight ($P<0.01$) and anthracnose pathogen ($P<0.001$). The differences among genotypes were even highly significant when referring to computed AUDPC values ($P<0.001$) regardless of the pathogens.

Table 5.3. Mean squares of incidence and severity scores for the root rot pathogens on elite bean lines at the 21st day after seedling emergence

Sources of variation	DF	FRR		RRR		PRR	
		Incidence	Severity	Incidence	Severity	Incidence	Severity
Replication	3	46889.4	140.6	159810	0.76	4170.9	36.3
Genotype	35	226.1^{ns}	2.2^{ns}	16^{ns}	1.7^{ns}	1235.2^{ns}	1.6^{ns}
Residual	35	204.8	1.7	16	1.0	173.0	0.95
Total	73						
Mean		74.2	5.0	52.9	2.2	50.9	3.5
$LSD_{0.05}$		29.0	2.7	8.1	2.0	26.7	2.0
CV (%)		19.3	26.4	7.5	45.1	25.9	27.9

DF=degree of freedom, $LSD_{0.05}$=least significant difference at 5% P-value threshold, CV=coefficient of variation, ns=no significant. FRR=*Fusarium* root rot, RRR=*Rhizoctonia* root rot, PRR=*Pythium* root rot.

Table 5.4. Mean squares of incidence and severity scores for the foliar pathogens on elite bean lines at the final score (28th days after inoculation)

Sources of variation	DF	ALS		BCMV		CBB		ANTH	
		Incidence	Severity	Incidence	Severity	Incidence	Severity	Incidence	Severity
Replication	3	5605.6	62.3	2322.2	6.1	4170.9	100.3	5.6	13.3
Genotype	35	712.4^{ns}	1.7*	1504.9^{ns}	3.1**	1235.2***	3.4**	952.1***	2.8 ^{ns}
Residual	35	493.5	0.78	864.6	0.92	173.0	1.0	2.1	2.4
Total	73								
Mean		28.7	2.7	75.1	3.5	50.9	3.6	28.9	2.6
$LSD_{0.05}$		45.1	1.8	59.7	1.9	26.7	2.0	2.9	59.1
CV (%)		77.5	32.9	39.2	27.8	25.9	27.5	5.0	52.1

DF=degree of freedom, $LSD_{0.05}$=least significant difference at 5% P-value threshold, CV=coefficient of variation, ns=no significant, *, **, ***=significant at P = 0.05, 0.01 and 0.001, respectively. ALS=angular leaf spot, BCMV=bean common mosaic virus, CBB=common bacterial blight, ANTH=anthracnose.

Table 5.5. Mean squares of incidence aand severity AUDPC for the foliar pathogens on elite bean lines under greenhouse conditions

Sources of variation	DF	ALS		BCMV		CBB		ANTH	
		Incidence	Severity	Incidence	Severity	Incidence	Severity	Incidence	Severity
Replication	3	17564.	741.1	122896.	115.0	158109.	5270.2	345	1378.1
Genotype	35	81206.***	78.8***	133628.***	364.9***	207554.***	418.4***	195616***	337.6^{ns}
Residual	35	8782.	16.6	21915.	18.8	20882.	74.5	153	274.6
Total	73								
Mean		486.5	32.2	1002	41.7	614.7	42.8	342.7	31.8
$LSD_{0.05}$		190.2	8.3	300.5	8.8	293.4	17.5	25.1	33.6
CV (%)		19.3	12.7	14.8	10.4	23.5	20.2	3.6	52.1

DF=degree of freedom, $LSD_{0.05}$=least significant difference at 5% P-value threshold, CV=coefficient of variation, ns=no significant, ***=significant at P = 0.001. ALS=angular leaf spot, BCMV=bean common mosaic virus, CBB=common bacterial blight, ANTH=anthracnose.

5.3.3. Reaction to root rot diseases

The *Fusarium* root rot was the most damaging disease on tested materials, its incidence ranged from 43.3% (on KMA13-27-31) to 96.1% (on the check variety BRB191) (Table 5.6). The disease severity was also high and ranging from 2.8 on KMA13-27-31 to 6.9 on KMA13-17-25. KMA13-27-31, a red kidney genotype, was the only elite bean line which showed resistance to *Fusarium* root rot. *Rhizoctonia* root rot affected more than 50% of plants for all the genotypes but the severity was very low. The incidence ranged from 50% to 61.6% on KMA13-31-6.2 while the severity ranged from 1.5 to 5.0. The *Pythium* root rot incidence was also very high and ranged from 53.9% to 84.6%. Severity of *Pythium* root rot varied from 2.1 on KMA13-32-28 to 5.8 on the check variety KATB1. The results showed that none of the elite lines or the check varieties had combined concurrently resistance to the three root rot-causing agents. However, 6 elite lines (KMA13-21-11; KMA13-23-14; KMA13-25-9; KMA13-28-5; KMA13-30-14 and KMA13-32-28) had combined resistance to *Rhizoctonia* and *Pythium* root rots simultaneously while KMA13-27-31 had concurrent resistance to *Fusarium* and *Rhizoctonia* root rots. Fortunately, more than 80% (21 of the 26) of the elite lines combined moderate resistance (scores of 4 to 6) for reaction to the three root rots.

Table 5.6. Incidence and severity of *Fusarium*, *Rhizoctonia* and *Pythium* root rots on inter-racial elite common bean lines grown in a greenhouse at Kabete, University of Nairobi.

Genotype	*Fusarium*			*Rhizoctonia*			*Pythium*		
	Incidence (%)	Severity	RC	Incidence (%)	Severity	RC	Incidence (%)	Severity	RC
KMA13-17-17	69.3	4.2	I	53.9	2.0	R	69.3	3.6	I
KMA13-17-25	92.3	6.9	S	50.0	1.5	R	84.6	4.4	I
KMA13-21-10	73.1	3.9	I	53.9	3.0	R	65.4	3.6	I
KMA13-21-11	65.4	6.1	S	50.0	1.5	R	61.6	2.9	R
KMA13-21-20	73.1	4.9	I	53.9	4.2	I	65.4	3.4	I
KMA13-22-21	73.1	4.7	I	53.9	4.0	I	53.9	2.3	R
KMA13-22-30	76.9	5.4	I	53.9	3.2	I	73.1	4.4	I
KMA13-23-13	69.3	4.1	I	53.9	2.3	R	69.3	3.6	I
KMA13-23-14	73.1	5.2	I	53.9	3.0	R	61.6	2.9	R
KMA13-23-22	84.6	6.2	I	57.7	2.1	R	61.6	3.3	I
KMA13-24-7	61.6	3.8	I	50.0	1.5	R	57.7	3.1	I
KMA13-25-9	65.4	4.6	I	53.9	2.5	R	53.9	2.5	R
KMA13-26-32	69.3	5.0	I	53.9	1.8	R	69.3	3.9	I
KMA13-27-12	84.6	5.9	I	57.7	3.1	I	69.3	4.5	I
KMA13-27-27	80.8	5.5	I	50.0	1.5	R	59.1	3.9	I
KMA13-27-31	49.3	2.8	R	50.0	1.5	R	57.7	3.9	I
KMA13-28-13	80.8	6.5	S	53.9	2.0	R	65.4	3.3	I
KMA13-28-2	61.6	4.1	I	50.0	1.5	R	57.7	3.9	I
KMA13-28-21	65.4	3.4	I	53.9	5.0	I	53.9	2.8	R
KMA13-28-5	80.8	6.0	I	53.9	3.0	R	59.1	2.6	R
KMA13-29-21	69.3	5.0	I	53.9	2.0	R	73.1	4.4	I
KMA13-29-24	76.9	4.9	I	50.0	1.5	R	61.6	3.4	I
KMA13-30-14	88.5	5.9	I	53.9	3.0	R	53.9	2.5	R
KMA13-30-22	80.8	5.6	I	53.9	1.8	R	84.6	5.6	I
KMA13-31-62	73.1	4.9	I	61.6	3.7	I	65.4	4.1	I
KMA13-32-28	61.6	4.9	I	53.9	2.0	R	57.7	2.1	R
AND1062	69.3	4.4	I	50.0	1.5	R	73.1	3.6	I
BRB191	96.2	6.5	S	53.9	1.8	R	80.8	4.9	I
G10909	80.8	6.1	S	57.7	2.1	R	69.3	3.4	I
G2333	57.7	3.9	I	50.0	1.5	R	53.9	2.3	R
GLP585	61.6	2.9	R	50.0	1.5	R	69.3	3.6	I
GLP92	92.3	5.9	I	50.0	1.5	R	69.3	3.9	I
KATB1	69.3	3.9	I	53.9	2.3	R	80.8	5.8	I
KATB9	80.8	5.9	I	50.0	1.5	R	57.7	3.0	R
Mex54	88.5	6.1	S	50.0	1.5	R	61.6	2.4	R
RWR719	76.9	4.2	I	50.0	1.5	R	57.7	2.6	R
Mean	74.2	5.0		52.9	2.2		64.9	3.5	
$LSD_{0.05}$	29.1	2.7		8.1	2.0		25.0	1.9	
CV (%)	19.3	26.4		7.5	45.1		18.9	27.9	

RC=reaction category; R=resistant; I=intermediate; S=susceptible; LSD=least significant difference at P-value threshold of 0.05; CV=coefficient of variation

Figure 5.2 presents symptoms of the three root rot pathogens as observed on susceptible genotypes.

