INHERITANCE AND SELECTION FOR YIELD COMPONENTS AND MULTIPLE DISEASE RESISTANCE IN SNAP BEAN

Joan Josephine Cheptoo Kimutai

(B. Sc. Biotechnology, Kenyatta University)

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Department of Plant Science and Crop Protection
Faculty of Agriculture
College of Agriculture and Veterinary Sciences
UNIVERSITY OF NAIROBI

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DECLARATION

I hereby declare that this is my original work. To the best of my knowledge, the work presented here has not been presented elsewhere for examination, award of a degree or publication.

…… ……

Joan Josephine Cheptoo Date

Department of Plant Science and Crop Protection, University of Nairobi.

This thesis was submitted with our approval as University supervisors:

Signature: …….. Date: …….

Prof. Paul M. Kimani,
Department of Plant Science and Crop Protection, University of Nairobi

Signature: …….. Date: …….

Prof. Rama D. Narla,
Department of Plant Science and Crop Protection, University of Nairobi

DEDICATION

I dedicate this work to God for continued sustenance and providence throughout my research work. To my loving husband, Chris Shimba and daughter Catina Jayden, I dedicate this research to you. Thank you both for enduring my absence and for your overwhelming support and encouragement. Thanks to God for my twins Jaylen and Jaylah and for my lastborn Jaydah who came along the way and gave me motivation to work harder. My special appreciation to Quinter Atieno who took care of my babies as I was studying, together we have realized the results. I appreciate the unwavering support of my dad, Pr. Jacob Kimutai Beles and my parents in love, Mr. and Mrs Robert Rotch for their unrelenting prayers.

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ABSTRACT

Snap bean (*Phaseolus vulgaris* L.) cultivation has gained popularity in East and Central Africa and more particularly in Kenya due to its potential as an alternative source of food and income generation. However, snap bean production by smallholder farmers is mostly limited by low yields and disease prevalence. Bush snap beans varieties cultivated by smallholder farmers are low yielding and highly susceptible to disease. The objectives of this study were: to i) establish the mode of inheritance of climbing capacity and pod yield in snap beans; ii) select for high yield, disease resistance and market preferred pod traits in locally developed climbing snap bean populations; and iii) select for high yield, disease resistance and market preferred pod traits in locally developed bush snap bean populations.

Three field experiments were conducted between 2012 and 2014. In the first field experiment, six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) of snap beans were developed from crosses between six climbing snap bean lines which showed multiple disease resistance and eight susceptible bush varieties. The parents and their progenies were evaluated at Kabete Field Station in 2014. Data was collected on 50% days to flowering, plant height, internode length, number of pods per plant and pod length. The data collected was subjected to generation means analysis using Genstat software. Estimates of genetic variance and components of phenotypic variance. Correlation analysis was for all traits under study. In the second and the third trials, 20 climbing snap bean lines and 25 advanced bush snap lines were evaluated for disease resistance and marketable pod qualities at Mwea and Embu during the 2013 short rain season and at Kabete during the 2014 long rain season. Data was collected on plant vigour, days to 50% flowering, days to first picking, rust, anthracnose and angular leaf spot severity, pod loadplant^{-1}, pod length and pod yield. Analysis of variance was used to establish if there are genotypic and location effects on the traits studied.

The results of the first trial indicated that six-parameter model (m + a + d + aa + ad + dd) of genetic analysis gave the best fit for all the traits tested based on the coefficient of determination (R^2) (>82.1%) and t-test. Estimates of genetic parameters indicated that additive gene effects were responsible for climbing capacity and pod yield in all crosses. High broad and narrow sense heritability were realized in plant height (91.7%; 83.3%) in Morgan x HAV 130 cross and days to 50% flowering (72.5%; 71.5%) in Star 2053 x HAV 131 cross. Narrow sense heritability (70.68%) was high for plant height among crosses compared to other traits (<27.9%). There were significant

(P≤0.05) positive correlations among the traits under study. Days to 50% flowering was significantly and positively associated with plant height in Paulista x HAV 133 (r = 0.9776**); internode length in Teresa x HAV 131 (r = 0.9737**); and number of pods per plant in Morelli x HAV 133 (r = 0.9386**). Plant height on the other hand showed a significantly (P≤ 0.05) positive relationship with internode length in Morgan x HAV 130 (r = 0.9974**); and number of pods per plant in Morelli x HAV 133 (r = 0.9951**). Internode length also showed a highly significant positive correlation with the number of pods per plant in Star 2053 x HAV 131 (r = 0.9039**).

The evaluation of advanced climbing snap bean lines indicated that there were genotypic variations for most traits under study. The climbing snap bean lines flowered ten days later than the bush varieties. The test lines showed resistance to rust, anthracnose and angular leaf spot (1.23) in comparison to the check varieties which showed intermediate resistance (4.3). The climbing snap bean lines had higher yield compared to the bush varieties with averages of 9,831.6 kg ha^{-1} and 1,858.6 kg ha^{-1} respectively. The climbing snap bean out yielded the check varieties fourfold with an average of 54% premium pods. Fifteen promising climbing snap bean lines were selected based on high yield (10, 088.5 kg ha-1), multiple disease resistance (1.2), high proportion of premium pod yield (58.2%) and good pod quality. KSV04-2-2M was the most outstanding since it met all the market preferred pod characteristics among the test lines.

Results indicated that there were genotypic variations in most traits among advanced snap bean bush lines. The advanced bush snap bean test lines flowered 3 days later than the check varieties. The test lines reduced disease severity to rust, anthracnose and angular leaf spot by 25.8%, 39.7% and 51.3% respectively while the check varieties showed intermediate resistance (3.8) to the three diseases. The bush snap bean lines had higher yields compared to the check varieties with averages of 9,609.6 kg ha^{-1} and 7,402.3 kg ha^{-1} respectively. The test lines out yielded the check varieties by 29.8% with an average of 80.6% premium grades. Sixteen promising bush snap bean lines were selected based on yield (10, 470.9 kg ha^{-1}), multiple disease resistance (2.3), Pod length (10.2 cm), premium pods (80.9%) and pod quality (green, round and straight). The lines KSB12-143-3-1M, KSB22-3-1T, KSB39-3M and KSB46-2M were the most outstanding lines among the test lines. All these lines had green, straight and round pods suitable for the export market. The promising lines yielded more than the check varieties by 41.5%.

Key words: climbing capacity, disease resistance, snap bean, pod quality, pod yield

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LIST OF ABBREVIATIONS AND ACRONYMS

AFA	Agriculture and Food Authority
ANOVA	Analysis of Variance
ASARECA	Association for Strengthening Agricultural Research in Eastern and Central Africa
AYT	Advanced Yield Trials
BCMV	Bean common mosaic virus
CBB	Common bacterial blight
CIAT	International Center for Tropical Agriculture
DUS	Distinctive, uniform and stable
ECABREN	Eastern and Central African Bean Research Network
FAO	Food and Agricuture Organization
FAOSTAT	Food Agricultural Organization Statistics
GAP	Good agricultural practices
GLOBALGAP	Global Good agricultural practices
HB	Halo Blight
HCDA	Horticultural Crops Development Authority
HVR	Horticultural Validated Report
KALRO	Kenya Agricultural and Livestock Research Organization
KARI	Kenya Agricultural Research Institute
KEPHIS	Kenya Plant Health Inspectorate
KMD	Kenya Meteorological Department
LSD	Least significant difference
MRLs	Maximum residue levels
NARS	National Agricultural Research Systems
NPTs	National Performance Trials
NVRC	National Variety Release Committee
PYT	Preliminary Yield Trials

QTL	Quantitative Trait Loci
RUFORUM	Regional Universities Forum for Capacity Building in Agriculture
t ha^{-1}	Tons per hectare
USA	United States of America
USAID	United States of Agency for International Development

CHAPTER ONE

INTRODUCTION

1.1 Background

Snap bean, a strain of common bean, *Phaseolus vulgaris L*. is a vegetable crop that grows well in lower midland to lower highland regions with an altitude of 1500m-2100m above sea level. It is also known as 'French bean', 'string bean' or 'green bean' (Kimno *et al*., 2016; Singh and Singh, 2015). Snap bean is an economically important horticultural crop worldwide. Romero-Arenas *et al*. (2013) asserts that snap bean production generates income for millions of smallholder farmers globally. Some countries grow snap beans for export thereby generating income to the farmers as well as the host country in terms of revenue. On the other hand, other countries grow snap bean for domestic consumption since it is a good source of protein and therefore important for nutritional value to the community (Singh and Singh, 2015). Most countries serve both export and domestic markets. African countries, more particularly East Africa, grow snap bean for export to the European markets.

Snap bean contributes to 30.7% of horticultural crops worldwide (FAOSTAT, 2017). Snap bean production has been associated with a vast production area worldwide. The world produces up to 1.5 million ha of snap beans with a yield of 13, 647.8 kg ha^{-1} amounting to 20.7 million tonnes annually. China was reported as the leading snap bean producer with an average yield of 16.2 million tonnes and 40.3% of the world total production between 2010 and 2014 (FAOSTAT, 2014). Other major snap bean producers include Indonesia (887,300 tonnes) and Turkey (617, 700 tonnes). Other countries with outstanding snap bean yields include India, Thailand, Egypt, Italy and Bangladesh (Table 1.1). Among them are selected ASACRECA countries with an average yield of 9,600 tonnes. A tremendous worldwide increase in snap bean export volumes (217.6%) and values (193%) from 2009 and 2013 has been reported (Agriculture and Food Authority, AFA, 2014). Myanmar is the lead supplier of snap beans with 51.68% market share globally (Gitta and Kata, 2012). Other countries that form the world's top suppliers include China with 20.43% market share; Colombia (7.07%); Thailand (5.53%) and Australia (2.85%). There was a worldwide increase of 46.3% in values and 24.7% in volumes between 2009 and 2013 with India registering the largest market share of 49.4% (FAOSTAT, 2017). However, there has been consistent low market shares in East Africa and Kenya in particular.

Table 1. 1 Annual snap bean production volumes in selected countries worldwide, 2010 to 2014

	Production ('000'tonnes)					
Country	**2010**	**2011**	**2012**	**2013**	**2014**	**Mean**
Bangladesh	88.6	94.8	94.4	93.0	110.0	96.1
CÃ´te d'Ivoire	4.4	4.6	4.8	4.8	4.8	4.7
Cameroon	3.9	3.9	4.0	4.1	4.3	4.0
China	15169.3	15650.9	16410.4	16675.2	17031.7	16187.5
Congo	3.8	4.0	4.2	4.2	4.2	4.1
Democratic Republic of Congo	4.1	4.3	4.5	4.6	4.7	4.4
Egypt	270.7	305.6	251.3	257.5	253.1	267.6
Ethiopia	6.3	6.0	6.2	6.2	6.5	6.2
India	586.1	601.0	620.0	620.0	636.1	612.6
Indonesia	942.4	885.5	871.2	881.6	856.0	887.3
Italy	183.0	163.7	134.1	155.0	139.9	155.2
Kenya	36.6	45.0	37.7	40.5	43.8	40.7
Madagascar	1.0	1.2	1.3	1.2	1.1	1.1
Rwanda	5.6	8.0	5.8	6.6	7.3	6.7
Sudan	0.2	47.6	47.6	1.0	1.0	19.5
Thailand	310.4	301.1	305.0	305.0	305.0	305.3
Turkey	588.0	614.9	615.0	632.3	638.5	617.7
United Republic of Tanzania	3.2	3.5	4.2	5.0	5.7	4.3

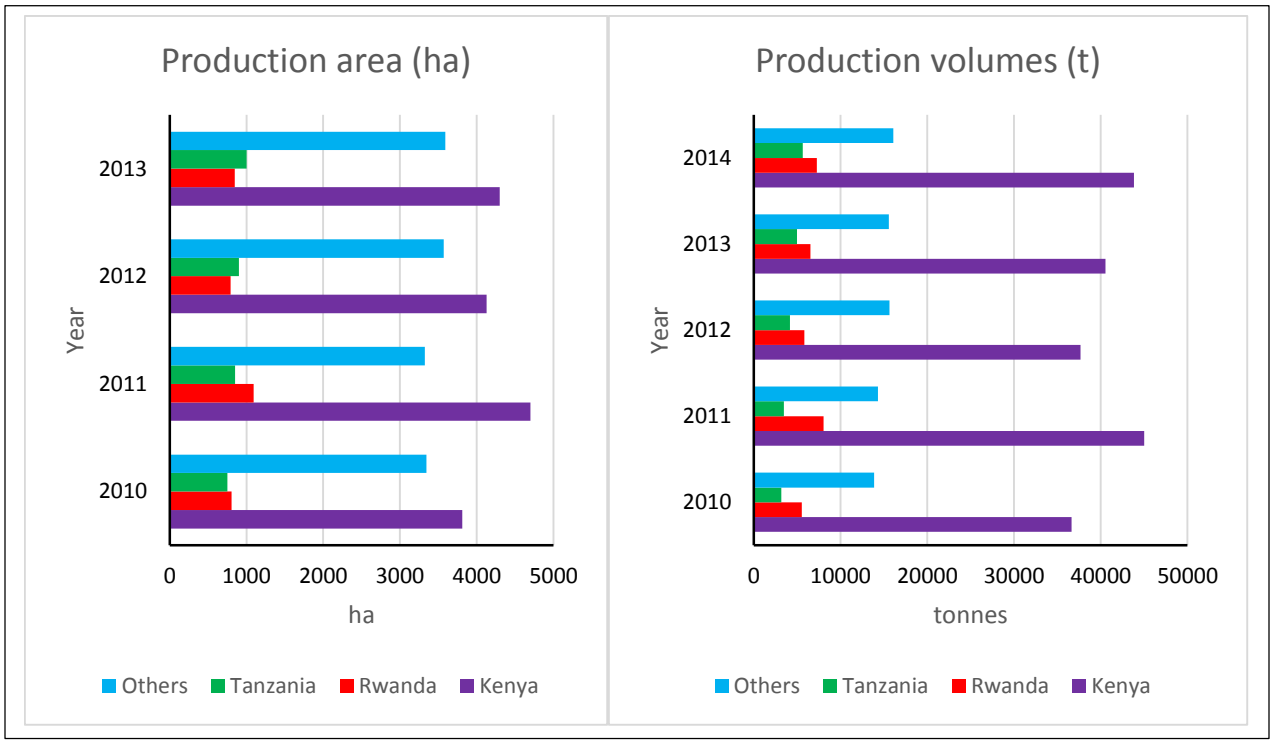
Source: FAOSTAT, 2017

Out of the world's 1.5 million ha, Africa's production area was 74,659 ha 12.8% of which was covered by East Africa between the years 2010 and 2014 (FAOSTAT, 2017). In general, Africa produced an average of 4.9% of the total world snap bean production volumes. Of this, 12.2% was produced in East Africa from 2010 to 2014 (Figure 1.1). Agriculture being the economic pillar among East African countries benefits from snap bean production thereby boosting the host country's economy through revenues and employment opportunities.

Source: FAOSTAT, 2017.

Figure 1. 1 World snap bean production between 2010 and 2014

In East Africa, snap bean production area is approximately 9,521.4 ha with a yield of 7,428.1 kg ha^{-1}. Snap bean is produced in Rwanda, Tanzania, and Uganda and is gaining popularity in South Sudan. However, these Countries have small market shares: Tanzania (1.48%), Kenya (0.19%), Rwanda (0.31%), and Uganda (0.07%). This is owing to low production volumes that result from production constraints and post-harvest losses (FAO, 2012).



Source: FAOSTAT, 2017.
Figure 1. 2 Regional snap bean production between 2010 and 2014

Kenya has the largest snap bean production area and volumes in East Africa accounting for 44.2% and 60.9% respectively (Figure 1.2). Snap bean production is labour intensive and offers employment to a good percentage of the Kenyan population (Kimani et al., 2006). Out of the total production volumes in East Africa, 96,772 metric tonnes was produced in Kenya and was valued at Kenya US $96.772 in 2013 (Otim *et al*., 2016). Kenya is among the top 30 world producers of snap bean (FAOSTAT, 2017). However, Kenya is among the lowest producers in production area, yields and volumes (FAOSTAT, 2017).

Snap bean is among major horticultural crop contributing 20% of the total export horticultural crop earnings in Kenya (Chemining'wa *et al*., 2012). The agricultural sector generally employs 0.01%

of Kenya's population. Of this, 80% work in the horticultural sub-sector (Muma, 2016). Horticultural crop production has been a good source of livelihood to 0.1-0.13% population in Kenya through generation of income and provision of on-farm and post-harvest employment opportunities (FAO, 2018). Kenya's snap bean production is dominated by smallholder farmers either individually or subcontracted by export companies (Kimani *et al*., 2006). Snap bean smallholder production requires use of casual labour during land preparation, planting, weeding, harvesting and post-harvest grading and packaging thus acting as a source of employment. Consequently, snap bean production in Kenya employs 45,000 to 60,000 people depending on the seasons (AFA, 2014). With a 75.7% increase in snap bean values from 2008 to 2013, Kenya has earned increased benefits to the farmers and the country as a whole (AFA, 2014). This makes snap bean an economically important crop nationally. For instance, Kenya produced 84, 112 and 123 metric tonnes (t) of snap beans valued at 5.2, 4.4 and 5.0 billion Kenyan shillings in 2012, 2013 and 2014 respectively AFA, 2014). Snap bean consumption is gaining popularity in the Kenyan domestic market thus explaining the disparity between production and export volumes observed between the years 2009 to 2013 (Table 1.2). This suggests that snap beans provide an alternative source of proteins and dietary fibre for the Kenyan population.

Table 1. 2 Snap bean production and export trends in East Africa, 2009-2013.

	Kenya					Rwanda					Tanzania				
	Production			Exports		Production			Exports		Production			Exports	
Year	Unit Area (ha)	Yield (Kg/ha)	Production (Tonnes)	Unit (Tonnes)	Value ($'000')	Unit Area (ha)	Yield (Kg/ha)	Production (Tonnes)	Unit (Tonnes)	Value ($'000')	Unit Area (ha)	Yield (Kg/ha)	Production (Tonnes)	Unit (Tonnes)	Value ($'000')
2009	3336.0	13937.6	46496.0	12447.0	34403.0	700.0	6608.6	4626.0	2501.0	334.0	730.0	4109.6	3000.0	388.0	1440.0
2010	3810.0	9616.5	36639.0	18935.0	55843.0	805.0	6904	5561.0	1770.0	208.0	750.0	4266.7	3200.0	699.0	1648.0
2011	4700.0	9574.5	45000.0	37517.0	132983.0	1092.0	7367	8048.0	7937.0	1178.0	850.0	4117.6	3500.0	1914.0	2072.0
2012	4128.0	9124.8	47667.0	38780.0	135062.0	793.0	7367.8	5841.0	4870.0	1611.0	900.0	4666.7	4200.0	3869.0	5431.0
2013	4300.0	9428.8	40544.0	32081.0	96772.0	849.0	7728.1	16561.0	11715.0	1434.0	1000.0	5000	5000.0	4912.0	7997.0

Source: FAOSTAT, 2017

Snap bean in Kenya is mainly grown for export market thus earning revenue to the country. Snap bean production in Kenya is done either in large scale or through smallholder production for commercial purposes. Production is concentrated in eight out of the 47counties (Kirinyaga, Muranga, Taita Taveta, Meru, Embu, Machakos, Nyeri and Narok) (Mulanya, 2016). There was an increase in production area (7%), quantities (33.1%) and in values (K. Shs) (83.9 %) from the year 2011 to 2014 (Mulanya, 2016). This denotes that snap bean production is gaining importance in Kenya. With a market share of 47.7%, Kirinyaga County is the lead producer of snap bean in Kenya. Between 2011 and 2013, Kirinyaga County produced an average of 12,639.7 tonnes annually from 1,740 ha which was valued at K. Shs. 472.9 million (Mulanya, 2016). It is also indicated that there has been a consistent and tremendous increase in the value of snap bean in Kirinyaga County with a 13.2% increase in 2012 rising to 92.8% in 2013 (Mulanya, 2016). This could be as a result of the increasing world snap bean market, increased domestic market and/or both.

Even though Kenya is the lead producer and exporter of snap bean in East Africa, snap bean exports slightly leveled off between 2011 and 2013 (Figure 1.3). This could be attributed to snap bean production challenges such as stringent market regulations and post-harvest losses or as a result of the increasing domestic market (Odhiambo, 2012). Generally, Kenya produces and exports higher volumes of snap beans than other East African countries.

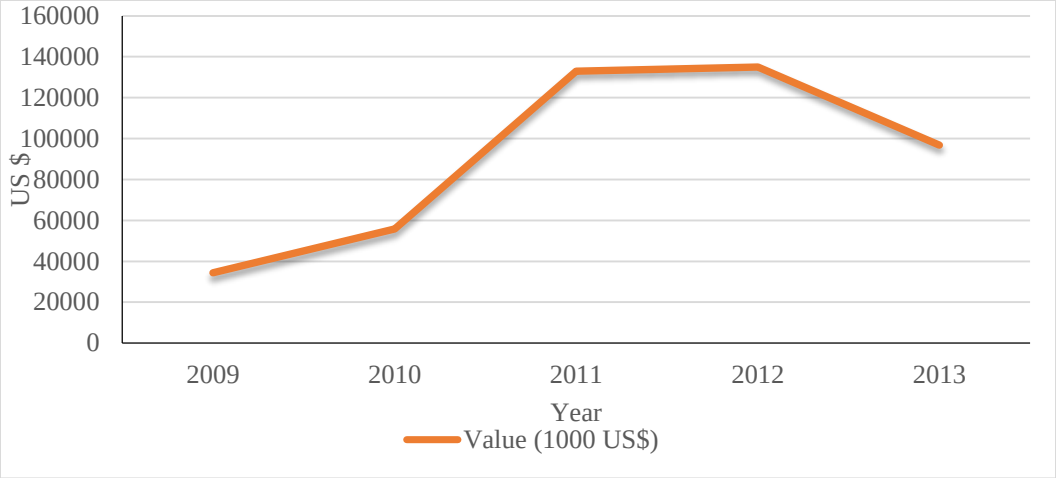


Figure 1. 3 Snap bean export export trends in volumes and values in Kenya between the years 2009 and 2013

Snap bean production is dominated by bush types. Climbing types which have an outstanding three times productivity compared to bush types are of critical interest to smallholder farmers wishing to maximize returns using family labour (CIAT, 2008). The small scale farmers obtain lower yield of bush snap bean because of disease constraints that lead to excessive use of pesticides which are costly (Chemining'wa *et al*., 2012). Furthermore, there are no commercial cultivars of climbing snap bean with marketable pods suitable for export market at present in Kenya. Climbing snap beans are commercially available in Latin America but they have flat pods and hence unsuitable for Kenya's export market (Schoonhoven and Voysest, 1991). However, research on climbing snap bean was started recently at the University of Nairobi (Wahome, 2011). These studies showed that the new climbing snap bean lines were more tolerant to diseases such as angular leaf spot (*Phaeoisareopsis griseola*), anthracnose (*Colletotrichum lindemuthianum*) and rust (*Uromyces appendiculatus*) as compared to commercial bush types. In addition, they could be a good source of the climbing growth habit and disease resistance for further breeding (Wahome *et al*., 2013).

While European markets prefer round podded snap beans, the American markets prefer the flat podded ones (CIAT, 2008). Snap bean pods can either be consumed fresh, canned or frozen (Abate, 2006). Pod traits are therefore considered to be the most important economic traits in snap bean (Singh and Singh, 2015). Pod colour, texture, shape and curvature are among the commonly considered market requirements (Alemu *et al*., 2017).

Much has been done to develop improved snap bean varieties, in relation to climbing habit, multiple disease resistance and good pod quality with little success (Lenne *et al*., 2005). In an attempt to develop climbing snap bean, Wahome (2011) evaluated advanced climbing snap beans that had been developed from crosses with BelDakMi, L227, Beltigrade RR2, Awash 1, G2333, BelMiNeb and Roba-1 which conferred disease resistance to anthracnose, angular leaf spot and rust. They found that these lines exhibited multiple disease resistance implying that they had inherited resistance genes from the parental lines. However, this study did not establish the mode of inheritance of the disease resistance genes among the study lines.

Besides, evaluation for pod quality and yield among advanced snap bean lines indicated that although climbing snap bean was high yielding with 13.4% yield advantage over the commercial check varieties, they had wider pod widths (1.1mm) making them unsuitable for export market (Wahome *et al*., 2013). This study sought to establish the mode of inheritance of climbing capacity and pod yield by evaluating six generations developed from crosses between bush and climbing snap beans. Further, components of genetic variance were established as well as broad and narrow sense heritability. The work done contributes towards the development of new high yielding disease resistant bush and climbing snap bean varieties with good marketable pod traits and hence contribute to increased productivity, sustainable natural resource use, innovative capacity of communities participating in variety selection and knowledge generation.

1.2 Problem statement

Smallholder farmers in Kenya generally rely on the low yielding bush snap bean varieties which are susceptible to various diseases and pests (Otim *et al.*, 2016). The interest in climbing growth habit in snap bean was influenced by their high productivity and multiple disease resistance (Checa *et al*., 2006; Wahome *et al*., 2011). Climbing snap bean popular in some of the North and South American markets have flat pods that are not suitable for European markets. Thin, round podded climbing snap bean varieties have not been developed for farmers in Kenya and other countries in East, Central and Southern Africa (Chemining'wa *et al*., 2012).

Smallholder snap bean production is constrained by lack of high yielding pest and disease resistant commercial snap bean varieties. Resistance to diseases such as rust, angular leaf spot, root rots, bean common mosaic virus (BCMV) and pests like bean stem maggots, thrips and nematodes could substantially improve snap bean productivity (Nderitu *et al*., 2007; Kimani *et al*., 2004).

Additionally, production is constrained by high costs of seed since most of the varieties produced by multinational companies are protected by legislation (Chemining'wa *et al*., 2012; Ugen *et al*., 2012). Excessive use of fungicides to control snap bean diseases increases production costs and reduces their profitability and acceptability in export destinations. Excessive use of pesticides is environmentally unfriendly and is now considered as inconsistent with modern good agricultural practices (GAP). Besides, this is no longer feasible because of the instituted stringent maximum residue levels (MRLs) in all export oriented agricultural produce.

Unlike their counterparts in South America, East African farmers normally do not grow the indeterminate snap bean (Kimani *et al*., 2006). Breeding for high yielding, disease and pest resistant climbing snap bean varieties, tolerant to abiotic stresses, exhibiting general adaptation to tropical conditions and acceptable market quality is a critical component of an integrated strategy to address constraints to snap bean production in the region.

1.3 Justification

Global preference for organic crop produce is on the rise (Lwayo and Obi, 2014). Use of disease resistant varieties is probably the most efficient and cost effective strategy for managing snap bean diseases and reducing reliance on expensive fungicides. Good sources of resistance to angular leaf spot (Namayanja *et al.*, 2006), anthracnose (Miklas *et al.*, 2006) and rust (Kimani *et al.*, 2002) have been reported in snap bean. Additionally, climbing snap bean forms a good source of multiple disease resistance despite its poor pod traits and late maturity (Wahome *et al*., 2011).

Development of climbing snap bean with combined genetic resistance to rust, anthracnose and angular leaf spot, and good pod traits will be economically important especially to smallholder farmers since the cost of production will be reduced while maximizing returns. However, information on the genetic inheritance of climbing capacity and pod yield in snap bean is deficient in the literature yet climbing snap bean would be expected to increase productivity. This is owing to the longer harvest periods and genetic disease resistance which drastically reduce the overdependence on fungicides hence meeting market regulations with regards to MRLs. Genetic information generated in this study is therefore useful in designing an effective snap bean breeding program. Increased productivity will empower smallholder farmers economically while enabling them to compete with large scale production at relatively low costs. Local seed production and

release will further reduce the smallholder famers' cost of production. Besides knowledge will be generated to fill the research gaps that currently exist.

1.4 Objectives

1.4.1 Overall objective

The overall objective of this study is to contribute to enhanced productivity and competitiveness of snap bean in East Africa.

1.4.2 Specific objectives

1. To establish the mode of inheritance for climbing capacity and pod yield in snap bean.
2. To evaluate and select for pod quality, pod yield and multiple disease resistance from advanced climbing snap bean segregating populations.
3. To evaluate and select for pod quality, pod yield and multiple disease resistance from advanced bush snap bean segregating populations.

1.5 Null hypothesis

(i) Climbing capacity and pod yield in snap bean is not genetically controlled.

(ii) There is no variation in pod quality, pod yield and multiple disease resistance in between the new advanced climbing snap bean lines and the check varieties.

(iii) The new advanced bush snap bean lines are not any different in pod quality, pod yield and multiple disease resistance from the commercial check varieties.

CHAPTER TWO

LITERATURE REVIEW

2.1 Origin of snap bean

Snap bean is a strain of common bean which is grown for its fresh tender pods with reduced fibre. Snap bean was derived from common bean which originated from southern Mexico to Mesoamerica and Ecudor, Peru and Bolivia as the secondary origin (Gepts 1998; Singh and Singh, 2015; Vidyakar *et al.*, 2017). Snap bean was originally developed from Andean genetic resources from southern Europe in the 19th century within which it was made a household vegetable with the name 'French' bean (Singh and Singh, 2015). Snap bean is thought to have been a result of continuous selection for tender, stringless and low fibre pods from the common bean rather than the wild beans. Other researchers suggest that snap bean has resulted from crosses between Mesoamerican and Andean gene pools in an attempt to introduce disease resistance to beans followed by selections for fleshy, tender and succulent pods with reduced fibre (Gepts, 1998; Myers and Baggett, 1999).

The first snap bean cultivars to be released in the mid to late 1800s had round and stringless pods (Singh and Singh, 2015). In the early to mid-1900s, Blue Lake green pods and Tendercrop were developed and released for canned and frozen bean processing industries (Silbernagel, 1986; Singh and Singh, 2015). Since then there have been continuous breeding programs and selection of snap bean mainly for yield, pod quality, adaptability and resistance to both biotic and abiotic stresses (Araujo *et al*., 2012; Singh and Sing, 2015; Beshir *et al*., 2015; Pevicharova *et al*., 2015; Sofkova *et al*., 2010; Wahome *et al*., 2011; Wahome *et al*., 2013).

2.2 Botanical characteristics of snap bean

Snap bean (*Phaseolus vulgaris* L.) belongs to the Fabaceae family as a true autogamous diploid species with 22 chromosomes (Singh and Singh, 2015). It is a self-pollinated crop with minimal or zero chance of outcrossing (Singh and Schwartz, 2010). The snap bean flowers have ten stamens which are diadelphous and free with equal lengths and uniform anthers. The standard is reflexed with wings of same length or slightly longer with a spirally coiled keel (Wahome, 2011).

Snap beans are either determinate or indeterminate with trifoliate leaves (Nassar *et al*., 2010). Determinate beans grow up to 60cm high, have short internodes, and do not require any support,

flower and pod within 35 to 40 days. The indeterminate beans on the other hand are as a result of modification of terminal leaflets leading to the stems and pickle tendrils (Calvo *et al*., 2017). They grow up to 3m high and require support by use of stakes or trellises (Wahome *et al*., 2011). Climbing snap beans have longer harvest periods due to continued flowering as the crop erects vertically (Checa *et al*., 2006).

2.3 Production constraints

East and Central African countries produce low volumes of snap beans due to common production constraints which include high pest and disease pressure, poor infrastructure, high cost of agricultural inputs, unfavourable global trends, inadequate control systems, lack of modern technology and stringent regulatory policies (Chemining'wa *et al*., 2012). Besides, lack of easy access to credit facilities, inadequate technical expertise to cope with the market and production standards, market fluctuations, lack of improved cultivars and climate change poses a great challenge to smallholder farmers (Birachi *et al*., 2011). Inadequate local and regional market leads to overdependence on international market which is protected by strict legislations thus adversely influencing the performance of smallholder farmers who are the major producers (Chemining'wa *et al*., 2012).

In Kenya, snap bean production is limited by ecological and agronomic practices as well as biotic stresses that include pathogens, insects and weeds (Elhag and Hussein, 2014; Muthomi *et al*., 2017). The optimal temperature for bean production ranges from 14-24°C with rainfall requirements of 900-1200mm well spread throughout the growing season. Snap beans grow well at an optimal soil pH of 6.5-7.5. Kenya is made up of various agro ecological zones with varied altitudes, temperatures, rainfall patterns and soil types. This limits the production of snap beans to areas that meet the crop's ecological requirements (Kimani *et al*., 2004).

Furthermore, Kenyan smallholder farmers are dependent on casual labour for all snap bean production processes. Large scale production of the bush snap beans is highly favored by mechanization and good infrastructure that is hardly available to the smallholder farmers (Schoonhoven and Voysest, 1991). As a result, snap bean yield in smallholder farms is very low varying from 2 to 8 t ha^{-1} compared to 14 t ha^{-1} for large scale producers (Kimani, 2006). Snap beans produced by smallholder farmers therefore vary with commercial production in volumes

and values. This is because smallholder production is limited by unfavorable global trends including competition, application of modern technology, inadequate control systems, poor infrastructure, stringent consumer policies, high pest and disease pressure, lack of local seed systems, low soil fertility, lack of improved cultivars and unstable market trends (Kamanu *et al*., 2012; Ugen *et al*., 2012).

2.4 Genetics of snap bean

Studies on the inheritance of important agronomic traits of snap beans are scarce. Genetic studies are required to establish the mode of inheritance, gene action and gene effects of major qualitative traits in snap beans. Genetic studies on bush snap beans have often concentrated on traits such as high yield potential, wider adaptability, better pod quality, earliness, stress tolerance and resistance to major diseases (Silva *et al*., 2004; Hagerty *et al*., 2016).

While there has been huge investment in these efforts the success rate has been slow and very low and therefore the challenge of bush bean productivity persists. One way of addressing this is to establish gene effects responsible for climbing ability, higher pod yield, good pod quality and multiple disease resistance in snap bean lines for successful genetic exploitation and appropriate selection methods in breeding. Unfortunately, there are no studies on the mode of inheritance, components of genetic variance and heritability of climbing capacity, pod yield and multiple disease resistance for snap bean improvement in Eastern Africa.

2.5 Review of global snap bean improvement

The ultimate goal of any breeding program is whether the end result appeals to the farmer, the processors and seed companies and the consumers (Silbernagel, 1986). Lack of premium market value snap beans has been critical component of snap bean underperformance in Kenya (Kimani *et al*., 2004). Chemining'wa *et al*. (2012) states that snap bean quality characteristics compliant with the target markets is critical for increasing snap bean consumption and export value. The breeders should therefore consider the needs of their target market and how sustainable they can be over time (Silbernagel, 1986).

Snap bean improvement dates back to the mid 1860s when the first round-podded and stringless cultivar was released and has been an on-going process due to variations in the requirements of either farmers, seed production and processing companies and the consumers as well as changing breeding objectives and market demands. High concentration of snap bean breeding has laid

emphasis on quality seed production, plant characteristics that foster crop adaptation and ease of handling and resistance to both biotic and abiotic stresses (Silbernagel, 1986; Wahome *et al*., 2011; Arunga *et al*., 2010).

2.5.1 Breeding for disease resistance

The development of high yielding varieties with good pod qualities and resistance to disease is attracting the attention of the researchers and the smallholder farmers in order to reap the benefits of reduced costs of production that lead to maximizing on yields and returns. Genetic resistance has a great impact on variety production since the market depends on product quality. Disease resistant cultivars are not only environmentally friendly but also meet the market preferred pod quality in terms of Global Good Agricultural practices (GLOBALGAP) and stringent policies on MRLs. By providing high yielding resistant varieties, smallholder farmers could substantially increase production in order to meet the growing domestic and international market demands and regulations (Birachi *et al*., 2011).

Snap bean production, dominated by smallholder farmers, is challenged by diseases such as rust, angular leaf spot and anthracnose which are the most limiting and widely distributed in Eastern Africa (Wahome, *et al*., 2011). Most of the commercial varieties such as Julia, Morelli, Samantha, Paulista, Morgan among others are highly susceptible to rust, angular leaf spot and anthracnose (Kimani *et al.*, 2006). These diseases can cause up to 100% yield losses and hence the smallholder farmers depend on fungicides to salvage the crop yields (Sofkova *et al*., 2010; Kimani *et al*., 2004). Breeding for multiple disease resistance boosts production by reducing overdependence on fungicides and hence reduced postharvest losses (Otim, 2011; Nderitu *et al.*, 2007). Overdependence on fungicides increases the risk of rejection of the farmers' produce if it exceeds the export market recommended MRLs (Odong, 2012).