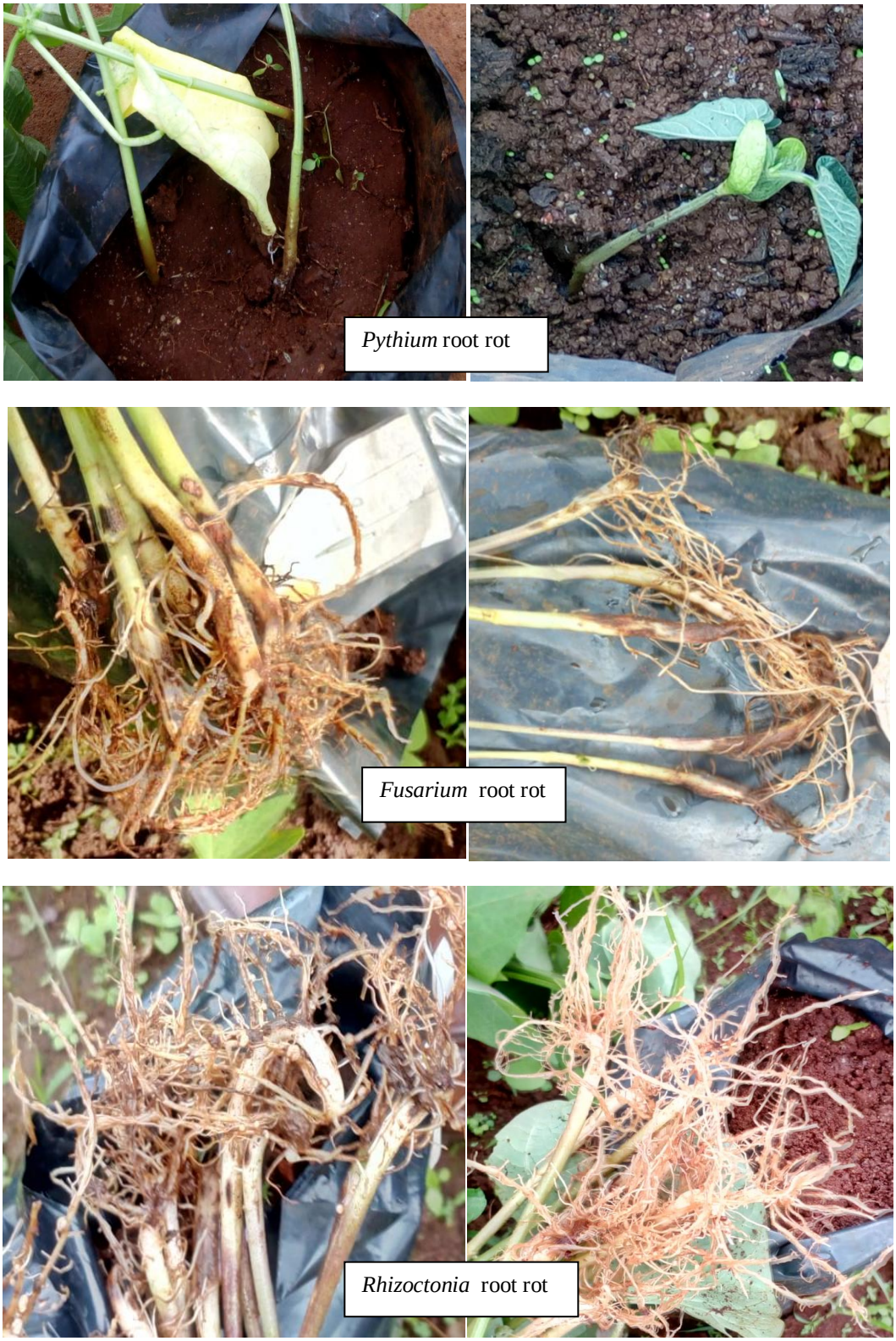

Figure 5.2. Root rot symptoms on susceptible genotypes

5.3.4. Reaction to bean common mosaic virus

Table 5.7 shows that 13 elite lines were resistant to bean common mosaic virus (BCMV) while the other 13 were moderately resistant. However, none of the lines was completely immune or highly susceptible to BCMV. Four of the 10 checks were resistant, five were intermediate and one (KATB1) was highly susceptible. The BCMV incidence was very high and increased over time from 34.8 percent 14 days after inoculation, to 88.2 percent after 21 days and to 93.4 percent on the 28th day after inoculation. The disease severity score increased from 2.5 on the 14th day after inoculation to 3.0 and 3.5 on the 21st and 28th days after inoculation, respectively. There were highly significant differences among genotypes for their reaction to BCMV when referring to computed severity AUDPCs ($P<0.001$). The highest levels of infection were recorded on the check variety KATB1 (82.2) (Figure 5.3). Line KMA13-30-14 (24.5) was the most resistant genotype compared to all the other elite lines and checks. Other elite lines with low levels of infection were KMA13-22-21, KMA13-23-22, KMA13-27-12, and KMA13-28-21 with an AUDPC value of 26.2.

Table 5.7. Incidence and severity of bean common mosaic virus on inter-racial elite common bean lines grown in a greenhouse at Kabete, University of Nairobi.

Genotype	14 Days after inoculation		21 Days after inoculation		28 Days after inoculation		Severity AUDPC	RC
	Incidence (%)	Severity	Incidence (%)	Severity	Incidence (%)	Severity		
KMA13-17-17	16.7	1.5	100.0	3.0	100.0	4.5	42.0	I
KMA13-17-25	50.0	2.0	100.0	2.0	100.0	4.0	35.0	I
KMA13-21-10	16.7	2.0	66.6	4.0	80.0	5.5	54.2	I
KMA13-21-11	35.0	4.0	94.5	4.0	100.0	4.5	57.8	I
KMA13-21-20	25.0	2.0	100.0	3.0	100.0	4.0	42.0	I
KMA13-22-21	8.4	1.5	33.3	2.0	58.4	2.0	26.2	R
KMA13-22-30	35.0	3.0	33.3	4.0	80.0	3.5	50.8	I
KMA13-23-13	41.7	3.5	91.7	3.0	98.4	2.5	42.0	R
KMA13-23-14	28.6	2.0	100.0	3.0	100.0	3.5	40.2	I
KMA13-23-22	50.0	1.5	100.0	2.0	100.0	2.0	26.2	R
KMA13-24-7	21.7	2.5	100.0	3.0	100.0	4.0	43.8	I
KMA13-25-9	43.8	2.0	100.0	2.0	100.0	2.5	29.8	R
KMA13-26-32	54.6	3.0	100.0	3.0	100.0	4.0	45.5	I
KMA13-27-12	8.4	1.5	100.0	2.0	100.0	2.0	26.2	R
KMA13-27-27	16.7	1.5	40.0	2.0	55.0	2.5	28.0	R
KMA13-27-31	50.0	2.5	100.0	2.0	100.0	4.5	38.5	I
KMA13-28-13	31.3	3.0	37.5	3.0	68.8	2.5	40.2	R
KMA13-28-2	28.6	4.5	100.0	5.5	100.0	5.5	73.5	I
KMA13-28-21	10.0	1.5	100.0	2.0	100.0	2.0	26.2	R
KMA13-28-5	54.8	3.5	28.6	2.0	56.0	3.0	36.8	R
KMA13-29-21	50.0	1.5	100.0	3.0	100.0	2.5	35.0	R
KMA13-29-24	16.7	1.5	100.0	2.0	100.0	3.0	29.8	R
KMA13-30-14	12.5	1.5	87.5	2.0	90.0	1.5	24.5	R
KMA13-30-22	12.5	1.5	75.0	3.0	82.5	3.5	38.5	I
KMA13-31-62	20.6	2.5	87.5	4.0	94.3	3.0	47.2	R
KMA13-32-28	57.5	3.5	100.0	5.0	100.0	4.5	63.0	I
AND1062	50.0	4.0	100.0	4.0	100.0	5.5	61.2	I
BRB191	47.9	4.0	100.0	4.0	100.0	3.5	40.2	I
G10909	87.5	4.0	100.0	3.0	100.0	2.5	43.8	R
G2333	14.3	1.5	100.0	2.0	100.0	3.0	29.8	R
GLP585	8.4	1.5	100.0	2.0	100.0	2.0	26.2	R
GLP92	18.4	2.0	100.0	3.0	100.0	2.5	36.8	R
KATB1	90.0	4.5	100.0	6.0	100.0	7.0	82.2	S
KATB9	25.0	2.0	100.0	3.0	100.0	4.5	43.8	I
Mex54	50.0	2.5	100.0	4.0	100.0	3.5	49.0	I
RWR719	66.7	3.0	100.0	3.0	100.0	4.0	45.5	I
Mean	34.8	2.5	88.2	3.0	93.4	3.5	41.7	
$LSD_{0.05}$	62.1	1.8	13.8	1.2	29.7	1.9	8.8	
CV (%)	87.9	34.9	17.7	13.9	19.2	27.8	10.4	

RC=reaction category; R=resistant; I=intermediate; S=susceptible; LSD=least significant difference at P-value threshold of 0.05; CV=coefficient of variation

A chart comparing the BCMV progression on a resistant elite line and on a susceptible commercial cultivar is present in Figure 5.3. This was to show the progress made in breeding for resistance. Field illustration of the disease progression is also presented in Figure 5.4 for the 14^{th}, 21^{st} and 28^{th} day after inoculation.

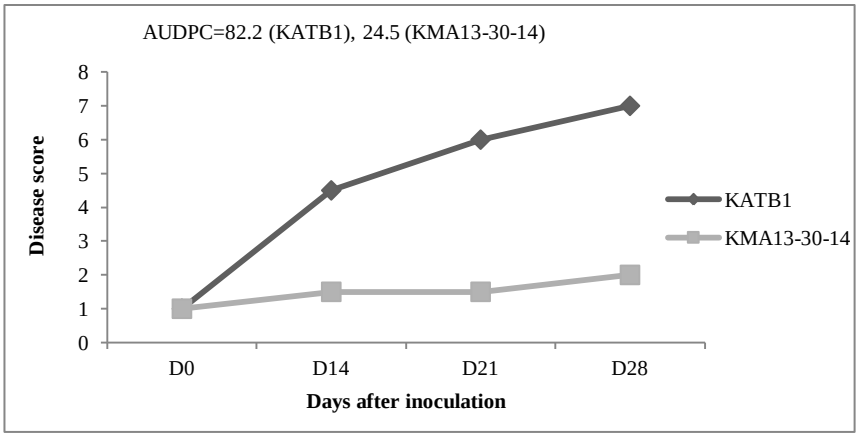

Figure 5.3. Comparative BCMV severity progression between a resistant line (KMA13-30-14) and a susceptible check variety (KATB1)

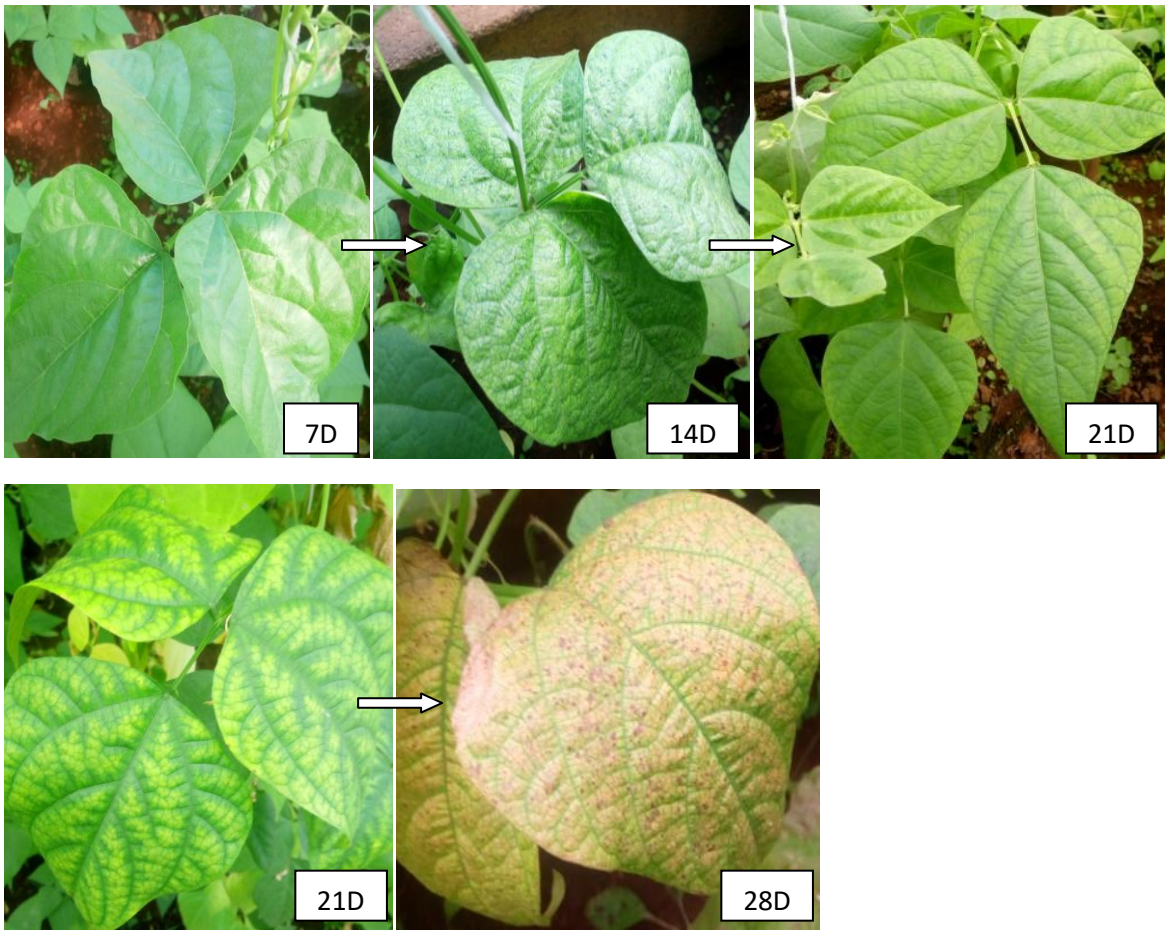

Figure 5.4. BCMV disease progression on susceptible cultivar (KATB1)

5.3.5. Reaction to angular leaf spot pathogen

Table 5.8 shows that 18 of the 26 elite lines were resistant to infection by angular leaf spot (ALS) pathogen, *Pseudocercospora griseola*; eight were intermediate, and none was highly susceptible. The pathogen effects were almost static (stable) over time as the severity scores were 2.0, 2.5 and 2.8 at 14^{th}, 21^{st} and 28^{th} days after inoculation, respectively. However, disease incidence increased from 35.1% on the 14^{th} day after inoculation to 45.7% on the 21^{st} day, and to 51.5% on the 28^{th} day. Computed AUDPCs, showed that there were highly significant differences among the genotypes for reaction to the ALS infections ($P<0.001$). The elite line KMA13-17-25, with an AUDPC value of 14.0, was the most resistant genotype to ALS compared to all other lines and parental checks. Other elite lines with low levels of infection were KMA13-27-12 (24.5), KMA13-17-17, KMA13-23-14, KMA13-26-32, and KMA13-28-21, all with an AUDPC value of 26.2.

Table 5.8. Incidence and severity of angular leaf spot on inter-racial elite common bean lines grown in a greenhouse at Kabete, University of Nairobi.

Genotype	14 Days after inoculation		21 Days after inoculation		28 Days after inoculation		Severity AUDPC	RC
	Incidence (%)	Severity	Incidence (%)	Severity	Incidence (%)	Severity		
KMA13-17-17	33.4	2.0	36.7	2.0	36.7	1.5	26.2	R
KMA13-17-25	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-21-10	56.3	2.0	62.9	2.5	69.3	4.0	36.7	I
KMA13-21-11	38.1	2.0	38.6	4.0	50.0	3.5	40.2	I
KMA13-21-20	42.9	2.0	50.0	3.0	56.8	3.0	35.0	R
KMA13-22-21	59.1	3.0	64.4	3.5	68.9	4.5	49.0	I
KMA13-22-30	22.8	2.0	28.1	2.0	59.1	4.5	36.8	I
KMA13-23-13	87.5	2.0	95.0	3.5	97.5	4.5	42.0	I
KMA13-23-14	10.0	2.0	20.0	1.5	20.0	2.0	26.2	R
KMA13-23-22	64.3	2.0	72.9	4.0	72.9	4.0	42.0	I
KMA13-24-7	83.4	2.0	83.4	3.0	90.8	3.0	35.0	R
KMA13-25-9	53.6	2.0	62.2	3.5	68.6	3.0	36.8	R
KMA13-26-32	25.0	2.0	33.3	2.0	36.7	1.5	26.2	R
KMA13-27-12	0.0	2.0	33.3	1.0	38.4	2.0	24.5	R
KMA13-27-27	32.5	2.0	37.5	2.0	40.0	2.5	29.8	R
KMA13-27-31	37.5	2.0	37.5	2.5	38.8	2.5	31.5	R
KMA13-28-13	33.3	2.0	44.4	2.0	52.2	3.0	31.5	R
KMA13-28-2	42.9	2.0	42.8	2.0	55.7	2.5	29.8	R
KMA13-28-21	8.4	2.0	42.9	1.5	44.3	2.0	26.2	R
KMA13-28-5	30.3	2.0	33.3	2.0	37.5	2.5	29.8	R
KMA13-29-21	12.5	2.0	25.0	1.5	32.5	2.5	28.0	R
KMA13-29-24	18.8	2.0	25.0	2.0	28.6	3.5	33.2	I
KMA13-30-14	28.4	2.0	33.3	3.5	50.0	3.5	38.5	I
KMA13-30-22	20.0	2.0	40.0	2.0	46.7	2.0	28.0	R
KMA13-31-62	44.3	2.0	46.4	3.0	51.6	2.0	31.5	R
KMA13-32-28	12.5	2.0	25.0	1.5	33.6	2.5	28.0	R
AND1062	37.5	2.0	40.0	2.0	45.0	3.5	29.8	I
BRB191	62.5	2.0	70.0	2.5	77.5	3.0	29.8	R
G10909	63.1	2.0	67.1	2.0	68.6	2.0	38.5	R
G2333	25.0	2.0	50.0	2.0	56.7	3.5	29.8	I
GLP585	43.8	2.0	47.5	3.5	48.8	3.5	35.0	I
GLP92	0.0	3.0	50.0	1.0	50.0	4.0	28.0	I
KATB1	41.7	2.0	66.6	3.0	70.0	3.5	33.2	I
KATB9	26.8	2.0	35.0	2.5	42.5	3.5	28.0	I
Mex54	50.0	2.0	60.0	2.0	65.0	2.2	35.0	R
RWR719	15.6	2.0	44.4	3.0	51.7	4.6	35.0	I
Mean	35.1	2.0	45.7	2.5	51.5	2.9	32.5	
$LSD_{0.05}$	29.0	0.7	28.1	1.2	45.1	1.8	8.3	
CV (%)	40.7	14.4	23.0	24.6	37.5	32.9	12.7	

RC=reaction category; R=resistant; I=intermediate; S=susceptible; LSD=least significant difference at P-value threshold of 0.05; CV=coefficient of variation

Figure 5.5 compares in a chart, the ALS disease progression on a resistant line (KMA13-17-25) and on a susceptible check (RWR719). The disease progression on a susceptible genotype at the 14^{th}, 21^{st} and 28^{th} days after inoculation is illustrated in Figure 5.6.

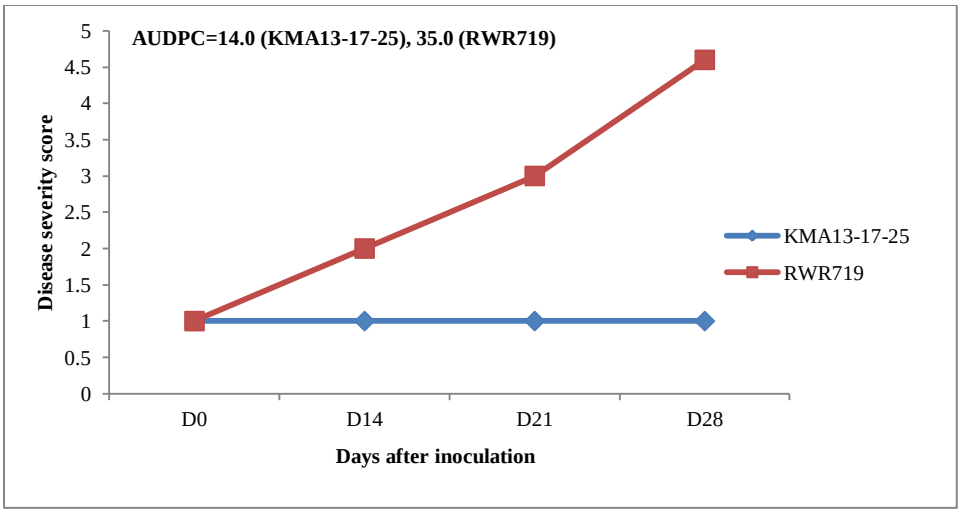

Figure 5.5. Comparative ALS severity progression between a resistant line (KMA13-17-25) and a susceptible check variety (RWR719)

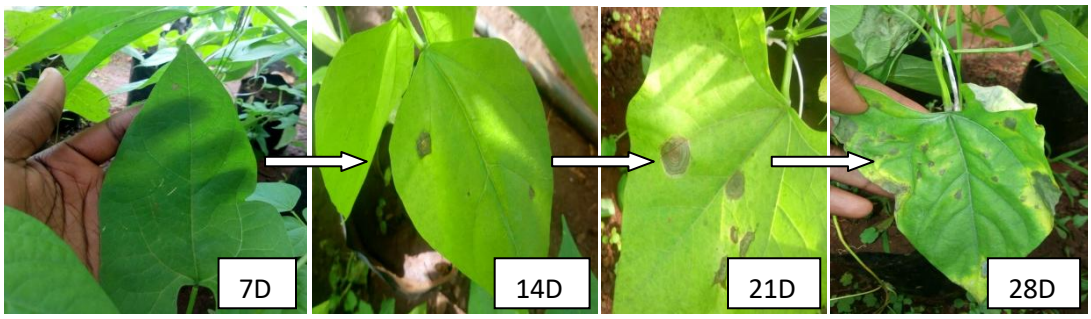

Figure 5.6. ALS disease progression on susceptible cultivar (RWR719)

5.3.6. Reaction to common bacterial blight

Table 5.9 shows that six of 26 elite lines were resistant to common bacterial blight (CBB), among which KMA13-17-17, KMA13-28-2, KMA13-28-21 and KMA13-30-14 were completely immune as not a single plant showed CBB symptoms. Eighteen (18) of the 26 elite lines had moderate resistance (3.1 to 6.0) while only 2 were highly susceptible (6.1 to 9).