In order to breed for disease resistance, it is important to understand disease dynamics in terms of the disease causing pathogens, their races, conditions promoting disease development and their economic importance. Bean diseases such as rust and anthracnose have various races of pathogens hence disease resistance keeps breaking down due to the emergence on new races of disease causing pathogens (Arunga *et al*., 2010). Some diseases are more severe compared to others based on the environmental conditions that favour the growth of disease pathogens. However sources of

resistance against major snap bean diseases have been identified (Wahome *et al*., 2011; Kimno *et al*., 2016). Developing varieties resistant to pests and diseases is probably the most cost effective way of diseases prevention in beans. However, disease resistance is less durable due to the emergence of new pathotypes of disease causing pathogens (Arunga *et al*., 2010; Sofkova *et al*., 2010). This indicates that apart from using disease resistant cultivars, other management practices should be employed for disease prevention.

It is suggested that there is need to pyramid variable race-specific genes with those that confer resistance to disease at late plant stages, those that slow disease development and those that cause reduced disease effects (Souza *et al*., 2013). Besides, Singh and Singh (2015) stipulate that it is important to integrate several breeding approaches in order to broaden the genetic base and introgress quantitatively inherited genes. In an attempt to select for multiple disease resistance, Wahome *et al.* (2011), found that rust was the most limiting disease recording the highest severity upon evaluation of bush and climbing snap bean varieties in Mwea and KALRO- Thika. Two bush lines (KSB 10 W and KSB 10 BR) and one climbing snap bean line, HAV 130 showed combined resistance to the three diseases. However, these lines were not the highest yielding. Further, HAV 130 had thick and flat pods hence poor pod quality (Wahome *et al.*, 2013).

2.5.2 Breeding for pod yield

Snap bean yield is a complex quantitative trait whose heritability is low (Singh and Singh, 2015). Snap bean pod yield, pod quality and stability makes snap bean breeding complicated. Pod yield components include plant height, growth habit, hypocotyl diameter, leaf number, leaf size, number of primary branches, number of reproductive nodes, duration to flowering, internode lengths, number of pods per plant and number of nodes per plant among others (Singh and Singh, 2015). Pod characteristics on the other hand include pod length, color, texture, width, shape, curvature and rate of pod development. While Checa and Blair (2012) reported significant negative correlation between days to flowering and pod length ($r = -0.30^{*}$); number of pods per plant and internode length ($r = -0.45^{**}$) in Darien HP bean cross, Alemu *et al*., 2017 found a significant positive correlation between days to 50% flowering and days to first pick ($r = 0.631^{**}$). Due to the existence of either positive or negative correlation among the yield traits and pod quality traits and many genes involved, breeding for yield and yield components in snap beans cannot be underestimated.

Several factors affect snap bean yields including climatic conditions, diseases (rust, BCMV), halo blight (HB), common bacterial blight (CBB), anthracnose, angular leaf spot and root rots), insect pests, weeds, population density and types of varieties grown (Field and Nkumbula, 1986; Checa *et al.*, 2006; Wahome *et al*., 2011). These factors basically lower snap bean yields. Smallholder farmer yields are further limited by lack of proper technology for post-harvest handling (Cheming'wa *et al*., 2012).

Snap bean is mainly grown for pods in their green state. Snap bean pods can either be consumed fresh, canned or frozen. Therefore pod qualities are of paramount importance depending on the target market. The market requirements vary but there are common pod traits that cut across the regions. While dry bean market classes are principally based on seed characteristics and less on horticultural traits, snap bean market classes are based on pod characteristics (Myers and Baggett, 1999). The most common pod traits include shape (oval, round, flat, crease-back), curvature (straight, curved), length, color (light, dark green, yellow or purple) and snapping ability among others.

Pod shape is normally influenced by pod length, cross sectional shape, the diameter and the length of the spur. Pods for processing range from 10 to16cm beyond which they can't fit to the processors. Myers and Baggett (1999) reported that the pod's cross-sectional shape is determined by the pod's wall thickness and the crop stage of development. This shows quantitative variation contributing to round, flat or crease-back pod shapes. Oval or round pods are good for fresh market due to durability for shipping and attractive appearance. Shape depends on the harvest time while oval or round pods determine the sieve size or market classes, quality and maturity. When over mature, pods become more fibrous and none palatable (Ferreira, *et al.*, 2006). In Kenya, snap bean grading is based on the pod width and pod cross-section. The main classes are extra fine (< 6mm), fine (6-8mm) and bobby (>8mm) (HCDA, 2011).

Pods can be curved or straight. The market export requires straight pods for neat cuts or whole pack products. Pod curvature is determined by the plant type. Straight bush lines and climbers normally produce straight pods. The market further requires long pods ranging from 9 to16cm (Myers Baggett, 1999). The most preferred market colors are light or dark green. The beans should not have fiber and they should snap easily.

2.5.3 Breeding for processing industry

Snap bean pods can be consumed canned or frozen. Snap bean pod texture is the best pod quality indicator for consumers although it changes with canning or freezing (Pevicharova *et al*., 2015; Brown, 1977). According to Singh and Singh (2015), pod texture is determined by the firmness, crispness, stringlessness, parchment layer, succulence and stringlessness. The interaction between genotypes and disease casing pathogens tend to affect the pod texture quality in snap beans (Kimno *et al*., 2016). According to Hagerty *et al*. (2016) and Okello *et al.* (2007) snap bean cultivars that meet the food safety standards of the vegetable processing industry should be developed.

2.5.4 Breeding for growth habit and other horticultural traits

Snap bean growth habit has been classified as either type I, II, III or type IV. Type I are the bush, and type IV are the climbers while type II and III fall in between (Wahome, 2011). Various studies have suggested that climbing growth habit could play a critical role in crop productivity. For example, Checa and Blair (2012) stated that climbing growth habit contributes to higher yields in dry bean leading to a yield advantage of 3:1 over bush bean. Climbing beans are associated with continuous growth of the guide shoots, continuous flowering, need for vertical support, high productivity and longer harvest periods (Checa *et al*., 2006). Although climbing habit may be of paramount importance in snap bean production by smallholder farmers, the mode of inheritance of this trait has not been established.

Researchers have also appreciated the economic importance of earliness in snap beans for reduced cost of production (Traka-Mavrona *et al*., 2000). Growth vigour and good seedling emergence contribute to consistent and maximum production in snap beans (Silbernagel, 1986). Breeding for pod quality in terms of colour, texture, low fibre content, pod curvature is critical since pods ought to have good sensory characteristics and appeal to the consumers.

Research at University of Nairobi centered on the development and selection of snap bean lines with marketable pod traits, development of segregating population and evaluation of advanced bush and climbing snap beans (Kimani, 2006; Kimani *et al*., 2008; Cheminin'gwa *et al.*, 2012; Mulanya, 2016; Kimani *et al.*, 2016). Evaluation and selection was carried out on pod traits, growth habit and disease resistance over replicated trials in space and time to ensure accurate selection of varieties that are distinct, uniform and stable (DUS). This led to the recommendation of Kenya

Amboseli and Kenya Safari to the National Variety Release Committee (NVRC) for release by the Kenya Plant Health Inspectorate Services (KEPHIS, 2015). These varieties were released in 2018 (KEPHIS, 2018).

2.5.5 Snap bean improvement in Eastern Africa

Several studies have been conducted in East and Central Africa on various aspects of snap bean production all aimed at the crop's improvement in terms of quality, adaptation and productivity (Chemining'wa *et al*., 2012). Snap bean improvement is a relatively recent activity in East Africa which started in 2005 though snap bean breeding is advanced in Latin America, USA, Europe and China. Within East and Central Africa, the research activities have been carried out in Kenya, Uganda, Rwanda and Tanzania (Kimani *et al*., 2009).

Snap bean improvement activities in Kenya started in 1998 in KARI (currently KALRO), a program that was supported by CIAT and Eastern and Central African Bean Research Network (ECABREN) (Chemining'wa *et al*., 2012). The breeding activities were performed in three locations; University of Nairobi, KALRO- Thika and Moi University. Research involved performing crosses and advancing to later generations accompanied by evaluation, screening and selection of promising lines.

University of Nairobi in collaboration with KALRO- Thika evaluated and selected bush and climbing snap bean lines with good pod quality, marketability, shelf-life, high productivity, growth habit, resistance to common bacterial blight, angular leaf spot, anthracnose, rust, root rots as well as thrips, bean fly, aphids and nematodes (Kimani *et al*., 2009). This work involved evaluation of 44 bush and 15 climbing snap bean lines of which upon selection 6 climbers and 15 bush lines were promising. Crosses were also developed in KALRO between commercial varieties and locally improved rust resistant variety *Kutuless* by Ndegwa (Chemining'wa *et al*., 2012). Eight promising lines were identified (Kimani *et al*., 2009). The breeding activities in KALRO-Thika were led by Agnes Ndegwa and resulted in the development of a rust resistant variety, with good snapping ability and extra fine pods known as *Kutuless* (J12) in 2000 (KEPHIS, 2009). In 2001, ECABREN supported a small program to develop improved snap beans with high yield potential, good pod traits and resistant to biotic stresses for smallholder farmers (CIAT, 2006). At Moi University, 10 snap bean lines were developed and evaluated and 4 locally adapted varieties were developed between 2003 and 2004. These test lines were evaluated in national performance trials (NPTs) and were found to have improved pod yield, marketable pod quality and resistant to

anthracnose, angular leaf spot and rust. However, the lines were not officially released (Chemining'wa *et al*., 2012).

A study conducted in Rwanda in 2006-2007 by Musoni involved the evaluation of 40 advanced climbing lines and 18 bush lines and selection for pod traits (Kimani *et al*., 2009). Climbing lines were found to be better yielding with "Boon, G685, Ncekarkonnigia, Saxa, Khaki and Loriet" as the most promising lines. These lines were however adversely affected by diseases such as root rots, rust, angular leaf spot and BCMV as well as pests including aphids, bean stem maggots, spider mites and crickets. As a result these lines have never been released (CIAT, 2008).

Through its 'Improved Beans for the Developing World' program in Cali Colombia, CIAT through the University of Nairobi Bean Program conducted on-farm screening for combined disease resistance, resistance to economic pests and development of production packages. This involved evaluation of 11 snap bean accessions from CIAT and Kenya for resistance to rust, angular leaf spot and common bacterial blight. Surveys showed that rust was the most limiting. Six lines; HAB 433, BC 4.8, A 20, J 12, L 1 and L 12 showed combined disease tolerance to rust, angular leaf spot and anthracnose though all were of type II growth habit which is associated with relatively low yields compared to climbing beans with type IV growth habit (CIAT, 2008).

In Tanzania, a baseline survey was carried out by F. S. Ngulu on major constraints regarding agronomic and crop protection management practices for snap bean production and marketing environment. It was indicated that good agronomic and crop protection practices improved snap bean performance (CIAT, 2008).

2.6 Conceptual Framework of snap bean breeding programme

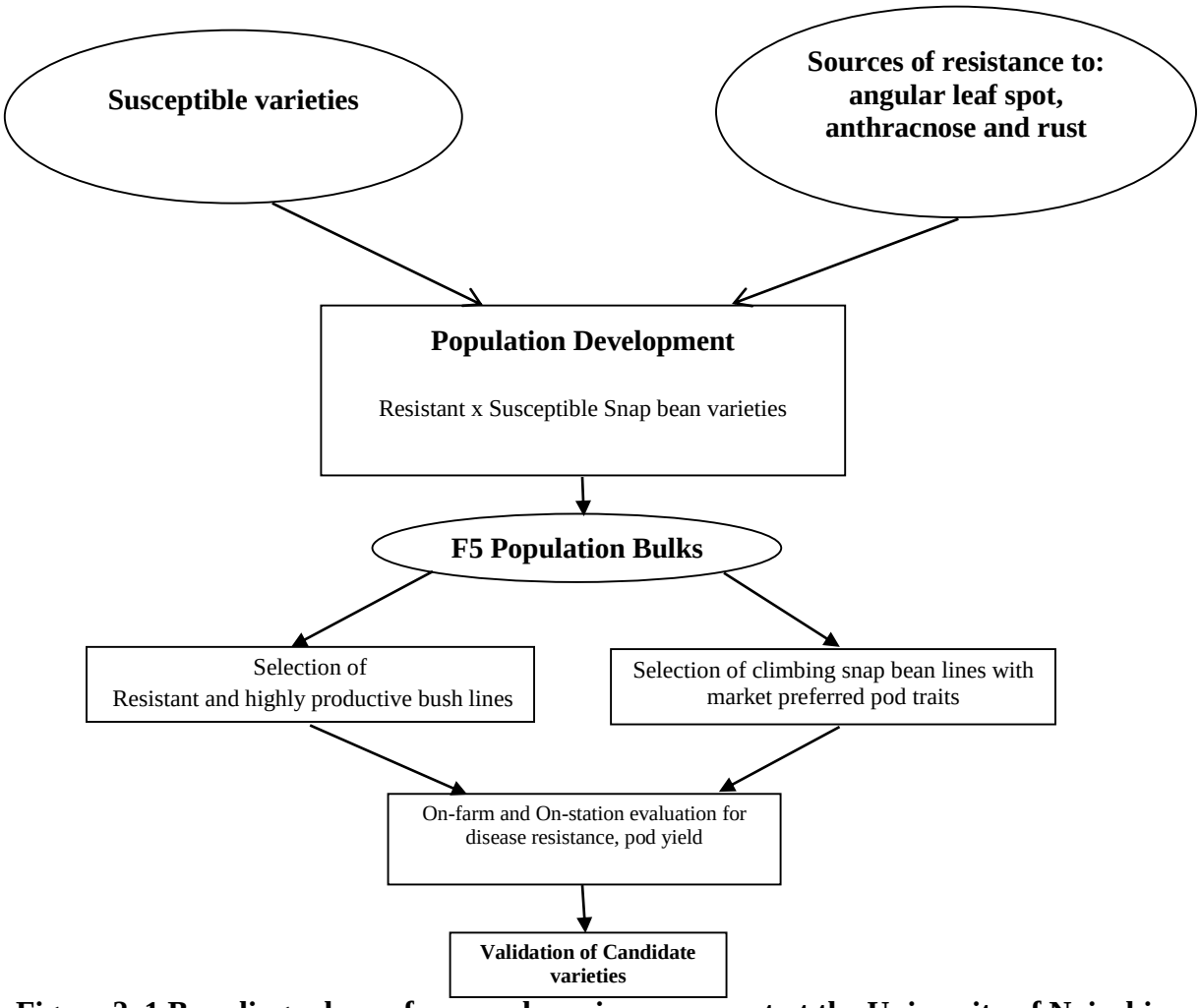


Figure 2. 1 Breeding scheme for snap bean improvement at the University of Nairobi.

The snap bean breeding programme at the University of Nairobi adopted the scheme to develop and select for high yielding disease resistant snap bean varieties (Figure 2.1). Crosses were carried out between susceptible commercial snap bean varieties and sources of resistance to rust, anthracnose and angular leaf spot (Figure 2.1). The susceptible commercial varieties included Amy, Foskelly, Paulista, Morgan, Morelli, Julia, Kutuless, Teresa, Alexandria, and Vernandon (Kimani, 2006) while the sources of resistance were Beldakmi, Belmineb, and Beltgrade lines (against rust), G2333 (against anthracnose), Mex 54 and L227-10 (against angular leaf spot) and L227-10 (against root rots). The F_1 progenies were then advanced through bulk population and pedigree methods to F_5 generation and/or backcrossed to their recurrent commercial parents (Kimani, 2006). Wahome (2011) evaluated 674 (F_6, $F_{7.9}$ and F_8) single plants for growth habit and

multiple disease resistance. The lines were artificially inoculated with rust, angular leaf spot and anthracnose isolates and advanced as Progeny I and II nurseries at Mwea and Thika in 2009 and 2010. Wahome (2011) realized that six climbing lines were more resistant to rust, anthracnose and angular leaf spot than the check varieties and the advanced bush lines. However, these lines were not the highest yielders and had poor pod quality. Further on-farm and on-station evaluations were performed in 2012. Validation of the candidate varieties was carried out in this study.

CHAPTER THREE

GENETIC ANALYSES OF CLIMBING ABILITY AND POD YIELD IN SNAP BEAN

ABSTRACT

Climbing snap beans have often been associated with high productivity compared to bush types. Breeding for climbing capacity in snap beans for increased productivity is limited by scarcity of information on gene action, genetic variability and heritability of climbing ability and pod yield. The objectives of this study were to determine genetic mechanisms responsible for climbing ability and pod yield in snap bean. Six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) were developed for each of 11 eleven crosses between climbing and bush snap bean genotypes. The generations were evaluated at Kabete Field Station. Data collected on days to 50% flowering, plant height, internode length, number of pods per plant and pod length was subjected to analysis of variance using Genstat statistical software (14th Ed.). Regression analysis was carried out to determine the estimates of genetic effects and components of phenotypic variance. Correlation analysis was carried out in order to determine the strength and direction of association among the traits under study.

There were significant genotypic differences ($P \leq 0.05$) in all the traits under study. The bush parents (P_1) and the climbing parents (P_2) varied significantly with extreme values in all the traits under study. F_1 progenies were within the parental ranges in all traits except in pod lengths of F_1 plants in Paulista x HAV 133 and Morgan x HAV 130 crosses where F_1 pods were longer that the pods of both parents. In most crosses, F_1 plants outperformed the F_2 plants in all traits. The backcross progenies (BC_1P_1 and BC_1P_2) were close to their recurrent parents in all traits. Regression analysis showed that 6-parameter model was appropriate for all the traits studied. Digenic duplicate epistasis was responsible for plant height in all crosses except in Samantha x HAV 131 cross. Morelli x HAV 130 and Serengeti x HAV 132 showed duplicate epistasis in all traits as compared to the other crosses. All traits had high additive genetic variance in all crosses Plant height had high broad (65.6-91.7%) and narrow (57.9-83.3%) sense heritability. Days to 50% flowering in Star 2053 x HAV 131 cross had the highest broad sense and narrow sense heritability (72.64% and 71.47% respectively). Internode length, number of pods per plant and pod length showed low heritabilities (<30%) in all crosses. Most traits revealed high additive variance

component in all crosses implying that these traits can easily be selected for in order to improve snap bean yields. Due to the presence of both fixable and non-fixable genes playing a role in the control of the traits under study, selection methods such as pedigree or single seed decent can be employed in selection for days to 50% flowering, plant height, internode length, number of pods per plant and pod length in snap bean breeding program. High positive heterosis was noted in days to 50% flowering for Morgan x HAV 130 (70.2%) and Star 2053 x HAV 131 whereas in plant height, heterosis was high for Samantha x HAV 131 (60.1%) and Serengeti x HAV 132 (80.9%). Positive heterosis was also realized in internode length (Samantha x HAV 131, 84.0%; and Serengeti x HAV 132, 93.5%) and number of pods per plant in Star 2053 x HAV 131 (80.6%) and Teresa x HAV 131 (88.1). The high positive heterosis is an evidence of the superior performance of F_1 progenies relative to the better-parental value and that these parents suitable for snap bean breeding since they have high potential for the performance of the segregating progenies in the respective traits.

There was a significant positive ($P \leq 0.05$) correlation between days to 50% flowering and plant height (Morelli x HAV 130, r = 0.9271**; Paulista x HAV 133, r = 0.9776**; Samantha x HAV 132, r = 0.9507**; and Morgan x HAV 130, r = 0.9688**). Correlation between 50% days to flowering and internode length were positive and significant ($P \leq 0.05$) for five out of eleven crosses with r values ranging from 0.9226** to 0.9737**. It is only in Morelli x HAV 133 that highest significant positive correlation ($P \leq 0.05$) was observed between days to 50% days to flowering and number of pods per plant (r = 0.9386**). Plant height and internode length had a high significant ($P \leq 0.05$) positive correlation in Morgan x HAV 130 (r = 0.9974**), Samantha x HAV 132 (r = 0.9292**), Star 2053 x HAV 135 (r = 0.9731**) and Star 2053 x HAV 131 (r = 0.9482**). Plant height showed a positively significant ($P \leq 0.05$) association with number of pods per plant in Morelli x HAV 133 (r = 0.9951**) and Teresa x HAV 131 (r = 0.9662**) crosses. Internode lengths were significantly and positively associated with the number of pods per plant in Star 2053 x HAV 131 cross (r = 0.9039**). However, negative correlation was noted between pod lengths and all other traits. Positive correlation among the studied traits indicates that these traits can be selected for in the snap bean breeding program.

Key words: Climbing capacity, correlation, gene effects, generation mean analysis, heritability.

3.1 INTRODUCTION

Snap bean, also referred to as green bean, string bean or French bean, is grown for its immature edible pods (Richardson, 2012). Its pods are consumed as vegetable while young and tender, snap easily before the seeds mature. Snap bean has both nutritional and economic value. It is a good source of carbohydrates, dietary fibre, proteins and vitamins C, K and B_6 in proportions of 15%, 14% and 11% respectively. It is also a good source of minerals such as manganese, calcium, iron, magnesium, potassium and zinc among others (Pattung *et al*., 2016). Romeo-Arenas *et al*. (2013) reported that snap bean has chromium salts which have anti-diabetic effects. Besides, snap bean farming is a good source of income and hence good for economic empowerment (Kimani *et al*., 2004; Araujo *et al*., 2012; Romeo-Arenas *et al*., 2013).

According to Checa and Blair (2012), growth habit in beans contributes to its yields. Consequently, climbing beans are higher yielding compared to bush beans. Snap beans can be determinate or indeterminate. Climbing (indeterminate) and bush (determinate) snap beans are morphologically distinct (Figure 3.1). Indeterminacy in dry beans has been associated with high yields (Checa and Blair, 2012) but in snap beans, Wahome *et al*. (2013) found that climbing snap beans which exhibited multiple disease resistance to rust, anthracnose and angular leaf spot were not the highest yielders.

Climbing beans are generally erect and require support by use of trellises or stakes and/ or support crops like maize in case of intercropping while determinate types do not require support. Apart from yield, climbing snap beans have been found to exhibit multiple disease resistance to anthracnose, rust and angular leaf spot compared with their bush counterparts (Wahome *et al*., 2011). However, available climbing snap bean varieties are not suitable for export markets due to poor pod qualities for the European market. Most of the available commercial bush snap bean varieties such as Paulista, Amy and Samantha popular in eastern Africa are not only low yielding but also susceptible to diseases such as rust, anthracnose, angular leaf spot, BCMV, and common bacterial blight and therefore producers rely on fungicides for disease control. However, this not only increases production costs but also poses health hazards to growers and consumers, and may adversely affect the environment. Besides, farmers are faced with lack of seeds that are resistant to diseases leading to reduced yields (Chemining'wa *et al*., 2012).

Snap bean yield is a polygenic complex trait since it is a result of interaction of many genes affecting yield components. On evaluating genetic correlations between yield and yield traits and determining the quantitative trait loci (QTL) controlling phenological and yield traits in dry bean, Checa *et al.*, 2012 found that four QTLs controlled yield while 12 QTLs controlled yield and yield components. Despite being polygenic, Checa and Blair (2012) stated that yield and yield components are easily and highly heritable. According to Singh and Singh (2015), snap bean yield components include plant height, growth habit, internode length, duration to flowering, and number of pods per plant among others. While climbing capacity can be measured by plant height and internode length (Checa *et al*., 2006), pod yield can be measured by the number of pods per plant. Araujo *et al*. (2012) found that the number of pods per plant had the most significant effect on productivity. This confirms the reports of Chung and Goulden (1971) who stated that number of pods per plant was the main component determining yield in beans. They argued that selection for high yield in beans can be based on the number of pods per plant.

A=climbing beans, B= bush beans

Figure 3. 1 Climbing and bush Snap beans

In order to breed for climbing ability, gene action controlling growth habit and adequate genetic variability of parents can contribute to the development of an effective breeding program. This can be achieved by measuring the plant genotypic performances of quantitative traits responsible for

growth habit and yield on several individual plants through generation means analysis. Generation mean analysis has been found to be the best and most effective method for generating information on the type and magnitude of gene action (Dhar, 2016); detecting presence or absence of epistasis (Sharmila *et al*., 2007); estimating genetic components of variation and heritability (Dvojkovic *et al*., 2010); and selecting parents and breeding methods for an effective breeding strategy (Abedi *et al*., 2015). Generation means analysis has been used to determine the genetic basis for yield and yield traits in wheat (Dvojkovic *et al*., 2010; Saidi, 2014), maize (Shahrokhi *et al*., 2013), chickpea (Deshmukh and Gawande, 2016), Okra (Patel *et al*., 2010), common bean (Checa *et al*., 2006; Hinkossa *et al*., 2013; Akhshi *et al*., 2014; Kunkaew *et al*., 2010), cowpea (Gupta *et al*., 2017) and tomatoes (Zdravkovic *et al*., 2011; Saidi *et al*., 2008) among other crops.

However, the literature is devoid of the information on the type, nature and magnitude of gene actions influencing quantitative traits responsible for climbing capacity and pod yield in snap beans. Components of genetic variability and heritability of these traits is also yet to be established. Correlation among the various quantitative traits responsible for yield could be used to identify the best traits to breed for, breeding methods and selection procedures in snap bean breeding. In order to generate this information, generation means analysis was applied on snap bean populations developed by crossing the climbing snap beans and bush commercial varieties. The objective of this study therefore was to determine the inheritance of climbing ability, pod yield and pod length in snap beans and to determine the relationships among these traits.

3.2 MATERIALS AND METHODS

3.2.1 Experimental site

This study was conducted on-station at the Kabete Field Station situated at 01.24256°S and 036.74186°E with an elevation of 1856 m above sea level. It falls under agro-ecological zone III (Medium potential). Kabete experiences bimodal rainfall patterns with long rain season occurring between March and June and short rain season between October and December. The annual rainfall at Kabete is 1000mm. Kabete has dominant soils classified as humic nitisols (Jaetzold *et al*., 2006). The average monthly temperature at Kabete is 19°C (Mulanya, 2016).

3.2.2 Plant materials

Bush parental lines were 8 commercial varieties (Paulista, Morgan, Samantha, Morelli, Serengeti, Star 2053, Teresa and Vernadon). Most of these varieties are susceptible to diseases or have intermediate resistance to diseases (Wahome, 2011). The seed color of these varieties varied from white (Paulista, Teresa, Serengeti, Star2053 and Samantha) to brown (Morgan) to black (Vernadon) and to black speckled (Morelli). Morelli has purple flowers while Serengeti and Morgan have yellow flowers. All the other commercial varieties have white flowers (Table 3.1). Teresa has been reported to possess *ur-5* genes that confer resistance to rust pathogens (Pasto-Corrales, 2010).

The second set of parents were 6 climbing snap bean lines previously characterized by Wahome (2011) (Table 3.1). They were obtained from the Bean Research Program, Department of Plant Science and Crop Protection of the University of Nairobi. These lines were selected from crosses between commercial varieties and several sources of resistance to rust, angular leaf spot, root rots and anthracnose (BelDakMi, L227, Beltigrade RR2, Awash 1, G2333, BelMiNeb and Roba-1) (Wahome *et al*, 2011). The segregating lines were advanced to F_4, $F_{4.5}$ and F_6 generations at Thika and Mwea. Single plants were selected and advanced as progeny rows during the 2010 short rain season at Mwea and Thika (Wahome *et al*, 2011). The progeny rows were evaluated in farmer participatory trials at Thika during the 2011 long rain season. Among the 160 lines selected, six (HAV 130, HAV 131, HAV 132, HAV 133, HAV 134 and HAV 135) exhibited climbing growth habit and multiple disease resistance to rust, angular leaf spot and anthracnose and high pod yield. However, HAV 130 was highly resistant to rust, anthracnose and angular leaf spot but low yields.

HAV 131 was the only climbing bean with extra fine pods and the highest percentage of premium pods (56%) (Table 3.1).

Table 3. 1 Characteristics of study parental lines.

Parental lines	Growth Habit	Origin#	Resistance genes			Days to 50% flowering	Pod color	Pod length (cm)	Pod curvature	Pod yield (kg ha^{-1})	Pod Quality (%)		
			Rust	Angular leaf spot	Anthracnose						Extra Fine	Fine	Bobby
Paulista	II	Monsanto	5.4	4.5	2.8	39	G	10.5	S	2836.7	29.9	65.1	4.9
Morgan	II	Unknown	5.5	4.3	3.7	38	P	9.7	S	2446.7	100	0	0
Samantha	II	Monsanto	6.4	5.0	3.8	39	G	11.9	S	3967.0	86.0	14	0
Morelli	II	Unknown	4.1	4.9	2.7	38	V	9.9	S	3229.5	12.4	56.8	30.8
Serengeti	II	Syngenta/ Kenya Highland Seed Company	3.8	6.2	4.1	39	G	5.8	S	2375	63.3	36.7	0
STAR 2053	II	Safari Seed Company	2.8	4.6	4.5	39	G	10.8	S	3364.4	58.9	41.1	0
Teresa	II	Monsanto	5.0	4.7	4.0	39	G	11.2	S	4221.1	85.8	14.2	0
Vernandon	II	Unknown	5.5	4.2	2.5	38	G	9.6	S	3677.8	0	67.1	32.9
HAV 130	IV		1.8	2.9	1.7	46	G	11.4	SC	2286.7	0	45.5	54.5
HAV 131	IV		3.0	3.1	1.8	48	G	10.5	S	3803.9	5.5	50.5	43.9
HAV 132	IV	UON Bean Program.	3.4	2.7	1.8	46	G	10.6	S	2251.1	0	36.5	63.5
HAV 133	IV		3.1	2.4	1.8	48	G	10.6	S	1935.6	0	31.6	63.4
HAV 134	IV		3.7	3.4	1.3	46	P	10.5	SC	1864.4	0	48.6	51.4
HAV 135	IV		3.4	3.4	2.5	49	V	10.6	S	1982.2	0	40.5	59.5

Source: Wahome *et al*., 2011: II- bush growth habit; IV- Climbing growth habit, Disease severity scale (van Schoonhoven and Pastor-Corrales, 1987), Chemining'wa *et al*., 2012.

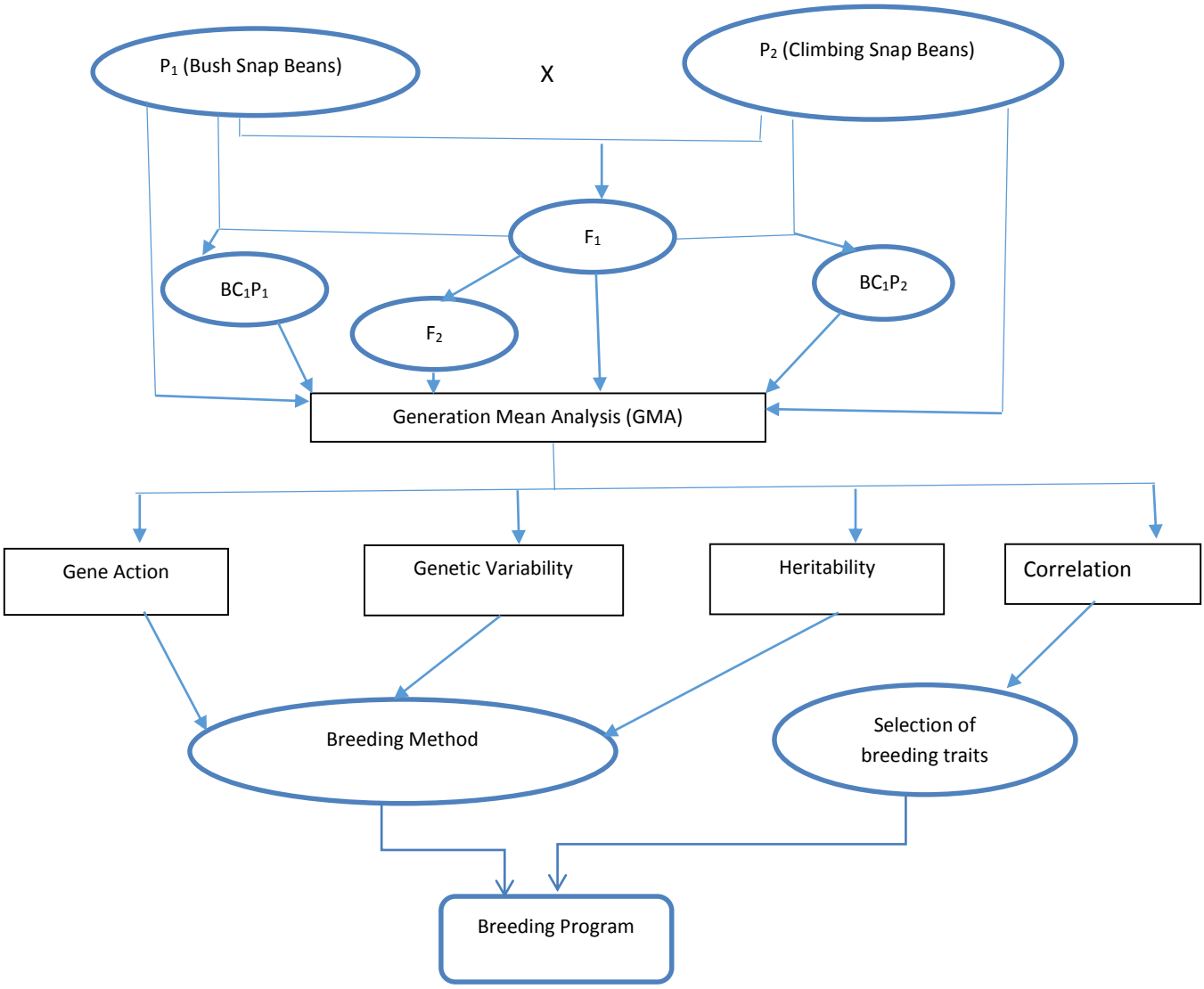


Figure 3. 2 Procedure followed in developing study populations for the generation mean analysis

3.2.3 Population Development

A step-by-step hybridization was carried out to generate the six generations P_1 (Bush parent), P_2 (Climbing parent), F_1 (First filial generation), F_2 (Second filial generation), BC_1P_1 (F_1 backcross to the bush parent) and BC_1P_2 (F_1 backcross to the climbing parent) of eleven populations (Figure 3.2). To determine the inheritance of climbing ability and pod yield in snap beans, crosses were made between six climbing and eight commercial bush varieties (Table 3.1). Three seeds of each parental line were planted in plastic pots filled with sterilized soil in an insect proof screen house at Kabete Field Station between December, 2012 and February, 2013. Before sowing, soil in each pot was mixed with 5g of di-ammonium phosphate (DAP). Ten seeds of each parental line were planted at 10 days intervals for one month to synchronize flowering and to ensure that adequate pollen was available for pollinations. Plants were top dressed with 5g of calcium ammonium nitrate (CAN) applied four weeks after planting. Climbing parents were staked using trellises (Figure 3.3). The crop was irrigated three times a week using a watering can. Insect pests such as whiteflies, spider mites and leaf miners were controlled by alternate application of Cyclone® (10% cypermethrin + 35% chlorypriplant heightos) and Confidor® (imidacloprid) at the rate of 1.5ml L^{-1} every two months.

During flowering, pollen was harvested from the male plants while hand emasculation was employed on female plants to prevent self-pollination. The stamens containing mature pollen were picked from the male plants using a forceps that was constantly cleansed using alcohol. The pollen were then rubbed on the stigma of the female plant. Upon hybridization, a tag containing the names of the two parents used for crossing was tied to the pedicel of the female flower for identification. Only 10 pods per plant for bush females from crosses were allowed to develop to maturity while all other flowers and pods were removed to ensure reduced competition between pods from crosses and selfs. The seeds were then harvested and planted to give rise to F_1 between March and June, 2013.

The resulting F_1 seeds were planted to obtain F_2 and backcrossed to each parent to generate BC_1P_1 and BC_1P_2 in September to December, 2013. At least 100 F_1 seeds, 200 seeds of F_2 and 50 backcross seeds were produced. The F_1, F_2 and backcrosses were then evaluated in the field for climbing capacity, pod yield and pod length during the long rain season, 2014.

Single crosses between P_1 and P_2	F_1 at germination stage	Morelli and Teresa crosses	F_1-All climbers staked with trellises

Figure 3. 3 Snap bean population development for generation mean analysis.

3.2.4 Field evaluations

3.2.4.1 Experimental Design and Treatments

The P_1, P_2, F_1, F_2 and BC_1P_1, BC_1P_2 progenies were evaluated for climbing ability, pod yield and pod length at Kabete Field Station between March and June 2014. Land preparation took place just before planting in the month of March. Each population was planted in a 4 x 8.5m plot. Spacing was 10cm within rows and 50cm between rows. The non-segregating populations (P_1, P_2 and F_1) were planted in two rows each, backcrosses three rows and F_2 progenies were planted in 4 rows. The trial was laid out in randomized complete block design with the six treatments in each population replicated two times.

Normal agronomic management practices were followed. Supplemental irrigation was provided every three times a week using sprinklers. Di-ammonium phosphate fertilizer was used during planting at a rate of 60 kg ha^{-1} while calcium ammonium nitrate (26% N) was applied during flowering at a rate of 5g per plant. Insect pests, mainly white flies, were controlled by alternate application of Cyclone® (10% cypermethrin + 35% chlorypriplant heightos) and Confidor® (imidacloprid) at the rate of 1.5ml L^{-1} twice during the experimental period. Climbing beans were supported using stakes.

3.2.4.2 Data Collection

Generations from each cross were evaluated for climbing ability, pod yield and pod length. Data was collected on days to 50% flowering, plant height, internode length, number of pods per plant and pod length. Pod yield data was based on number of pods per plant. The number of plants evaluated varied with treatments; 8 plants were randomly selected from non-segregating populations (P_1, P_2 and F_1); 12 plants from backcrosses (BC_1P_1 and BC_1P_2) and 20

plants from the segregating F_2 progenies in order to obtain the desired variability among populations. The non-segregating populations (P_1, P_2 and F_1) are fairly uniform in their performance while moderate to maximum variability is expected in the backcross progenies (BC_1P_1 and BC_1P_2) and F_2 progenies respectively. Data was subjected to analysis of variance followed by separation of means using Tukey's *w* procedure (Steel *et al*., 1999). Upon separation of means, it was determined whether each trait was qualitatively or quantitatively inherited. The six generations (P_1, P_2, F_1, F_2 and BC_1P_1, BC_1P_2) means were compared in order to determine the type of gene action and heritability of the climbing ability, pod yield and pod length. The type of epistasis was established using dominance and additive x dominance gene actions.

3.2.4.2.1 Days to 50 percent flowering

Days to 50 percent flowering was recorded as the duration from planting to the date when 50 percent of the plants in each plot had at least one flower. Eight plants of the non-segregating populations (P_1, P_2 and F_1), 12 plants of the backcross progenies (BC_1P_1 and BC_1P_2) and 20 plants of the second filial generation (F_2) were evaluated for days to 50% flowering.

3.2.4.2.2 Plant height

Plant height was measured in centimetres from the ground level of the plant stem to the last leaf axis along the main stem. Eight plants of the non-segregating populations (P_1, P_2 and F_1), 12 plants of the backcross progenies (BC_1P_1 and BC_1P_2) and 20 plants of the second filial generation (F_2) were evaluated for plant height.

3.2.4.2.3 Internode length

Internode length was evaluated by counting all the internodes and finding the median then using it as the internode along the main stem of the plant and recording its length in centimetres. Eight plants of the P_1, P_2 and F_1, 12 plants of the BC_1P_1 and BC_1P_2 and 20 plants of the F_2 progenies were evaluated for internode length.

3.2.4.2.4 Number of pods per plant

Number of pods per plant per treatment in each population were counted and recorded. The plants at the edges were however not evaluated in order to eliminate border effects. Evaluation for the number of pods per plant was administered on 8 plants of the non-segregating populations (P_1, P_2 and F_1), 12 plants of the backcross progenies (BC_1P_1 and BC_1P_2) and 20 plants of the second F_2 generation.

3.2.4.2.5 Pod length

Pod length per treatment in each population was measured using a calibrated ruler and recoded in centimetres Eight plants of the non-segregating populations (P_1, P_2 and F_1), 12 plants of the backcross progenies (BC_1P_1 and BC_1P_2) and 20 plants of the second generation (F_2) were evaluated for pod length.

3.2.4.3 Data Analysis

Step-wise data analysis was carried out as follows:

I. Analysis of Variance:

Analysis of variance (ANOVA) was carried out separately for generations within a cross and repeated for the eleven populations. Tukey's *w* procedure was used for separation of means (Steel *et al.*, 1999). Populations which showed significant genotypic variations (F_{pr}= <0.01) were further subjected to genetic analyses.

II. Genetic analysis:

Genetic analyses were performed for traits showing significant differences among generations in each cross. Joint scaling test was carried out to determine the presence or absence of epistasis while regression analysis was carried out to identify genes responsible for the expression of significant quantitative traits in snap bean. Components of phenotypic variance were also computed to identify their contribution to the expression of traits under study.

(i) Joint scaling test:

The models (3 and 6 parameter models) were tested to determine which gave the best fit in terms R^2 values and t-tests. The tests were carried out using the Mather and Jinks (1982) scaling tests in order to determine whether 3-parameter model (m+a+d) or 6-parameter model (m+a+d+aa+ad+dd) was appropriate for the explanation of the expression of the traits under study. The joint scaling test was done as follows

$A = 2\overline{BC_1P_1} - \overline{F_1} - \overline{P_1}$ and $V_A = 4V_{BC_1P_1} + V_{P_1} + V_{F_1}$

$B = 2\overline{BC_1P_2} - \overline{F_1} - \overline{P_2}$ and $V_B = 4V_{BC_1P_2} + V_{P_2} + V_{F_1}$

$C = 4\overline{F_2} - 2\overline{F_1} - \overline{P_1} - \overline{P_2}$ and $V_C = 16V_{F_2} + 4V_{F_1} + V_{P_1} + V_{P_2}$

Where:

$\overline{P_1}$, $\overline{P_2}$, $\overline{F_1}$, $\overline{F_2}$, $\overline{BC_1P_1}$ and $\overline{BC_1P_2}$ referred to the generations means and V_{P1}, V_{P2}, V_{F1}, V_{F2}, V_{BC1P1} and V_{BC1P2} referred to the generation variances estimated according to Mather and Jinks (1971).

The t- test values were calculated as:

$$\pm t = \frac{\text{Deviation}}{\text{standard error}} = \frac{\text{Deviation (Values of A or B or C)}}{\sqrt{\text{Variation of deviation}}}$$

$$\pm t_A = \frac{A}{\sqrt{V_A}} \text{ and } t_B = \frac{B}{\sqrt{V_B}} \text{ and } t_c = \frac{C}{\sqrt{V_C}}$$

The t-tests were calculated at 5% and 1% probability levels. Where either the A, B or C values were statistically significant, the 3-parameter model (m+a+d) was insufficient in the explanation of genetic effects among traits thus implying that the six parameter model (m+a+d+aa+ad+dd) was appropriate due to the presence of non-allelic or epistatic gene effects (Singh and Chaudhary, 1985).

(ii) Generation means analysis (GMA):

This methodology was applied as proposed by Mather and Jinks (1971) for genetic analyses.

Generation mean analysis was based on the following model:

$$g_k = m + (\alpha_k)a + (\delta_k)d + (\alpha_k)2aa + (\alpha_k\delta_k)ad + (\delta_k)2dd.$$

Where

g_k = mean of generation k

m = mean of the parental homozygotes

α_k and δ_k = coefficients determined by the degree of relationship of generation k

a = additive gene effects

d = dominant gene effects

aa = additive x additive gene effects

ad= additive x dominant gene effects

dd= dominant x dominant gene effects .

The fixed (**a, aa**) and non-fixed (**d, ad and dd**) gene parameters were estimated in a stepwise linear regression analysis using Genstat software version 14. Regression analysis was weighted based on the inverse of the population variance and the coefficient of genetic effects as shown in Table 3.2 (Mather and Jinks 1971). Coefficient of determination (R^2), goodness of fit (F-test) and

t-test were used to determine the genetic effects that were adequate within the model (Ceballos *et al*. 1998).

Table 3. 2 Coefficients of genetic effects used in the construction of 9 models in generation mean analysis.

Generation	Genetic effects					
	m	a	d	aa	ad	dd
P_1	1	-1	0	1	-1	0.25
P_2	1	1	0	1	1	0.25
F_1	1	0	1	0	0	0.25
F_2	1	0	0.5	0	0	0
BC_1P_1	1	-0.5	0.5	0.25	0	0
BC_1P_2	1	0.5	0.5	0.25	0	0

m-mean effect of parental homozygotes, a=additive gene effects, d=dominance gene effects, aa= additive x additive gene effects, ad=additive x dominant gene effects and dd= dominance x dominance gene effects

Source: Mather and Jinks, 1971

Genetic effect estimates were then computed upon identification of the appropriate model at 5% and 1% t-test levels of significance (Singh and Roy, 2007).

III. Components of phenotypic variance for the most segregating populations (F_2) were also estimated based on Mather and Jinks (1971) formula as follows;

i. Phenotypic variance (p): $\sigma^2_p = \sigma^2_g + \sigma^2_e$

ii. Environmental variance or error (e): $\sigma^2_e = ¼\{(\sigma^2_{P1} + \sigma^2_{P2} + (2\sigma^2_{F1})\}$

iii. Genotypic variance (g): $\sigma^2 g\ (F_2) = \sigma^2_{F2} - \sigma^2_e$

iv. Additive variance (a): $\sigma^2 a\ (F_2) = (2\sigma^2_{F2}) - [\sigma^2_{BC1\ P1} + \sigma^2_{BC1P2}]$

v. Dominance variance (d): $\sigma^2 d\ (F_2) = \sigma^2 g\ (F_2) - \sigma^2 a\ (F_2)$

vi. Additive x Dominance variance (ad): $\sigma^2 ad = 0.5(\sigma^2_{\ BC1P2} - \sigma^2_{\ BC1P1})$

Where: σ^2 = variance; P_1- parent 1; P_2= parent 2; F_1= First filial generation; F_2= second filial generation; BC_1P_1= backcross to parent 1; and BC_1P_2= backcross to parent 2

IV. Broad and narrow sense heritabilities were calculated as;

(i) Broad sense heritability (h^2_b)= $100(\sigma^2 g\ (F_2)/ \sigma^2_{F2})$

(ii) Narrow sense heritability (h^2_n)= $100(\sigma^2 a\ (F_2)/ \sigma^2_{F2})$

V. The performance of F_1 hybrids (Heterosis) was established as follows:

BPH (%) = {(F1-BP)/BP} x 100

Where: BPH= Better parent heterosis, F_1= mean of first filial progenies and BP= mean of the better parent.

VI. Phenotypic correlation was carried out using Genstat version 15 in order to establish how strong the associations among the studied traits are and whether these characters can be genetically improved based on the suitability of the parents. Tests of significance for r values were done at 1 and 5% probability levels. Correlation among traits for F_2 was calculated as follows;

$$r = n(\sum xy) - (\sum x)(\sum y)/[\sqrt{[n\sum x^2 - (\sum x)^2][n(\sum y^2) - (\sum y)^2]}]$$

Where:

r= correlation coefficient

n= sample size

xy= variables

3.3 RESULTS

3.3.1 Weather conditions

Weather data for Kabete was obtained from Kenya Meteorological Department (KMD) (www.meteo.go.ke) in 2015 (Appendix 1). The temperatures during the experimental period ranged from 13.2°C to 27.3°C with an average of 20.3°C, (Appendix 1). Although the annual temperatures in Kabete were slightly higher than expected, the mean temperatures during flowering and podding period were 19.8°C. Kabete experienced a total of 402.9mm during the 2014 experimental period with average percentage humidity of 76.95%. Monthly temperatures ranged between 19.1°C to 21.1°C while rainfall was highest in June (163.7mm) and lowest in January (4.1mm) (Figure 3.4).

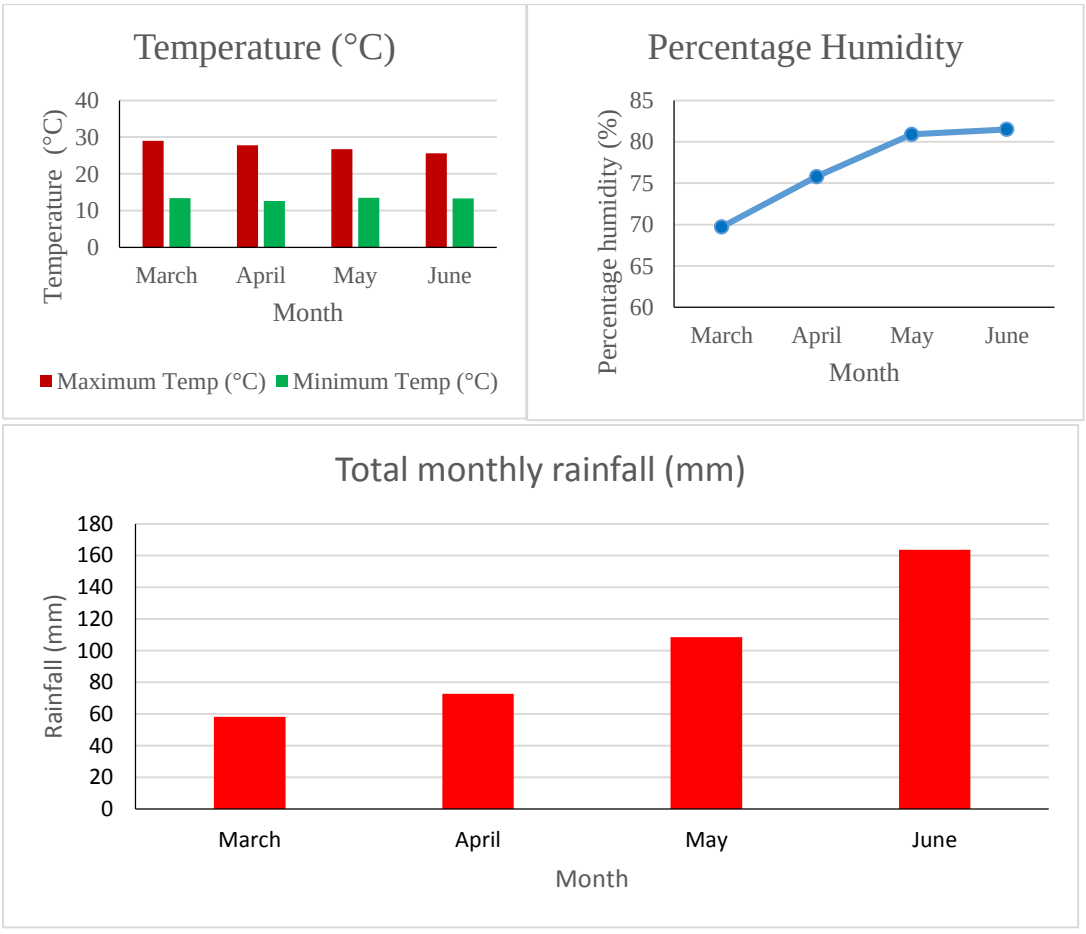


Figure 3. 4 Climatic conditions during the experimental period at Kabete, 2014.

3.3.2 Generation means

Table 3. 3 Mean squares for all traits studied in eleven populations

		Mean squares				
Cross	Df	50% days to flowering	Plant height (cm)	Internode length (cm)	Pods plant^{-1}	Pod length (cm)
Paulista x HAV 133	5	264.2**	151925.3**	231.984**	748.55**	11.6537**
Morgan x HAV 130	5	596.67**	117576.8**	374.401**	457.897**	71.4062**
Samantha x HAV 132	5	459.957**	106935.7**	450.79**	583.71**	18.2756**
Morelli x HAV130	5	182.04**	110193.3**	856.672**	407.314**	59.9124**
Samantha x HAV 131	5	261.89**	86458.99**	247.879**	82.62**	60.7422**
Serengeti x HAV 132	5	313.766**	90676.68**	715.982**	128.99**	119.3468**
Star 2053 x HAV 135	5	467.6**	112683.1**	804.718**	352.88**	26.6446**
Star 2053 x HAV 131	5	154435.7**	81916.55**	431.406**	540.62**	69.1236**
Teresa x HAV 134	5	283.19**	117256.2**	421.113**	794.31**	49.083**
Teresa x HAV 131	5	518.2**	51934.39**	443.09**	191.472**	36.3737**
Vernadon x HAV 134	5	422.436**	85567.09**	314.123**	134.296**	88.1973**

DF= Degrees of freedom, **= Significance at 1%

3.3.2.1 Days to 50% flowering

Duration to 50% flowering varied significantly between treatments in all populations (Table 3.3; Appendix 2). Days to 50% flowering of the bush parents (P_1) and climbing parents (P_2) varied significantly in all crosses where bush parental lines flowered earlier between 36 to 38 days with a mean of 37.4 days while C flowered later in 46 to 53 days (mean, 48.8 days). Among bush parental lines, Morelli and Star 2053 flowered earlier (36 days) while Serengeti flowered in 38 days. Days to 50% flowering were not statistically different among the bush parental lines. The earliest flowering among bush parental lines were HAV 131 (46.4 days) whereas HAV 130 flowered latest (53 days) (Table 3.4).

Duration to 50% flowering of F_1 plants varied significantly from those of bush and climbing parental lines in six out of eleven crosses. F_1 progenies flowered between 42 to 49 days. The F_1 progenies of Teresa x HAV 134 cross were early flowering compared to those of Morgan x HAV 130 which were late flowering (49 days). Duration to 50% flowering of F_1 progenies fell within the parental range in all crosses. However, F_1 and bush parental lines' days to 50% flowering did not vary significantly in Morelli x HAV 130 and Teresa x HAV 134 crosses. F_1 and climbing parental lines' days to 50% flowering showed no significant variation in Paulista x HAV 133, Morgan x HAV 130 and Serengeti x HAV 132 crosses (Table 3.4).

Duration to 50% flowering among F_2 progenies ranged from 41 to 48 days with a mean of 45 days. F_2 progenies of Morgan x HAV 130 and Star 2053 x HAV 135 were early flowering while those of Vernadon x HAV 134 were late flowering. Only four out of eleven crosses showed significant variations in days to flowering between F_1 and F_2 progenies. These crosses were Serengeti x HAV 132, Star 2053 x HAV 135, Star 2053 x HAV 131 and Vernadon x HAV 134. The rest of the crosses showed that the number of days to 50% flowering were not statistically significant between F_1 and F_2.

Table 3. 4 Days to 50% flowering in six generations of eleven snap bean crosses

	Days to 50% flowering										
Populations	**Paulista X HAV 133**	**Morgan X HAV130**	**Samantha X HAV132**	**Morelli X HAV130**	**Samantha X HAV131**	**Serengeti X HAV132**	**Star2053 X HAV135**	**Star2053 X HAV131**	**Teresa X HAV134**	**Teresa X HAV131**	**Vernadon X HAV134**
P_1	37.6	38.1	37.8	36.4	37.8	38.3	37.1	36.4	37.6	36.9	37.6
BC_1P_1	42.9	41.9	39.5	39.8	46.6	42.1	40.5	39.8	43.6	40.9	42.8
F_2	45.1	48.1	45.9	41.0	46.8	43.4	45.4	41.0	42.5	47.0	48.3
F_1	45.8	49.1	47.0	42.1	46.9	47.6	47.7	42.1	41.6	45.8	43.1
BC_1P_2	47.1	49.9	48.0	42.4	48.0	47.8	48.3	40.9	48.3	50.0	49.2
P_2	48.8	53.0	49.6	46.4	48.4	47.8	49.4	46.4	47.3	50.0	49.3
Mean	44.7	47.0	45.0	41.4	46.1	45.1	45.2	41.17	43.6	45.5	45.7
$LSD_{0.05}$	1.9	2.5	1.3	2.7	1.9	1.7	1.2	3.3	2.3	2.2	1.7
CV (%)	7.2	8.9	5.0	11.1	7.1	6.4	4.7	13.7	9.1	8.3	6.4

P_1= female parents (Paulista, Morgan, Samantha, Morelli, Serengeti, Star2053, Teresa and Vernadon), P_2= male parents (HAV130, HAV131, HAV132, HAV133, HAV134 and HAV135), BC_1P_1 =backcross to female parent, BC_1P_2 = backcross to male parent, LSD= least significance difference at 5%

Days to 50% flowering among the backcrosses varied from 40 to 47 days in BC_1P_1 with a mean of 42 days and 41 to 50 days in BC_1P_2 (mean, 47 days). Among BC_1P_1, Morelli x HAV 130 and Star 2053 x HAV 135 were early flowering while Samantha x HAV 131 were late flowering. On the other hand, BC_1P_2 progenies of Star 2053 x HAV 131 flowered earlier whereas Teresa x HAV 131 flowered later.

Days to 50% flowering in the backcross progenies were all within the parental range and were close to their recurrent parents. In most cases, there were no significant variations between the backcross progenies and their recurrent parents (Table 3.4).

3.3.2.2 Plant height

The results showed significant variation in plant height in all crosses (Table 3.3; Appendix 2). Eight parental lines were determinate. These were Paulista, Morgan, Morelli, Samantha, Serengeti, Star 2053, Teresa and Vernadon. Plant height of the bush lines varied from 28.8 to 43.3 cm with a mean of 34.2 cm. Among bush plants, Teresa was the shortest with 28.8cm while Vernadon was the tallest with 43.3cm. The other six parental lines were indeterminate. Plant height of these plants varied from 182 to 284.2 cm with a mean of 245.61cm. HAV 130 had a plant height of 182.9 while HAV 133 was the tallest with plant height of 284.3cm (Table 3.5).

Plant heights of F_1 progenies differed significantly in most crosses. All F_1 plants exhibited type IV growth habit ranging from 149.0 to 214.7 cm with a mean of 194.7 cm. Teresa x HAV 131 F_1 progenies were shorter while F_1 progenies of Vernadon x HAV 134 were the taller than all other F_1 progenies. F_1 progenies were generally taller than bush and shorter than climbing parental lines in all crosses (Table 3.5).

Plant heights among F_2 progenies ranged from 116.6 to 235.8cm with a mean of 188.3cm. Teresa x HAV 131 were shorter while Star 2053 x HAV 135 were the tallest among F_2 progenies in all crosses. There were statistically significant variations in plant heights between F_1 and F_2 progenies in all crosses. In most crosses, F_2 progenies were shorter than F_1 progenies except in Samantha x HAV 132, Samantha x HAV 131 and Star 2053 x HAV 131 where F_2 progenies were taller than F_1s.

Plant heights among the backcrosses ranged from 101.7 to 200.2cm in BC_1P_1 with a mean of 149.1cm and 169.8 to 240.8cm in BC_1P_2 (mean, 211.6cm). Among BC_1P_1, Paulista x HAV 133 were shorter while Vernadon x HAV 134 were the tallest. On the other hand, BC_1P_2 progenies of Teresa x HAV 131 were short whereas Morelli x HAV 130 were the tallest. Plant heights of the backcross progenies were all within the parental range and were close to their recurrent parents. There were significant variations between the backcross progenies and their recurrent parents in

all crosses except in Star 2053 x HAV 131 where BC_1P_2 and the climbing parental lines were not significantly different (Table 3.5).

Table 3. 5 Plant height (cm) of six generations of 11 snap bean crosses

	Plant height (cm)										
Populations	**Paulista x HAV 133**	**Morgan x HAV130**	**Samantha x HAV132**	**Morelli x HAV130**	**Samantha x HAV131**	**Serengeti x HAV132**	**Star2053 x HAV135**	**Star2053 x HAV131**	**Teresa x HAV134**	**Teresa x HAV131**	**Vernadon x HAV134**
P_1	29.9	29.7	30.1	32.9	37.1	36.1	39.9	39.2	29.6	28.8	43.4
BC_1P_1	101.7	146.9	180.2	161.2	140.0	144.2	162.9	162.9	111.1	129.1	200.2
F_2	166.8	200.6	185.4	188.1	171.9	234.6	235.8	185.8	207.9	116.6	178.5
F_1	201.3	209.5	209.9	177.8	187.3	203.4	188.8	201.2	199.0	149.0	214.7
BC_1P_2	230.7	215.3	215.0	240.8	220.2	172.0	237.2	220.2	179.0	169.8	226.9
P_2	284.2	270.6	266.1	261.4	228.8	220.2	268.3	222.1	259.9	182.9	237.2
Mean	174.5	184.5	188.2	180.0	170.2	173.4	190.1	179.4	168.2	129.5	186.1
$LSD_{0.05}$	3.7	4.0	3.4	3.8	4.3	3.8	3.8	3.9	4.0	4.2	4.1
CV (%)	3.6	3.7	3.1	3.7	4.3	3.8	3.4	3.7	4.1	5.5	3.7

P_1= female parents (Paulista, Morgan, Samantha, Morelli, Serengeti, Star2053, Teresa and Vernadon), P_2= male parents (HAV130, HAV131, HAV132, HAV133, HAV134 and HAV135), BC_1P_1 =backcross to female parent, BC_1P_2 = backcross to male parent, LSD= least significance difference at 5%

3.3.2.3 Internode Length

The results showed significant variation in internode lengths in all crosses (Table 3.3; Appendix 2). Internode lengths among parental lines were significantly different ranging from 5.1 to 8.4cm in P_1 and 19.2 to 26.4cm in P_2. P_1 plants had shorter internodes (6.9cm) whereas P_2 had longer internodes with a mean of 21.1cm. Among P_1 plants, Morelli had the shortest internodes (5.1cm) while Serengeti had the longest internodes (8.4cm). On the other hand, HAV 133 had the shortest internodes of 19.2cm while HAV 132 had the longest internodes of 26.4cm (Table 3.6).

Internode lengths of F_1 progenies differed significantly in most crosses. All F_1 progenies had internode lengths ranging from 14.6 to 18.0cm with a mean of 16.2cm. F_1 progenies of Samantha x HAV 131 had shorter internodes while those of Vernadon x HAV 134 had longer internodes than all other F_1 progenies. Internode lengths of F_1 progenies varied significantly with those of the parents except in Paulista x HAV 133 and Teresa x HAV 134 where F_1 and P_2 progenies were not statistically significant. Internode lengths of F_1 progenies were generally longer than those of P_1 plants but shorter than those of P_2 plants in all crosses (Table 3.6).

Internode lengths among F_2 progenies ranged from 13.0 to 18.6cm with a mean of 16.4cm. Internode lengths of Samantha x HAV 131 were shorter while those of Star 2053 x HAV 135 were the longer among F_2 progenies in all crosses. The internode lengths of F_1 and F_2 progenies were not statistically significant in all crosses except in Samantha x HAV 132, Serengeti x HAV 132, Star 2053 x HAV 135 and Star 2053 x HAV 134. In most crosses, internode lengths of F_2 progenies were shorter than internode lengths of F_1 progenies except in Samantha x HAV 131, Serengeti x HAV 132, Star 2053 x HAV 131, Star 2053 x HAV 135 and Teresa x HAV 134 where F_2 progenies had longer internodes than F_1s.

Internode lengths among the backcrosses ranged from 5.4 to 16.1cm in BC_1P_1 with a mean of 12.8cm and 16.3 to 21.9cm in BC_1P_2 (18.4cm). Among BC_1P_1, Morelli x HAV 130 had short internodes while Paulista x HAV 133 had long internodes. On the other hand, BC_1P_2 progenies of Paulista x HAV 133 had short internodes whereas internodes of Star 20533 x HAV 135 were long. Internode lengths of the backcross progenies were all within the parental range and were close to their recurrent parents. There were significant variations in internode lengths between the backcross progenies and their recurrent parents in most crosses. However, internode lengths of Morelli x HAV 130 and Samantha x HAV 131crosses and those of P_1 were not statistically

significant as well as internode lengths of BC_1P_2 and P_2 in Samantha x HAV 132, Teresa x HAV 134 and Teresa x HAV 131 crosses (Table 3.6).

Table 3. 6 Internode length (cm) in six generations of eleven snap bean crosses

	Internode lengths (cm)										
Population	**Paulista x HAV 133**	**Morgan x HAV130**	**Samantha x HAV132**	**Morelli x HAV130**	**Samantha x HAV131**	**Serengeti x HAV132**	**Star2053 x HAV135**	**Star2053 x HAV131**	**Teresa x HAV134**	**Teresa x HAV131**	**Vernadon x HAV134**
P_1	8.2	6.4	5.8	5.1	8.1	8.4	5.8	5.7	6.5	7.9	8.3
BC_1P_1	16.1	12.9	10.8	5.4	16.0	12.9	14.1	14.1	14.9	10.3	13.3
F_2	16.4	16.0	13.0	15.5	16.5	18.5	18.6	17.9	17.2	14.6	16.2
F_1	16.8	16.3	16.9	16.0	14.6	15.8	16.5	15.6	15.7	15.5	18.0
BC_1P_2	16.3	17.5	17.9	17.2	16.9	21.4	21.9	16.9	20.1	19.0	17.3
P_2	19.2	19.7	26.4	21.2	19.5	26.4	25.7	20.8	19.7	20.6	20.7
Mean	15.7	15.1	13.8	13.6	15.3	17.0	17.1	15.3	15.9	14.6	15.7
$LSD_{0.05}$	1.4	1.2	1.5	1.3	1.6	1.5	1.3	1.4	1.6	1.2	1.4
CV (%)	15.7	13.1	19.0	16.9	18.4	15.1	13.2	16.1	17.4	14.5	14.9

P1= female parents (Paulista, Morgan, Samantha, Morelli, Serengeti, Star2053, Teresa and Vernadon), P2= male parents (HAV130, HAV131, HAV132, HAV133, HAV134 and HAV135), BC1P1 =backcross to female parent, BC1P2 = backcross to male parent, LSD= least significance difference at 5%

3.3.2.4 Number of Pods per Plant

Number of pods per plant varied significantly between treatments in all populations (Table 3.3; Appendix 2). P_1 and P_2 number of pods per plant varied significantly in all crosses where P_1 had fewer number of pods per plant ranging from10 to 19 pods with a mean of 14 pods while P_2 had more number of pods per plant, 20 to 32 pods (27 pods). Among P_1 plants, Teresa had the fewest number of pods (10 pods) while Vernadon had 19 pods. Number of pods per plant were not statistically different among P_1 plants. HAV 135 had the fewest number of pods per plant among P_2 (20 pods) whereas HAV 134 had the highest number of pods per plant (32 pods) (Table 3.7).

Number of pods per plant of F_1 progenies varied significantly from those of P_1 and P_2 in all crosses. The number of pods per plant of F_1 progenies ranged from 15 to 26 pods. The F_1 progenies of Serengeti x HAV 132 cross were fewer (15 pods) compared to those of Star 2053 x HAV 135 (26 pods). Number of pods per plant of F_1 progenies were within the parental range in all crosses. The variation between the F_1 progenies and the parental lines were statistically significant in all crosses (Table 3.7).

The number of pods per plant among F_2 progenies ranged from 15 to 26 pods with a mean of 20 pods. Number of pods per plant in Teresa x HAV 131 cross were the fewest whereas those of Star 2053 x HAV 135 were more among the F_2 progenies. There were no significant variations in number of pods per plant between F_1 and F_2 progenies in all crosses except in Teresa x HAV 134 and Teresa x HAV 131 crosses.

Number of pods per plant among the backcrosses ranged from 13 to 26 pods in BC_1P_1 with a mean of 18 pods and 18 to 27 pods in BC_1P_2 (21 pods). Paulista x HAV 133 had few number of pods while Star 2053 x HAV 135 had more pods among the BC_1P_1 progenies. On the other hand, BC_1P_2 progenies of Teresa x HAV 131 had fewer pods whereas Star 2053 x HAV 135 had more pods. The number of pods per plant in the backcross progenies were all within the parental range. Number of pods per plant of the backcross progenies were close to their recurrent parents. There were significant variations in number of pods per plant between the backcross progenies and their recurrent parents in most crosses. However, the number of pods per plant of Paulista x HAV 130, Samantha x HAV 131 and Serengeti crosses and those of P_1 were not statistically significant as well as BC_1P_2 and P_2 number of pods per plant in Morelli x HAV 130 crosses (Table 3.7).

Table 3. 7 Number of pods per plant in six generations of eleven snap bean crosses

Population	Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
P_1	11.9	11.4	14.1	13.0	17.1	12.5	22.8	12.1	10.1	10.1	17.6
BC_1P_1	13.0	17.1	18.2	20.5	17.9	16.8	25.7	16.7	15.1	15.7	21.6
F_2	19.3	17.1	20.0	22.3	19.3	17.7	26.1	17.4	17.9	15.4	23.1
F_1	19.6	16.9	20.4	23.2	18.9	14.9	26.4	24.3	22.6	15.8	25.4
BC_1P_2	21.0	19.1	26.1	25.1	20.3	19.0	27.2	19.1	17.9	17.7	23.2
P_2	30.1	27.6	30.0	27.2	23.3	19.9	31.6	27.9	30.4	20.4	31.6
Mean	18.9	18.0	21.3	22.1	19.4	17.1	26.5	19.0	18.1	15.8	23.5
$LSD_{0.05}$	2.0	1.7	2.0	1.8	1.8	1.6	1.6	1.9	2.1	1.7	1.9
CV (%)	18.5	15.7	16.1	13.9	15.5	15.6	10.6	16.8	19.0	18.6	13.7

P_1= female parents (Paulista, Morgan, Samantha, Morelli, Serengeti, Star2053, Teresa and Vernadon), P_2= male parents (HAV130, HAV131, HAV132, HAV133, HAV134 and HAV135), BC_1P_1 =backcross to female parent, BC_1P_2 = backcross to male parent, LSD= least significance difference at 5%, CV= Coefficient of Variation

3.3.2.5 Pod Lengths

The results showed significant variation in pod lengths in all crosses (Table 3.3; Appendix 2). Pod lengths among parental lines varied significantly ranging from 10.3 to 13.7cm in P_1 and 7.9 to 10cm in P_2. P_1 plants formed longer pods (12.0cm) whereas P_2 formed shorter pods with a mean of 9.0cm. Among P_1 plants, Paulista x HAV 133 had the shortest pods (10.3cm) while Morelli had the longest pods (13.7cm). On the other hand, HAV 131 had the shortest pods of 7.9cm while HAV 135 had the longest pods of 10.0cm (Table 3.8).

Pod lengths of F_1 progenies differed significantly in most crosses. All F_1 progenies had pod lengths ranging from 9.2 to 12.9cm with a mean of 10.7cm. Samantha x HAV 132 F_1 progenies had shorter pods while F_1 progenies of Morgan x HAV 130 had longer pods than all other F_1 progenies. Pod lengths of F_1 progenies varied significantly with those of the parents except in Samantha x HAV 132 where F_1 and P_2 progenies were not statistically significant. Pod lengths of F_1 progenies were generally longer than those of P_2 plants and shorter than those of P_1 plants in all crosses except in Paulista x HAV 133 and Morgan x HAV 130 where F_1 progenies formed longer pods than the better parent, P_1(Table 3.8).

The pod lengths among F_2 progenies ranged from 6.5 to 10.1cm with a mean of 8.8cm. Pod lengths of Serengeti x HAV 132 were shorter while those of Teresa x HAV 131 were the longest among F_2 progenies in all crosses. The pod lengths of F_1 and F_2 progenies were statistically significant in all crosses. In most crosses, pod lengths of F_2 progenies were shorter than pod lengths of F_1 progenies except in Samantha x HAV 132 cross where F_2 progenies had slightly longer pods than F_1s.

Pod lengths among the backcrosses ranged from 9.4 to 13.0cm in BC_1P_1 with a mean of 11.0cm and 7.1 to 10cm in BC_1P_2 (9.2cm). Among BC_1P_1, Paulista x HAV 133 formed short pods while Vernadon x HAV 134 formed longer pods. On the other hand, BC_1P_2 progenies of Star 2053 x HAV 131 had short pods whereas pods of Vernadon x HAV 134 were long. Pod lengths of the backcross progenies were all within the parental range and were close to their recurrent parents except in Samantha x HAV 132 where BC_1P_1 formed longer pods than P_1 and Star 2053 x HAV 131 where BC_1P_2 formed shorter pods than P_2. There were significant variations in pod lengths between the backcross progenies and their recurrent parents in most crosses. However, pod lengths

of Paulista x HAV 133, Morgan x HAV 130, Morelli x HAV 130 and Star 2053 x HAV 135crosses and those of P_2were not statistically significant (Table 3.8).