None of the check varieties was resistant to CBB; eight of the 10 checks were moderately resistant while two were highly susceptible (Mex54 and G2333). The CBB severity and incidence on tested lines increased over time (Figure 5.7 and Figure 5.8). The overall mean incidences were 33.6%, 48.1% and 54.4% of diseased plants at 14th, 21st and 28th days after inoculation, respectively. The severity means were 2.7, 3.0 and 3.6 at 14th, 21st and 28th days after inoculation, respectively. There were highly significant differences among genotypes for

their reactions to CBB when comparing their severity AUDPCs (*P<0.001*). Based on computed AUDPC values, the check variety Mex54 was the most susceptible. It had the highest AUDPC value (71.8) compared to all the elite lines and other checks. The lowest infection levels (14.0) were recorded on elite lines KMA13-17-17, KMA13-28-2 and KMA13-30-14.

Table 5.9. Incidence and severity of common bacterial blight on inter-racial elite common bean lines grown in a greenhouse at Kabete, University of Nairobi.

Genotype	14 Days after inoculation		21 Days after inoculation		28 Days after inoculation		Severity AUDPC	RC
	Incidence (%)	Severity	Incidence (%)	Severity	Incidence (%)	Severity		
KMA13-17-17	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-17-25	12.5	1.5	50.0	3.0	50.0	4.0	36.8	I
KMA13-21-10	45.2	3.0	69.1	4.0	74.6	6.0	56.0	I
KMA13-21-11	18.8	2.0	50.0	3.0	56.3	4.0	38.5	I
KMA13-21-20	56.3	4.0	56.3	4.0	62.5	7.0	59.5	S
KMA13-22-21	31.3	2.5	60.7	3.5	60.7	5.0	47.2	I
KMA13-22-30	75.0	4.5	75.0	3.5	75.0	5.0	54.2	I
KMA13-23-13	66.7	4.5	100.0	4.5	100.0	8.0	68.2	S
KMA13-23-14	58.3	4.5	83.3	4.5	83.3	6.0	61.2	I
KMA13-23-22	39.3	3.0	53.5	3.5	65.3	6.0	50.8	I
KMA13-24-7	58.4	3.5	66.7	3.5	66.7	5.0	50.8	I
KMA13-25-9	33.3	2.5	33.3	3.0	44.5	5.0	42.0	I
KMA13-26-32	31.3	2.0	38.8	2.0	45.0	2.0	28.0	R
KMA13-27-12	37.5	2.5	55.0	3.5	62.5	5.0	45.5	I
KMA13-27-27	37.5	3.5	50.0	3.5	56.3	6.0	52.5	I
KMA13-27-31	37.5	2.0	37.5	1.5	37.5	2.0	22.8	R
KMA13-28-13	43.8	3.0	43.8	2.5	43.8	5.0	42.0	I
KMA13-28-2	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-28-21	0.0	1.0	8.4	1.5	0.0	1.0	17.5	R
KMA13-28-5	44.4	3.5	66.7	4.5	74.5	6.0	61.2	I
KMA13-29-21	16.7	1.5	33.3	2.0	83.3	5.0	31.5	I
KMA13-29-24	75.0	3.5	87.5	3.0	87.5	5.0	49.0	I
KMA13-30-14	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-30-22	31.3	2.5	56.3	3.0	68.8	5.0	45.5	I
KMA13-31-62	42.9	3.5	64.3	2.5	71.4	5.0	43.8	I
KMA13-32-28	25.0	3.5	35.0	3.0	36.7	6.0	47.2	I
AND1062	20.0	2.0	30.0	2.5	50.0	4.0	35.0	I
BRB191	30.0	2.5	30.0	3.5	40.0	6.0	47.2	I
G10909	10.0	1.5	46.7	2.5	56.7	6.0	36.8	I
G2333	13.4	2.0	25.9	3.5	52.7	8.0	50.8	S
GLP585	5.6	1.5	18.1	2.5	22.2	5.0	35.0	I
GLP92	46.7	3.5	75.0	3.0	76.7	5.0	47.2	I
KATB1	31.3	3.5	56.3	3.0	56.3	4.0	43.5	I
KATB9	40.0	3.0	60.0	3.0	70.0	5.0	47.2	I
Mex54	52.7	5.0	72.3	5.0	79.5	8.0	71.8	S
RWR719	41.0	2.0	42.5	2.5	47.8	4.0	35.0	I
Mean	33.6	2.7	48.1	3.0	54.4	3.6	42.8	
$LSD_{0.05}$	37.4	1.3	31.1	1.7	26.7	2.0	17.5	
CV (%)	54.9	23.1	33.6	28.8	25.8	27.5	20.2	

RC=reaction category; R=resistant; I=intermediate; S=susceptible; LSD=least significant difference at P-value threshold of 0.05; CV=coefficient of variation

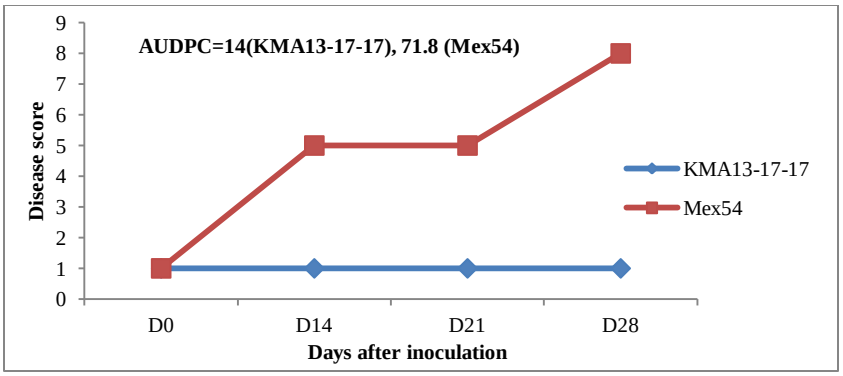

Figure 5.7. Comparative CBB severity progression between a resistant line (KMA13-17-17) and a susceptible check variety (Mex54)

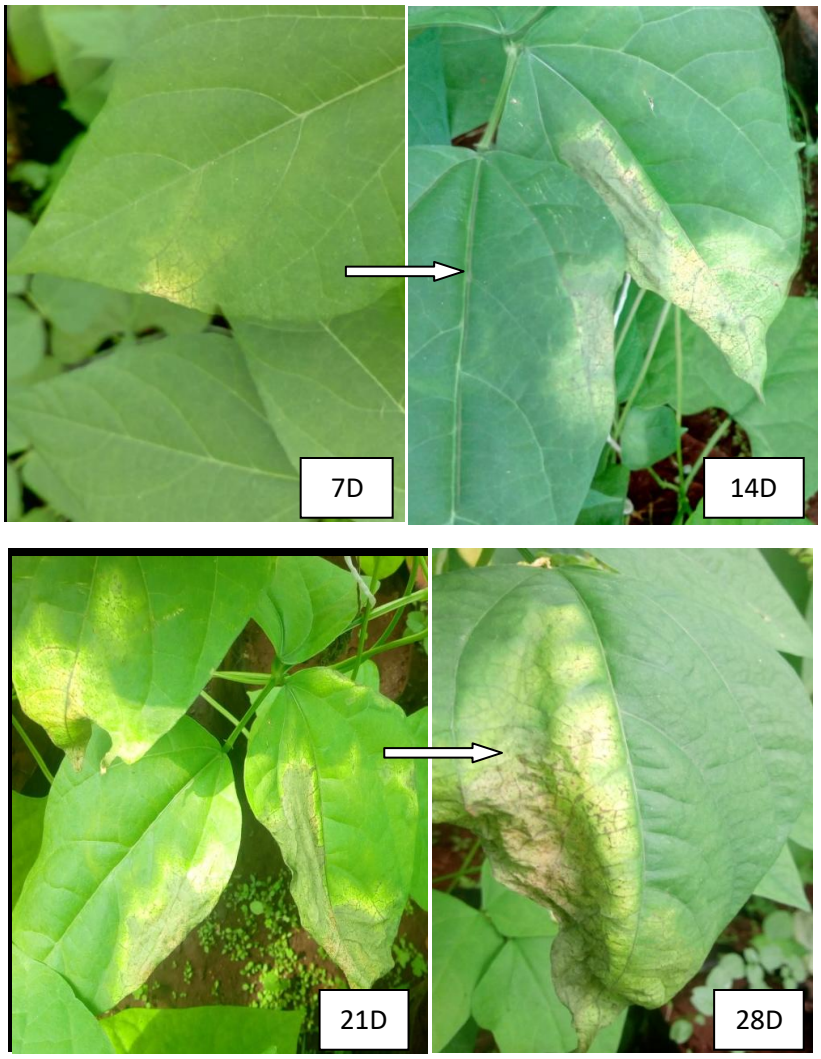

Figure 5.8. CBB disease progression on susceptible cultivar (Mex54)

5.3.7. Reaction to anthracnose pathogen

Table 5.10 shows that most of the elite lines were resistant to anthracnose. The disease severity ranged from 1.0 on elite lines KMA13-21-20, KMA13-28-21, and KMA13-29-21 to 6.0 on the check variety KATB1. Disease incidences were also low; averages were 20.9%, 24.1%, and 28.9% at 14^{th}, 21^{st} and 28^{th} days after inoculation. Referring to the AUDPC values, KMA13-21-20, KMA13-28-21, and KMA13-29-21 were the most resistant as they recorded the lowest infection levels (14.0). The highest levels of infection were recorded on check varieties KATB1 (70.0) and KATB9 (66.6). Figure 5.9 compares the disease progression in a susceptible check variety (KATB1) to a resistant elite line (KMA13-21-20). Figure 5.10 illustrates the disease progression on the susceptible check KATB1.

Table 5.10. Incidence and severity of anthracnose on inter-racial elite common bean lines grown in a greenhouse at Kabete, University of Nairobi.

Genotypes	14 Days after inoculation		21 Days after inoculation		28 Days after inoculation		Severity AUDPC	RC
	Incidence (%)	Severity	Incidence (%)	Severity	Incidence (%)	Severity		
KMA13-17-17	20.0	2.0	22.0	2.0	27.0	2.0	28.0	R
KMA13-17-25	9.0	2.0	11.0	2.0	19.0	2.0	28.0	R
KMA13-21-10	16.7	2.0	19.0	2.0	22.0	3.0	31.5	R
KMA13-21-11	16.7	2.0	17.5	2.0	22.0	2.0	28.0	R
KMA13-21-20	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-22-21	57.1	2.0	64.0	3.0	69.0	3.0	38.5	R
KMA13-22-30	40.0	2.0	43.0	2.0	44.0	2.0	28.0	R
KMA13-23-13	33.3	2.0	39.0	2.0	39.0	3.0	31.5	R
KMA13-23-14	36.4	2.0	38.0	2.0	40.0	3.0	31.5	R
KMA13-23-22	71.4	3.0	77.0	4.0	77.0	4.0	52.5	I
KMA13-24-7	75.0	3.0	87.0	3.0	100.0	3.0	42.0	R
KMA13-25-9	0.0	1.0	0.0	1.0	11.0	2.0	17.5	R
KMA13-26-32	40.0	2.0	48.0	2.0	52.0	2.0	28.0	R
KMA13-27-12	18.2	2.0	20.0	2.0	26.0	2.0	28.0	R
KMA13-27-27	22.2	2.0	25.0	2.0	27.0	2.0	28.0	R
KMA13-27-31	0.0	1.0	0.0	1.0	11.0	2.0	17.5	R
KMA13-28-13	37.5	2.0	38.0	3.0	40.0	3.0	38.5	R
KMA13-28-2	14.3	2.0	15.0	2.0	19.0	2.0	28.0	R
KMA13-28-21	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-28-5	10.0	2.0	15.0	2.0	22.0	2.0	28.0	R
KMA13-29-21	0.0	1.0	0.0	1.0	0.0	1.0	14.0	R
KMA13-29-24	16.7	2.0	18.0	2.0	24.0	2.0	28.0	R
KMA13-30-14	20.0	2.0	22.0	2.0	32.0	3.0	31.5	R
KMA13-30-22	50.0	2.0	55.0	2.0	62.0	2.0	28.0	R
KMA13-31-62	11.1	2.0	15.0	2.0	17.0	2.0	28.0	R
KMA13-32-28	0.0	1.0	9.0	2.0	14.0	2.0	24.5	R
AND1062	0.0	1.0	11.0	3.0	24.0	5.0	42.0	I
BRB191	6.0	2.0	17.0	4.5	22.0	5.0	56.0	I
G10909	25.0	2.0	30.0	2.0	37.0	2.0	28.0	R
G2333	25.0	2.0	25.0	2.5	29.0	2.5	33.2	R
GLP585	27.3	2.0	32.0	3.0	38.0	3.5	40.2	I
GLP92	0.0	1.0	11.0	2.0	19.0	2.0	24.5	R
KATB1	16.7	3.0	18.0	5.5	25.5	6.0	70.0	I
KATB9	5.5	2.5	14.5	5.5	25.5	5.5	66.5	I
Mex54	0.0	1.0	0.0	1.0	12.0	2.0	17.5	R
RWR719	11.1	2.0	14.0	2.0	16.0	3.0	31.5	R
Mean	20.9	1.8	24.1	2.3	28.9	2.6	31.8	
$LSD_{0.05}$	2.6	1.0	1.7	2.8	2.9	3.1	33.6	
CV (%)	6.2	25.6	3.4	60.7	5.0	59.1	52.1	

RC=reaction category; R=resistant; I=intermediate; S=susceptible; LSD=least significant difference at P-value threshold of 0.05; CV=coefficient of variation

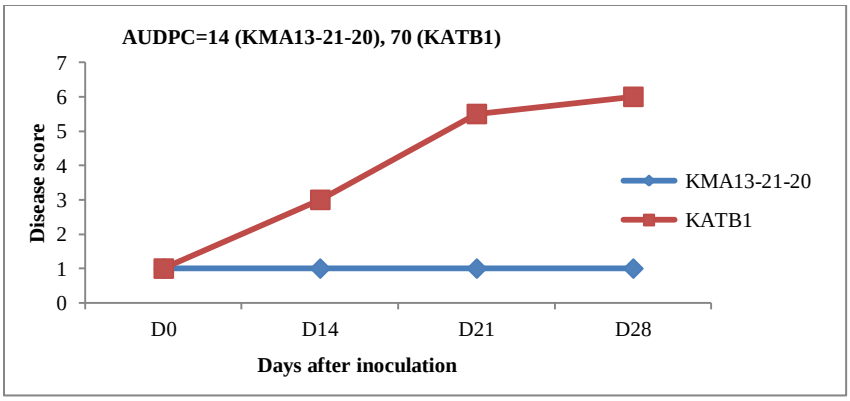

Figure 5.9. Comparative anthracnose severity progression between a resistant line (KMA13-21-20) and a susceptible check variety (KATB1)

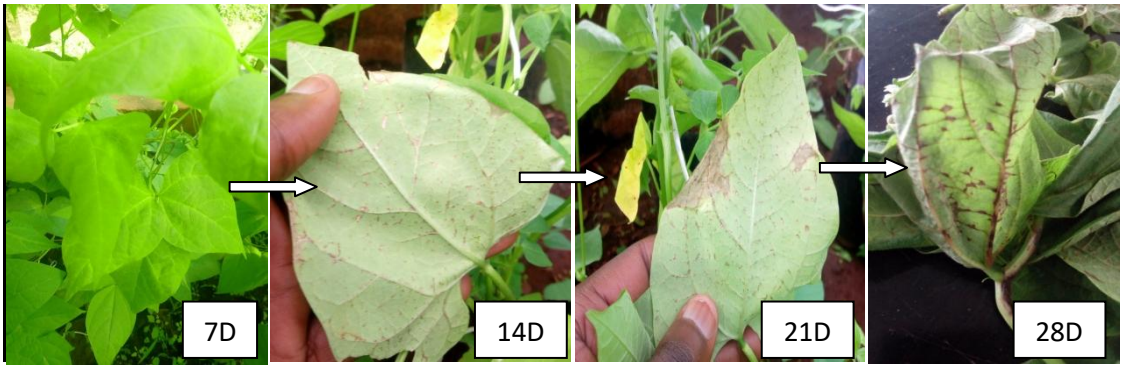

Figure 5.10. Anthracnose disease progression on susceptible cultivar (KATB1)

5.3.8. Multiple resistance in elite lines

From Table 5.11, all the elite lines possessed a resistance to at least one of the pathogens. In summary, five of the 26 elite lines possessed a multiple resistance to five pathogens (KMA13-25-9, KMA13-27-31, KMA13-28-21, KMA13-28-5, and KMA13-30-14); eight genotypes were resistant to four pathogens (KMA13-17-17, KMA13-23-14, KMA13-26-32, KMA13-27-27, KMA13-28-13, KMA13-28-2, KMA13-29-21, and KMA13-32-28); nine genotypes were resistant to three pathogens, three of the 26 elite lines possessed resistance to two pathogens and one had a resistance to one disease. Table 5.12 shows that there were no significant correlations in reaction of tested genotypes to the seven diseases used in this study, except the significant correlation ($P<0.05$) between the reaction of genotypes to bean common mosaic virus and the angular leaf spot (r=0.3942*).

Table 5.11. Multiple disease resistance of elite bean lines grown under greenhouse conditions at Kabete Field Station, University of Nairobi

Genotypes	[1]Pathogens							[2]Resistances	Number
	ALS	BCMV	CBB	ANT	*Fusarium*	*Rhizoctonia*	*Pythium*		
KMA13-17-17	R	I	R	R	I	R	I	A, C, AN, R	4
KMA13-17-25	R	I	I	R	S	R	I	A, AN, R	3
KMA13-21-10	I	I	I	R	I	R	I	AN, R	2
KMA13-21-11	I	I	I	R	S	R	R	AN, R, P	3
KMA13-21-20	R	I	S	R	I	I	I	A, AN	2
KMA13-22-21	I	R	I	R	I	I	R	B, AN, P	3
KMA13-22-30	I	I	I	R	I	I	I	ANT	1
KMA13-23-13	I	R	S	R	I	R	I	B, AN, R	3
KMA13-23-14	R	I	I	R	I	R	R	A, R,AN, P	4
KMA13-23-22	I	R	I	I	I	R	I	B, R	2
KMA13-24-7	R	I	I	R	I	R	I	A, AN, R	3
KMA13-25-9	R	R	I	R	I	R	R	A, B,AN, R, P	5
KMA13-26-32	R	I	R	R	I	R	I	A, C, AN, R	4
KMA13-27-12	R	R	I	R	I	I	I	A, AN, B	3
KMA13-27-27	R	R	I	R	I	R	I	A, B, AN, R	4
KMA13-27-31	R	I	R	R	R	R	I	A, C, AN, F, R	5
KMA13-28-13	R	R	I	R	S	R	I	A, B, AN, R	4
KMA13-28-2	R	I	R	R	I	R	I	A, C, AN, R	4
KMA13-28-21	R	R	R	R	I	I	R	A, B, C, AN, P	5
KMA13-28-5	R	R	I	R	I	R	R	A, B, AN, R, P	5
KMA13-29-21	R	R	I	R	I	R	I	A, B, AN, R	4
KMA13-29-24	I	R	I	R	I	R	I	B, AN, R	3
KMA13-30-14	I	R	R	R	I	R	R	B, C, AN, R, P	5
KMA13-30-22	R	I	I	R	I	R	I	A, AN, R	3
KMA13-31-62	R	R	I	R	I	I	I	A, B, AN	3
KMA13-32-28	R	I	I	R	I	R	R	A, AN, R, P	4

1: R=resistant; I=intermediate; S=susceptible

2: A=ALS; B=BCMV; C=CBB; AN=anthracnose; F=*Fusarium*; R=*Rhizoctonia* and P=*Pythium*

Table 5.12. Pearson's correlation coefficient among pathogens for disease resistance

Parameters	ALS	ANT	BCMV	CBB	FRR	PRR
ANT	0.1604^{ns}					
BCMV	0.3942*	-0.1099^{ns}				
CBB	0.1171^{ns}	0.0301^{ns}	0.1780^{ns}			
FRR	-0.1755^{ns}	-0.0185^{ns}	-0.0705^{ns}	0.1848^{ns}		
PRR	-0.1933^{ns}	0.0401^{ns}	0.0725^{ns}	-0.1040^{ns}	0.0849^{ns}	
RRR	-0.0145^{ns}	-0.0656^{ns}	-0.2251^{ns}	0.0293^{ns}	0.0691^{ns}	-0.1989^{ns}

ns=not significant; *=significant at 0.05 P-value threshold; ALS=angular leaf spot; ANT=anthracnose; BCMV=bean common mosaic virus; CBB=common bacterial blight; FRR=*Fusarium* root rot; PRR=*Pythium* root rot; RRR=*Rhizoctonia* root rot

5.4. DISCUSSION

This study confirmed the effectiveness of marker-assisted gamete selection to concurrently improve the common bean resistance to major diseases in Eastern and Central Africa. In fact, during the population development, markers were only used in early generations (F_1 while selecting male gametes to be involved in final crosses and $F_{1.1}$ to confirm desirable genes are found in the multiple-parent F_1). From these disease phenotypic validation experiments in controlled environments, more than 96% of the tested elite bean lines (25 of the 26) combined concurrent resistance to at least two pathogens. Five of them combined resistance to five different pathogens. This implied that markers were effective in the identification and transfer of resistance genes to susceptible commercial varieties in early generations. From these results, efficient use of markers in the gamete selection method at early generations is enough for pyramiding resistance genes into susceptible genotypes.