Table 3. 8 Pod lengths (cm) in six generations of eleven snap bean crosses

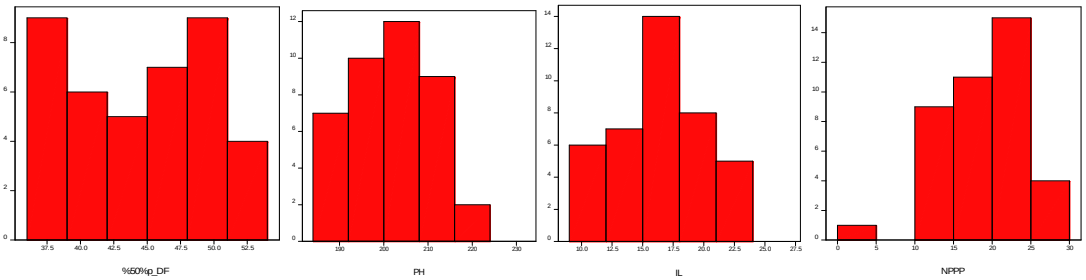
	Pod length (cm)										
Population	**Paulista x HAV 133**	**Morgan x HAV 130**	**Samantha x HAV 132**	**Morelli x HAV 130**	**Samantha x HAV 131**	**Serengeti x HAV 132**	**Star 2053 x HAV 135**	**Star 2053 x HAV 131**	**Teresa x HAV 134**	**Teresa x HAV 131**	**Vernadon x HAV 134**
P1	10.3	11.4	10.8	13.7	12.4	12.0	12.1	12.3	13.4	12.5	11.4
BC1P1	9.4	9.9	11.4	11.2	10.5	11.5	11.5	10.6	10.9	11.2	13.0
F2	9.4	8.3	9.8	9.7	7.9	6.5	9.4	8.7	9.3	10.1	7.9
F1	11.3	12.9	9.2	12.1	9.3	10.9	11.1	9.4	9.9	11.3	10.8
BC1P2	9.2	8.4	9.5	9.3	8.7	10.0	9.6	7.1	9.6	9.5	10.5
P2	9.9	8.5	9.0	9.1	7.9	9.3	10.0	8.0	9.1	8.5	9.8
Mean	9.8	9.5	10.0	10.6	9.2	9.5	10.4	9.2	10.1	10.4	10.2
$LSD_{0.05}$	0.3	0.2	0.3	0.3	0.3	0.3	0.3	0.2	0.3	0.4	0.3
CV (%)	5.2	4.5	4.8	4.1	4.8	4.6	4.2	4.5	5.8	6.5	5.1

P_1= female parents (Paulista, Morgan, Samantha, Morelli, Serengeti, Star2053, Teresa and Vernadon), P_2= male parents (HAV130, HAV131, HAV132, HAV133, HAV134 and HAV135), BC_1P_1 =backcross to female parent, BC_1P_2 = backcross to male parent, LSD= least significance difference at 5%, CV= Coefficient of Variation

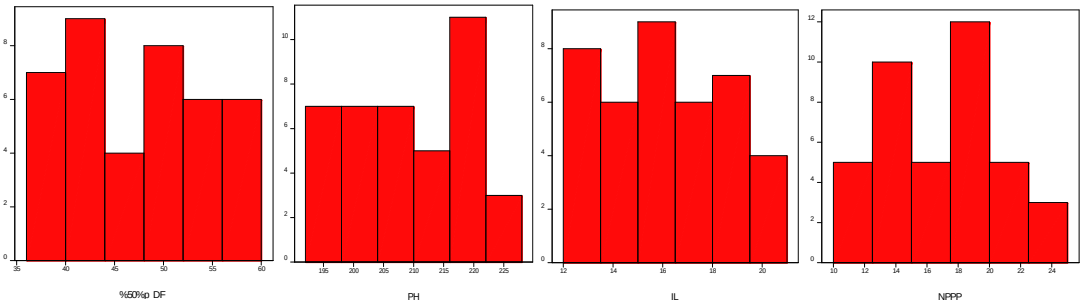
3.3.3 Quantitative inheritance

Tukey's *w* procedure of the separation of means indicated that the traits under study were quantitatively inherited. This implies that the traits are polygenic in nature and exhibit continuous variation. This was shown by the distribution of F_2 generations as follows:

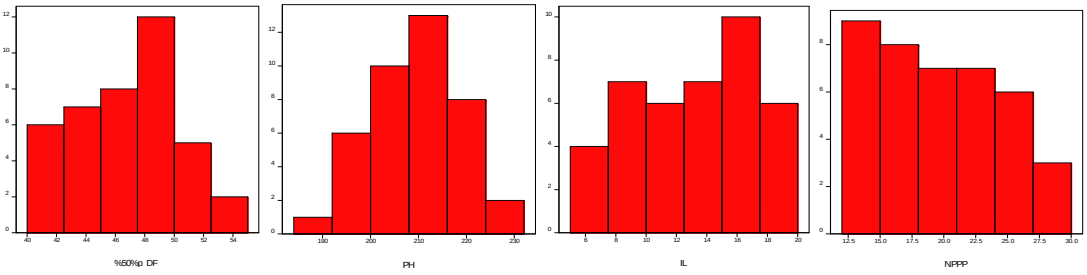
Paulista x HAV 133



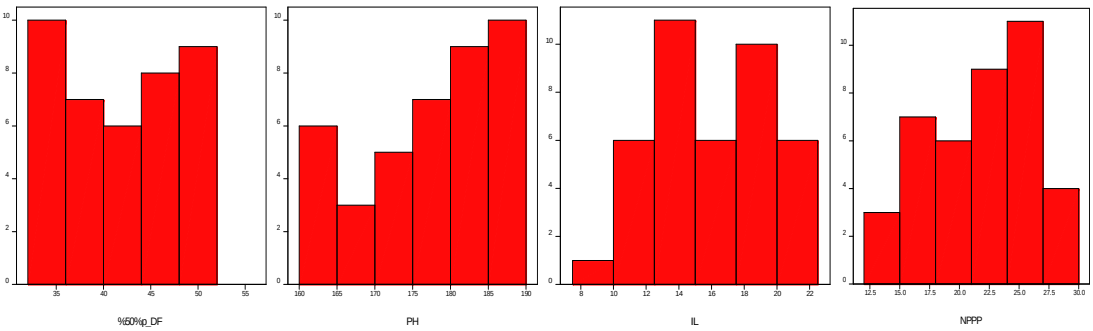
Morgan x HAV 130



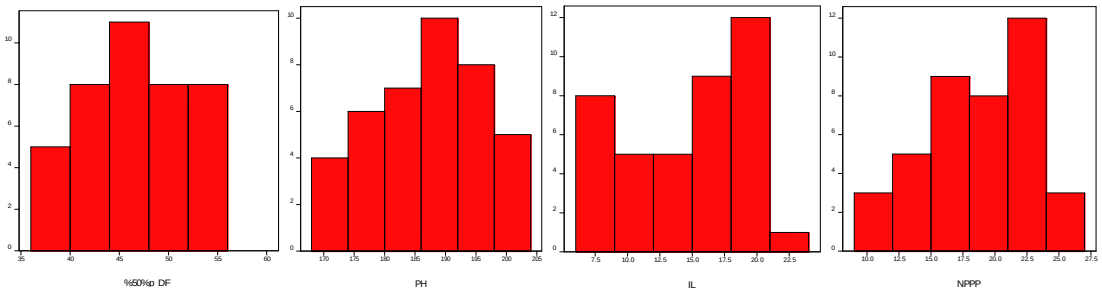
Samantha x HAV 132



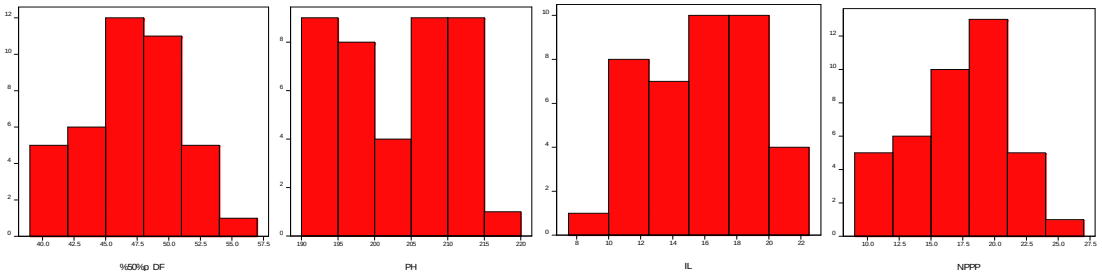
Morelli x HAV 130



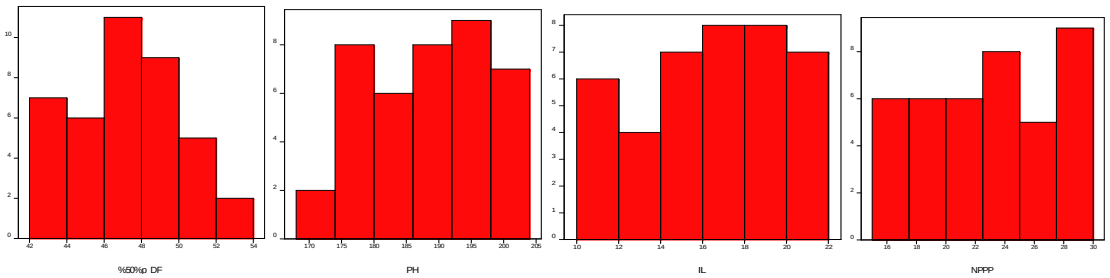
Samantha x HAV 131



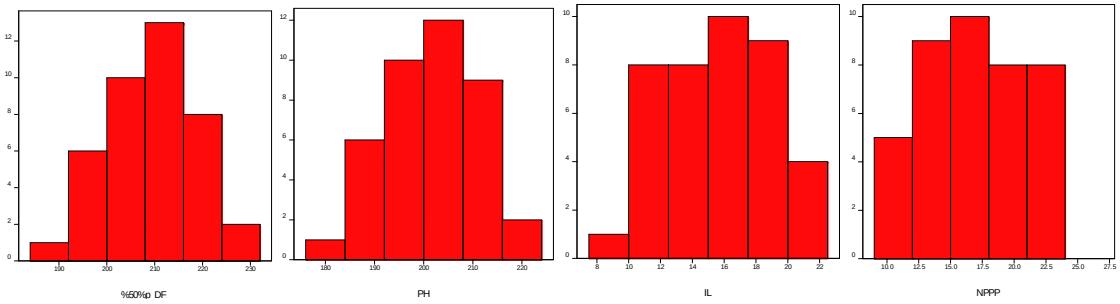
Serengeti x HAV 132



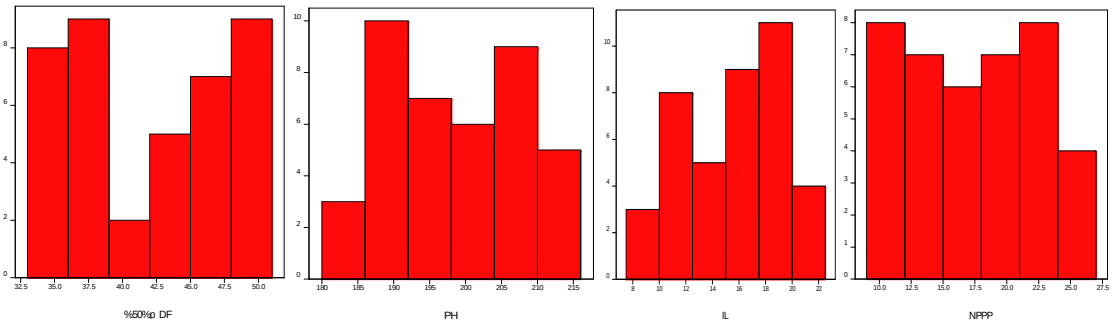
Star 2053 x HAV 135



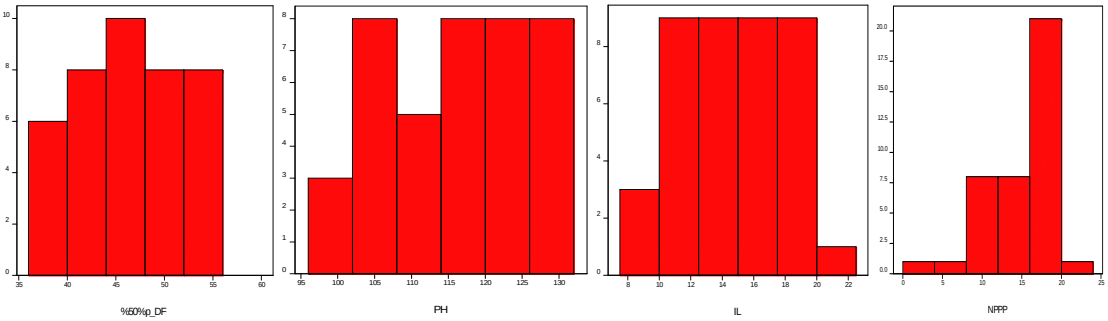
Star 2053 x HAV 131



Teresa x HAV 134



Teresa x HAV 131



Vernadon x HAV 134

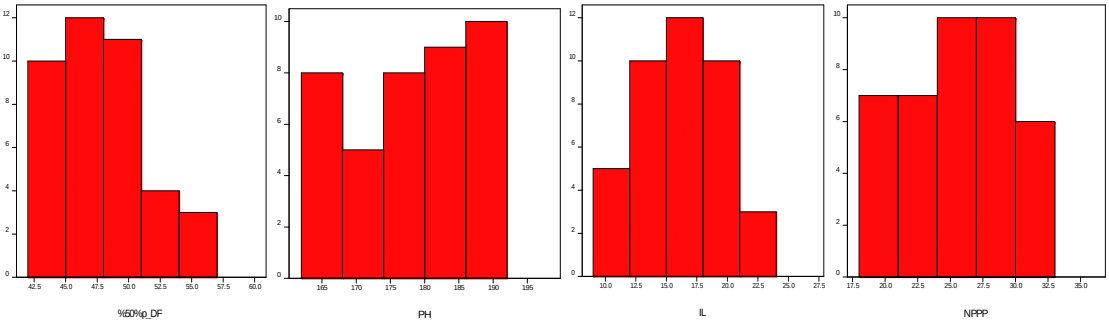


Figure 3. 5 Frequency distribution for days to 50% flowering, plant height, pod length, and number of pods per plant among the F2 generations in 11 crosses

3.3.4 Generation Means Analysis

The traits under study (days to 50% flowering, plant height, internode length, number of pods per plant and pod length) were quantitatively inherited as evidenced by the distribution of F_2 progenies. This implies that these traits are controlled by several genes influencing their expression. Quantitative inheritance of these traits formed the prerequisite for subsequent genetic analyses. With multiple genes at play, epistasis was confirmed using joint scaling tests.

3.3.4.1 Joint scaling tests

Joint scaling tests showed that there were significant variations in days to 50% flowering, plant height, internode lengths, number of pods per plant and pod lengths for all crosses at either 1% or 5% t-test (Table 3.9). The joint scaling tests revealed that additive-dominance model was inadequate for days to 50% flowering, plant height, internode lengths, number of pods per plant and pod lengths as evidenced by the significance of one, two or all the scaling tests (A, B and C) in all crosses showing the presence of non-allelic gene actions in the expression of the traits under study (Mather, 1949). This implies that the traits under study are quantitatively inherited due to the interaction of various genes thus indicating that the Hayman's six parameter model (m+a+d+aa+ad+dd) showed the best fit for traits under study in all crosses.

Table 3. 9 Joint scaling test for snap bean days to 50% flowering, plant height, internode length, number of pods per plant and pod length in eleven crosses

Trait		Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
Days to 50% Flowering	A	4.58589 **	0.376772 ns	-0.95231 ns	-0.70927 ns	3.57351 **	-0.86713 ns	0.66806 ns	-0.26864 ns	-0.1979 ns	1.83658 *	-0.15262 ns
	B	-0.04882 ns	1.997072 *	0.128667 ns	2.343 **	0.107611 ns	0.674169 ns	0.444562 ns	1.937642*	1.84349 *	0.560568 ns	0.944149 ns
	C	0.118271 ns	0.234824 ns	6.3313 **	0.124263 ns	0.423083 ns	1.654175 **	1.9741*	19.21461**	0.08755 ns	0.420885 ns	1.64932 *
Plant height	A	2.30803*	3.937822**	16.66609**	7.354839**	3.944633**	1.192018 ns	3.724964**	7.470911**	-1.04948 ns	5.962479**	9.314391**
	B	-1.74445 ns	-3.4679ns	-1.70335 ns	2.19124*	2.464603**	-6.80797 ns	-2.21851 ns	2.20143*	-6.66015 ns	0.444871 ns	0.121782 ns
	C	-1.367 ns	2.092401*	4.887618**	1.113021 ns	3.561596**	2.468433**	-0.65353 ns	4.620011**	2.354716**	-1.12436 ns	0.10747 ns
Internode length	A	1.615502 *	1.684233 *	2.655694 **	-0.49334 ns	2.02749 *	-0.21671 ns	4.32189 **	0.729782 ns	0.968607 ns	1.935776*	-0.61145 ns
	B	-0.67871 ns	-0.21687 ns	-0.00868 ns	2.59302 **	-0.00959 ns	3.37703 **	-0.11757 ns	-1.11339 ns	0.477549 ns	0.531669 ns	2.98651 **
	C	0.324646 ns	0.530649 ns	-0.42086 ns	0.435484 ns	1.7238 *	-0.61472 ns	-0.20104 ns	2.90761 **	2.130194 *	-0.07305 ns	3.01777 **
Number of pods per plant	A	3.86458 **	1.911136*	0.291221 ns	0.764031 ns	1.7384 *	1.191863 ns	2.01617 *	-0.40889 ns	-4.09283 ns	1.997425 *	0.362274 ns
	B	2.34952 *	-0.90525 ns	4.604906**	2.92287 **	-0.25652 ns	1.714338 *	-1.49631 ns	-1.98473 ns	2.36977 **	-0.12786 ns	-0.69456 ns
	C	-0.19329 ns	-0.2983 ns	0.769018 ns	3.136661**	2.06629 *	0.546885 ns	-0.42151 ns	1.90661 *	-0.70145 ns	-0.03043 ns	2.17153 *
Pod length	A	2.10839 *	4.68608 **	2.150367 *	3.30878 **	-0.67206 ns	-0.02401 ns	-0.1954 ns	-0.35304 ns	-1.00046 ns	-0.80037 ns	2.630688**
	B	-5.05787 ns	-1.5375 ns	1.527562 ns	4.28726 **	0.314133 ns	-0.1745 ns	3.28202 **	6.54348 **	0.376706 ns	-0.70358 ns	0.453696 ns
	C	2.06757 *	5.94406 **	0.533607 ns	-3.65611 ns	2.7939 **	3.21378 **	-2.95943 ns	-2.13529 ns	1.67142 **	2.10458 *	-4.91853 ns

3.3.4.2 Regression Analysis

Table 3. 10 Mean squares for six parameter model of all traits under study in eleven populations.

Cross	DF	Days to 50% Flowering	Plant Height	Internode Length	Number of pods per plant	Pod length
Paulista x HAV 133	5	31.5903**	16796.48**	28.468**	85.546**	1.22817**
Morgan x HAV 130	5	61.5621**	13774.07**	45.5547**	56.2169**	7.33897**
Samantha x HAV 132	5	50.6995**	12807.37**	50.6995**	65.2741**	1.80352**
Morelli x HAV130	5	21.6975**	12945.19 **	87.5515**	48.4651**	6.486428**
Samantha x HAV 131	5	31.284**	15344.32**	30.0572**	9.6563 **	5.97932**
Serengeti x HAV 132	5	31.2105**	10555.09**	81.2285**	14.9515**	8.00387**
Star 2053 x HAV 135	5	47.8214**	13492.74**	93.9968**	43.1198**	2.32256**
Star 2053 x HAV 131	5	9172.904**	9430.654**	53.071**	64.203**	7.09946**
Teresa x HAV 134	5	29.763**	13381.73**	48.809**	96.053**	5.38859**
Teresa x HAV 131	5	54.6662**	6067.55**	47.7955**	23.0763**	4.1639**
Vernadon x HAV 134	5	43.615**	10273.76**	37.4492**	16.4097**	5.82021**

DF= Degrees of freedom, **= Significance at 1%

Results of the regression analysis showed significant variations ($P \leq 0.05$) in 50% days to flowering (Table 3.10; Appendix 4). Mean effect was significant for 50% days to flowering in all crosses (Table 3.11). Additive gene effects (m + a) were found to account for 50% days to flowering in 8 out of 11 crosses with R^2 values ranging from 82.1 to 99.7%. Additive and additive x dominance (m + a + ad) gene effects accounted for 50% days to flowering in Morgan x HAV 130 cross while additive and additive x additive (m + a + aa) gene effects explained 50% days to flowering in Samantha x HAV 132 cross. Both fixable and non-fixable genes (m + a + d + aa + ad + dd) accounted for earliness in Star 2053 x HAV 131 cross with R^2= 100% (Table 3.11). The coefficient of determination for all other crosses was >91%.

Plant height mean effect was significant ($P \leq 0.05$) for all crosses (Table 3.10; Appendix 4). Additive (a), dominance (d) and all epistatic gene effects (aa, ad and dd) better explained plant height in almost all crosses except in Star 2053 crosses. In Star 2053 x HAV 135, the epistatic gene effects (aa and dd) failed to account for plant height whereas in Star 2053 x HAV 131 cross only additive x additive (aa) gene effects did not account for plant height (Table 3.12). The coefficient of determination (R^2) ranged from 99.5% to 100% in all crosses which indicated better goodness of fit of the 6-parameter model and hence presence of epistatic gene effects.

Mean effect of internode length was significant (P≤0.05) in all crosses (Table 3.13). For most crosses, additive gene effects explained internode lengths except in Morelli x HAV 130 and Samantha x HAV 131 crosses. With a coefficient of determination of 99%, only additive x dominance (ad) gene effects failed to account for internode length in Morelli x HAV 130 cross. On the other hand, additive and additive x dominance (m + a + ad) gene effects were found to be responsible for internode length in Samantha x HAV 131 cross. Generally, the coefficient of determination for internode length in all crosses ranged from 91.3% to 99% (Table 3.13).

The number of pods per plant on the other hand showed significant mean effects (P≤0.05) in all crosses (Table 3.10; Appendix 4). Additive gene effects (m + a) were responsible for number of pods per plant in all crosses at 5% probability except in Star 2053 x HAV135 where additive, additive x dominance and dominance x dominance (m + a + ad + dd) accounted for the number of pods per plant (R^2= 99.1%). Additive and dominance x dominance genes (m + a + dd) were significant in the expression of number of pods per plant in Teresa x HAV 134 (R^2= 97.4%). Dominance and epistatic gene effects were not significant for most crosses (Table 3.14). The coefficient of determination (R^2 value) ranged from 88.6 to 99.2% for the number of pods per plant.

Regression analysis showed that there were significant (P≤0.05) variations in pod length in all crosses (Table 3.10; Appendix 4). Six parameter model gave a better goodness of fit with R^2 values ranging from 97.9 to 99.9%. The mean effects were significant in all crosses. Additive gene effects contributed to the expression of pod lengths in all crosses except in Paulista x HAV 133 (m + ad + dd) and Morgan x HAV 130 (m + d + ad) crosses. Dominance genes did not contribute to the expression of pod length in only four crosses including Morgan x HAV 130, Morelli x HAV 131 (m + a + aa + dd), Teresa x HAV 134 (m + a + aa) and Teresa x HAV 131 (m + a). All the epistatic gene effects (aa, ad and dd) accounted for pod lengths in Samantha x HAV 132 and Vernadon x HAV 134 crosses. The additive x additive and dominance x dominance gene effects were significant in Morelli x HAV 130, Paulista x HAV 133, Samantha x HAV 131 and Serengeti x HAV 132 crosses. Additive x additive and additive x dominance epistatic gene effects were significant in Star 2053 x HAV 135 while epistatic gene effects were not significant in the expression of pod length in Teresa x HAV 134 cross (Table 3.15).

Table 3. 11 Estimates of gene effects (6-parameter model) for days to 50% flowering in eleven snap bean crosses

	Days to 50% Flowering										
Gene effects	Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
m	42.9±0.7*	46.8±1.8*	56.7±2.2*	45.5±3.3*	41.3±4.0*	53.7±2.7*	56.3±2.5*	698.0±2.4*	28.9±5.7*	49.8±2.9*	52.6±4.0*
a	-5.6±0.1*	-5.9±0.3*	-5.9±0.3*	-5.0±0.5*	-5.3±0.6*	-4.8±0.49*	-6.1±0.4*	-5.8±0.3*	-4.8±0.8*	-6.5±0.4*	-5.8±0.6*
d	5.9±1.7	3.1±4.3	-28.1±5.2	-9.2±7.9	17.0±9.7	-14.0±6.6	-23.6±5.9	-1297.5±5.7*	41.7±13.8	-7.2±7.0	-7.8±9.5
aa	0.3±0.7	-2.8±1.8	-13.0±2.1*	-4.2±3.3	1.8±4.0	-10.7±2.7	-13.0±2.4	-654.4±2.3*	13.6±5.7	-6.4±2.9	-9.2±3.9
ad	2.2±0.4	-10.3±1.1*	-5.4±1.4	4.7±2.1	7.7±2.6	-1.9±1.7	-3.5±1.6	-14.9±1.5*	0.2±3.7	-5.2±1.9	-1.0±2.5
dd	-3.0±1.0	-0.7±2.6	17.2±3.2	4.7±4.9	-11.5±6.0	3.7±4.1	12.7±.63	642.9±3.5*	-29.1±8.5	3.2±4.3	-1.8±5.9
R^2	99.7	99.1	98.2	91.4	91.1	95.8	97.8	100	82.1	97.2	93.7

Days to 50% flowering= 50% days to flowering; m= Mean effect; a= Additive; d= Dominance; aa= Additive X Additive; ad= Additive X Dominance; and dd= dominance X Dominance gene effects, Coefficient of determination, * significance at 5% t-probability values respectively

Table 3. 12 Estimates of gene effects (6-parameter model) for plant height in eleven snap bean crosses

	Plant Height										
Gene effects	Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
m	297.5±3.1*	263.6±5.8*	197.2±2.1*	55.3±2.8*	367.0±8.2*	309.1±10.5*	109.2±7.8*	169.3±7.2*	360.4±8.0*	-25.5±13.5*	-0.2±5.6*
a	-127.2±0.5*	-120.5±0.8*	-118.0±0.30*	-114.3±0.4*	-95.9±1.2*	-92.1±1.5*	-114.3±1.12*	-91.4±1.0*	-115.2±1.2*	-77.0±1.93*	-96.9±0.8*
d	-254.0±7.6*	-153.4±1*	62.7±5.09*	357.3±6.7*	-523.2±19.7*	-348.4±25.2*	191.8±18.8*	111.2±17.3*	-493.1±19.3*	393.8±32.5*	499.5±13.5*
aa	-140.4±3.1*	-113.5±5.8*	-49.1±2.1*	91.9±2.8*	-234±8.1*	-181±10.4*	44.9±7.8	-38.6±7.1	-215.6±7.9*	131.3±13.4*	140.4±5.6*
ad	512.1±2.0*	104.3±3.7*	166.3±1.4*	68.3±1.8*	-173.7±5.2*	128.7±6.7*	80±5*	68.2±4.6*	94.6±5.1*	72.9±8.7*	140.2±3.6*
dd	123.3±4.7*	90.4±8.7*	-74.6±3.1*	-224.5±4.2*	328.1±12.2*	273.9±15.6*	-65.2±11.6	-94.7±10.7*	340.7±11.9*	-219.3±20.1*	-284.7±8.4*
R^2	100	100	100	100	99.9	99.8	99.9	99.9	99.9	99.5	99.9

m= Mean effect; a= Additive; d= Dominance; aa= Additive X Additive; ad= Additive X Dominance; and dd= dominance X Dominance gene effects, Coefficient of determination, * significance at 5% t-probability values respectively

Table 3. 13 Estimates of gene effects (6-parameter model) for internode length in eleven snap bean crosses

	Internode Length										
Gene effects	Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
m	14.7±3.5**	16.7±1.8**	6.8±2.4**	31.9±2.2**	6.4±2.5*	12.0±3.2**	9.5±1.9**	13.5±4.1*	5.7±5.0*	14.2±2.7*	17.9±1.6**
a	-5.5±0.5**	-6.9±0.3**	-6.6±0.3**	-8.0±0.3**	-5.7±0.4**	-9.0±0.5**	-9.9±0.3**	-7.5±0.6**	-6.6±0.7**	-6.3±0.4**	-6.2±0.2**
d	4.9±8.5	-2.1±4.3	14.4±5.8	-47.1±5.3**	22.7±6.0	8.8±7.7	18.6±4.6	3.8±9.9	28.2±12.0	0.4±6.5	-7.1±3.9
aa	-1.0±3.5*	-3.4±1.8	5.5±2.4	-18.7±2.2**	7.4±2.5	5.5±3.2	6.2±1.9	-0.2±4.1	7.4±4.9	0.1±2.7	-3.5±1.6
ad	10.7±2.3	4.4±1.1	-1.1±1.5	-7.5±1.4	9.5±1.6**	1.0±2.1	4.3±1.2	9.6±2.6	2.8±3.2	-4.7±1.7	4.4±1.0
dd	-2.8±5.3	1.7±2.6	-4.3±3.6	30.8±3.3**	-12.6±3.7	-2.2±4.8	-9.6±2.8	0.6±6.1	-16.7±	0.9±4.0	7.2±2.4
R^2	92.4	98.8	98	99	96.3	97.7	99.3	94.4	91.3	97.3	98.8

m= Mean effect; a= Additive; d= Dominance; aa= Additive x Additive; ad= Additive x Dominance; and dd= dominance x Dominance gene effects, Coefficient of determination, * Significance at 5% and ** Significance at 1% t-probability values.

Table 3. 14 Estimates of gene effects (6-parameter model) for number of pods per plant in eleven snap bean crosses

	Number of Pods per Plant										
Gene effects	Paulista x HAV 133	Morgan x HAV130	Samantha x HAV132	Morelli x HAV130	Samantha x HAV131	Serengeti x HAV132	Star2053 x HAV135	Star2053 x HAV131	Teresa x HAV134	Teresa x HAV131	Vernadon x HAV134
m	30.2±3.8*	15.4±3.5*	13.3±1.7*	17.8±2.2*	20.9±2.5*	15.4±3.2*	27.5±1.5*	17.9±4.5*	25.9±0.5*	9.9±2.1**	25.8±3.0*
a	-9.1±0.5*	-8.1±0.5*	-8.0±0.2*	-7.1±0.3*	-3.1±0.4*	-3.7±0.5*	-7.0±0.2*	-7.9±0.6*	-10.2±0.5*	-5.2±0.3*	-4.4±0.4*
d	-33.2±9.1	5.3±8.3	19.4±4.2	12.6±5.2	-4.4±6.0	9.8±7.7	-15.5±3.6	-8.4±10.9	-28.7±9.0	16.0±5.2	0.7±7.2
aa	-9.2±3.7	4.1±3.4	8.7±1.7	2.3±2.1	-0.7±2.5	0.8±3.2	-2.9±1.5	2.1±4.5	-5.6±3.7	5.4±2.1	1.4±3.0
ad	2.3±2.4	12.2±2.2	0.1±1.1	5.0±1.4	1.3±1.6	3.1±2.0	10.8±1.0*	11.1±2.9	14.7±2.4	6.2±1.4	5.8±1.9
dd	22.6±5.6	-3.8±5.1	-12.3±2.6	-7.1±3.2	2.5±3.7	-10.3±4.7	13.4±2.2*	14.8±6.7	25.4±5.6*	-10.2±3.2	-0.1±4.4
R^2	97	96.3	99.2	98.3	89.2	88.6	99.1	94.4	97.4	96.5	90.8

m= Mean effect; a= Additive; d= Dominance; aa= Additive x Additive; ad= Additive x Dominance; and dd= dominance x Dominance gene effects, Coefficient of determination, * Significance at 5% and ** Significance at 1% t-probability values.

Table 3. 15 Estimates of gene effects (6-parameter model) pod length in eleven snap bean crosses

	Pod length										
Gene effects	**Paulista x HAV 133**	**Morgan x HAV130**	**Samantha x HAV132**	**Morelli x HAV130**	**Samantha x HAV131**	**Serengeti x HAV132**	**Star2053 x HAV135**	**Star2053 x HAV131**	**Teresa x HAV134**	**Teresa x HAV131**	**Vernadon x HAV134**
Constant	10.6±0.6*	6.5±0.5*	7.1±0.4*	9.2±0.2*	3.1±0.9*	-6.4±0.6*	6.6±0.5*	9.4±0.5*	7.2±0.7*	9.2±1.2*	-4.9±0.4*
A	0.2±0.1	1.4±0.0	0.9±0.1*	2.3±0.0*	2.2±0.1*	1.4±0.1*	1.0±0.0*	2.1±0.1*	2.2±0.1*	2.0±0.2*	0.8±0.1*
D	-5.4±1.5	0.7±1.2*	8.6±0.9*	-0.9±0.6	12.9±2.2*	34.1±1.5*	6.9±1.3*	-2.9±1.1*	5.5±1.8	1.5±2.8	35.4±1.0*
Aa	-0.5±0.6*	3.5±0.5*	2.8±0.4*	2.2±0.2*	7.0±0.9*	17.0±0.6*	4.5±0.5*	0.7±0.5	4.0±0.7*	1.3±1.2	15.6±0.4*
Ad	0.2±0.4	0.2±0.3	1.9±0.2*	-0.8±0.1	-0.9±0.6	0.1±0.4	1.6±0.3*	2.9±0.3*	-1.9±0.5	-0.7±0.7	3.4±0.3*
Dd	6.1±0.9*	5.7±0.7	-6.5±0.6*	3.7±0.3*	-6.6±1.4*	-16.8±0.9*	-2.5±0.8	2.9±0.7	-2.9±1.1	0.7±1.7	-19.6±0.6*
R^2	94.4	99.4	98.6	99.9	97.5	99.1	97.9	99.5	98.2	94.4	99.4

m= Mean effect; a= Additive; d= Dominance; aa= Additive x Additive; ad= Additive x Dominance; and dd= dominance x Dominance gene effects, Coefficient of determination, * Significance at 5% and ** Significance at 1% t-probability values.

3.3.4.3 Components of phenotypic variance, heritability and heterosis

3.3.4.3.1 Days to 50% flowering

There were higher additive variances in days to flowering for all crosses (Table 3.16). The dominance variance was negative in all crosses. Consequently, genetic variance had lower values compared to additive variances in all crosses. Days to 50% flowering was not influenced by the environmental effects as evidenced by low environmental values and high phenotypic values. Duplicate epistasis was also revealed in days to 50% flowering of 7 out of the eleven crosses. The remaining four crosses showed complementary epistasis. Broad and narrow sense heritability of days to 50% flowering was low for most cross (<30%).

Table 3. 16 Phenotypic variance components, heritability and heterosis in snap bean days to 50% flowering

	50% Days to Flowering								
Cross	**V_E**	**V_A**	**V_D**	**V_{AD}**	**V_G**	**V_P**	**h^2_b**	**h^2_n**	**%BPH**
Paulista x HAV 133	3.2	37.6	-16.5	-0.3	21.1	24.3	23.5	22.9	-26.9
Morgan x HAV130	5.2	69.4	-31.1	0.8	38.3	43.5	42.2	41.3	70.2
Samantha x HAV132	2.0	16.4	-7.2	0.9	9.3	11.3	10.8	10.5	26.9
Morelli x HAV130	10.6	45.1	-17.1	9.0	28.0	38.6	35.9	34.6	-28.4
Samantha x HAV131	4.0	39.2	-17.6	-1.4	21.6	25.6	24.6	24.1	-39.7
Serengeti x HAV132	4.0	17.3	-5.3	1.5	11.9	15.9	14.9	14.1	22.0
Star2053 x HAV135	2.2	11.6	-5.0	0.3	6.6	8.8	8.3	8.1	-14.4
Star2053 x HAV131	3.6	130.5	-60.5	1.3	69.9	73.5	72.6	71.5	76.7
Teresa x HAV134	7.2	43.1	-17.6	-4.3	25.6	32.7	31.0	29.9	-3.8
Teresa x HAV131	3.1	39.2	-11.6	1.2	27.6	30.7	29.9	27.9	43.9
Vernadon x HAV134	3.6	12.0	-1.1	-0.3	10.9	14.5	13.6	12.4	22.5

V_E= Environmental variance, V_A= Additive variance, V_D=Dominance Variance, V_{AD}= Additive dominance variance, V_G= Genetic variance, V_P= Phenotypic variance, H^2_b= Broad sense heritability and h^2_n= narrow sense heritability.