The preliminary test confirmed the donor parents used as sources of resistance to target diseases: AND1062 and RWR719 for *Pythium* root rot, BRB191 for BCMV, G10909 and Mex54 for ALS, and G2333 for anthracnose. The fact that phenotypic resistance to target pathogens has been observed on elite lines developed using those parents proved how effective was the breeding programme initiated by the Universisty of Nairobi Bean Research Programme from 2009. We can confirm that the primary objective of that breeding programme was reached: sources of resistance to emerging pathotypes were identified; resistance genes were pyramided into susceptible popular cultivars; the genetic base of Andean large-seeded bean cultivars was broadened using Mesoamerican small-seeded counterparts; and the breeding methodology was improved the by incorporating markers in the selection procedure which allowed to accelerate and add precision in cultivar development.

As multiple coinfections are reported in farmers' fields, developing these cultivars with multiple resistance to major pathogens threatening bean production in Eastern Africa is a great achievement. Wortmann *et al.* (1998) estimated the annual production losses in the region attributed to angular leaf spot at 281,300 t; anthracnose at 247,400 t; root rot at 179,800 t; common bacterial blight at 145,900 t and bean common mosaic virus at 144,600 t. Pyramiding genes for disease resistance in a genotype is, therefore, more durable and sustainable strategy to control these diseases (Singh, 2001; Valentini *et al.*, 2017; Okii *et al.*, 2018). While developing

inter-gene pool multiple-parent genotypes, Okii *et al.* (2017) showed the effectiveness of marker-assisted selection to pyramid resistance genes as well as improving the agronomic qualities. In their study, disease resistance was associated with small-seeded Mesoamerican genotypes, except for the BCMV where the Andean and Mesoamerican genotypes behaved similarly. This could explain the growing interest for inter-racial crosses among genotypes belonging to these two gene pools. Thus, the low levels of disease infection recorded on tested elite lines could be attributed to inter-gene and inter-racial crosses performed between Andean and Mesoamerican cultivars as they allowed to broaden the genetic base and increased levels of resistance to both biotic and abiotic stresses (Welsh *et al.,* 1995; Singh *et al.,* 2002; Singh and Schwartz, 2010; Singh, 2013).

Gamete selection method was effective as it allowed pyramiding resistance genes to target pathogens and thus, reaching the primarly objective of this breeding programme which was to ascertain the effectiveness of the gamete selection in pyramiding resistance genes to ALS, BCMV, Pythium root rot, CBB and the anthracnose in susceptible popular cultivars. Many other successful applications of the gamete selection method to improve the common bean disease resistance have been reported by Singh *et al.* (1998); Asensio-S.-Manzanera *et al.* (2005; 2006); Singh *et al.* (2008); and Terán and Singh (2009). The use of markers in this breeding programme allowed to accelerate, increase precision and efficiency and, therefore, made easy pyramiding of desirable genes as previously stated by Miklas *et al.* (2006). In fact, markers used in early generations to select male gametes and multiple-parent F_1 with requisite resistance genes proved to be effective when validating phenotypically developed lines at advanced generations.

From our findings, there were no significant correlations in the reaction of tested genotypes to the seven pathogens used in this study, except the significant correlation between the reaction of genotypes to BCMV and the ALS. This could suggest that most of the genes controlling resistance to these major bean diseases were in different chromosomes and inherited independently. Even though no significant correlation was reported between ALS and BCMV and between anthracnose and the BCMV, results found by Okii *et al.* (2017) demonstrating a co-segregation of resistance genes for anthracnose (*Co-5*) and angular leaf spot (*Phg-2*) within the pyramided population is opposed to our findings which did not reveal any significant correlation among them. More surprising were reactions of elite lines to root rot-causing agents. The

Fusarium root rot was the most damaging among common bean root rots, both for disease incidence and severity. Only one elite line from the 26 tested and one check variety of the 10 used were resistant to *Fusarium* root rot. A study carried out by Mukankusi (2008) confirmed the virulence of the *Fusarium* root rot as, among the 147 accessions evaluated in that study, none of them had shown resistance to this pathogen. Spence (2003) found that *F. solani* was more damaging than the two common species of *Pythium* (*P. torulosum* and *P. spinosum*) in Uganda. Although the plant materials used in this study were improved for *Pythium* root rot, its incidence and severity were still very high. Only 8 out of 26 elite lines possessed the *Pythium* root rot resistance. This confirmed it as one of the most damaging in common bean production (Bodah, 2017). In Kenya and Rwanda, bean losses attributed to *Pythium* root rot of up to 70% were reported if susceptible cultivars are grown (Nzungize *et al.,* 2012). None of the genotypes had shown concurrent resistance to *Pythium* and *Fusarium* root rot. Similar results were reported by Mukankusi *et al.* (2018) as only 21.5% of tested inter-specific lines combined resistance to *Fusarium* and *Pythium* root rot concurrently. Ongom *et al.* (2012) concluded that, although quantitative trait loci (QTLs) linked to *Fusarium solani* resistance have been mapped on the same chromosome as that on which gene for resistance to *Pythium ultimum* had been found, their resistances were inherited independently and the correlation between them was very low. This could explain why breeding for *Pythium* root rot resistance did not improve significantly the *Fusarium* root rot resistance even if a donor parent (RWR719) resistant to both pathogens was involved in the crosses. Damages due to *Rhizoctonia* root rot were very low, more than 80% of lines being resistant despite a high incidence recorded. This study confirmed findings from other authors on *Rhizoctonia solani* Kuhn as a pathogen causing substantial yield losses on common bean worldwide but less economically important than *Pythium* and *Fusarium* root rots (Marcenaro and Valkonen, 2016; Paparu *et al.,* 2018).

5.5. CONCLUSION

This study confirmed the effectiveness of inter-racial crosses and marker-assisted gamete selection to concurrently improve resistance of common bean to major diseases in Eastern and Central Africa. From the 26 elite lines tested in this experiment, five lines possessed a concurrent resistance to five pathogens; eight were resistant to four pathogens; nine were resistant to three pathogens, three showed resistance to two pathogens and one had a resistance to only one pathogen. However, there were no significant correlations in the reaction of tested genotypes to the seven pathogens used in this study, except the significant correlation between the reaction of genotypes to bean common mosaic virus and the angular leaf spot. This could suggest that most of the genes controlling resistance to these major bean diseases were inherited independently.

This study allows to confirm that the primary objective of this breeding programme was reached as it has been possible to identify sources of resistance to emerging pathotypes, to pyramid resistance genes to susceptible genotypes, to broaden the genetic base of Andean large-seeded bean cultivars using Mesoamerican small-seeded counterparts, and to improve the breeding methodology by incorporating markers in the selection procedure.

Further field experiments in areas with a high prevalence of these diseases should be conducted to confirm the multiple disease resistance of these elite lines before releasing to farmers. In addition, more sources of resistance to these pathogens should be identified and introgressed for durable resistance, especially to common bacterial blight and *Fusarium* root rot.

CHAPTER 6: CONCLUSIONS AND RECOMMENDATIONS

6.1. GENERAL DISCUSSION

6.1.1. Agronomic performance of inter-racial populations of common bean

There were significant differences among the 16 inter-racial populations for seed yield and other agronomic traits. Transgressive segregants for seed yield was identified in most of the populations, confirming the effectiveness of inter-racial crosses to improve the common bean productivity as previously demonstrated by Welsh *et al.* (1995) and Singh *et al.* (2002). Blair *et al.* (2010) showed that inter-gene pool introgressions provide interesting combinations of traits along with higher adaptability to environmental stresses, diseases and pests' resistance and nutritional quality. Vandemark *et al.* (2014) concluded that the enhancement of seed yield of common beans in the future will depend on continued inter-racial crosses which should provide new sources of genetic diversity. The number of pods per plant was the most significant component related to seed yield, implying that it can be used by bean breeders as an indirect selection criterion for seed yield (Darkwa *et al.*, 2016; Rao *et al.*, 2017; Assefa *et al.*, 2017). Crosses involving the parental variety KATB9, a drought-resistant variety (Kimani *et al.*, 2012; Ruraduma *et al.*, 2016), showed the best for seed yield potential and other traits. The variety KATB9 seemed to have transmitted to its progenies the drought resistance which allowed reasonable yields under drought conditions at Mwea. Results from Mwea experiment indicated that, small-seeded genotypes give better yields than their large-seeded counterparts. Singh *et al.* (2002) also reported that in Colombia, small-seeded lines produced 40 to 60% more yield than large-seeded lines. Lima *et al.* (2005) explained that delayed leaf senescence, higher net assimilation rate, the greater number of pods per plant or the number of seeds per pod could allow to small-seeded genotypes to achieve more yield than the large-seeded beans. However, the G x E experiment in this study did not confirm the same trends as there were positive correlations between the seed size and the seed yield. Differences were more pronounced among market classes than within. Market classes with larger seeds (red kidney and red mottled) achieved significantly higher yields than small-seeded market classes (pinto, small red, mixed color). These results are similar to those previously found by Mushagalusa *et al.* (2016). Lima *et*

al. (2005) explained that sowing larger seeds improves the early-season plant growth which is advantageous for crop establishment in stressed environments.

6.1.2. Stability analysis and G x E effects on the seed yield of inter-racial advanced lines

The G x E effects on common bean seed yield revealed significant effects of the interaction between the site and the genotype on all the traits for all the market classes, implying that the tested lines behaved differently from one site to another and their ranking varied significantly across the 3 sites (Mukankusi *et al.,* 2015; Ashango *et al.,* 2016). This showed the diversity of sites and the existence of significant genetic differences among the advanced lines for seed yield (Tamene and Tadesse, 2014; Ashango *et al.,* 2016). The effect of the environment was responsible for the largest part of the variability, a result similar to those previously found by Mwale *et al.* (2009) in Malawi and Ashango *et al.* (2016) and Tadesse *et al.* (2017; 2018) in Ethiopia. Best yields were recorded from Tigoni in the high altitude. This was attributed to cooler conditions and higher rainfall which led to slower plant growth and delayed maturity favoring, therefore, higher yields as previously reported by Singh *et al.* (2002). In fact, higher yields are often associated with delayed maturity, which allows development of more pods and more seeds per pod (Welsh *et al.,* 1995; Lad *et al.,* 2017). However, opposite results were found in drought stress environments where higher yield was negatively correlated with the days to maturity (Polania *et al.,* 2016; Gereziher *et al.,* 2017). Although the environment is a very broad term and includes many factors (predictable and unpredictable); it was the temperature and the amount and distribution of rainfall that had mainly contributed to observed results. Tigoni in high altitude experienced cooler conditions (15.8°C) with a relatively well-distributed rainfall along the growing season (506 mm). Kabete experienced mean monthly temperatures of 18.2°C and an amount of rainfall of 372 mm. Mwea in low altitude was warmer (24°C) with erratic rainfall as described previously (311 mm). Other key environmental factors (e.g. soil type, nutrients, pH, etc.) were not significantly different among the three sites. Another key aspect from the G x E experiment was that the higher yielding lines were the most unstable across sites. This is supporting results found by Swegarden *et al.* (2016) and Tadesse *et al.* (2017; 2018) which showed that the stable lines are not always the better yielding. Lin *et al.* (1986) demonstrated that a satisfactory Type I stability parameter (i.e., CV) is often linked with reduced yield performance.

6.1.3. Multiple disease resistance of inter-racial elite lines to major bean pathogens

Pyramiding genes for disease resistance in a genotype is a more durable and sustainable strategy to control diseases as multiple coinfections of pathogens are common in production fields and have been reported to substantially affect productivity of the common bean (Singh, 2001; Valentini *et al.,* 2017; Okii *et al.,* 2018). Inter-racial crosses and marker-assisted gamete selection method proved to be effective in pyramiding genes for disease resistance to major common bean diseases in Eastern and Central Africa. Results showed that 25 of the 26 elite lines possessed at least a resistance to two pathogens. Five of them were concurrently resistant to five pathogens. Many other successful applications of the marker-assisted gamete selection to improve the common bean for multiple disease resistance and other agronomic traits have been reported (Singh *et al.,* 1998; Singh, 2001; Asensio-S.-Manzanera *et al.,* 2005; 2006; Miklas *et al.,* 2006; Singh *et al.,* 2008; Terán and Singh, 2009). The low levels of disease infection (in greenhouse) recorded on test elite lines could be attributed to inter-gene and inter-racial crosses performed between Andean and Mesoamerican cultivars as they allowed to broaden the genetic base and increased levels of resistance to both biotic and abiotic stresses (Welsh *et al.,* 1995; Singh *et al.,* 2002; Singh and Schwartz, 2010; Singh, 2013). In fact, the resistance genes to most of the pathogens attacking Andean cultivars (intensively grown in Eastern Africa) were associated with the small-seeded Mesoamerican cultivars (Okii *et al.,* 2017). This rendered the use of inter-gene pool and inter-racial crosses very crucial to control major diseases of common beans. Absence of correlation for disease resistance suggested that the genes controlling resistance to target diseases were assorting independently. Consequently, there was no co-segregation of these genes. Results were more surprising for the root rot-causing pathogens as no genotype combined resistance to *Fusarium* and *Pythium* root rot, even though the parental line RWR719, which was used in study populations, has been reported to possess genes of resistance to both pathogens (Otsyula *et al.,* 2003; Mukankusi, 2015). These results supported those of Ongom *et al.* (2012) who concluded that, although quantitative trait loci (QTLs) linked to *Fusarium solani* resistance have been mapped on the same chromosome as that for resistance to *Pythium ultimum*, their resistances were inherited independently and the correlation between them was very low. In addition, resistance to *Fusarium solani* is believed to be much more complex as it is controlled by two or more genes (Schneider *et al.,* 2001; Romans-Aviles and Kelly, 2005; Mukankusi *et al.,* 2011; Obala *et al.,* 2012), while, the *Pythium ultimum* resistance

is only conditioned by a single dominant gene, marked by a dominant SCAR marker-PYAA19^{800} (Otsyula *et al.*, 2003; Mahuku *et al.*, 2005; Otsyula, 2010). This could explain why the *Fusarium* root rot was the most damaging on elite lines bred for *Pythium* root rot resistance.

6.2. CONCLUSION

This study was a continuation of a breeding programme initiated to determine whether marker-assisted gamete selection could be applied to pyramid genes for resistance to bean major diseases in Eastern Africa. The specific objectives of the study were: to determine the agronomic performance of $F_{1.3}$ to $F_{1.6}$ generations of 16 segregating inter-racial populations and select the most promising genotypes with respect to market classes; to analyze the effects of genotype-environment interaction (G x E) on seed yield of the selected $F_{1.7}$ elite lines across different agro-ecological conditions of central Kenya; and thereafter to validate the multiple resistance of the selected $F_{1.8}$ elite lines to infections by root rots, common bacterial blight, angular leaf spot, bean common mosaic virus and anthracnose pathogens using natural epiphytotics and artificial inoculation.

The presence of genotypes combining high yield potential, seed quality, wider adaptation, and multiple disease resistance confirmed the effectiveness of inter-racial crosses and marker-assisted gamete selection in common bean improvement, regardless of seed size and market class. The G x E effects were very high, reflecting diversity of experimental sites, and the existence of significant genetic differences among the advanced lines for seed yield. The environment was responsible for the largest part of the variability. The high altitude (Tigoni) was the most conducive to common bean production as most of the genotypes yielded higher compared to means recorded in medium and low altitudes. Among the 26 elite lines suggested by AMMI model, five lines possessed a concurrent resistance to five pathogens; eight were resistant to four pathogens; nine were resistant to three pathogens, three possessed resistance to two pathogens and one of the genotypes had only a resistance to one pathogen. However, there were no significant correlations in the reaction of tested genotypes to the 7 pathogens used in this study, except the significant correlation existing between the reaction of genotypes to bean

common mosaic virus and the angular leaf spot. This suggested that resistance genes for those pathogens were inherited independently.

6.3. RECOMMENDATIONS

- Further testing is necessary to confirm the yield performance and stability of these elite lines across a large number of contrasting environments as a huge variability has been observed among the lines across the environments.
- More sources of resistance should be identified to improve the level of resistance found in some of these genotypes especially for *Fusarium* root rot, common bacterial blight and bean common mosaic virus.
- Although weather conditions are unpredictable and often not conducive to the development of pathogens, field testings for disease resistance are crucial before the release of these lines to farmers.

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APPENDIX

Appendix 1. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-17 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	18.46	0.89	1.84	768.29	0.22	5.96	1762.12	6883219
Line	12	33.70*	1.99^{ns}	0.36^{ns}	53.58^{ns}	3.02**	148.13***	108.96ns	425629^{ns}
Error	62	13.67	1.72	0.25	44.24	0.98	31.40	89.90	351206
Total	75								
CV (%)		7.4	28.4	34.7	35.5	18.8	17.6	36.1	36.1

Appendix 2. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-18 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	7.50	0.56	1.68	798.24	0.09	5.86	1764.03	6891004
Line	10	35.09**	1.99^{ns}	0.37^{ns}	56.45^{ns}	2.80***	129.67***	111.97^{ns}	437387^{ns}
Error	60	13.32	1.35	0.25	44.99	1.01	31.43	89.94	351336
Total	71								
CV (%)		7.4	23.8	32.4	33.8	17.8	19.4	34.2	34.2

Appendix 3. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-19 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	6.55	0.56	2.16	880.42	0.02	25.78	2102.89	8214890
Line	14	33.03**	2.50*	0.34^{ns}	58.33^{ns}	2.47**	96.98***	125.58^{ns}	490618^{ns}
Error	65	12.28	1.19	0.24	42.72	0.92	29.75	87.29	340985
Total	80								
CV (%)		7.2	22.7	31.4	33.7	17.5	18.9	33.2	33.2

Appendix 4. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-20 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	9.08	0.24	1.83	800.35	0.29	17.36	2007.75	7842873
Line	11	35.19**	2.26^{ns}	0.39^{ns}	51.29^{ns}	2.71**	130.54***	96.81^{ns}	378135^{ns}
Error	62	12.94	1.27	0.25	43.95	0.94	29.96	92.78	362420
Total	74								
CV (%)		7.4	24.3	33.6	34.5	17.6	18.1	34.9	34.9

Appendix 5. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-21 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	18.21	5.93	3.66	1353.79	0.25	137.49	4807.09	1.878E+07
Line	35	19.51*	2.17*	0.41*	38.58^{ns}	2.01**	47.79**	79.22^{ns}	309445^{ns}
Error	87	10.55	1.18	0.22	35.79	0.95	23.77	84.01	328174
Total	123								
CV (%)		6.8	22.9	25.3	34.1	19.3	16.2	36.2	36.2

Appendix 6. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-22 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	97.97	0.95	0.79	824.26	0.18	1.32	2747.03	1.073E+07
Line	37	19.74 *	2.15*	0.83***	35.98ns	1.54**	39.99*	91.09^{ns}	355796^{ns}
Error	89	11.82	1.32	0.24	32.76	0.78	23.89	66.48	259687
Total	127								
CV (%)		6.9	23.7	23.1	27.2	16.9	16.8	28.2	28.2

Appendix 7. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-23 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	8.57	0.02	0.55	1504.55	0.00	89.89	3489.78	1.363E+07
Line	31	29.46**	1.60^{ns}	0.55**	65.91^{ns}	1.86**	49.97*	100.41^{ns}	392231^{ns}
Error	82	15.19	1.42	0.26	51.45	0.82	28.60	96.35	376407
Total	114								
CV (%)		7.6	24.6	27.7	32.3	17.5	18.0	32.1	32.1

Appendix 8. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-24 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	0.24	0.85	1.03	584.57	0.08	21.43	1230.16	4805946
Line	29	31.78**	2.30^{ns}	0.62**	54.12^{ns}	1.69*	75.01***	124.62^{ns}	486757^{ns}
Error	80	15.32	1.52	0.27	55.11	0.92	25.38	102.10	398835
Total	110								
CV (%)		7.8	23.4	27.8	37.8	18.3	18.3	39.6	39.6

Appendix 9. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-25 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	16.35	17.44	3.11	606.39	0.09	2.02	985.66	385040
Line	33	27.46**	1.59^{ns}	0.99***	28.32^{ns}	2.04**	56.54**	69.66^{ns}	272088^{ns}
Error	84	12.9	1.57	0.24	36.17	0.91	24.58	79.60	310942
Total	118								
CV (%)		7.5	27.0	22.3	30.1	17.9	16.1	30.7	30.7

Appendix 10. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-26 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	0.52	0.53	1.45	551.92	0.43	63.63	0.96	5486795
Line	24	33.90**	3.25**	0.41^{ns}	103.10**	3.14***	78.29**	232.99***	910141***
Error	75	13.83	1.38	0.25	41.45	0.96	35.74	85.24	332982
Total	100								
CV (%)		7.4	21.5	31.1	39.9	19.9	21.6	44.8	44.8