However, Star 2053 x HAV 131 had high broad and narrow sense heritability (72.64% and 71.47%) (Table 3.16). The hybrid vigour ranged from -39.7 to 76.7%. Six out of eleven crosses showed positive heterosis while the remaining 4 crosses showed negative heterosis. Morgan x

HAV 130 and Star 2053 x HAV 131 had high positive heterosis (70.2 and 76.7% respectively) (Table 3.16).

3.3.4.3.2 Plant height

There were higher additive variances (48.5 to 100.2) in plant height for all crosses (Table 3.17). The dominance variance was negative in 6 out 11 crosses while the remainder of the crosses had positive values of dominance variance. Where there were negative dominance variance, genetic variance had lower values compared to additive variances in all crosses. The genetic variance ranged from 46.2 to 83.7 (Table 3.17). Plant height was not influenced by the environmental effects as demonstrated by low environmental values and high phenotypic values (73.5 to 94.3). High additive variance further authenticates that the genetic effects played a key role in the expression of plant height among all the crosses.

Table 3. 17 Phenotypic variance components, heritability and heterosis in snap bean plant height

	Plant height								
Cross	**V_E**	**V_A**	**V_D**	**V_{AD}**	**V_G**	**V_P**	**h^2_b**	**h^2_n**	**%BPH**
Paulista x HAV 133	12.1	83.1	-17.7	5.2	65.4	77.5	74.5	68.5	-24.8
Morgan x HAV130	10.6	100.2	-16.5	0.6	83.7	94.3	91.7	83.3	9.1
Samantha x HAV132	11.5	99.8	-37.8	10.3	62.1	73.5	70.7	67.6	6.3
Morelli x HAV130	9.6	67.7	2.3	2.0	70.0	79.6	77.2	68.2	8.9
Samantha x HAV131	33.9	48.5	-2.2	-9.5	46.2	80.2	71.7	66.2	60.1
Serengeti x HAV132	19.9	39.8	10.9	5.3	50.7	70.6	65.6	57.9	80.9
Star2053 x HAV135	8.5	88.6	-12.0	0.1	76.6	85.1	83.0	74.9	17.3
Star2053 x HAV131	12.8	76.5	-7.5	2.9	69.0	81.8	78.6	70.9	-40.4
Teresa x HAV134	8.5	66.2	14.8	7.3	80.9	89.4	87.3	75.3	28.6
Teresa x HAV131	8.0	68.3	14.0	13.1	82.3	90.3	88.3	76.3	-85.7
Vernadon x HAV134	13.9	57.8	9.9	2.4	67.7	81.6	78.1	68.4	14.3

V_E= Environmental variance, V_A= Additive variance, V_D=Dominance Variance, V_{AD}= Additive dominance variance, V_G= Genetic variance, V_P= Phenotypic variance, H^2_b= Broad sense heritability and h^2_n= narrow sense heritability.

Digenic duplicate epistasis was important for plant height in 50% of the crosses while complementary epistasis accounted for plant height in the remainder of the crosses. There was high broad heritability of plant height in all cross (65.6-91.7%). Narrow sense heritability was also high (57.9-83.3%) as shown in Table 3.15. Morgan x HAV 130 had the highest broad (91.7%) and narrow (83.3%) sense heritability. Heterosis ranged from -85.7 to 80.9% in all crosses. Eight crosses showed positive heterosis while the remaining 3 had negative heterosis. Samantha x HAV 131 and Serengeti x HAV 132 had the highest positive heterosis (60.1 and 80.9% respectively) (Table 3.17).

3.3.4.3.3 Internode lengths

Additive variances were higher than the genetic variances in internode lengths for all crosses (Table 3.18). The dominance variance was negative hence genetic variance had lower values compared to additive variances in all crosses. The expression of internode length was not influenced by the environmental effects since the environmental values were lower than the phenotypic values. Further, the additive variance were high while the dominance variances were negative in all crosses. Duplicate epistasis was important for most crosses except Samantha x HAV 131 and Star 2053 x HAV 131 which showed complementary epistasis. There was low broad and narrow sense heritability of internode length in all cross (<30%). The superiority of F_1 hybrids compared to the better parent ranged from -5.8 to 93.5%. Only five crosses showed positive heterosis while the remaining had negative heterosis. Samantha x HAV 131 (84.0%) and Serengeti x HAV 132 (93.5%) had the highest positive heterosis (Table 3.18).

Table 3. 18 Phenotypic variance components, heritability and heterosis in snap bean internode length

	Internode length								
Cross	**V_E**	**V_A**	**V_D**	**V_{AD}**	**V_G**	**V_P**	**h^2_b**	**h^2_n**	**% BPH**
Paulista x HAV 133	2.3	15.2	-4.9	0.1	10.3	12.6	12.1	11.4	23.0
Morgan x HAV130	2.2	4.1	-0.4	0.1	3.6	5.8	5.3	4.9	-35.8
Samantha x HAV132	2.5	22.2	-9.6	0.0	12.7	15.2	14.6	14.2	-10.2
Morelli x HAV130	2.0	24.8	-12.8	0.9	12.0	14.0	13.5	13.6	-58.8
Samantha x HAV131	2.2	31.4	-13.9	-0.7	17.5	19.7	19.1	18.7	84.0
Serengeti x HAV132	2.8	9.9	-1.2	0.4	8.7	11.5	10.8	9.8	93.5
Star2053 x HAV135	2.4	17.7	-8.7	0.5	8.9	11.3	10.7	10.7	-22.8
Star2053 x HAV131	4.3	14.9	-8.0	-1.2	7.0	11.3	10.2	10.3	43.5
TeresaXHAV134	2.4	12.6	-1.1	2.9	11.4	13.8	13.2	11.9	-0.4
TeresaXHAV131	1.6	18.3	-8.8	0.3	9.5	11.2	10.7	10.7	-47.7
VernadonXHAV134	2.1	15.6	-6.1	-0.7	9.4	11.6	11.0	10.6	8.0

V_E= Environmental variance, V_A= Additive variance, V_D=Dominance Variance, V_{AD}= Additive dominance variance, V_G= Genetic variance, V_P= Phenotypic variance, H^2_b= Broad sense heritability and h^2_n= narrow sense heritability.

3.3.4.3.4 Number of pods per plant

Additive variances were higher than the genetic variances in number of pods per plant for all crosses (Table 3.19). The dominance variance was negative hence genetic variance had lower values compared to additive variances in all crosses.

The phenotypic variances are higher than the environmental variances while additive genetic variances were also higher than the dominance variances. This explains why the expression of number of pods per plant was not influenced by the environmental effects. Duplicate epistasis was important for Samantha x HAV 131, Star 2053 x HAV 135, Star 2053 x HAV 131 and Teresa x HAV 131 while most crosses showed complementary epistasis. There was low broad and narrow sense heritability of number of pods per plant in all cross (<30%). Percentage heterosis ranged from -78.1 to 88.1% in all crosses. Seven crosses showed positive heterosis while the remaining had negative heterosis. Star 2053 x HAV 131 (80.6%) and Teresa x HAV 131 (88.1%) had the highest positive heterosis (Table 3.19).

Table 3. 19 Phenotypic variance components, heritability and heterosis in snap bean number of pods per plant.

Number of Pods Per Plant									
Cross	**V_E**	**V_A**	**V_D**	**V_{AD}**	**V_G**	**V_P**	**h^2_b**	**h^2_n**	**%BPH**
Paulista x HAV 133	4.2	40.9	-20.3	-1.0	20.7	24.8	14.2	15.0	7.6
Morgan x HAV 130	3.5	8.4	0.8	1.5	9.2	12.7	12.5	12.6	-6.7
Samantha x HAV 132	3.5	32.3	-11.0	0.4	21.3	24.8	16.0	13.9	7.6
Morelli x HAV130	2.1	20.7	-3.9	-0.3	16.8	18.9	16.8	16.6	45.4
Samantha x HAV 131	2.5	17.6	-2.9	-0.2	14.7	17.2	14.4	14.5	-18.7
Serengeti x HAV 132	1.9	20.2	-7.0	-1.2	13.1	15.0	13.8	13.2	-78.1
Star 2053 x HAV 135	3.2	19.6	-3.5	1.4	16.2	19.3	17.6	18.3	0.4
Star 2053 x HAV 131	4.1	13.1	-0.3	0.0	12.8	16.9	12.5	13.6	80.6
Teresa x HAV 134	1.9	24.3	-1.4	-0.4	22.9	24.8	12.5	15.5	-27.8
Teresa x HAV 131	2.5	24.4	-8.3	0.1	16.1	18.6	11.5	11.2	88.1
Vernadon x HAV 134	2.2	17.5	-3.9	-1.3	13.6	15.7	19.4	19.5	14.4

V_E= Environmental variance, V_A= Additive variance, V_D=Dominance Variance, V_{AD}= Additive dominance variance, V_G= Genetic variance, V_P= Phenotypic variance, H^2_b= Broad sense heritability and h^2_n= narrow sense heritability.

3.3.4.3.5 Pod length

The expression of pod length was influenced by the environmental effects since the environmental values were higher than the genetic values in all crosses. The dominance variance was negative hence genetic variance had lower values compared to additive variances in all crosses. Additive variances were higher than the genetic variances in pod lengths for all crosses (Table 3.20). Complementary epistasis was important for most crosses except Samantha x HAV 131, Samantha x HAV 132, Teresa x HAV 134 and Vernadon x HAV 134 which showed duplicate epistasis. There was low broad and narrow sense heritability of pod length in all cross (<1%). The performance of F_1 hybrids ranged from -26.7 to 13.3%. Most crosses showed negative heterosis whereas the crosses of Paulista x HAV 133 and Morgan x HAV 130 had positive heterosis with 9.4% and 13.3% respectively (Table 3.20).

Table 3. 20 Phenotypic variance components, heritability and heterosis in snap bean pod lengths

	Pod Lengths								
Cross	**V_E**	**V_A**	**V_D**	**V_{AD}**	**V_G**	**V_P**	**h^2_b**	**h^2_n**	**%BPH**
Paulista x HAV 133	0.3	0.0	-0.2	-0.1	-0.2	0.2	0.1	0.1	9.4
Morgan x HAV 130	0.2	0.0	-0.1	-0.1	-0.1	0.1	0.1	0.1	13.3
Samantha x HAV 132	0.3	0.2	-0.4	0.0	-0.2	0.2	0.1	0.1	-14.3
Morelli x HAV130	0.1	0.2	-0.1	-0.1	0.1	0.2	0.2	0.2	-12.0
Samantha x HAV 131	0.2	-0.2	0.1	-0.1	-0.1	0.1	0.1	0.1	-24.4
Serengeti x HAV 132	0.2	-0.3	0.2	0.0	-0.2	0.1	0.0	0.0	-9.2
Star 2053 x HAV 135	0.2	0.2	-0.1	-0.1	0.0	0.2	0.2	0.2	-8.4
Star 2053 x HAV 131	0.2	0.1	-0.1	-0.1	0.0	0.2	0.1	0.1	-23.5
Teresa x HAV 134	0.4	-0.3	0.1	-0.1	-0.2	0.2	0.1	0.1	-26.7
Teresa x HAV 131	0.3	0.8	-0.5	-0.1	0.3	0.7	0.6	0.6	-9.7
Vernadon x HAV 134	0.4	0.0	-0.2	0.0	-0.2	0.2	0.1	0.1	-5.0

V_E= Environmental variance, V_A= Additive variance, V_D=Dominance Variance, V_{AD}= Additive dominance variance, V_G= Genetic variance, V_P= Phenotypic variance, H^2_b= Broad sense heritability and h^2_n= narrow sense heritability.

3.3.5 Correlation

3.3.5.1 Days to 50% flowering

There were positive correlation between days to 50% flowering and plant height in all crosses. Paulista x HAV 133 (r=0.9776**), Morgan x HAV 130 (r=0.9688**), Morelli x HAV 130 (r=0.9271**) and Samantha x HAV 131 (r=0.9507**) had strong positive correlation between 50% days to flowering and plant height at 1% level of significance (Table 3.21). Three crosses had strong positive correlation between 50% days to flowering and plant height at 5% level of significance.

Days to 50% flowering was strongly and positively correlated with internode length in most crosses. Days to flowering of Paulista x HAV 133, Morgan x HAV 130, Samantha x HAV 132, Teresa x HAV 135 and Teresa x HAV 131 crosses had strong positive correlations with internode length at 1% level of significance (Table 3.21). Additionally, 4 out of 11 crosses showed positive correlation between days to 50% flowering and internode lengths at 5% level of significance. Only Morelli x HAV 130 cross had strong positive correlation between 50% days to flowering and

number of pods per plant at (P≤ 0.05) level of significance (0.9386**). Five out of eleven crosses showed strong positive correlation between 50% days to flowering and number of pods per plant. A strong negative correlation between 50% days to flowering and pod length was observed in all crosses. Days to 50% flowering had significantly strong negative relationship with pod lengths at 1% (Samantha x HAV 132, r=-0.9371**) and at 5% (Samantha x HAV 131, r= -0.8729** and Teresa x HAV 131, r=-0.8710**) (Table 3.21).

3.3.5.2 Plant height

There were positive correlation between plant height and internode length in all crosses except in Serengeti x HAV 132. Morgan x HAV 130 (r=0.9974**, Samantha x HAV 132 (r=0.9292**), Star 2053 x HAV 135 (r=0.9731**) and Star 2053 x HAV 131 (r=0.9482**) had strong positive correlation between plant height and internode length at 1% level of significance (Table 3.21). Most crosses had strong positive correlation between plant height and internode length at 5% level of significance.

Plant height was strongly and positively correlated with number of pods per plant in most crosses. Plant height of Morelli x HAV 130 and Teresa x HAV 131 crosses had strong positive correlations with number of pods per plant at 1% level of significance (Table 3.21). Six out of 11 crosses showed strong positive correlation between plant height and number of pods per plant at 5% level of significance.

A strong negative correlation between plant height and pod length was observed in all crosses. Significant and strong negative relationship between plant height and pod lengths was noted in Morelli x HAV 130 (r=-0.9209**), Teresa (r=-0.9574**), and Teresa x HAV 131 (r=-0.9289**). There was also a strong and significant negative association between plant height and pod lengths in Samantha x HAV 131 (r=-0.9115*), Star 2053 x HAV 135 (r=-0.8796*) and Star 2053 x HAV 131(r=-0.9111*) (Table 3.21).

3.3.5.3 Internode lengths

There were positive relationship between internode length and number of pods per plant in almost all crosses (Table 3.21). The relationship was not significant at 1% for all crosses. A strong association between internode lengths and number of pods per plant was significant (P≤0.05) in most crosses.

The relationship between internode lengths and pod length was negative in all crosses. Internode lengths had significantly strong negative relationship with pod lengths in Teresa x HAV 134 (r=-

0.9583**) and Teresa x HAV 131 (r=-0.9450**). Significant negative relationship between internode length and pod lengths was observed in most crosses at 5% level of significance (Table 3.21).

3.3.5.4 Number of pods per plant

Number of pods per plant was negatively associated with pod length in all crosses. A strong, significant and negative correlation between number of pods per plant and pod length was noted in Morelli x HAV 130 (r=-0.9172**) and Teresa x HAV 134 (r=-0.9425**). Number of pods per plant had a significantly strong negative relationship with pod lengths in Teresa x HAV 131 (r=-0.8208*) (Table 3.21).

3.3.5.5 Pod lengths

There were negative associations between pod length and 50% days to flowering, plant height, internode lengths and number of pods per plant in all crosses. There was a strong negative association between pod lengths and: 50% days to flowering (Samantha x HAV 132: r=-0.9371**); plant height (Morelli x HAV 130 (r=-0.9209**), Teresa x HAV 134 (r=-0.9574**) and Teresa x HAV 131 (r=-0.9289**); internode length (Morelli x HAV 130 (r=-0.9172**), Teresa x HAV 134 (r=-0.9583**) and Teresa x HAV 131 (r=-0.9450**); and number of pods per plant in Teresa x HAV 131 (r=-0.9425**). A significant strong negative relationship between pod length and 50% days to flowering, plant height, internode lengths and number of pods per plant in some crosses at 5% level of significance (Table 3.21).

Table 3. 21 Correlation among plant height, 50% days to flowering, internode length, number of pods per plant and pod length for (F_2) generations of eleven populations.

Cross	Trait	Days to 50% flowering	Plant height	Internode length	Number of pods per plant	Pod length
Paulista x HAV 133	Days to 50% flowering	1.0000				
	Plant height	0.9776**	1.0000			
	Internode length	0.9413**	0.8657*	1.0000		
	Number of pods per plant	0.8701*	0.9370*	0.7475^{ns}	1.0000	
	Pod length	-0.2355^{ns}	-0.2336^{ns}	-0.2102^{ns}	-0.0438^{ns}	1.0000
Morgan x HAV 130	Days to 50% flowering	1.0000				
	Plant height	0.9688**	1.0000			
	Internode length	0.9720**	0.9974**	1.0000		
	Number of pods per plant	0.8252*	0.8581*	0.8471*	1.0000	
	Pod length	-0.493^{ns}	-0.4960^{ns}	-0.5001^{ns}	-0.5185^{ns}	1.0000
Samantha x HAV 132	Days to 50% flowering	1.0000				
	Plant height	0.8515*	1.0000			
	Internode length	0.9538**	0.9292**	1.0000		
	Number of pods per plant	0.8758*	0.8552*	0.8898*	1.0000	
	Pod length	-0.9371**	-0.6520^{ns}	-0.8411*	-0.7356^{ns}	1.0000
Morelli x HAV 130	Days to 50% flowering	1.0000				
	Plant height	0.9271**	1.0000			
	Internode length	0.9018*	0.8451*	1.0000		
	Number of pods per plant	0.9386**	0.9954**	0.8708*	1.0000	
	Pod length	-0.7923^{ns}	-0.9209**	-0.7495^{ns}	-0.9172**	1.0000
Samantha x HAV 131	Days to 50% flowering	1.0000				
	Plant height	0.9507**	1.0000			
	Internode length	0.7125^{ns}	0.8788*	1.0000		
	Number of pods per plant	0.6691^{ns}	0.8202*	0.8839*	1.0000	
	Pod length	-0.8710*	-0.9115*	-0.8916*	-0.7564^{ns}	1.0000
Serengeti x HAV 132	Days to 50% flowering	1.0000				
	Plant height	0.7696^{ns}	1.0000			
	Internode length	0.8282*	0.7789^{ns}	1.0000		
	Number of pods per plant	0.9145*	0.6453^{ns}	0.8224*	1.0000	
	Pod length	-0.2983^{ns}	-0.7435^{ns}	-0.5759^{ns}	-0.1163^{ns}	1.0000
Star 2053 x HAV 135	Days to 50% flowering	1.0000				
	Plant height	0.9052*	1.0000			
	Internode length	0.9226**	0.9731**	1.0000		
	Number of pods per plant	0.7908^{ns}	0.8643*	0.9007*	1.0000	
	Pod length	-0.7755^{ns}	-0.8796*	-0.8347*	-0.6886^{ns}	1.0000

	Correlation Continued……					
Star 2053 x HAV 131	Days to 50% flowering	1.0000				
	Plant height	0.2758^{ns}	1.0000			
	Internode length	0.0988^{ns}	0.9482**	1.0000		
	Number of pods per plant	-0.1385^{ns}	0.7278^{ns}	0.9039*	1.0000	
	Pod length	-0.0666^{ns}	-0.9111*	-0.8776*	-0.7341^{ns}	1.0000
Teresa x HAV 134	Days to 50% flowering	1.0000				
	Plant height	0.6889^{ns}	1.0000			
	Internode length	0.9015*	0.8845*	1.0000		
	Number of pods per plant	0.6195^{ns}	0.9167*	0.7630^{ns}	1.0000	
	Pod length	-0.7521^{ns}	-0.9574**	-0.9583**	-0.8208*	1.0000
Teresa x HAV 131	Days to 50% flowering	1.0000				
	Plant height	0.8836*	1.0000			
	Internode length	0.9737**	0.8834*	1.0000		
	Number of pods per plant	0.8811*	0.9662**	0.8994*	1.0000	
	Pod length	-0.8729*	-0.9289**	-0.9450**	-0.9425**	1.0000
Vernadon x HAV 134	Days to 50% flowering	1.0000				
	Plant height	0.7940^{ns}	1.0000			
	Internode length	0.8395*	0.9078 *	1.0000		
	Number of pods per plant	0.7849^{ns}	0.7872^{ns}	0.8942*	1.0000	
	Pod length	-0.2277^{ns}	-0.3367^{ns}	-0.5987^{ns}	-0.3601^{ns}	1.0000

**** Level of significance at 1%, * Level of significance at 5%, ns= Not significant**

3.4 DISCUSSION

Literature is scarce on inheritance of quantitative traits using generation means analysis in snap beans hence the present study seeks to fill this gap. Where genetic effects on yield and its related traits have been studied in French beans, different methodologies have been applied on varied populations. For example Sood and Pathania (2014) estimated genetic effects on snap beans using materials generated through induced mutation while Rainey and Griffiths (2005) used materials from diallele method to analyze gene effects on yield and its related traits in snap bean. Ashwini *et al*. (2015) estimated gene effects in yield and yield components of snap beans but in a cross between different varieties in India. Consequently, in addition to these studies, the results of this study are compared with results of inheritance studies on similar traits of other crops like common beans (Checa *et al*., 2006; Hinkossa *et al*., 2013;Akhshi *et al*., 2014) chickpea (Anbessa *et al*., 2006; Deshmukh and Gawande, 2016) and pigeon pea (Singh and Oswalt, 1992) using generation means analysis.

The variations recorded among generations in the eleven populations indicated that the parents chosen for this breeding programme were appropriate. This is because the parental lines sharply contrasted in all traits. The bush plants were early flowering (37.4 days) while the climbing parents were late flowering (48.8 days). The bush plants had shorter plants (34.2cm) with short internodes (6.9cm) as compared to climbing bean plants which were tall (245.6cm) with long internodes (21.1cm). Besides, the bush parents had fewer number of pods/plant (14) compared to their P_2 counterparts which had 27 number of pods per plant. P_1 plants formed longer pods than P_2 plants with means of 12.0cm and 9.0cm respectively. The sharp contrasts between the parental lines are primary requirements for the performance of generation means analysis since proper choice of parents facilitates the exploitation of genetic variability and production of superior recombinant genotypes. There was therefore evidence of appreciable variability in the materials tested (Checa *et al*., 2006; Hinkossa *et al*., 2013). The backcrosses and F_1 fell in between the parental progenies in almost all crosses for all traits and in each case, the respective backcrosses were close to their recurrent parents as expected.

The joint scaling tests revealed that the Hayman's six parameter model (m+a+d+aa+ad+dd) showed the best fit for traits under study in all crosses. The six parameter model was adequate for days to 50% flowering, plant height, internode lengths, number of pods per plant and pod lengths

as evidenced by the significance of one, two or all the scaling test values (A, B and C) in all crosses. This revealed the presence of non-allelic gene actions in the expression of the traits under study (Mather, 1949). Asrat and Kimani (2005) found that the six parameter model was appropriate in the expression of traits such as number of pods per plant, pod length and plant height. Contrawise, Checa *et al*. (2006) used 3-parameter model to explain the genetic effects of plant height and internode length in common beans. The six parameter model indicated that non-allelic gene actions which were confirmed by Asrat and Kimani (2006) and Hinkossa *et al*. (2013).

The mean effect (m- contribution due to the overall mean plus the locus effect and interaction of the fixed loci) was highly significant for all crosses and in all traits. This indicated that most of traits are quantitatively inheritable (Hinkossa *et al*., 2013). Additive-dominance gene action better explained 50% days to flowering (R^2=82.1-99.7%), internode length (R^2=91.3-99%), number of pods per plant (R^2=88.6-992%) and pod length (94.4-99.9%) whereas additive (a), dominance (d) and epistatic (aa, ad and dd) gene effects were responsible for plant height (R^2= 99.5-100%) in almost all crosses. Sundaram *et al*. (2018) states that epistatic gene effects accounted for days to 50% flowering, plant height and number of pods per plant in chickpea. Additive gene effects were higher than dominance gene effects in all crosses for 50% days to flowering, internode length and number of pods per plant. The results of this study agrees with the reports given by Hinkossa *et al*. (2013) and Akhshi *et al*. (2014) where they found that plant height in common beans was influenced by epistatic gene effects. The findings of Karami and Talebi (2013) contradicts the results of the current study by indicating that additive and non-additive gene effects were important for 50% days to flowering in chickpea. Plant height in common beans was controlled by additive x dominance gene effects at advanced growth stages with >99% R^2 values according to Checa *et al*. (2006).

Higher values of genetic variance were recorded in all crosses for almost all the traits studied in comparison to the environmental variance. Additive variance was greater than dominance variance in all crosses for all the traits except in pod lengths. This indicated that the 50% days to flowering, plant height, internode length and number of pods per plant were not under the influence of the environment while the expression of pod lengths was highly influenced by the environment (González *et al.*, 2010). Consequently, the segregating populations may be good for rapid improvement of yield components in snap bean. Digenic duplicate epistasis was responsible for

plant height, 50% days to flowering and internode length in most crosses as compared to number of pods per plant where most crosses exhibited complementary epistasis. Akhshi *et al*. (2014) reported that duplicate epistasis was more pronounced in common bean number of pods per plant.

High broad and narrow sense heritability was registered for plant height in all crosses indicating that this trait holds high genetic gain in snap bean. Checa *et al*. (2006) reported high broad (80.64-85.6%) and narrow (56.03-79.63%) sense heritability at advanced stages of plant growth in common beans. Osekita and Olorunfemi (2014) however found that broad sense heritability was low for plant height (3.9%) in soybean. Star 2053 x HAV 131 had the highest broad sense and narrow sense heritability (72.64% and 71.47%) for 50% days to flowering. This result agrees with the reports of Osekita and Olorunfemi (2014) who indicated that there was high heritability of 98.9% in 50% days to flowering in soybean. This indicates that early generation selection procedures such as single seed descent would yield successful results for this cross. Both broad and narrow sense heritabilities were low for internode length number of pods per plant and pod length in all crosses. This is attributed to the high environmental error meaning that selection for these traits could be done at advanced stages when there is increased fixable components of variance (a and aa) and decreased dominance (Singh, 2005). Similar results were reported by Vanda *et al*. (2013) where they found low heritability of number of pods per plant and 50% days to flowering in lentils.

The superior performance of F_1 hybrids was evident in days to 50% flowering, plant height, internode length, number of pods per plant and pod lengths for crosses that had positive heterosis. Although positive heterosis is highly significant in hybrid development, this is not feasible for snap bean due to the self-pollinating nature of the crop. However, this informations is highly significant in selection for high yield potential and superior performance of snap bean in the segregating populations. Selection should therefore be based on the studied traits where positive heterosis was realized. On the other hand, negative heterosis indicates that the segregrants can be selected for alternative traits.

The positive correlation observed between 50% days to flowering and plant height indicated that continuous flowering occurs with increase in plant height. This explains why climbing plants are late flowering and have longer harvest periods. Positive correlation between plant height and internode length in most crosses implied that as the guide shoots keep growing there is an

elongation of the internodes. The negative correlation noted between pod lengths and all other traits indicated that pod length reduces with increase in the number of days to 50% flowering, increased plant height and longer internode lengths. Increase in the number of pods reduces the pod lengths due to competition. This explains why the high yielding climbing snap beans have shorter pods (Wahome *et al*., 2013). Positive correlation is important to breeders in the selection of traits to be improved especially when the traits are complex. Highly significant positive correlation is important in the selection for such traits as stated by Jain (2011). Positive correlation was noted among all traits studied except in Morgan x HAV 13, Samantha x HAV 132, Morelli x HAV 133 and Teresa x HAV 134 crosses where there was no significant correlation between varied traits. This implies that improvement of any one of the traits under study is possible through indirect selection. Plant height however influenced almost all the traits in all the crosses except in Serengeti x HAV 132 cross where there was no significant correlation between plant height and internode length, 50% days to flowering, number of pods per plant and pod lengths. Similar findings were also reported in safflower (Gonzalez *et al*., 2016) whereas Ahmed (2011) found a negative correlation between plant height and days to 50% flowering.

Days 50% to flowering was positively associated with internode length in all crosses except in Samantha x HAV 132 and Star 2053 x HAV 131 crosses where there was no significant correlation. There was no correlation between 50% days to flowering and number of pods per plant in five crosses. The findings of the present study are similar to those obtained by Jain (2011) which indicated that there was highly significant positive correlation between days to flowering and number of pods in *Linum usitatissimum L.* However, Singh *et al*. (2017) found a negative correlation (r = -0.271**) between days to 50% flowering and number of pods per plant in Faba beans. Four of the crosses studied showed results similar to those of Konate *et al*. (2016) which indicated no significant correlation between plant height and days to 50% flowering though the remainder of the crosses indicated otherwise.

3.5 CONCLUSION AND RECOMMENDATION

This study indicated that the parental lines are genetically diverse and hence suitable for any breeding and selection program given that they varied significantly. There was an indication therefore that these snap bean progenies can be selected successfully for plant height and pod yield. The significance of the six-parameter model in the expression of traits under study based on regression (F_{pr}) value and coefficient of determination (R^2) showed that these trait are highly heritable and can easily be selected for in breeding for climbing capacity and improvement of pod yield in snap bean. The additive and dominance genes that accounted for 50% days to flowering, internode length and number of pods per plant in most crosses suggested that selection procedures such as single seed decent, recurrent selection, diallele selection and pedigree can be employed for an effective breeding program in snap bean. The high additive genetic variance that was observed in all crosses for all traits in the current study implies that 50% days to flowering, plant height, internode length, number of pods per plant and pod length can easily be inherited in snap beans. High heritability presents high genetic gain in plant height and 50% days to flowering. Low heritabilities obtained for internode length and number of pods per plant directs the selection procedures for breeders, hence vital information. The positive correlation among the studied characters indicates that improvement of snap bean yield is possible if these traits are utilized in a breeding program.

CHAPTER FOUR

EVALUATION OF ADVANCED CLIMBING SNAP BEAN LINES AND SELECTION FOR POD QUALITY, POD YIELD AND DISEASE RESISTANCE

ABSTRACT

Although climbing snap beans have the potential of increasing productivity and competitiveness in domestic and export markets, suitable varieties with market preferred pod quality characteristics and desirable agronomic traits are not available to smallholder farmers in Kenya and other countries in east, central and West Africa. The objective of this study was to select climbing snap beans with market preferred pod quality characteristics, high pod yield and multiple disease resistance from locally developed breeding populations and advanced lines. Fifty three advanced climbing snap bean lines were evaluated in preliminary yield trials at Mwea during the 2013 long rain season. Twenty lines were selected and evaluated in advanced yield trials at Mwea and Embu during the 2013 short rain season. Data was collected on plant vigour, days to 50% flowering, days to first picking, reaction to rust, anthracnose and angular leaf spot infection, pod length and yield per market class. Data was analyzed using Genstat Version 15.1.

Results showed that there were significant genotypic variations ($P<0.05$) for 50% days to flowering, days to first picking, resistance to rust, angular leaf spot and anthracnose, pod length, market grades and pod yield. Plant vigour scores at the two sites varied from 1 to 5 among the test lines compared to 3 to 4.5 for check varieties. However, differences in plant vigour were not significant. Rust, anthracnose and angular leaf spot were severe at Embu where sprinkler irrigation was used. Duration to 50% flowering varied from 42 to 48days in both sites. This may have contributed to differences in days to first picking which occurred 53 to 7 days after planting. Cumulative pod yield over 13 harvests in Embu varied from 8,164.0 to 15,191.0 kg ha-^{1}, compared with 5,459.0 to13, 398 kg ha-^{1} at Mwea. The test lines grown at Embu showed a yield advantage of 35%. While KSV27-145-1-1M had the highest percentage of premium pods (71.2%), KSV13-1-2-3M yielded three times (5,665.3 kg ha^{-1}, 43.7%) the average premium pods of the check varieties. KSV04-2-2M met all the market preferred pod characteristics among the test lines. Although KSV42-2M was highly vigorous, showed multiple disease resistance, had high yields (12, 705.0 kg ha^{-1}), formed straight round green pods, had a considerable percentage of premium

pods (66%), it formed shorter pods (7.1cm). Generally, the new climbing snap bean lines out-yielded commercial bush varieties four fold. The new lines produced an average of 54% premium grades. KSV04-2-2M and SV20-1-1T were the most outstanding lines since they met the recommended pod qualities. The results of this study indicate that new climbing snap bean varieties with market preferred pod characteristics, high yield potential and resistance to major diseases can be developed from the selected lines. Exploitation of the longer harvest period of climbing beans can contribute to higher yields and better returns to investment especially for smallholder farmers, and to the overall competitiveness of the snap bean sub-sector.

Key words: Snap bean, diseases resistance, pod quality, indeterminate snap beans.

4.1 INTRODUCTION

The snap bean originated from Peru and are either determinate (bush) or indeterminate (climbers) (Singh and Singh, 2015). Determinate snap bean grows up to 0.3m high, flower and pod within a short period of time, while indeterminate types growing up to 3m, have terminal vegetative buds, long vines and twining ability enabling them to climb easily and thus requiring support using stakes or trellises (Checa *et al.*, 2006). Climbing dry beans are three times more productive compared to bush beans (Checa *at al*., 2006). Previous work in Kenya showed that climbing snap bean selections were more tolerant to diseases such as angular leaf spot (*Phaeoisareopsis griseola*), anthracnose (*Colletotrichum lindemuthianum*) and rust (*Uromyces appendiculatus*) as compared to bush types and could be a good source of the climbing habit and disease resistance (Wahome *et al*., 2013). However, snap bean production in eastern Africa is dominated by determinate types. Most of the available bush varieties are susceptible to diseases like rust, bean stem maggots, bacterial blight, angular leaf spot and anthracnose which can lead to losses of up to 100%.

Indeterminate snap beans which have three times productivity advantage due to their longer harvest periods and plant size compared to determinate types have not been developed for smallholder farmers wishing to intensify return by use of family labour (CIAT, 2008). Additionally, indeterminate snap bean varieties that are popular in some of the North and South American markets have flat pods that are not suitable for European markets (Schoonhoven and Voysest, 1991). Thin, round podded and locally adapted climbing snap bean varieties have not been developed for farmers in eastern Africa (Chemining'wa *et al*., 2012). The objective of this study therefore was to select indeterminate snap beans with good pod quality, high pod yield and multiple disease resistance for commercial production.

Research on climbing capacity has only been done in common beans and it has been found to contribute to higher yields due to longer harvesting period and the erect nature of the plant. As to whether the same applies to snap bean is not yet known. It has been established that climbing snap beans have multiple disease resistance but have poor pod quality and low yields (Wahome *et al*., 2011).

4.2 MATERIALS AND METHODS

4.2.1 Experimental sites

Preliminary yield trials (PYT) were carried out in Wangúru, Mwea (Kirinyaga County) during the 2013 long rain season, while the advanced yield trials (AYT) of climbing snap bean test lines were conducted at Mwea and Embu during the 2013 short rain season. Wang'uru, Mwea (37^0 21.9'E; $0^0$36.1'S) is located in the lower altitude zones of Kirinyaga County. Runyenjes, Embu (0° 47'S; 37° 40'E) is located in the Upper Midlands 2 (UM2) Agro-Ecological Zone of Embu County. Mwea is located at a lower altitude of 1159 m whereas Embu is a high altitude zone of 1493m (Jaetzold *et al*., 2006). Due to the lower altitudes, Mwea experiences higher mean annual temperatures of 21.7°C (15.6 to 27.8°C) compared to Embu which experiences mean annual temperature of 16°C. Both sites have bimodal rainfall which occur between March and June, and from October to December. Mwea has mean annual rainfall of 1037mm compared with 1206 mm for Embu. Mwea has red sandy loam soils with low nitrogen levels while Embu has humic nitisol soils which are moderately fertile (Jaetzold *et al.*, 2006; Kamanu *et al*., 2012).

4.2.2 Plant materials

Fifty-three (53) advanced climbing snap bean lines, were evaluated in preliminary trials in Mwea during the 2013 long rain season (April-June) (Appendix 5). These genotypes collectively referred to as Progeny I Nursery were nearly homozygous $F_{6.9}$, F_8 and F_{10} lines. Twenty (20) advanced lines selected from the preliminary trials based on growth habit, disease resistance, good pod quality and yield were further evaluated in advanced yield trials at Mwea and Embu during the 2013 short rain season.

The materials were obtained from the University of Nairobi Bean Research Program, Department of Plant Science and Crop Protection, Kabete Campus. These lines originated from crosses between bush and climbing snap beans. The parental lines differed in resistance to major snap diseases. The parents included: BelDakMi, BelMiNeb and Beltigrade RR2 which conferred resistance to rust; Mex54 and L227-10 resistant to angular leaf spot; and G2333 which conferred resistance to anthracnose. Single crosses were performed between these lines and commercial varieties which were susceptible to the three diseases. The commercial varieties included Amy, Paulista, Morelli, Morgan, Julia, Foskelly, Teresa, Vernandon, Kutuless and Alexandria. The F_1 progenies obtained from these crosses were advanced to F_5 through bulk population method. They

were then evaluated for high productivity and multiple disease resistance. Growth habit and market preferred pod traits were also selected for among these populations (Figure 2.4).

The segregating populations were evaluated for two seasons in Mwea and Thika in the year 2009 to 2010. Firstly, the segregating populations (F_4, F_5 and F_6) were artificially inoculated with rust, angular leaf spot and anthracnose pathogens at the triofoliate stage (Wahome *et al*., 2011). Nine lines and 674 single plants with resistance to rust, angular leaf spot and anthracnose were selected. Secondly, fifty one F_2 populations that had been advanced to F5 and F6 generations were evaluated for yield and pod quality (Wahome *et al*., 2013). These lines were further advanced to $F_{6.8}$, $F_{7.9}$ and F_8 from which 53 climbing snap bean lines were selected and evaluated in preliminary yield trials at Mwea during the 2013 long rain season. Advanced yield trials were conducted at Mwea and Embu during the short rain seasons in 2013. Five commercial bush varieties (Teresa, Morgan, Star 2053, Samantha and Morelli) were used as checks.

4.2.3 Experimental design and Trial Management

The trials at Mwea and Embu were laid out in a randomized complete block design with two replicates. The plot sizes were 2 m wide and 4 m long. Spacing was 50 cm between rows, and 10 cm within rows. A plot consisted of four, 4m rows. Diammonium phosphate (DAP: 18:46:0) fertilizer was applied during planting at the rate of 225 kg ha^{-1}. The crops were top dressed with calcium ammonium nitrate (21% N) at the rate of 340 kg ha^{-1} four weeks after planting. Supplementary irrigation was provided using furrow irrigation in Mwea and with sprinklers at Embu. The plots were manually weeded at both sites. The crops were staked to offer support due to their erect growth habit. Insect pests such as aphids, white flies and leaf miners were controlled by alternate application of Cyclone® (10% Cypermethrin + 35% chlorpyriphos) and Confidor® (imidacloprid) at the rate of 1.5ml L^{-1}.

4.2.4 Data Collection

Data was collected on plant vigour, reaction to diseases (rust, anthracnose and angular leaf spot), total pod yield and pod quality (curvature, colour and pod shape) during the preliminary and trial. For advanced yield trial, data was collected on plant vigour, 50% days to flowering, reaction to infection by rust, anthracnose and angular leaf spot, and duration to first picking. Data on quality pod traits such as pod length, pod grades and pod yield was recorded at both sites.

Plant vigour was based on plant height and vegetative growth of ten plants per plot rated on a scale of 1 to 9, where 1=excellent vigour, 3=good vigour, 5= intermediate vigour, 7=poor and 9=very

poor vigour (van Schoonhoven and Pasto-Corrales, 1987). Duration to 50% days to flowering was recorded as the number of days from planting to the date when 50% of plants in a plot had one or more open flowers. Disease resistance was evaluated following procedures described by van Schoonhoven and Pastor-Corrales, (1987) as shown in Table 4.1. Reaction to rust, anthracnose and angular leaf spot were recorded at late pod maturity.

Table 4. 1 Disease severity scale used to evaluate the reaction of test lines to fungal diseases.

Rating	Category	Description	Comments
1-3	Resistant	No visible symptom or light symptoms (2% of the leaf)	Germplasm useful as a parent or commercial variety.
4-6	Intermediate	Visible and conspicuous symptoms (2-5% of the leaf) resulting only in limited economic damage.	Germplasm can be used as commercial variety or source of resistance to disease.
7-9	Susceptible	Severe to very severe symptoms (10-25% of the leaf) causing yield losses or plant death.	Germplasm in most cases not useful as parent or commercial variety

Source: van Schoonhoven and Pastor-Corrales, 1987.

Plots were harvested on Mondays, Wednesdays and Friday each week for five weeks. Pods were harvested from plants in the two inner rows of each plots during the short rain season at Mwea and Embu. Plots were harvested 13 times during the five week period. The harvested pods were classified into three standard commercial categories based on pod diameter defined as extra fine (6 mm), fine (6-8 mm) and bobby (>8 mm) according to HCDA (2009;Table 4.2). Pod length was measured in centimeters using a calibrated ruler. Total pod yield was determined by weighing the pods in each market grade using an A and D top pan balance (Model EK-6100i-EC, Hong Kong, China).

Table 4. 2 Marketable snap bean classes

Pods	Width (mm)	Other Characteristics	Comments
Extra Fine	6	-Tender - seedless - stingless	-Good marketable pod -Recommended for export market
Fine	6-9	-Small immature seeds	-Good marketable pod -Recommended for export market
Bobby	>8	-seeds -strings	-Unsuitable for export market

Source: HCDA (2009)

Total pod yield was calculated by summing up the pod mass of the three grades. Pod length was determined as the mean length of three randomly sampled pods per market class for four harvests. The average length for the four harvests was then calculated for each market class. The weather data for the experimental period was obtained from the Kenya Meteorological department at Embu and Mwea. Data on monthly rainfall, maximum temperature and minimum temperature was recorded.

4.2.5 Data analysis

Data on plant vigour, 50% days to flowering, days to first picking, reaction to rust, anthracnose and angular leaf spot, pod length and pod yield was subjected to combined analysis of variance using Genstat software 14th edition (VSN International, 2011). The differences among the means were compared using Fishers Protected Least Significance difference test at 5 and 1% probability levels.

4.3 RESULTS

4.3.1 Weather Conditions at Embu and Mwea Trial sites

This Embu and Mwea 2013 weather data was obtained from the Kenya Meteorological Department, 2015 (Appendix 6). The preliminary yield trials were carried out from April to June, 2013 at Mwea. Temperatures ranged between 11.0 to 33.3^{o}C with a mean of 22.8^{o}C during this period. The area received 456mm total rainfall during the experimental period (Figure 4.1).

During the AYT trials, temperatures ranged from 18.5 to 20.0°C at Embu with a mean of 19.4^{o}C, and from 21.0 to 24.5°C at Mwea with mean of 22.8°C (Figure 4.1). Mean temperatures were higher at Mwea compared to Embu. The mean temperatures during flowering and podding period were 18.0°C at Embu, and 21.8°C at Mwea. While temperatures were normal in Embu, the annual temperatures in Mwea were slightly higher than expected. Mwea and Embu received 528mm and 485.2mm respectively during the experimental period. Mwea received less than the expected annual rainfall. However, Embu received normal rainfall well distributed throughout the year. Embu and Mwea recorded the highest amounts of rainfall in April and November while Mwea had higher temperatures throughout the experimental period (Figure 4.1)

The observations indicate that of the two sites, Embu experienced both normal rainfall and temperatures. However, Mwea received low amounts of rainfall and experienced higher than normal mean temperatures.

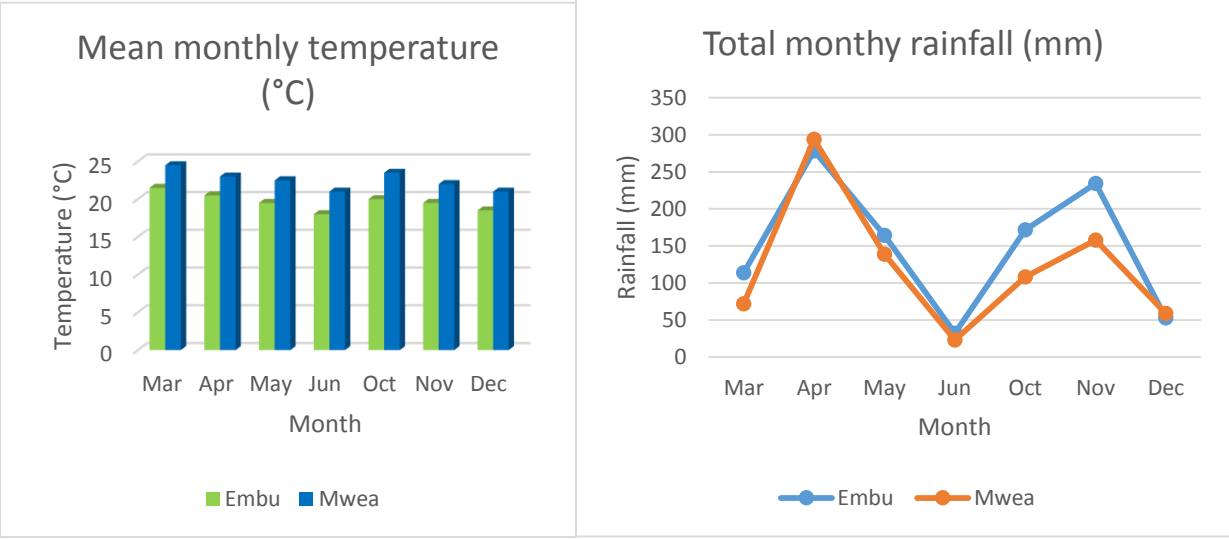


Figure 4. 1 Weather in Mwea during the PYT and AYT trials

4.3.2 Preliminary Yield Trials

Fifty three advanced climbing snap bean lines were evaluated for plant vigour, reaction to rust, anthracnose and angular leaf spot, total pod yield and pod quality in Mwea in 2013. Sixteen climbing snap bean lines failed to germinate due to water logging that resulted from excessive rains during the 2013 long rain season hence no data was recorded (Appendix 5). Twenty out of fifty three lines were selected for subsequent trials based on their resistance to disease rust, anthracnose and angular leaf spot; pod yield and pod quality as presented in Table 4.3.

Table 4. 3 Mean squares for plant vigor, reaction to diseases and pod yield of climbing lines grown at Mwea during the 2013 long rain season.

Sources of variation	Df	Plant vigour	Days to 50% flowering	Pod length	Reaction to Disease			Pod yield (kg ha^{-1})
					Rust	Anthracnose	ALS	
Replicates	1	1.1585	0.48	1.16	0.03774	0.03774	0.03774	1.86E+04
Genotype	51	2.5121**	74.91**	46.13**	0.41842**	0.41842**	0.41842**	3.88E+07**
Residual	53	0.3861	45.26	9143.1	0.01816	0.01816	0.01816	1.01E+06
CV (%)		26.6	18.1	22.8	19.3	19.3	19.3	27.6

Df= Degress of freedom, **= significant at 1% Probability, ALS- angular leaf spot

4.3.2.1 Plant vigour

Plant vigour varied significantly ($P \leq 0.01$) among the test lines and check varieties at Mwea (Table 4.3). The vigour of the test lines varied from good to excellent compared to the checks most of which showed intermediate vigour. About 13.5% of the test lines had excellent vigour with a score of 1 (Table 4.4). Eighty five percent (85%) of the selected lines had an excellent vigour with KSV46-2, KSV41-2-1-1M, KSV41-1-2-3M, KSV29-2M and KSV17-145-1-1M being the most vigorous lines.

4.3.2.2 Reaction to rust

Rust reaction varied significantly ($P \leq 0.01$) among the 53 evaluated lines (Table 4.3). All the lines showed resistant reactions to rust in comparison to the check varieties. With rust scores of 1, it indicates that despite the high disease pressure during the experimental period the test lines exhibited multiple disease resistance. Morelli with a score of 7 was the most susceptible variety among the check commercial checks (Table 4.4). However, most check varieties showed intermediate resistance to rust.

4.3.2.3 Reaction to anthracnose

The test lines and check varieties showed significant differences ($P \leq 0.01$) in their reaction to infection by anthracnose (Table 4.3). However, disease pressure was low (Appendix 5). Disease scores varied from 1 to 5. The test lines and Morelli showed resistance to anthracnose in comparison to other check varieties which had intermediate resistance. Teresa had the highest score (4.8) while all the test lines were resistant to anthracnose (Table 4.4).

4.3.2.4 Reaction to angular leaf spot

Reaction to angular leaf spot varied significantly ($P \leq 0.01$) among test lines although the disease pressure appeared low (Table 4.3). All the test lines were resistant to angular leaf spot in comparison with the check varieties. The check varieties showed intermediate resistance to angular leaf spot except Morgan and Samantha which were resistant (Table 4.4). Samantha was more susceptible to angular leaf spot (5.0 score).

4.3.2.5 Total pod yield

The total pod yield varied significantly among the 53 genotypes evaluated in the preliminary yield trials at Mwea (Table 4.3; Appendix 5). Pod yield of the varied from 234 to13, 689 kg ha^{-1}. The pod yield of the check varieties varied from 2513.9 to 3610.6 kg ha^{-1} with a mean of 2938.9 kg ha^{-1}. Twenty (20) test lines out-yielded the best check varieties with 204.3% yield advantage. Thirty-two percent (32%) of the test lines had lower pod yield than the check varieties and therefore they were omitted in the advanced yield trials selections. The selected lines out yielded the check varieties threefold with a mean yield of 8, 942.85 kg ha^{-1} compared to 2, 938.94 kg h^{-1} among the check varieties.

While 85% of the selected test lines had pod yield ranging from 5,494 to 9,955 kg ha^{-1}, KSV04-1-2M, KSV13-1-2-3M, KSV42-2M and KSV44-1M emerged to be the best yielders with more than10, 000 kg ha^{-1} (Table 4.4). The lowest yielder of the selected test lines yielded more than the checks by 86.9%. The 20 selected test lines were the highest yielders in comparison to the check varieties and hence the rationale for their selection.

Table 4. 4 Characteristics of selected snap bean test lines in the preliminary yield trials at Mwea (Wang'uru), Kirinyaga County During the long rains season, 2013

Test Line	Trait Scores and Pod Quality									
								Pod Quality		
	Vigour	Days to 50% Flowering	Pod length (cm)	Rust	Anthracnose	Angular Leaf Spot	Total Pod Yield ($kgha^{-1}$)	Pod Colour	Pod curvature	Pod shape
KSV01-1M	2.0	45.5	9.6	1.0	1.0	1.0	9955.0	Green	Straight	Round
KSV04-1-2M	1.5	55.0	5	1.0	1.0	1.0	12240.0	Green	Straight	Round
KSV04-2-2M	2.0	47.5	6	1.0	1.0	1.0	9943.0	Green	Straight	Round
KSV08-2-2-1T	3.0	45.5	8.3	1.0	1.0	1.0	6447.0	Green	Straight	Round
KSV13-1-2-3M	2.0	42.5		1.0	1.0	1.0	13689.0	Green	Straight	Round
KSV14-1-4M	1.5	52.0	6.4	1.0	1.0	1.0	8190.0	Green	Straight	Round
KSV17-145-1-1M	2.0	44.0	6.2	1.0	1.0	1.0	8739.0	Green	Straight	Round
KSV17-2-1-1T	1.0	49.0	5.3	1.0	1.0	1.0	7243.0	Green	Straight	Round
KSV19-1-2M	2.0	50.5	4.7	1.0	1.0	1.0	5494.0	Green	Straight	Round
KSV25-1-1T	3.0	46.1	10.1	1.0	1.0	1.0	6213.0	Green	Straight	Round
KSV27-145-1-1M	2.0	52.5	6.2	1.0	1.0	1.0	8702.0	Green	Straight	Round
KSV27-69-4-1-2T	2.0	47.0	5.1	1.0	1.0	1.0	7508.0	Green	Straight	Round
KSV29-2M	1.0	51.2	7.5	1.0	1.0	1.0	9934.0	Light Green	Straight	Flat
KSV41-1-2-3M	1.0	48.5	6.8	1.0	1.0	1.0	9718.0	Green	Straight	Round
KSV41-1-2T	3.0	48.0	8.9	1.0	1.0	1.0	9132.0	Green	Straight	Round
KSV41-2-1-1M	1.0	49.5	7.8	1.0	1.0	1.0	7689.0	Green	Straight	Round
KSV42-2M	1.5	49.0	9.3	1.0	1.0	1.0	11737.0	Green	Straight	Round
KSV43-1T	1.5	45.5	8.7	1.0	1.0	1.0	8574.0	Green	Straight	Round
KSV44-1M	2.0	50.1	6.9	1.0	1.0	1.0	10056.0	Green	Straight	Round
KSV46-2M	1.0	49.4	9.8	1.0	1.0	1.0	7654.0	Green	Straight	Round
Checks										
Morelli	4.3	37.9	11.6	7.0	3.5	3.0	2513.9	Purple	Straight	Round
Morgan	3.8	38.4	10.9	5.3	3.3	4.3	2641.5	Green	Straight	Round
Samantha	4.5	38.1	11.2	5.0	2.5	5.0	2907.9	Light Green	Straight	Flat
Star 2053	4.5	37.6	10.9	5.0	4.0	3.5	3020.8	Green	Straight	Round
Teresa	3.5	39.4	11.6	4.8	4.8	3.5	3610.6	Light Green	Straight	Round
Grand Mean	1.4	43.8	9.6	0.7	0.7	0.7	3643.0			
$LSD_{0.05}$	1.2	4.9	8.1	0.2	0.2	0.2	1744.5			
CV (%)	26.6	18.1	22.8	19.3	19.3	19.3	27.6			

LSD= least significant difference, CV= coefficient of variation, Plant vigour scale, disease severity scale (van Schoonhoven and Pastor-Corrales, 1987)

4.3.2.6 Pod characteristics

Pod quality in terms of colour, curvature and shape varied among the genotypes. Most genotypes had green pods with only 9.4% having purple and 13.2% light green pods (Table 4.4). More than half of the evaluated test lines had straight pods while the remaining lines had pods that were either curved or slightly curved. Eight of the 53 test lines had flat pods. The check varieties on the other hand had straight round pods except Samantha whose pods were flat. The pod colours of the check varieties were purple (Morelli), light green (Samantha and Teresa) and green (Morgan and Star). All the twenty selected test lines had straight, round green pods except KSV29-2M which had flat pods (Figure 4.1, Table 4.4)

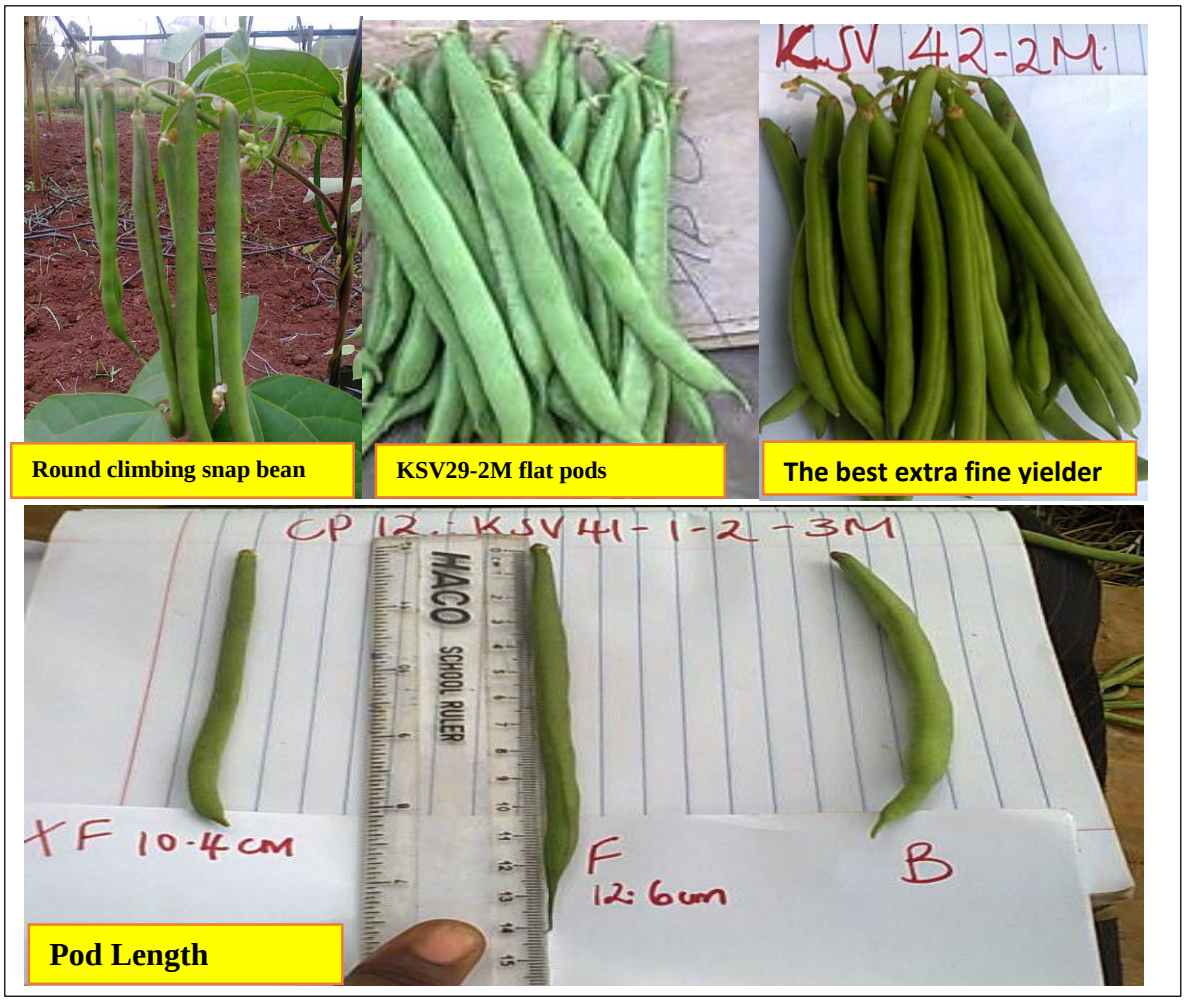


Figure 4. 2 Climbing snap bean pods in Embu

4.3.3 Advanced yield trials

Out of the 53 test lines evaluated in the preliminary yield trials, 20 were selected for advanced yield trials evaluations in Mwea and Embu during the 2013 short rain season. Selection was based on all the traits studied in the PYT evaluations in Mwea.

Table 4. 5 Means squares for climbing lines in advanced yield trials at Mwea and Embu

					Disease severity			Pod length			Pod yield			
Sources of variation	**Df**	**Plant Vigor**	**50%DF**	**Days to 1st pick**	**Rust**	**Anthracnose**	**ALS**	**EF**	**F**	**B**	**EF**	**F**	**B**	**Total pod yield**
Rep	1	64	2.29	246.49	3.24	0.25	0.01	102.08	66.11	40.36	3.25E05	3.10E+07	1.53E+05	3.89E+07
Genotype	24	4.021	58.25**	153.61	12.70**	4.681*	5.525	28.33	14.96	43.58	9.31E+06**	2.29E+08	2.39E+08	7.07E+08**
Location	1	27.04*	670.81**	8.41	2.56	0.25	0.091	0.37	38.04	145.51	2.82E+07**	1.13E+09	3.86E+09	7.20E+08**
Genotype x Location	24	5.728	10.75	96.29	2.685**	1.27	1.09	17.7	9.62	17.45	6.64E06**	2+08E+07	5.45E+07	3.97E+07*
Residual	49	6.571	10.62	94.88	0.8727	1.862	1.302	12.54	15.46	19.8	6.71E+05	1.05E+07	4.49E+07	2.56E+07
CV (%)		17.3	7.6	19.4	22.8	20.2	19.2	38.9	45.6	24.4	16.9	12.6	21.9	42.1

Rep= Replication, Df= Degress of freedom, 50% DF= Days to 50% flowering, ALS= Angular leaf spot, EF= Extra fine, F= Fine, B= Bobby

4.3.3.1 Agronomic traits

4.3.3.1.1 Plant vigour

The analysis of variance ($P \leq 0.05$) revealed that there were no significant variations among genotypes at Mwea and Embu trial sites. Plant vigour was influenced by location whereas interaction between genotypes and location have no effect on plant vigour (Table 4.5; Appendix 8). The test lines exhibited good plant vigour that ranged from 1-4 in Mwea while 50% of the test lines showed intermediate plant vigour in Embu. Plant vigour ranged from1 to 7 at Embu (Table 4.6).

4.3.3.1.2 Days to 50% Flowering

There were significant genotypic differences ($P \leq 0.05$) in days to 50% flowering in Mwea and Embu (Table 4.5). Combined analysis of variance showed that duration to 50% flowering was influenced by both genotypic and location effects (Appendix 8). However, the interaction between genotype and the location had no significant effects on earliness among the test lines and the check varieties. The check varieties flowered earlier (34-38 days) than the test lines which flowered between in 40 to 44 days at Mwea, and 43 to52 days in Embu (Table 4.5). On average, 70% of the test lines flowered by the 45^{th} day with KSV29-2M flowering later in both sites. Most test lines flowered later at Embu as compared to Mwea (Table 4.6).

4.3.3.1.3 Days to first picking

There were no significant genotypic differences ($P<0.01$) for number of days to first picking at the two sites (Table 4.5). This was however neither influenced by location nor interactions between genotypes and location (Appendix 8).The number of days to first picking among the check varieties ranged from 40 to 44 at Mwea, and from 42 to 45 at Embu.

The number of days to first picking for the test lines varied from 51 to 54 in Mwea and 56 to 60 in Embu indicating that the test lines were late maturing. Days to first picking ranged from 41 to 44 for check varieties, and from 53 to 57 for the test lines in both sites (Table 4.6). It was noted that days to first picking were earlier in Mwea than Embu.

Table 4. 6 Plant vigour, days to 50% flowering and days to first picking of new climbing snap bean lines and check varieties at Mwea and Embu during short rains in 2013

	Plant vigour scores			50 % Days to Flowering			Days to first Picking		
Genotype	**Mwea**	**Embu**	**Mean**	**Mwea**	**Embu**	**Mean**	**Mwea**	**Embu**	**Mean**
KSV01-2M	1.0	5.0	3.0	40.0	52.0	46.0	50.5	59.5	55.0
KSV04-1-2M	2.0	5.0	3.5	42.0	48.0	45.0	51.5	56.0	53.8
KSV04-2-2M	2.0	1.0	1.5	40.0	48.0	44.0	50.5	56.0	53.3
KSV08-2-2-1T	3.0	7.0	5.0	41.5	50.5	46.0	53.0	58.0	55.5
KSV13-1-2-3M	2.0	5.0	3.5	40.5	49.0	44.8	52.0	56.0	54.0
KSV14-1-4M	4.0	3.0	3.5	43.0	47.0	45.0	52.5	56.0	54.3
KSV17-145-1-1M	3.0	5.0	4.0	40.5	48.5	44.5	53.0	56.0	54.5
KSV17-2-1-1T	2.0	5.0	3.5	43.0	47.0	45.0	53.0	56.0	54.5
KSV19-1-2M	1.0	5.0	3.0	40.0	43.5	41.8	51.5	56.0	53.8
KSV25-1-1T	3.0	2.0	2.5	42.5	50.0	46.3	53.0	56.0	54.5
KSV27-145-1-1M	3.0	5.0	4.0	42.5	50.0	46.3	53.0	58.0	55.5
KSV27-69-4-1-2T	1.0	1.0	1.0	41.5	45.0	43.3	52.0	57.0	54.5
KSV29-2M	3.0	5.0	4.0	43.5	52.0	47.8	54.0	59.5	56.8
KSV41-1-2-3M	3.0	6.0	4.5	42.5	49.5	46.0	53.0	58.0	55.5
KSV41-1-2T	3.0	1.0	2.0	42.0	49.0	45.5	52.0	57.0	54.5
KSV41-2-1-1M	2.0	5.0	3.5	42.5	47.0	44.8	52.0	56.0	54.0
KSV42-2M	1.0	3.0	2.0	40.0	44.5	42.3	50.5	58.0	54.3
KSV43-1T	2.0	4.0	3.0	41.0	48.5	44.8	51.5	57.0	54.3
KSV44-1M	2.0	3.0	2.5	42.0	47.0	44.5	52.0	56.0	54.0
KSV46-2M	2.0	3.0	2.5	42.5	44.5	43.5	53.0	58.0	55.5
Checks									
Morelli	5.0	3.5	4.3	35.0	34.5	34.8	40.5	42.0	41.3
Morgan	5.0	2.5	3.8	35.5	36.0	35.8	40.5	42.5	41.5
Samantha	6.5	2.5	4.5	36.0	36.0	36.0	42.0	43.0	42.5
Star 2053	3.0	6.0	4.5	35.5	36.5	36.0	40.5	42.5	41.5
Teresa	5.0	2.0	3.5	37.5	38.5	38.0	43.5	45.0	44.3
Grand Mean	2.8	3.8	3.3	40.5	45.7	43.1	50	50.6	50.3
$LSD_{0.05Gen}$	3.3	6.4	5.2	5	8.1	6.5	4.2	27.9	19.6
CV (%)	11.4	12.1	17.3	6.0	8.6	7.6	4.1	26.7	19.4

LSD= least significant difference, CV= coefficient of variation, Plant vigour scale: van Schoonhoven and Pasto-Corrales, 1987.

4.3.3.2 Reaction to diseases

4.3.3.2.1 Rust

Genotypic reaction to rust varied significantly in both sites. These variations were significantly influenced by both the genotype and interaction between genotype and location (Table 4.5; Appendix 7 and 8). The test lines were resistant to rust in Mwea and Embu (1-3). The check varieties showed intermediate resistance in Mwea. However, they showed susceptibility in Embu except Samantha and Star 2053 which showed intermediate resistance. The test lines and the check

varieties showed resistance to rust in both sites except Morelli which was susceptible with a mean score of 7. Seventy percent (70%) of the test lines showed complete resistance to rust with a score of 1.0 (Table 4.7).

Table 4. 7 Disease severity scores of advanced climbing snap bean lines at Mwea and Embu during short rains in 2013

Genotype	Rust			Anthracnose			Angular Leaf spot		
	Mwea	Embu	Mean	Mwea	Embu	Mean	Mwea	Embu	Mean
KSV01-2M	1.0	1.5	1.3	1.0	1.0	1.0	1.0	1.0	1.0
KSV04-1-2M	1.0	1.0	1.0	1.0	2.5	1.8	2.0	1.0	1.5
KSV04-2-2M	1.0	1.0	1.0	2.0	1.0	1.5	1.0	1.0	1.0
KSV08-2-2-1T	1.0	1.0	1.0	2.0	1.0	1.5	1.0	1.0	1.0
KSV13-1-2-3M	1.0	1.0	1.0	3.0	1.0	2.0	1.0	1.0	1.0
KSV14-1-4M	1.0	1.0	1.0	1.0	1.0	1.0	2.0	1.0	1.5
KSV17-145-1-1M	2.0	1.0	1.5	2.0	1.0	1.5	2.0	1.0	1.5
KSV17-2-1-1T	3.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV19-1-2M	2.0	1.5	1.8	1.0	1.0	1.0	1.0	1.0	1.0
KSV25-1-1T	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV27-145-1-1M	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV27-69-4-1-2T	1.0	1.0	1.0	3.0	3.0	3.0	2.0	1.0	1.5
KSV29-2M	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV41-1-2-3M	3.0	1.0	2.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV41-1-2T	1.0	1.0	1.0	1.0	2.0	1.5	1.0	1.0	1.0
KSV41-2-1-1M	2.0	1.0	1.5	1.0	1.0	1.0	1.0	1.0	1.0
KSV42-2M	1.0	1.0	1.0	2.0	1.0	1.5	3.0	1.0	2.0
KSV43-1T	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0	1.0
KSV44-1M	1.0	1.0	1.0	1.0	1.0	1.0	0.9	1.0	1.0
KSV46-2M	1.0	1.0	1.0	2.0	1.0	1.5	1.0	1.0	1.0
Checks									
Morelli	6.0	8.0	7.0	2.0	5.0	3.5	2.0	4.0	3.0
Morgan	2.5	8.0	5.3	3.0	3.5	3.3	3.0	5.5	4.3
Samantha	4.5	5.5	5.0	2.5	2.5	2.5	5.0	5.0	5.0
Star 2053	4.5	5.5	5.0	2.5	5.5	4.0	4.5	2.5	3.5
Teresa	2.5	7.0	4.8	4.5	5.0	4.8	2.5	4.5	3.5
Grand Mean	1.9	2.2	2.0	1.7	1.8	1.8	1.7	1.7	1.7
LSD0.05	2.2	1.7	1.9	2.3	3.3	2.7	2.3	2.4	2.3
CV (%)	12.4	15.7	22.8	18.3	14.9	20.2	16.8	11.1	19.2

LSD= least significant difference, CV= coefficient of variation, Disease severity scale, 1 to 3= resistant, 4 to 6= intermediate resistance, 7 to 9= susceptible (van Schoonhoven and Pastor-Corrales, 1987)

4.3.3.2.2 Anthracnose

There was significant variation for reaction to anthracnose infection among genotypes at Embu and at Mwea trial sites (Table 4.5). Genotypes showed anthracnose infection in Embu compared to Mwea. This variation was genotypic with no location or G x E effects. All the test lines were rated resistant to anthracnose in both sites. However, the check varieties had intermediate resistance in Embu (Mean: 4.3) and resistance in Mwea (2.9) except Teresa (Table 4.7).

4.3.3.2.3 Angular leaf spot

Results revealed that reaction to angular leaf spot infection did not vary among genotypes at the two trial sites (Table 4.5). The test lines showed resistance (1-3) to angular leaf spot in Mwea and Embu while the checks showed intermediate resistance (3-4) in both sites (Table 4.7).

4.3.3.3 Pod traits

4.3.3.3.1 Pod Length

Pod lengths of extra fine pods were not significantly different at the two trial sites (Table 4.5). Genotypes formed fine and bobby pods that had no variations in lengths at both sites (Table 4.5). The significant differences in pod length among the study lines was attributed to genotypes. The test lines formed shorter pods (7.7cm) as compared to the check varieties (10.0cm) in both sites. Genotypes formed longer pods at Embu than Mwea in all market grades (Table 4.8).

Extra fine, fine and bobby pod lengths were not significantly ($P \leq 0.05$) different among genotypes at both sites (Table 4.5; Appendix 8). However, 15% of the test lines had pod that were >10cm in Embu and therefore met a key requirement of the extra-fine class. None of the lines' extra fine pods attained the HCDA required pod length at Mwea, suggesting a strong genotype x environment on pod length. KSV04-2-2M, KSV19-1-2M and KSV25-1-1T exceeded the extra fine check varieties' pod lengths in Embu.

In fine pods, eleven out of twenty genotypes at Embu and only KSV27-69-4-1-2T at Mwea had the recommended pod length. On average, only 20% of the test lines' fine pods met the required pod length in both sites. About 50% of the climbing bean lines at Embu and KSV14-1-4M and KSV27-69-4-1-2T at Mwea had the recommended pod length. The premium pods of two test lines, KSV25-1-1T and KSV04-2-2M, had market required pod length among the test lines (Table 4.8). All bush commercial check varieties had the recommended minimum length of 10cm in both sites with averages of 10.8cm extra fine and 11.4cm fine pods. However, bobby pods of the check

varieties were shorter (7.8cm). Morelli formed the longest premium pods among the check varieties in both sites.