Appendix 11. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-27 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	17.76	1.44	7.39	3008.42	0.27	27.82	5459.63	2.133E+07
Line	36	25.16^{ns}	2.18*	0.39*	37.93^{ns}	1.46*	53.48**	99.25^{ns}	387685^{ns}
Error	87	17.94	1.12	0.24	46.65	0.88	25.29	106.65	416630
Total	124								
CV (%)		8.4	21.6	25.8	35.5	18.0	16.8	38.9	38.9

Appendix 12. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-28 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	1.72	8.41	2.49	697.31	1.89	0.00	828.10	3234157
Line	22	25.91*	2.03^{ns}	0.77***	51.10^{ns}	2.14**	82.67***	119.22^{ns}	465679^{ns}
Error	73	12.45	1.56	0.26	44.664	0.87	26.85	107.15	465679
Total	96								
CV (%)		7.3	27.9	26.0	31.6	17.9	17.6	36.1	36.1

Appendix 13. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-29 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	91.57	2.31	0.32	387.12	1.31	0.96	822.24	3212285
Line	32	15.85^{ns}	1.63	0.90***	56.11^{ns}	2.03***	74.86***	85.18^{ns}	332744^{ns}
Error	83	12.59	1.60	0.25	55.68	0.86	28.10	110.33	431009
Total	116								
CV (%)		7.2	24.9	24.4	33.6	18.5	17.3	37.4	37.4

Appendix 14. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-30 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	12.70	0.24	2.72	749.02	0.09	11.10	1620.88	6331171
Line	22	25.09*	1.69^{ns}	0.58**	61.13^{ns}	2.33***	73.12***	167.48*	654260*
Error	73	13.91	1.25	0.24	39.20	0.84	26.85	85.71	334814
Total	96								
CV (%)		7.7	22.6	27.3	28.6	17.1	17.8	29.4	29.4

Appendix 15. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-31 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	4.94	0.17	1.97	648.39	0.36	6.74	1333.59	5209323
Line	14	28.15*	2.21*	0.57*	69.74^{ns}	2.21**	99.41**	171.11*	668418
Error	65	12.50	1.19	0.24	41.76	0.91	29.62	90.33	352857
Total	80								
CV (%)		7.3	23.7	29.4	29.9	16.8	19.2	30.0	30.0

Appendix 16. Mean squares for seed yield and seed yield related parameters of lines within population KMA13-32 of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	100SW	SWP	SY
Replication	1	5.07	0.24	1.71	573.19	0.41	13.48	1346.18	5258591
Line	13	37.06**	2.03^{ns}	0.50*	94.71*	2.77***	118.64***	241.15**	941934**
Error	64	13.55	1.46	0.24	42.28	0.91	28.91	87.93	343486
Total	78								
CV (%)		7.4	25.6	28.9	29.4	17.3	17.7	29.3	29.3

Appendix 17. Mean squares for seed yield and seed yield related parameters of lines among populations of bean grown at Mwea in 2016

Source of variation	DF	DTF	VIG	UNIF	PP	SP	SWP	100SW	SY
Population	25	65.84***	4.53***	2.00	222.22***	3.57***	561.1***	139.24***	2191841.***
Line	239	13.53^{ns}	1.41^{ns}	0.25	30.34^{ns}	0.74^{ns}	74.0^{ns}	21.15^{ns}	289004.^{ns}
Error	230	17.01	1.94	0.30	56.34	0.88	125.0	24.07	488282.
Total	495								
CV (%)		8.3	28.1	27.0	36.6	18.6	39.8	16.4	39.8

Appendix 18. Mean squares for seed yield and seed yield components of pinto bean lines grown at Mwea, Tigoni and Kabete in 2017 short rain season

Source of variation	DF	GC	VIG	DTF	DTM	PP	SP	100SW	HI	SY
Replication	3	17.74	0.45	15.80	15.08	0.95	0.55	1.88	25.9	434411
Site	2	9526.12***	97.06***	1009.33***	4255.49***	7959.69***	31.86***	736.32***	17416.1***	2.041E+08***
Line	12	317.20^{ns}	1.32*	4.95***	18.71***	76.57**	1.73***	28.34***	140.5*	1972916**
Site x Line	24	199.73^{ns}	0.93^{ns}	3.56***	11.35***	48.01*	0.91**	10.48**	111.9^{ns}	1688507**
Error	114	180.78	0.70	0.86	2.34	28.23	0.42	4.64	70.6	797560
Total	155									
CV (%)		19.8	19.2	2.2	1.6	33.6	12.7	8.0	18.0	42.4

Appendix 19. Mean squares for seed yield and seed yield components of red kidney bean lines grown at Mwea, Tigoni and Kabete in 2017 short rain season

Source of variation	DF	GC	VIG	DTF	DTM	PP	SP	100SW	HI	SY
Replication	3	254.87	0.36	3.34	0.19	0.05	0.12	39.05	4.2	1306067
Site	2	8930.39***	94.84***	1460.82***	4177.21***	5013.33***	7.02***	770.78***	20369.2***	2.503E+08***
Line	14	698.22***	3.08***	11.24***	17.81**	162.16***	2.43***	266.77***	438.7***	3579133***
Site x Line	28	488.32***	1.27**	7.86***	11.90*	52.04***	0.93***	47.81***	175.8***	1412214***
Error	132	202.49	0.6035	2.14	7.50	20.54	0.30297	10.199	23.3	432658
Total	179									
CV (%)		23.9	23.8	3.2	2.8	33.7	12.5	7.5	12.5	28.9

Appendix 20. Mean squares for seed yield and seed yield components of red mottled bean lines grown at Mwea, Tigoni and Kabete in 2017 short rain season

Source of variation	DF	GC	VIG	DTF	DTM	PP	SP	100SW	HI	SY
Replication	3	572.4	0.80	18.78	62.67	133.1	4.74	46.64	286.90	788594
Site	2	14380.1***	97.9***	1262.4***	4338.8***	11603.7***	15.9***	1602.2***	9155.5***	2.895E+08***
Line	15	320.5*	3.3***	48.0***	102.9***	181.7***	3.7***	813.6***	705.0*	2525709***
Site x Line	30	403.0***	1.4^{ns}	18.7***	31.7***	126.5***	2.3***	81.5***	630.4*	1841186***
Error	141	176.4	0.97	2.58	5.64	33.9	0.57	31.1	399.8	523332
Total	191									
CV (%)		22.1	23.7	3.5	2.3	37.3	17.1	14.6	57.1	34.4

Appendix 21. Mean squares for seed yield and seed yield components of small red bean lines grown at Mwea, Tigoni and Kabete in 2017 short rain season

Source of variation	DF	GC	VIG	DTF	DTM	PP	SP	100SW	HI	SY
Replication	3	1421.15	5.44	0.25	72.34***	589.1	3.50	23.60	109.0	1.575E+07
Site	2	8672.22***	142.88***	2561.91***	6977.17***	11035.9***	3.37**	454.73***	13434.4***	2.398E+08***
Line	23	295.74^{ns}	1.67**	43.51***	112.43***	153.4***	7.29***	205.57***	940.7***	5324158***
Site x Line	46	453.38***	0.86^{ns}	3.17***	24.30***	90.3***	1.24***	14.46***	671.3***	2219643***
Error	213	208.83	0.79	1.44	8.33	37.1	0.51	6.07	112.5	620933
Total	287									
CV (%)		21.4	23.4	2.7	3.0	44.1	12.0	9.3	22.7	39.8

Appendix 22. Mean squares for seed yield and seed yield components of mixed color bean lines grown at Mwea, Tigoni and Kabete in 2017 short rain season

Source of variation	DF	GC	VIG	DTF	DTM	PP	SP	100SW	HI	SY
Replication	3	2079.3	1.960	1.22	1.9	51.35	0.09	0.57	62.7	760215
Site	2	16831.3***	171.34***	3225.65***	13118.3***	3034.81***	3.08***	1965.77***	31255.4***	1.089E+08***
Line	32	314.6^{ns}	3.04***	59.10***	146.0***	232.09***	5.06***	210.65***	886.9***	3260277***
Site x Line	64	291.9^{ns}	1.34***	16.04***	47.7***	85.94***	1.62***	48.18***	444.6***	1835605***
Error	294	226.2	0.63	1.76	3.3	6.08	0.26	4.18	35.8	101005
Total	395									
CV (%)		21.5	21.6	2.9	1.8	19.8	10.0	6.2	13.9	18.7

Appendix 23. Summary ANOVA for AUDPC for the pathogens on elite bean lines tested under controlled environment at Kabete in 2018

Sources of variation	DF	ALS		BCMV		CBB		ANTH	
		Incidence	Severity	Incidence	Severity	Incidence	Severity	Incidence	Severity
Replication	1	17564.	741.1	122896.	115.0	158109.	5270.2	345	1378.1
Genotype	35	81206.***	78.8***	133628.***	364.9***	207554.***	418.4***	195616***	337.6^{ns}
Residual	35	8782.	16.6	21915.	18.8	20882.	74.5	153	274.6
Total	71								
Mean		486.5	32.2	1002	41.7	614.7	42.8	342.7	31.8
$LSD_{0.05}$		190.2	8.3	300.5	8.8	293.4	17.5	25.1	33.6
CV (%)		19.3	12.7	14.8	10.4	23.5	20.2	3.6	52.1

Appendix 24. Mean temperature and rainfall for the short rain season 2016 at KALRO-MWEA

Month	Rainfall (mm)	Temperature (°C)
September 2016	70.1	24.8
October 2016	111.3	23.8
November 2016	102.0	22.6
December 2016	15.1	23.7
January 2017	27.3	25.1
February 2017	21.2	25.7
Total	347.0	145.7
Mean	57.8	24.3

Appendix 25. Mean temperature and rainfall during the short rain season 2017 at Mwea, Kabete and Tigoni

Month	KALRO-MWEA		KALRO-TIGONI		KABETE	
	Rainfall (mm)	Temperature (°C)	Rainfall (mm)	Temperature (°C)	Rainfall (mm)	Temperature (°C)
September 2017	32.1	21.9	31.0	14.7	13.7	17.3
October 2017	152.8	24.0	82.0	15.9	128.7	18.5
November 2017	111.6	22.5	176.0	15.7	161.7	18.4
December 2017	14.9	21.8	102.0	15.6	14.7	18.1
January 2018	0	22.3	58.0	16.0	40.5	18.0
February 2018	0	22.9	57.0	16.7	12.6	18.8
Total	311.4	135.4	506.0	94.6	371.9	109.1
Mean	51.9	22.6	84.3	15.8	62.0	18.2

Appendix 26. Mean temperature and rainfall from March to June 2018 at Kabete Field Station

Month	Rainfall (mm)	Temperature (°C)
March 2018	382.2	19.4
April 2018	361.9	19.2
May 2018	291.8	17.8
June 2018	66.7	16.3
Total	1,102.6	72.2
Mean	275.7	18.2