Table 4. 8 Pod lengths (cm) of advanced climbing snap bean lines at Mwea and Embu in 2013

	Pod lengths of genotypes for each market grades								
	Extra Fine			Fine			Bobby		
Genotype	**Embu**	**Mwea**	**Mean**	**Embu**	**Mwea**	**Mean**	**Embu**	**Mwea**	**Mean**
KSV01-2M	8.8	7.0	7.9	9.5	7.9	8.7	9.3	5.1	7.2
KSV04-1-2M	0.0	7.2	3.6	10.6	8.4	9.5	5.7	8.2	6.9
KSV04-2-2M	11	8.4	9.7	12.9	9.8	11.4	10.9	3.9	7.4
KSV08-2-2-1T	8.2	3.9	6.1	11	4.7	7.9	11.3	3.8	7.6
KSV13-1-2-3M	8.5	4.2	6.4	5.6	5.3	5.5	5.9	4.4	5.2
KSV14-1-4M	9.3	6.6	8.0	11.7	9.3	10.5	12.7	10.4	11.6
KSV17-145-1-1M	7.8	4.8	6.3	5.2	6.0	5.6	7.2	5.8	6.5
KSV17-2-1-1T	3.6	6.0	4.8	8.6	9.5	9.1	4.5	8.5	6.5
KSV19-1-2M	13.6	4.3	9.0	12.7	6.3	9.5	11.9	6.7	9.3
KSV25-1-1T	14.6	8.4	11.5	12.5	8.6	10.6	15.6	6.4	11.0
KSV27-145-1-1M	6.0	4.6	5.3	12.8	5.8	9.3	12.0	1.2	6.6
KSV27-69-4-1-2T	3.9	8.1	6.0	6.2	10	8.1	5.8	10.7	8.3
KSV29-2M	5.2	6.6	5.9	5.6	7.3	6.5	11.5	6.8	9.3
KSV41-1-2-3M	3.7	4.8	4.3	8.3	5.6	6.9	10.1	5.5	7.8
KSV41-1-2T	0.0	8.8	4.4	5.7	9.7	7.7	4.3	6.3	5.3
KSV41-2-1-1M	0.0	5.9	2.9	10.3	8.7	9.5	7.3	2.1	4.7
KSV42-2M	3.3	7.0	5.15	10	8.2	9.1	5.8	6.2	6.0
KSV43-1T	3.8	5.9	4.9	5.2	9.1	7.1	4.7	9.4	7.1
KSV44-1M	4.6	8.1	6.4	11.9	9.1	10.5	12.4	8.1	10.3
KSV46-2M	4.4	6.6	5.5	11.8	7.9	9.85	10.8	8.4	9.6
Checks									
Morelli	12.5	11.6	12.1	14.8	12.1	13.5	10.2	8.9	9.6
Morgan	10.7	9.8	10.3	11.5	11.3	11.4	9.9	10.2	10.1
Samantha	11.4	9.4	10.4	10.9	11.5	11.2	5.1	9.3	7.2
Star 2053	11.0	10.1	10.6	8.5	11.2	10.0	3.7	10.6	7.2
Teresa	10.3	11.0	10.7	11.3	10.7	11.0	0.0	9.9	5.0
Grand Mean	7.8	8.7	7.2	6.8	8.9	9.1	5.8	6.2	6.5
$LSD_{0.05G}$	4.6	4.9	5.0	5.3	7.5	5.9	9.7	6.6	6.6
$LSD_{0.05L}$	0.8	1.1	1.4	2.4	1.2	1.7	1.7	1.6	1.9
$LSD_{0.05GXL}$	6.4	8.1	7.1	9.3	6.4	8.3	9.1	8.7	9.4
CV (%)	24.3	32.6	38.9	39.6	40.1	45.6	22.8	19.4	24.4

LSD= least significant difference, CV= coefficient of variation

4.3.3.3.2 Pod yield

Total pod yield varied significantly among genotypes and in in extra fine grade (Table 4.5). The genotypic variations revealed that there were locations and interaction (genotype x location) influences on extra fine market classes as well as the total pod yield (Appendix 8). The fine and the bobby pod yields showed no significant genotypic variations. Check varieties had a higher proportion (74.1%) of extra fine pods in both sites compared to the test lines (5.5%). However, KSV01-2M equally produced relatively higher yield (18.6%) of extra fine pods compared to the rest of the test lines in Mwea. On average, KSV01-2M was the highest of extra fine pods in both sites (10.6%). About half of the test lines produced more than 50% fine pods in both sites with KSV27-145-1-1M being the highest producer (64.9%). Pod yield ranged from 8,164 to 15,191 kg ha^{-1} at Embu and from 5,459 to 13,398 kg ha^{-1} at Mwea. Mean pod yield of the climbing snap bean lines was higher at Embu (10, 515.5 kg ha^{-1}) than Mwea (9,147 kg ha^{-1}). The pod yield of the check varieties averaged at 1, 858.6 kg ha^{-1} in both sites. This indicates that the climbing lines were five times high yielding compared to the check varieties.

Sixty five percent of the test lines had a total pod yield above 10,000 kg ha^{-1} at Embu as compared to 30% of the lines in Mwea. KSV01-2M, KSV04-2-2M, KSV13-1-2-3M, KSV19-1-2M, KSV29-2M, KSV41-2-1-2T, KSV42-2M and KSV44-1M were the highest yielding genotypes in both sites. KSV13-1-2-3M was the highest yielding line (15, 191.0 kg ha^{-1}) in Embu and KSV42-2M (13, 398.0 kg ha^{-1}) at Mwea. KSV25-1-1T had the lowest yield (8, 164.0 kg ha^{-1}) at Embu, and KSV17-2-1-1T with 7, 231.0 kg ha^{-1} at Mwea (Table 4.9; Figure 4.1).

Grade distribution

Eighty five percent (85%) of the test lines produced an average of 59.7% premium pods. KSV42-2M had the highest proportion of premium pods (66%). KSV17-145-1-1M produced the lowest proportion of premium grades (fine and extra fine) (Table 4.9). Although KSV13-1-2-3M had the highest total pod yield in both sites, about 56.3% of its pods were bobby. However, KSV13-1-2-3M had 43.7% premium pods which was higher than the total amount of premium pods of 60% of the test lines. Additionally the premium pods of KSV13-1-2-3M (5, 665.3 kg ha^{-1}) were three times the average amount of premium pods of all the check varieties. KSV01-2M, KSV19-1-2M, KSV27-145-1-1M, KSV29-2M and KSV42-2M were found to be the best due to high yield of premium pods (>6500 kg ha^{-1}).

Table 4. 9 Total Pod yield (kg ha^{-1}) and yield as market classes of snap bean lines at Mwea and Embu in 2013 short rains

	Total pod yield and Grade (%) distribution and pod yield											
	Extra Fine			Fine			Bobby			Total Yield		
Genotype	**Embu**	**Mwea**	**Mean**	**Embu**	**Mwea**	**Mean**	**Embu**	**Mwea**	**Mean**	**Embu**	**Mwea**	**Mean**
KSV01-2M	**2.6**	**18.6**	**10.6**	**43.7**	**64.5**	**54.1**	**53.7**	**16.8**	**35.3**	**10070.0**	**11893.0**	**10982.0**
KSV04-1-2M	1.6	7.0	4.3	23.0	54.1	38.6	75.4	38.9	57.1	11822.0	8151.0	9987.0
KSV04-2-2M	1.7	6.0	3.8	32.8	65.5	49.2	65.5	28.5	47.0	11085.0	9201.0	10143.0
KSV08-2-2-1T	2.0	8.5	5.2	27.0	55.9	41.4	71.0	35.7	53.3	9266.0	6708.0	7987.0
KSV13-1-2-3M	1.8	7.4	4.6	23.0	55.2	39.1	75.3	37.4	56.3	15191.0	10737.0	12964.0
KSV14-1-4M	1.4	5.7	3.5	26.7	59.3	43.0	71.9	35.1	53.5	11202.0	8224.0	9713.0
KSV17-145-1-1M	0.8	4.4	2.6	15.9	43.1	29.5	83.2	52.5	67.9	9608.0	5459.0	7534.0
KSV17-2-1-1T	2.8	10.2	6.5	36.6	62.3	49.5	60.6	27.4	44.0	8833.0	7231.0	8032.0
KSV19-1-2M	3.0	9.2	6.1	41.2	70.2	55.7	55.7	20.6	38.1	11500.0	11371.0	11435.0
KSV25-1-1T	3.0	9.3	6.1	37.1	67.3	52.2	59.9	23.4	41.7	8164.0	7828.0	7996.0
KSV27-145-1-1M	3.6	8.9	6.3	52.7	77.1	64.9	43.7	14.0	28.8	8494.0	10248.0	9371.0
KSV27-69-4-1-2T	2.0	7.2	4.6	35.7	67.1	51.4	62.3	25.7	44.0	10392.0	9189.0	9791.0
KSV29-2M	3.0	12.6	7.8	38.8	66.1	52.5	58.2	21.3	39.7	10810.0	10801.0	10806.0
KSV41-1-2-3M	2.2	6.6	4.4	39.6	71.7	55.6	58.2	21.7	40.0	10062.0	9921.0	9991.0
KSV41-1-2T	2.5	8.5	5.5	35.2	65.6	50.4	62.3	25.9	44.1	9646.0	8505.0	9076.0
KSV41-2-1-1M	1.4	6.5	4.0	19.2	49.3	34.3	79.4	44.1	61.7	12320.0	7846.0	10083.0
KSV42-2M	3.6	10.9	7.3	45.1	72.3	58.7	51.2	16.8	34.0	12011.0	13398.0	12705.0
KSV43-1T	2.0	7.5	4.8	32.0	63.2	47.6	66.0	29.3	47.7	10162.0	8313.0	9237.0
KSV44-1M	3.2	10.0	6.6	37.2	66.9	52.1	59.6	23.0	41.3	10487.0	9914.0	10201.0
KSV46-2M	2.7	9.2	5.9	34.8	64.5	49.6	62.5	26.4	44.5	9184.0	8010.0	8597.0
Checks												
Morelli	88.7	73.3	81.0	8.8	20.7	14.7	2.6	6.0	4.3	2613.9	1107.8	1860.9
Morgan	82.8	75.0	78.9	16.8	24.2	20.5	0.4	0.8	0.6	2739.5	1351.4	2045.5
Samantha	76.9	64.3	70.6	22.0	34.0	28.0	1.1	1.6	1.4	1987.4	1386.8	1637.1
Star 2053	67.3	75.7	71.5	32.2	23.4	27.8	0.5	0.9	0.7	2340.9	1404.3	1872.6
Teresa	71.	65.6	68.7	26.9	32.7	29.8	1.4	1.7	1.5	2060.3	1693.4	1876.9
Grand Mean			58.9			43.6			37.1	8882.1	7595.7	8143
$LSD_{0.05}$Gen			115.6			245.2			186.4	3015.1	2247.3	1945.2
$LSD_{0.05}$Loc			89.1			52.9			79.6	486.2	348.9	550.2
$LSD_{0.05}$ (GX L)			45.6			49.8			85.4	3569.1	2463.5	2750.9
CV (%)			16.9			12.6			21.9	32.8	34.6	42.1

$LSD_{0.05}$= least significant difference at 5% level of significance, $LSD_{0.05}$Gen= LSD Genotype, $LSD_{0.05}$Loc= LSD location, $LSD_{0.05}$ (GX L)= LSD Genotype x Location, CV= coefficient of variation

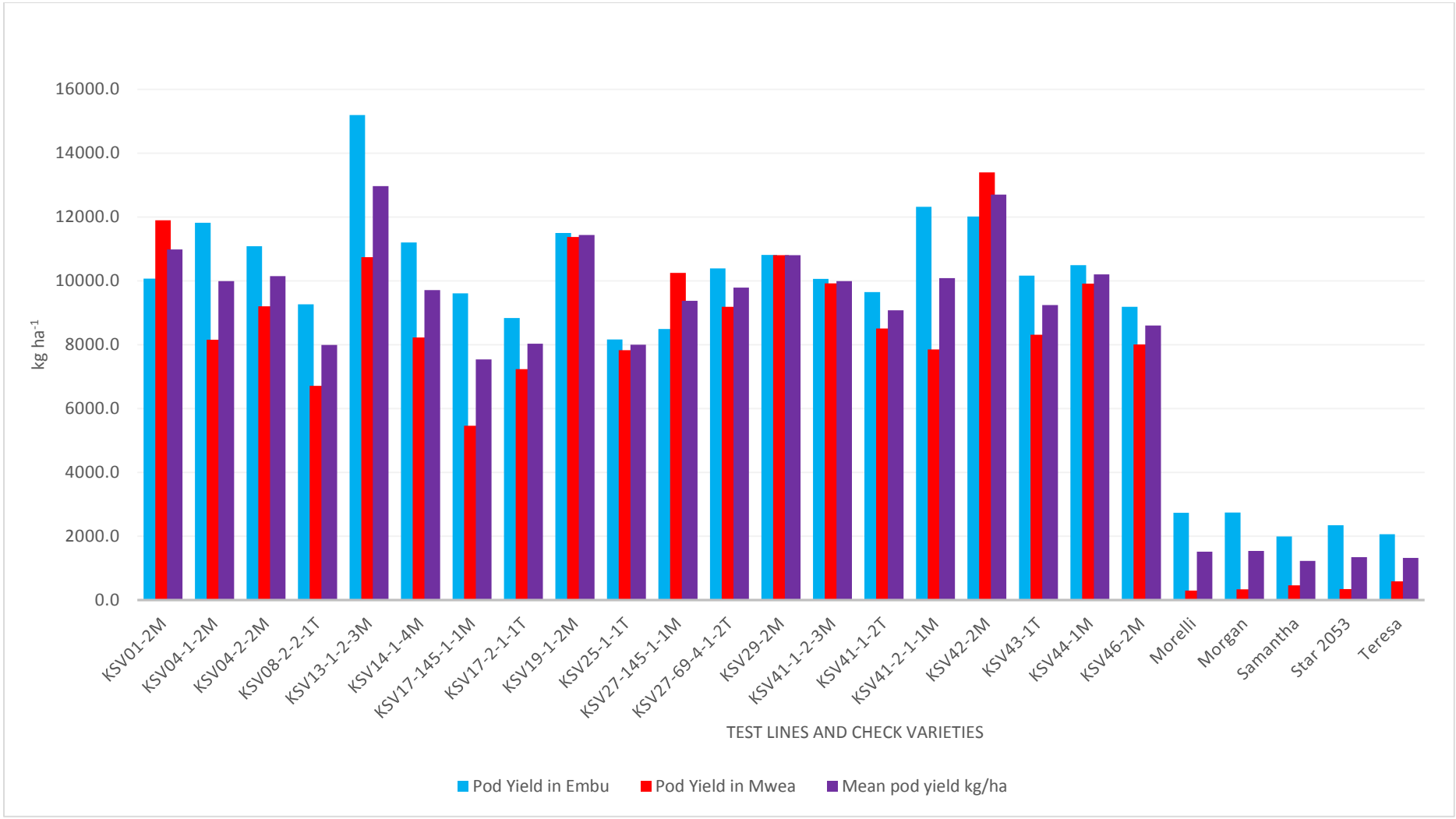


Figure 4. 3 Pod yield (kg ha^{-1}) of climbing snap bean lines at Embu and Mwea

4.3.4 Promising advanced climbing snap bean lines

Out of the 20 advanced climbing snap bean lines evaluated in AYT, the best 15 lines were identified based on disease resistance to rust, anthracnose and angular leaf spot; pod quality (pod length, pod shape, pod curvature and pod colour), pod yield and grade distribution (% premium pods) (Table 4.10). The selection was done based on the mean performance of the lines at the two sites for all studied traits. The promising lines had good to excellent plant vigour (1-3) and flowered between 41-48 days. All the lines exhibited multiple disease resistance to rust, anthracnose and angular leaf spot with scores of 1-3. Although only two out of fifteen of the promising lines attained the HCDA (2009) recommended pod length, 93.3% of the lines had >50% of premium pods out of the total pod yield in both sites. However, KSV13-1-2-3M had 43.7% of the premium pods despite being the highest yielder. On the other hand KSV27-145-1-1M had the highest percentage of premium pods but the pods were flat and light green (Table 4.10)

The total pod yield of the promising lines ranged from 7996 to 12964 kg ha^{-1} with an average of 10,088 kg ha^{-1}. The lines therefore out yielded the checks by 81.6% in both sites. Additionally, the test lines had good pod quality based on pod shape, pod curvature and pod colour with straight (86.6%), round (80%) and green (86.6%) pods (Table 4.10).

Table 4. 10 Vigour, duration to flowering, days to first pciking, disease resistance, pod yield and grade distribution of elite most climbing snap bean lines grown in three environments.

The best selected climbing beans														
									Pod yield (kg ha^{-1})			Pod quality		
Genotypes	**Vigour**	**50%DF**	**Days to first picking**	**Rust**	**Angular Leaf Spot**	**Anthracnose**	**Pod length (cm)**	**Premium pods (%)**	**Mwea**	**Embu**	**Mean**	**Pod curvature**	**Pod shape**	**Pod colour**
KSV01-2M	3.0	46.0	55.0	1.3	1.0	1.0	8.3	64.7	10070.0	11893.0	10982.0	Straight	Round	Green
KSV04-2-2M	1.5	44.0	53.3	1.0	1.0	1.5	10.5	53.0	11085.0	9201.0	10143.0	Straight	Round	Green
KSV13-1-2-3M	3.5	44.8	54.0	1.0	1.0	2.0	5.9	43.7	15191	10737	12964	Straight	Round	Green
KSV17-2-1-1T	3.5	45.0	54.5	2.0	1.0	1.0	6.9	56.0	8833.0	7231.0	8032.0	Straight	Round	Green
KSV19-1-2M	3.0	41.8	53.8	1.8	1.0	1.0	9.2	61.8	11500.0	11371.0	11435.0	Straight	Round	Green
KSV25-1-1T	2.5	46.3	54.5	1.0	1.0	1.0	11.0	58.3	8164.0	7828.0	7996.0	Straight	Flat	Green
KSV27-145-1-1M	4.0	46.3	55.5	1.0	1.0	1.0	7.3	71.2	8494.0	10248.0	9371.0	Straight	Flat	Light Green
KSV27-69-4-1-2T	1.0	43.3	54.5	1.0	1.5	3.0	7.1	56.0	10392.0	9189.0	9791.0	Straight	Round	Green
KSV29-2M	4.0	47.8	56.8	1.0	1.0	1.0	6.2	60.3	10810.0	10801.0	10806.0	Slightly curved	Flat	Light Green
KSV41-1-2-3M	4.5	46.0	55.5	2.0	1.0	1.0	5.6	60.0	10062.0	9921.0	9991.0	Straight	Round	Green
KSV41-1-2T	2.0	45.5	54.5	1.0	1.0	1.5	6.1	55.9	9646.0	8505.0	9076.0	Slightly curved	Round	Light Green
KSV42-2M	2.0	42.3	54.3	1.0	2.0	1.5	7.1	66.0	12011.0	13398.0	12705.0	Straight	Round	Green
KSV43-1T	3.0	44.8	54.3	1.0	1.0	1.0	6.0	52.4	10162.0	8313.0	9237.0	Straight	Round	Green
KSV44-1M	2.5	44.5	54.0	1.0	1.0	1.0	8.4	58.7	10487.0	9914.0	10201.0	Straight	Round	Green
KSV46-2M	2.5	43.5	55.5	1.0	1.0	1.5	7.7	55.5	9184.0	8010.0	8597.0	Straight	Round	Green
Checks														
Morelli	4.3	34.8	41.3	7.0	3.0	3.5	12.8	95.7	2613.9	1107.8	1860.9	Straight	Round	Purple
Morgan	3.8	35.8	41.5	5.3	4.3	3.3	10.8	99.4	2739.5	1351.4	2045.5	Straight	Round	Green
Samantha	4.5	36.0	42.5	5.0	5.0	2.5	10.8	98.6	1987.4	1286.8	1637.1	Straight	Flat	Light Green
Star 2053	4.5	36.0	41.5	5.0	3.5	4.0	10.2	99.3	2340.9	1404.3	1872.6	Straight	Round	Green
Teresa	3.5	38.0	44.3	4.8	3.5	4.8	10.8	98.5	2060.3	1693.4	1876.9	Straight	Round	Light Green

4.4 DISCUSSION

4.4.1 Preliminary Yield Trials

Out of the 53 advanced lines evaluated, 16 failed to germinate due to excessive rains while 17 had poor performance. The plant vigour of the 20 selected lines ranged from good to excellent despite the water logging stress that resulted from heavy rains. The selected lines showed high levels of resistance to rust, anthracnose and angular leaf spot which they inherited from their parents. The parental lines included sources of resistance to rust (Beldakmi, Belmineb, and Beltgrade lines), angular leaf spot (Mex 54 and L227-10), root rots (L227-10) and anthracnose (G2333), and susceptible commercial varieties (Amy, Paulista, Morelli, Morgan, Julia, Foskelly, Teresa, Vernandon, Kutuless and Alexandria) (Wahome *et al*., 2011). The lines had 304% higher pod yield compared to the check varieties. The higher pod yield could be attributed to the outstanding growth vigour and multiple disease resistance (Wahome *et al*., 2011; Wasonga, 2010). This validates the reports given by Wahome *et al*. (2011; 2013), where they found that climbing lines exhibited multiple disease resistance compared to bush varieties. Besides, the selected test lines had the best pod qualities in terms of pod colour, curvature and shape (Myers and Baggett, 1999). This however contradicts the results obtained by Wahome *et al*. (2011) where they found that climbing snap bean lines had poor pod qualities ranging from colour, pod curvature to pod shape. Besides, the climbing lines with multiple disease resistance were low yielders according to Wahome *et al*. (2011)

4.4.2 Advanced yield trials

4.4.2.1 Agronomic traits

The absence of significant variations in growth vigour among genotypes in both sites implies that the climatic conditions in both sites are suitable for the cultivation of snap beans. Check varieties including test lines in Mwea showed intermediate plant vigour which could be attributed to harsh temperatures and limited soil moisture in Mwea (Shaban, 2013).

Advanced climbing snap bean showed variations in number of days to 50% flowering in both sites. Location effects played a significant role in the differences in the number of days to 50% flowering hence advanced climbing snap bean varieties flowered earlier under warmer temperatures as compared to cool temperatures. Labuda and Brodaczewska (2007) suggest that the flowering in snap beans is mainly influenced by environmental conditions besides planting dates and genetic features of the genotypes under study. They found out that prolonged high temperatures during

flowering impacts negatively on flowering and pod setting. Poor pod setting ultimately leads to poor pod yield. Water deficits in Mwea could have also contributed to early flowering compared to Embu where there was a reliable irrigation system. Poor pod yield of the test lines at Mwea could have been as a result of flower falling and disease pressure. Al-Suhaibani (2009) and Ntatsi *et al*. (2018) found that water deficits during the onset of flowering led to decrease in number of days to 50% flowering in faba beans which also negatively affected pod setting leading to poor pod yield.

Earlier or late flowering of genotypes is directly proportional to the number of days to first picking. In the present study, days to first picking were influenced by genotypic effects in Mwea as compared to Embu. The delay in the number of days to first picking in Embu were as a result of cool temperatures that led to delayed flowering. These results confirm the findings of Al-Suhaibani (2009) which indicated that reduced number of days to flowering affects the maturity of faba beans. Home Vegetable Gardening on the other hand confirm these results when they found that pole lima beans matured 10-15 days after bush lima beans.

The commercial varieties otherwise used as checks in this study had intermediate vigour in both sites despite the favorable climatic conditions. Favorable climatic conditions contribute to excellent vigour in crops (Finch-Savage and Bassel, 2015). This indicates that commercial varieties' establishment is limited by other factors other than environmental conditions. The growth vigour of the commercial varieties may have been influenced by genetic factors such as those that confer resistance to diseases. When seeds are not genetically resistant to diseases, crop establishment is likely to be poor. This is substantiated by Teresa which had a good plant vigour under favorable conditions in Embu compared to other check varieties. This good plant vigour could be attributed to the *ur-5* genes in Teresa which confer resistance to rust (Pastor-Corrales, 2010). Besides, good to excellent growth vigour was noted in climbing snap bean lines which could be as a result of multiple disease resistance to anthracnose, rust and angular leaf spot.

Although commercial varieties are early flowering and have good pod qualities, their yield is limiting. Low yields experienced by farmers in the cultivation of commercial check varieties has been attributed to their susceptibility to diseases. Commercial check varieties are susceptible to diseases such as rust, angular leaf spot, bacterial wilt, BCMV, anthracnose and root rots among other diseases. These diseases have been found have economic losses that contribute to up to 100% yield loss in beans (Muthomi *et al*., 2017). Besides, high disease pressure leads to overdependence

of fungicides which reduces snap been pod quality. Besides, the export market has stringent policies on maximum residue levels. Use of resistant varieties could be very economical especially to smallholder farmers. Genetic resistance to multiple diseases is of great advantage to snap bean production (Wahome *et al*., 2011). Therefore the adoption of the new climbing lines with market desirable pod traits guarantees farmer of reduced costs of production and increased yield since the lines are high yielding and are resistant to major snap bean diseases.

4.4.2.2 Genotypic reaction to diseases

There was high rust pressure at both experimental sites indicated by the susceptibility of Morelli to rust (score of 7). The significant variations among genotypes in reaction to rust in Embu was influenced by the environment. Rust prevalence in Embu could be attributed to sprinkler irrigation that was used to supplement inadequate rains during the experimental period. Although there were rust infections in Embu, they were not very virulent confirming the results obtained by Arunga *et al*., (2012) who reported low rust incidences in Mwea and Embu. Test lines showed resistance to rust, anthracnose and angular leaf spot confirming the results obtained by Wahome *et al*., (2011) where they found climbing snap beans to show multiple disease resistance. The check varieties however showed intermediate resistance or susceptibility to rust, anthracnose and angular leaf spot in Mwea and Embu. The drier conditions in Mwea did not favour disease development as compared to Embu where sprinkler irrigation was used coupled with cool weather conditions which promote pathogen virulence (Wahome *et al*., 2011).

Although moisture improves plant growth by enhancing plant water use efficiency, high humidity is said to promote disease development and spread of foliar fungal infections in beans which ultimately affects crop yield (Monda *et al*., 2003). Rust, anthracnose and angular leaf spot are known to cause up to 100% yield loss in snap beans depending on their severity (Kimani, 2002). This explains the low snap bean yield in 85% of the genotypes in Embu compared to Mwea.

Besides environmental conditions, the genetic features of the genotypes play a critical role in determining the severity of disease effects. The low disease reaction severity scores observed among the test lines demonstrates that there could be a considerable amount of disease resistance genes (*ur* genes for rust resistance, *co* genes for anthracnose and genes resistant to ALS inherited from Mex 54) among the lines. Whereas *Ur-11* confers resistance to 98.9% of the rust races according to Pasto-Corrales (2002); and Araya *et al*. (2004), *Co* genes in G2333 confers resistance

to anthracnose (Pastor-Corrales *et al*., 1994). Check varieties like Teresa normally possesses *ur-5* genes which confer resistance to rust but still showed intermediate resistance in both sites (Arunga *et al*., 2012; Pastor-Corrales *et al.*, 2010). This could be attributed to the emergence of new rust races or broken rust resistance in Teresa leading to higher than expected severity scores (Arunga *et al*., 2012).

Diseases resistance established in the climbing lines is attributed to their parental lines from which they were developed. Resistance to rust can be traced back to *ur* genes found in Beldakmi (*Ur-3, U-4, ur-6* and *ur-11*), Belmineb (*ur-4* and *ur-11*) and Beltgrade (*ur-4* and *ur-11*). Further resistance was inherited from the climbing line G2333 which has *Co* genes (*Co-4*, *Co-4*, *Co-5* and *Co-6)* known for resistance to anthracnose (Checa *et al*., 2006). Moreover, Mex 54 used in the development of these populations offered resistance to angular leaf spot.

4.4.2.3 Pod quality

The results indicated that there were no significant variations between genotypic lengths as well as location effects. However, most test line produced premium pods which meet HCDA (2009) specifications. Only KSV25-1-1T extra fine pods attained the recommended pod length while the 95% of the test lines had extra fine pod lengths of <10cm. On the other hand, 30% and 20% of the fine and bobby pods of the test lines had the recommended pod length in both sites. This could be as a result of the planting pattern and weed interference as suggested by Esmaeilzade and Aminpanah (2015) where they found that common bean spatial square planting pattern and absence of weed enhanced pod length in common beans. Akter *et al*. (2013) also reported that weed interference reduced pod length in mungbean. According to Myers and Baggett (1999), there is always a positive relationship between pod length, pod shape, quality and maturity of snap beans.

Hagerty *et al*. (2016) in USA, Beshir *et al*. (2015) in Ethiopia and Kamanu *et al*. (2012) in Kenya found that decreased availability of nutrients such as nitrogen and plant senescence negatively affect snap bean pod length and pod width hence pod quality. However, the test lines in Embu and Mwea were supplied with sufficient amounts of nitrogen by application of DAP and CAN fertilizer. This therefore implies that the observed short pod lengths among the advanced climbing snap bean lines were genetically controlled leading to lower than recommended pod lengths. Other pod traits include pod colour, shape, pod curvature and snapping ability.

The test lines had light green to green pod colour matching the market preferred pod colour specifications as indicated by Myers and Baggett (1999). According to Snodgrass *et al*. (2011), high pod yield and deep green colour are the most desired characteristics of snap beans in Florida. Kahn and McGlynn, (2009) agrees with these results stating that deep green pod colour in snap beans is more appealing to consumers. Test lines' pods were either round or flat in both sites except for KSV25-1-1T which has flat pods. The test lines' pods also ranged from straight to slightly curved though 90% of the test lines had straight pods. Hagerty *et al*., (2016) noted that there is a positive correlation between pod length and pod width (r= 0.8214), while Myers and Baggett (1999) state that pod quality and pod maturity is a function of pod length, pod width and snapping ability in marketable pod grades.

4.4.2.4 Pod Yield

Results of this study indicated that there were significant genotypic and location effects for pod yield among the test lines and in the various market classes. There was a higher proportion of premium pods (extra-fine and fine) in Embu compared to Mwea despite the fact that total pod yields in Mwea were higher than pod yield in Embu. This could be as a result of varied climatic conditions between the two sites such as higher altitudes in Embu.

Pod yields in Mwea ranged from 5,459.0 to13, 398.0 kg ha^{-1} as compared to 8,164.0 to 15,191 kg ha^{-1} at Embu. Low yields in Mwea are as a result of moisture stress that resulted from drier climatic conditions and that may have led to poor flower and pod setting (Pattung *et al*., 2016; Vadez *et al*., 2011). Labuda and Brodaczewska (2007) postulated that low soil moisture and high temperatures as experienced in Mwea during the experimental period leads to 73.9% pod setting as opposed to high soil moisture and low temperatures. On the other hand, high yields realized in Embu is an indication that humid conditions favored pod and flower setting resulting in optimal productivity of climbing snap beans.

On average, 65% of the climbing lines had yield >10,000 kg ha^{-1} with 35% yield advantage in Embu. KSV01-2M, KSV13-1-2-3M, KSV19-1-2M, KSV27-145-1-1M, KSV29-2M and KSV42-2M were found to be the best of the climbing lines as shown in Figure 4.2 since they produced highest amounts of premium pods. These test lines had good-excellent plant vigour and exhibited multiple disease resistance to rust, anthracnose and angular leaf spot. They flowered between 40-45 days and had pod yield of 9,371-12,705 kg ha^{-1}.

All the test lines out yielded the checks in the production of premium pods. Although the yield percentages among the climbing lines were lower than those of the check varieties, the actual amounts of premium pods among the test lines exceeded those of the check varieties by 89.2%. The lowest yielder of premium pods among the test lines out yielded the average yield of the check by 14.8%. This confirms the reports that were given by Checa *et al*. (2006) who found that climbing beans have more yield advantage compared to the bush varieties. The high yields among the test lines is attributed to the inheritance of disease resistance genes (Beldakmi, Belmineb and Beltgrade against rust; Mex54 and L227-10 against angular leaf spot; and G2333 against anthracnose) coupled with good pod traits inherited from the parents by the high yielding climbing test lines (Wahome *et al*., 2011). The results suggest that these test lines can be validated in national performance trials and availed to smallholder farmers for increased productivity.

4.5 CONCLUSION AND RECOMMENDATIONS

The new climbing snap bean lines had good to excellent plant vigour scores as compared to intermediate to very poor vigour of commercial bush checks as observed in both sites. The climbing lines took longer time to flower than the checks in both sites. The test lines exhibited multiple disease resistance to rust, anthracnose and angular leaf spot; better pod quality; and high total marketable pod yields. This indicates that these genotypes can be validated in national performance trials and made available to farmers for increased production. These genotypes can also be exploited in breeding programs for the development of high yielding disease resistant snap bean varieties with excellent pod qualities to match the vast growing market as well as economic empowerment of smallholder farm.

CHAPTER FIVE

VALIDATION OF NEW BUSH SNAP BEAN LINES AND SELECTION FOR POD QUALITY, POD YIELD AND DISEASE RESISTANCE OF IN KENYA

ABSTRACT

Bush snap beans cultivated by commercial and smallholder farmers are highly constrained by diseases such as rust, angular leaf spot, BCMV, root rots and anthracnose leading to over-dependence on costly fungicides. Productivity of bush snap beans is further constrained by low yielding cultivars in comparison to climbing snap beans which have a 3:1 yield advantage. The objective of this study was to validate resistance to rust, angular leaf spot and anthracnose among locally developed advanced bush snap bean lines, and to determine their pod yield and pod quality. Twenty five $F_{6.9}$ bush snap bean lines were evaluated at Mwea and Embu during the 2013 short rain seasons, and at Kabete during the 2014 long rain season. Data was collected on plant vigour, days to 50% flowering, days to first picking, reaction to rust, anthracnose and angular leaf spot, number of pods per plant, pod length and total pod yield per market class. Data was subjected to analysis of variance using Genstat Version 14.

Results indicated that there were genotypic variations for all traits studied. Plant vigour scores of the new lines varied from 1 to 4 compared to 3 to 7 for the check varieties in all sites. Among the test lines, duration to 50% flowering varied from 37 to 43 days while days to first picking varied from 46 to 52 days after planting in the three sites. Rust, anthracnose and angular leaf spot were most severe in Embu and Kabete where overhead irrigation was used. Number of pods per plant, pod length and pod yield varied with sites with Kabete having the highest yields. Mean pod yield over 13 harvests was 7,210.0 kg ha-^{1} at Embu, 8,886.0 kg ha-^{1} at Mwea, and 12,260.0 kg ha^{-1} at Kabete. The new lines had mean yield advantage of 29.8% over the commercial checks. The new lines produced an average of 80.6% premium grades compared to 77.2% for the commercial check varieties. However, this varied with genotypes and was significantly influenced by the trial site. The lines KSB12-143-3-1M, KSB22-3-1T, KSB39-3M and KSB46-2M were the most outstanding lines among the test lines. While KSB12-143-3-1M was the earliest flowering (37.8), revealed the strongest multiple disease resistance (1.2) and had the highest number of podsplant^{-1}, KSB22-3-1T was the most vigorous (1.3) and formed the longest pods (12.0cm). KSB39-3M on the other

hand had the highest yields (13, 359.7 kg ha^{-1}) and KSB46-2 had the highest percentage of premium pods per plant (93.2%). The outstanding lines had green, straight and round and pods suitable for the export market. The results of this study indicate that new advanced bush snap bean varieties with market preferred pod characteristics, high yield potential and resistance to major diseases can be developed from the selected lines. Exploitation of the good pod traits, high pod yield and multiple disease resistance of advanced bush beans can contribute to better returns to investment for smallholder farmers.

Key words: Snap bean, diseases resistance, pod quality, pod yield

5.1 INTRODUCTION

Snap bean is an important horticultural export crop in East and Central Africa contributing up to 60% of Kenya's vegetable exports, and 21% horticultural exports yearly (Kamanu, 2012; HCDA, 2010; Nderitu, 2007). About 1% of Kenya's population benefits from snap bean production as a source of income. Snap bean farming offers on-farm employment opportunities to up to 0.13% of Kenya's total population (Odhiambo, 2009). Approximately >90% of the snap bean produced annually is exported to regional and international markets (Kimani *et al*., 2006). Bush snap bean cultivars are dominantly produced in Kenya by both smallholder farmers and commercial companies for export to United Kingdom, France, Netherlands and Belgium. Besides, snap bean domestic market is on the rise implying that the Kenyan population also reaps the benefits of the snap bean nutritional value.

Production of snap bean by smallholder farmers in eastern Africa is constrained by diseases especially rust, angular leaf spot and anthracnose (Chemining'wa *et al*., 2012; Wahome *et al*., 2011; 2013). Rust is the most limiting disease to snap bean farmers in Kenya resulting in up to 100% yield loss (Arunga *et al*., 2010). The intensive nature of cultivation of this crop leads to high disease and pest pressure, and consequently excessive use of pesticides. This does not only increase production cost but is also environmentally unfriendly and reduces the quality of the produce. Smallholder production is further constrained by high cost of seed, reliance on susceptible varieties, stringent pesticide residue regulations and quality requirements (Otim *et al*., 2016).

Much has been done to develop improved bush snap bean varieties with good pod quality and multiple disease resistance but they have not been made freely available to smallholder farmers and informal seed producers in eastern Africa. In Kenya, snap bean improvement has been done at the University of Nairobi and Moi University. Crosses were performed between sources of disease resistance to rust, anthracnose and angular leaf spot. Selections were done for multiple disease resistance and growth habit at the University of Nairobi and for adaptability at Moi University, Eldoret. These materials have not been released and made available to smallholder farmers in Kenya. Therefore, the objective of this study was to conduct preliminary and advanced yield trials in order to evaluate and select promising advanced bush snap lines with high yields, multiple disease resistance and good marketable pod qualities.

5.2 MATERIALS AND METHODS

5.2.1 Plant Materials

The purpose of this study was to evaluate advanced snap lines for productivity, pod quality and disease resistance. Evaluation was done on existing Progeny-I bush Nursery lines that were segregating for growth habit and pod traits as well as resistance to anthracnose, rust and angular leaf spot. These materials (Progeny I) were obtained from the University of Nairobi Bean Research Program, Department of Plant Science and Crop Protection, Kabete Campus. The progeny I lines had been developed from BelDakMi, BelMiNeb and Beltigrade RR2 which conferred resistance to rust; Mex54 and L227-10 resistant to angular leaf spot; and G2333 which conferred resistance to anthracnose. Several crosses were carried out in 2006/2007 between the sources of disease resistance and commercial varieties including Teresa, Samantha, Amy, Julia, Morgan, Kutuless, Vernadon, and Maasai Red among others. The main objective of carrying out these crosses was to transfer resistance to rust, anthracnose, angular leaf spot and root rots from the source to susceptible commercial varieties (Wahome *et al*., 2013).

The segregating lines were then advanced to $F_{6.8}$ and F_7 generations at the University of Nairobi where 674 single plants were selected during the 2009/2010 short rain season at Mwea and Thika as Progeny 1 lines (Wahome *et al.*, 2011). Progeny I nursery were segregating for growth habit and disease resistance to rust, angular leaf spot, anthracnose and root rots. Wahome *et al*. (2013) evaluated these lines and selected them based on multiple disease resistance (to rust, angular leaf spot and anthracnose) as well as good pod quality. In 2011, the selected lines were evaluated in farmer participatory trials at Mwea and Thika (KALRO) (Kimani *et al.*, 2012). A total of 59 lines bush snap beans were selected and evaluated for multiple disease resistance, pod quality and pod yield. In 2012, these lines were evaluated in preliminary trials reported in the present study. From 59 lines that were evaluated, 25 advanced lines were selected and evaluated in advanced yield trials at Mwea, Embu and Kabete. Two commercial varieties, Teresa and Samantha, were used as checks.

5.2.2 Experimental sites

The experimental materials were evaluated at Wanguru, Mwea in Kirinyaga County and Runyenjes in Embu County during the 2013 short rain season, and at Kabete, Kiambu County during the 2014 long rain season. Mwea is located at 37º 20’ East and an elevation of 1159m above

sea level (Jaetzold *et al*., 2006). It receives bimodal rainfall with an annual mean of 1037 mm. Long rains fall between March and May with a mean of 71mm while short rains are received between October and December with a mean of 50mm. The mean annual maximum and minimum temperatures are 27.8 ^{0}C and 15.6 ^{0}C respectively (Jaetzold *et al*., 2006). Runyenjes in Embu County is located at 0°47'S, 37°40'E at an elevation of 1493m above sea level. It has a bimodal rainfall which occurs between March and May (long rains) and from October to December (short rains) with an annual mean of 1206mm. Annual temperatures range from 9.6°C to 28.8°C. Kabete on the other hand is located at an altitude of 1840m above sea level and is classified under agro-ecological zone III. Kabete experiences bimodal rainfalls in March to June and October to December with an annual rainfall of about 1000mm. The site has average annual temperatures of 19^{o}C (Jaetzold *et al*., 2006).

5.2.3 Experimental design and trial management

The preliminary yield trials were carried out in Mwea during the 2013 long rain season whereas advanced yield trials were conducted at Mwea, Embu (2013 short rain season) and Kabete (2014 long rain season. The trials were laid out in a randomized complete block design with two replications in each location. Each plot measured plot 2 m x 4 m and had four rows. Spacing was 50 cm between rows, and 10 cm within rows. Approximately 40 seeds were planted in four rows two of which were sampled for pod yield and pod quality in both PYT and AYT. Diammonium phosphate (18:46:0) fertilizer was applied at the rate of 225.0 kg ha^{-1}. The crops were top dressed with calcium ammonium nitrate (21% N) at the rate of 340.0 kg ha^{-1}. Furrow irrigation was used for supplementary irrigation at Mwea. Sprinklers were used at Embu and Kabete. Plots were irrigated twice a week at Mwea and Embu while supplementary irrigations were done in Kabete once a week for the three weeks when rains failed. Manual weeding was done twice in all sites. Insect pests such as aphids, white flies and leaf miners were controlled by alternate application of Cyclone® (10% Cypermethrin + 35% chlorpyriphos) and Confidor® (imidacloprid) at the rate of 1.5ml L^{-1}.

5.2.4 Data collection

During the preliminary yield trials, data was collected on plant vigour, 50% days to flowering, rust, anthracnose and angular leaf spot severity, pod yield, pod colour, pod curvature and pod shape. In addition to these traits, data was collected on days to first picking, number of pods per plant and pod length during the advanced yield trials at Mwea, Embu and Kabete.

Plant vigour was based on plant height and vegetative growth of ten plants per plot rated on a scale of 1 to 9, where 1=excellent vigour, 3=good vigour, 5= intermediate vigour, 7= poor vigour and 9=very poor vigour (van Schoonhoven and Pastor-Corrales, 1987). Duration to 50% flowering was recorded as the number of days after planting to the date when 50% of plants in a plot had one or more open flowers. To determine pod quality, data was collected on pod quality traits including pod length, pod grade distribution and pod yield at both sites. Pod quality was based on pod traits like pod length, width, pod colour and pod curvature. Pod length was measured using a calibrated ruler and recorded in centimeters. The pods were classified as extra fine, fine or bobby (Wahome *et al*., 2011). Pod colour was recorded as green, light green or purple as observed. Pod curvature was recorded as either straight or curved (S/SC) upon phenotypic observation. Disease resistance was evaluated following procedures of van Schoonhoven and Pastor-Corrales, (1987), which are summarized in Table 5.1. Reaction to rust, anthracnose and angular leaf spot were recorded at late pod maturity.

Table 5. 1 Disease severity scale used to evaluate the reaction of bean germplasm to fungal diseases

Rating	Category	Description	Comments
1-3	Resistant	No visible symptom or light symptoms (2% of the leaf)	Germplasm useful as a parent or commercial variety.
4-6	Intermediate	Visible and conspicuous symptoms (2-5% of the leaf) resulting only in limited economic damage.	Germplasm can be used as commercial variety or source of resistance to disease.
7-9	Susceptible	Severe to very severe symptoms (10-25% of the leaf) causing yield losses or plant death.	Germplasm in most cases not useful as parent or commercial variety

Source: van Schoonhoven and Pastor-Corrales, 1987.

Thirteen harvests were done during the five week period. Plots were harvested on Mondays, Wednesdays and Friday every week. Samples were taken from the two inner rows. The harvested pods were classified into three standard commercial categories based on pod widths defined as extra fine (6 mm), fine (6-8 mm) and bobby (>8 mm) according to HCDA (2009). Pod lengths were measured in centimeters using a calibrated ruler.

Pod yield was determined by weighing the pods in each market grade using an A and D top pan balance (Model EK-6100i-EC, Hong Kong, China). Total pod yield was calculated by summing

up the total yield of the three grades. Pod length was determined as the mean length of three randomly sampled pods per market class for four harvests .The average length for the four harvests was then calculated for each market class.

Table 5. 2 Marketable snap bean classes

Pods	Width (mm)	Other Characteristics	Comments
Extra Fine	6	-Tender - seedless - stingless	-Good marketable pod -Recommended for export market
Fine	6-9	-Small immature seeds	-Good marketable pod -Recommended for export market
Bobby	>8	-seeds -strings	-Unsuitable for export market

Source: HCDA (2009).

5.2.5 Data analysis

Separate analysis of variance was carried out for each site and combined analysis of variance was done for quantitative data collected at the three sites. Analysis of variance was performed using Genstat software 14th edition (VSN International, 2011). The differences among the means were compared using Fishers Protected Least Significance difference test at 5% probability level.

5.3 RESULTS

5.3.1 Climatic conditions at the trial sites in 2013 and 2014

The 2014 Kabete and 2013 Embu and Mwea weather data was obtained the Kenya Meteorological Department, 2015 (Appendix 1; Appendix 9). The preliminary yield trials were carried out from April to June, 2013 during which the temperatures ranged between 11.0-33.3^{o}C with a mean of 22.8^{o}C. The area received 456mm total rainfall during the experimental period.

During the advanced yield trials, weather data for Kabete, Embu and Mwea was obtained from Kenya Meteorological Department and is presented in Appendix 9. The temperatures during the experimental period ranged from 19.5-21.2°C at Kabete, 18.5-20.0°C at Embu and 21.0-24.5°C at Mwea with averages of 20.3°C, 19.4°C and 22.8°C respectively (Figure 5.1). Mean temperatures were therefore higher at Mwea compared to Kabete and Embu. The mean temperatures during flowering and podding period was 19.8°C at Kabete, 18.0°C at Embu and 21.8°C at Mwea. Temperatures were normal in Embu, but slightly higher than normal averages at Kabete and Kabete.

Amounts of rainfall received during the experimental period in 2014 varied with sites. Kabete received 402.9mm of rainfall compared with 528mm at Mwea and 485.2mm at Embu. Mwea and Kabete received below normal annual rainfall in 2013 and 2014. However, Embu received normal rainfall well distributed throughout the year. Embu recorded the highest amounts of rainfall among the trial sites. Mwea had higher temperatures compared to Embu and Kabete (Figure 5.1)

The observations indicate that of the three sites, Embu experienced both normal rainfall and temperatures in 2013. However, Kabete and Mwea received below normal rainfall in 2014 and 2013 respectively. However, both sites had higher than normal mean temperatures.

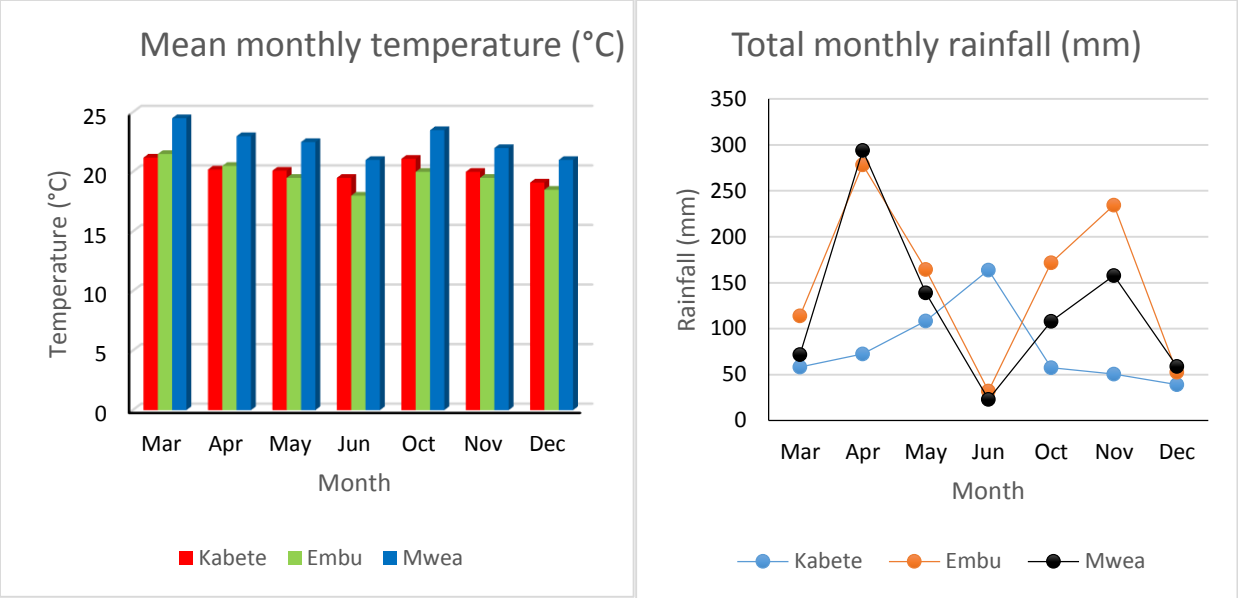


Figure 5. 1 Mean monthly temperatures (°C) and total Monthly rainfall (mm) at Kabete, Embu and Mwea trial sites during the experimental period

5.3.2 Preliminary Yield Trials

Fifty nine advanced bush snap bean lines were evaluated for plant vigour, days to 50% flowering, reaction to rust, anthracnose and angular leaf spot, total pod yield and pod quality (curvature, shape and colour) in Mwea in 2013 (Table 5.3). Eleven bush snap bean test lines failed to germinate hence data was recorded as zero (Appendix 10).

Table 5. 3 Mean squares for all traits in the PYT evaluations of advanced bush snap bean

Sources of variation	Df	Plant Vigour	Days to 50% flowering	Reaction to Disease			Pod yield State(kg ha^{-1})
				Rust	Anthracnose	ALS	
Replication	1	1.1613	0.65	0	5.452	0.29	1.84E+05
Genotype	60	17.207**	474.91**	8.458**	6.523**	13.352**	7.02E+07**
Residual	62	0.578	26.26	2.903	2.654	1.27	3.76E+06
CV (%)		22.4	16.4	58.0	75.9	39.9	25.3

Df= Degrees of freedom, ALS= Angular leaf spot, **= Significant at 1% probability

5.3.2.1 Plant vigour

Plant vigour varied significantly among the test lines and check varieties evaluated at Mwea during the long rain season ((Table 5.3); Appendix 11). The vigour of the test lines ranged from excellent

(score of 1) to very poor (score of 9) with a mean of 4.2. The vigour of the check varieties varied from 1 to 5 with a mean of 3. Among the new lines, eight (8) had a score of 1. These lines included KSB08-3-4M, KSB39-1-1M, KSB39-3M, KSB45-1M, KSB47-1-2M, KSB47-2-2M, KSB47-2 and KSB23-143-3-1M. However, 10 lines including KSB17-2-1-2M, KSB-18-2M, KSB21-2, KSB27-69-4-2-1T, KSB42-1-2M and KSB42-3M had very poor vigour. Among the check varieties, growth vigour ranged from excellent to good with Star 2053 being the most vigorous, and Teresa having intermediate vigour (Table 5.4).

5.3.2.2 Days to 50% flowering

Genotypes varied significantly in the number of days to 50% flowering (Table 5.3; Appendix 11). Days to 50% flowering among the test lines ranged from 19.3 to 44 days. Seventeen test lines flowered 3 days earlier than all the check varieties. The earliest maturing lines included KSB23-143-3-1M, KSB12-143-3-1M, KSB52-2M, KSB45-3M and KSB42-3M. All these lines flowered within 34 days. However, 18 genotypes were considered late flowering since they attained 50% flowering in more than 40 days. The test line KSB23-143-3-1M flowered earlier than all the test lines and the check varieties (Table 5.4). The check varieties flowered between 37 to 39 days. Star 2053 flowered earlier (37 days) among four checks while Samantha flowered later (39 days).

5.3.2.3 Reaction to diseases

5.3.2.3.1 Rust

There were significant genotypic differences for reaction to rust infection among the 59 lines (Table 5.3; Appendix 11). Reaction to rust pathogens ranged from 1 to 8 among the test lines and 2 to 5 among the check varieties. While 29 new lines showed resistance to rust (score of 1-3), three lines showed no reaction to rust despite the prevalence of rust pathogens in the field. These lines are KSB45-3M, KSB17-2-2T and KSB23-66-1-2-1T (Appendix 10). These lines were resistant to rust. Fifteen test lines showed intermediate resistance to rust while three were susceptible to rust (KSB14-1-2M, KSB06-1-2/1-1M and KSB21-2M). Among the check varieties, Teresa was resistant to rust (score of 2) while Star 2053 and Samantha had intermediate resistance to rust. The resistant lines reduced rust severity by 41.9%. The three susceptible lines were not selected for advanced trials.

5.3.2.3.2 Anthracnose

There were significant genotypic variations in reaction to anthracnose infection among the 59 evaluated lines (Table 5.3; Appendix 11). Reaction to anthracnose ranged from 1 to 8 among the

test lines and 1 to 5 among the check varieties (Appendix 10). Thirty four (34) new lines showed resistance to anthracnose (score of 1-3) 50% of which showed complete resistance (score of 1) (Appendix 10). Twelve test lines showed intermediate resistance to anthracnose. One line KSB18-2M was susceptible to anthracnose with a score of 8. Among the check varieties, Star 2053 and Samantha were resistant to anthracnose while Teresa (score of 5) showed intermediate resistance. Star 2053 showed complete resistance to anthracnose (Score of 1). The resistant lines reduced anthracnose severity by 40 %.

5.3.2.3.3 Angular leaf spot

There were significant genotypic reactions to angular leaf spot among the 59 evaluated lines (Tale 5.3; Appendix 11). Reaction to angular leaf spot pathogens ranged from 1 to 9 among the test lines and 1 to 5 among the check varieties (Appendix 10). Thirty new lines were resistant (score of 1-3), nine showed intermediate resistance and eight lines were susceptible to angular leaf spot. There was disease prevalence in the field as evidenced by the susceptible test lines. Susceptible lines include KSB45-1M, KSB46-2M, KSB39-3-1M, KSB30-3-1-3M, KSB42-2M, KSB42-1-2M, KSB42-3M and KSB21-1-1-3M (Appendix 10). Among the check varieties, Samantha (score of 1) and Teresa (score of 3) were resistant to angular leaf spot while Star 2053 had intermediate resistance to angular leaf spot. The resistant lines reduced angular leaf spot severity by 33.3%.

5.3.2.4 Pod yield

Pod yield varied significantly among the 59 genotypes evaluated in the PYT at Mwea (Appendix 11). The yield of the test lines varied from 2542.0 to 13,603.0 kg ha^{-1} with a mean of 8, 078.7 kg ha^{-1} while the yield of checks varied from 4149.0 to 6074.0 kg ha^{-1} with a mean of 5202.0 kg ha^{-1} (Appendix 10). Sixty six percent (66%) of the new lines yielded pods than the check varieties. The test lines out yielded the check varieties by 55.3%. Among the check varieties, Teresa was high yielding with a cumulative pod yield of 6074.0 kg ha^{-1}. Thirty three new lines had better pod yield that the best check variety. Twenty seven percent of the test lines emerged to be the best yielders with >10,000 kg ha^{-1}.

5.3.2.5 Pod Quality

Thirty four of the test lines had green pods, eleven had light green pods and two had purple pods (Appendix 10). Among the check varieties, Teresa and Star 2053 had green pods while Samantha had light green pods. Out of all the test lines, only eight had slightly curved pods while the rest

Table 5. 4 Characteristics of selected bush snap bean test lines in the preliminary yield trials at Mwea (Wang'uru), Kirinyaga County During the 2013 long rain season

Genotype	Plant Vigour	50%DF	Rust	Anthracnose	Angular leaf spot	Pod yield (kg ha^{-1})	Pod colour	Pod Curvature	Pod Shape
KSB 39-2-1-2M	2.0	35.0	2.0	1.0	2.0	10408.0	Green	Straight	Round
KSB04-1-1M	2.0	37.0	3.0	2.0	1.0	11763.0	Light Green	Straight	Round
KSB06-1-1-2M	3.0	38.5	5.0	1.0	1.0	13125.0	Green	Straight	Round
KSB08-3-4M	1.0	37.0	4.0	3.0	1.0	12613.0	Light Green	Straight	Round
KSB12-143-3-1M	3.0	33.0	3.0	3.0	2.0	11243.0	Green	Straight	Round
KSB13-1-1-1M	3.0	39.5	5.0	4.0	2.0	11088.0	Green	Straight	Round
KSB22-3-1T	2.0	39.0	3.0	1.0	2.0	9169.0	Green	Straight	Round
KSB23-143-3-1M	0.5	26.3	2.0	1.0	1.0	8664.0	Green	Straight	Round
KSB27-143-2-1M	3.0	38.0	3.0	1.0	1.0	8183.0	Green	Straight	Round
KSB30-3-1-2M	3.0	38.0	3.0	1.0	3.0	10235.0	Green	Straight	Round
KSB33-1-2M	3.0	42.0	2.0	1.0	3.0	7917.0	Green	Straight	Round
KSB33-3-1M	2.0	39.5	6.0	3.0	2.0	6294.0	Green	Straight	Round
KSB36-1-5M	2.0	41.0	5.0	6.0	4.0	7213.0	Green	Straight	Round
KSB39-1-1M	1.0	43.5	4.0	4.0	4.0	9245.0	Green	Straight	Round
KSB39-1-4M	2.0	37.5	2.0	1.0	1.0	8215.0	Green	Straight	Round
KSB39-2-4M	3.0	43.0	2.0	3.0	2.0	8764.0	Green	Straight	Round
KSB39-3M	1.0	39.0	3.0	1.0	3.0	11419.0	Green	Straight	Round
KSB39-4-4M	3.0	41.5	3.0	4.0	2.0	11428.0	Green	Slightly curved	Round
KSB42-2-2M	4.0	40.0	2.0	3.0	3.0	11964.0	Green	Straight	Round
KSB43-2M	5.0	38.5	2.0	4.0	2.0	10847.0	Green	Straight	Round
KSB46-2M	3.0	44.0	3.0	4.0	7.0	11465.0	Green	Straight	Round
KSB47-1-2M	1.0	39.0	3.0	5.0	2.0	13603.0	Green	Straight	Round
KSB47-2-2M	1.0	42.0	3.0	6.0	4.0	10464.0	Green	Straight	Round
KSB47-2M	1.0	36.5	3.0	2.0	1.0	11017.0	Green	Straight	Round
KSB52-2M	3.0	33.0	2.0	1.0	4.0	12621.0	Green	Straight	Round
Checks									
Samantha	3.0	39.0	5.0	3.0	1.0	5384.0	Light Green	Straight	Flat
Star 2053	1.0	37.5	6.0	1.0	5.0	4149.0	Green	Straight	Round
Teresa	5.0	38.0	2.0	5.0	3.0	6074.0	Green	Straight	Round
Grand Mean	3.4	31.3	2.9	2.2	2.8	6429.0			
$LSD_{0.05}$	1.3	8.9	3.0	2.8	2.0	2818.4			
CV (%)	22.4	16.4	58.0	75.9	39.9	25.3			

LSD= least significant difference, CV= coefficient of variation, DF= days to 50% flowering, Plant vigour scale (van Schoonhoven and Pastor-Corrales, 1987), Disease severity scale (van Schoonhoven and Pastor-Corrales, 1987)

had straight pods. On the other hand, all the check varieties had straight pods (Appendix 10). Seven test lines had flat pods while the remaining had round pods. Teresa and Star 2053 were round podded whereas Samantha had flat pods.

Reaction to rust, angular leaf spot and anthracnose were considered in the selection of test lines that were evaluated in advanced yield trial. Additionally, the selection of test lines for AYT evaluations were based on pod yield and pod quality. The 25 selected lines had higher pod yield than the best check. The yield ranged from 6294.0 to 13, 603.0 kg ha^{-1} with an average of 10, 358.7 kg ha^{-1} (Table 5.4). The selected lines had green, straight and round pods except KSB04-1-1M and KSB08-3-4M which had straight and round light green pods and KSB39-4-4M which had green, round and slightly curved pods. All the new lines had pod yield >10, 000 kg ha^{-1} (Table 5.4).

5.3.3 Advanced Yield Trials

Out of the 59 test lines evaluated in the preliminary yield trials, 25 were selected for advanced yield trials evaluations in Mwea and Embu during the 2013 short rain season and Kabete during the 2014 long rain season. The selections were mainly based on reaction to diseases (rust, angular leaf spot and anthracnose), pod yield and pod quality.

Table 5. 5 Mean squares for studied traits during the AYT evaluations at Kabete, Embu and Mwea

Source of variation	Df	Plant Vigour	50% DF	Days to first picking	Reaction to diseases			Pods plant^{-1}	Pod Length (cm)			Pod Yield (kg ha^{-1})
					Rust	Angular Leaf Spot	Anthracnose		Extra Fine	Fine	Bobby	
Replication	1	0.006	20.765	4.84	0.006	0.222	0.5	151128	13.64	69.27	106.89	6.61E+07
Genotype	26	4.072*	20.619**	34.763**	3.419*	4.849**	2.075	31173**	96.28**	118.45**	134.93**	1.87E+07
Location	2	53.784**	133.654**	127.154**	274.006**	13.654**	17.71**	351606**	2370.69**	4583.1**	3682.63**	3.58E+08**
Genotype x Location	52	3.566**	12.802**	8.718**	6.109**	3.75**	2.479*	18030	60.52**	107.71**	112.88**	2.62E+07**
Residual	80	1.906	5.715	3.852	1.931	1.272	1.55	26015	20.66	22.41	29.29	1.14E+07
CV (%)		12.1	8.8	8.5	15.3	10.5	10.7	13.3	25.3	43.4	22.1	39.7

DF= Degrees of freedom, 50%DF= Days to 50% flowering, **= Significant at 1%, *= Significant at 5% Probability

5.3.3.1 Plant Vigour

The location had significant effect on the variations in plant vigour among the test lines. Genotypes also varied significantly in all the three sites (Table 5.5). The interaction between location and genotype significantly contributed to the differences in growth vigour among the genotypes (Table 5.5; Appendix 12). The plant vigour of the new lines ranged from good to excellent for 80% lines at Kabete, 96% at Embu and 76% at Mwea (Table 5.6).

The check varieties on the other hand had an excellent vigour at the three sites. The test lines and the check varieties were more vigorous at Kabete and Embu compared to Mwea. In general, plant vigour of all the test lines and the check varieties was good in all trial sites.

5.3.3.2 Days to 50% flowering

The location effects contributed significantly to the variations in days to flowering among genotypes at the three trial sites (Table 5.5; Appendix 13). Equally, variations in the number of days to 50% flowering among genotypes was significant. The results also showed that the significant differences at $P \leq 0.05$ in number of days to 50% flowering were as a result of genotype x location interaction effect (Table 5.5; Appendix 13). The test lines attained the 50% flowering in 42 days at Kabete, 40 days at Embu and 38 days at Mwea. The test lines flowered in 36 to 46 days at Kabete, 34 to 47 days at Embu and 35-43 days at Mwea (Table 5.7). About 72% genotypes flowered in less than 40 days at Mwea compared to 40% at Kabete and 16% at Embu trial sites. KSB12-143-3-1M, KSB47-2-2M and KSB36-1-5M genotypes flowered earlier at the three sites while KSB47-2M flowered latest at Mwea and KSB04-1-1M at Kabete and Embu.

Mean number of days to 50% flowering was 40 days in all sites and the overall range of number of days to 50% flowering in all sites was 37-44 days. The check varieties were early flowering. They flowered in 35-40 days in all sites (Table 5.7). Hence the test lines were late flowering compared to the check varieties. The test lines consistently flowered later than the check varieties in both the PYT and the AYT trials.

Table 5. 6 Plant vigour scores for advanced bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Plant Vigour scores			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	3.0	1.0	3.0	2.3
KSB04-1-1M	3.0	1.0	2.0	2.0
KSB06-1-1-2M	2.0	1.0	3.0	2.0
KSB08-3-4M	3.0	1.0	2.0	2.0
KSB12-143-3-1M	3.0	3.5	2.0	2.8
KSB13-1-1-1M	2.0	1.0	4.0	2.3
KSB22-3-1T	2.0	1.0	1.0	1.3
KSB23-143-1-1M	3.0	1.0	2.0	2.0
KSB27-143-2-1M	5.0	1.0	5.0	3.7
KSB30-3-1-2M	9.0	1.0	3.0	4.3
KSB33-1-2M	3.0	1.0	5.0	3.0
KSB33-3-1M	3.0	1.0	2.0	2.0
KSB36-1-5M	1.0	1.0	2.0	1.3
KSB39-1-1M	2.0	1.0	2.0	1.7
KSB39-1-4M	1.0	1.0	3.0	1.7
KSB39-2-4M	2.0	1.0	3.0	2.0
KSB39-3M	3.0	1.0	2.0	2.0
KSB39-4-4M	1.0	1.0	3.0	1.7
KSB42-2-2M	5.0	1.0	4.0	3.3
KSB43-2M	1.0	1.0	2.0	1.3
KSB46-2M	8.0	1.0	4.0	4.3
KSB47-1-2M	2.0	1.0	2.0	1.7
KSB47-2-2M	1.0	1.0	4.0	2.0
KSB47-2M	2.0	1.0	2.0	1.7
KSB52-2M	5.0	1.0	2.0	2.7
Checks				
Samantha	5.0	1.0	1.0	2.3
Teresa	3.0	3.0	1.0	2.3
Mean	3.1	1.2	2.6	2.3
LSD $_{0.05Gen}$	3.9	0.3	2.9	1.6
LSD $_{0.05Loc}$				0.5
LSD $_{0.05GenXLoc}$				2.7
CV (%)	12.3	11.7	10.9	12.1

LSD= least significant difference, CV= coefficient of variation, Plant vigour scale (van Schoonhoven and Pastor-Corrales, 1987)

Table 5. 7 Days to 50% flowering scores for new bush snap bean lines at Kabete, Embu and Mwea in 2013 and 2014

	Scores of genotypic days to 50% flowering			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	40.0	37.5	37.5	38.3
KSB04-1-1M	46.0	47.0	39.5	44.2
KSB06-1-1-2M	42.0	39.5	38.0	39.8
KSB08-3-4M	45.0	37.5	37.5	40.0
KSB12-143-3-1M	36.5	34.5	42.5	37.8
KSB13-1-1-1M	42.0	44.0	36.5	40.8
KSB22-3-1T	40.0	36.0	38.0	38.0
KSB23-143-1-1M	43.0	41.0	40.0	41.3
KSB27-143-2-1M	45.0	42.5	39.5	42.3
KSB30-3-1-2M	45.0	38.0	39.0	40.7
KSB33-1-2M	37.0	44.5	38.5	40.0
KSB33-3-1M	40.0	39.0	39.0	39.3
KSB36-1-5M	41.0	43.0	35.5	39.8
KSB39-1-1M	39.0	40.5	38.5	39.3
KSB39-1-4M	38.0	40.0	37.5	38.5
KSB39-2-4M	41.0	41.5	40.5	41.0
KSB39-3M	42.0	41.0	38.5	40.5
KSB39-4-4M	45.5	37.5	37.5	40.2
KSB42-2-2M	46.0	42.0	39.0	42.3
KSB43-2M	42.5	41.0	40.0	41.2
KSB46-2M	46.5	39.5	40.5	42.2
KSB47-1-2M	46.0	43.0	41.0	43.3
KSB47-2-2M	45.0	34.0	39.5	39.5
KSB47-2M	43.5	41.5	43.0	42.7
KSB52-2M	40.0	40.5	37.0	39.2
Checks				
Samantha	36.5	37.5	38.5	37.5
Teresa	38.0	35.5	36.0	36.5
Mean	42.6	39.15	39.33	40.3
LSD $_{0.05Gen}$	3.1	7.0	3.8	4.1
LSD $_{0.05Loc}$				1.4
LSD $_{0.05GenXLoc}$				7.1
CV (%)	3.6	10.9	4.8	8.8

LSD= least significant difference, CV= coefficient of variation.

5.3.3.3 Days to first picking

There were significant location, genotypic and interaction (G x E) effects for the duration from planting to first picking in among the genotypes (Table 5.5; Appendix 13).

Table 5. 8 Days to first picking scores for new bush snap bean lines at Kabete, Embu and Mwea in 2013 and 2014

	Days to first picking			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	50.0	49.0	48.0	49.0
KSB04-1-1M	53.5	53.0	48.0	51.5
KSB06-1-1-2M	48.5	51.5	47.0	49.0
KSB08-3-4M	54.5	50.5	48.0	51.0
KSB12-143-3-1M	42.0	49.0	49.0	46.7
KSB13-1-1-1M	52.5	55.0	47.0	51.5
KSB22-3-1T	50.0	49.0	49.0	49.3
KSB23-143-1-1M	49.0	51.5	49.0	49.8
KSB27-143-2-1M	53.0	52.0	48.0	51.0
KSB30-3-1-2M	55.0	49.0	49.0	51.0
KSB33-1-2M	47.0	54.0	47.0	49.3
KSB33-3-1M	50.0	50.5	48.0	49.5
KSB36-1-5M	52.5	53.0	47.0	50.8
KSB39-1-1M	52.0	51.5	48.0	50.5
KSB39-1-4M	48.0	50.5	47.0	48.5
KSB39-2-4M	49.5	50.5	47.0	49.0
KSB39-3M	51.0	51.5	48.0	50.2
KSB39-4-4M	52.0	49.0	48.0	49.7
KSB42-2-2M	53.5	54.0	49.0	52.2
KSB43-2M	51.5	51.5	48.0	50.3
KSB46-2M	54.5	50.5	49.0	51.3
KSB47-1-2M	52.0	53.0	49.0	51.3
KSB47-2-2M	53.0	44.5	49.0	48.8
KSB47-2M	51.5	51.5	50.0	51.0
KSB52-2M	50.0	50.5	48.0	49.5
Checks				
Samantha	41.5	43.0	43.5	42.7
Teresa	43.5	41.0	41.0	41.8
Mean	51.4	48.5	50.0	49.
LSD $_{0.05Gen}$				4.9
LSD $_{0.05Loc}$				1.6
LSD $_{0.05GenXLoc}$				8.5
CV (%)	3.1	5.7	2.2	8.5

LSD= least significant difference, CV= coefficient of variation.

Pods were first picked in 42 to 55 days at Kabete, 44 to 55 days at Embu and between 47 to 50 days at Mwea. The mean number of days to first picking were 51 at Kabete and Embu and 48 at Mwea. This indicates that pods were first picked earlier at Mwea compared to Kabete and Embu. Table 5.8 shows that first picking among genotypes occurred in 46 days after planting with an average of 49 days in all sites.

5.3.3.4 Reaction to diseases

5.3.3.4.1 Rust

There were evidence of rust pathogens at the three sites. Rust infections were more severe in Kabete and Embu and less in Mwea. The disease pressure was low at Embu and Mwea where there were no susceptible lines. The rust severity scores ranged from 1 to 9 at Kabete, 1 to 6 at Embu and 1 to 4.6 at Mwea. The check varieties showed intermediate resistance to rust at Kabete and Mwea and resistance to rust at Embu. On average the mean rust severity score were 5.7 at Kabete, 2.6 at Embu and 1.7 at Mwea (Table 5.9). The mean rust severity scores for the three sites was 3.1.

There were significant location and interaction (G x E) effects on the genotypic reaction to rust severity in the three site (Table 5.5; Appendix 13). High rust severity was evident at Kabete (1-9) compared to Embu (1-6) and Mwea (1-4.2) trial sites. Consequently, only 16% of the test lines showed resistance to rust in Kabete compared to 84% at Embu and 86% at Mwea (Table 5.9). This implies that Kabete's conditions favored rust development compared with the other two locations, although there could be different races at the two sites.

Genotypic reactions to rust at Kabete ranged from resistant (16%) to susceptible (32%) with the remainder of the genotypes exhibiting intermediate reactions to rust infections. The most outstanding lines at Kabete were KSB-12-143-3-1M, KSB27-143-2-1M, KSB30-3-1-2M and KSB33-3-1M. These lines were resistant to rust despite the high rust prevalence and severity at Kabete. These lines were also resistant to rust at Mwea whereas KSB-12-143-3-1M and KSB30-3-1-2M were resistant to rust at Embu but KSB27-143-2-1M and KSB33-3-1M showed intermediate resistance.

Table 5. 9 Rust severity scores on bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Genotypic rust severity scores			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	6.5	3.0	1.0	3.5
KSB04-1-1M	9.0	1.5	4.2	4.9
KSB06-1-1-2M	5.0	2.0	1.0	2.7
KSB08-3-4M	5.5	3.0	1.0	3.2
KSB12-143-3-1M	1.0	1.5	1.0	1.2
KSB13-1-1-1M	5.5	3.5	3.0	4.0
KSB22-3-1T	7.0	1.0	3.8	3.9
KSB23-143-1-1M	8.0	2.0	4.6	4.9
KSB27-143-2-1M	1.0	5.0	1.0	2.3
KSB30-3-1-2M	1.0	3.0	1.0	1.7
KSB33-1-2M	5.0	4.0	1.0	3.3
KSB33-3-1M	3.0	6.0	1.0	3.3
KSB36-1-5M	7.0	2.0	1.0	3.3
KSB39-1-1M	9.0	2.0	3.6	4.9
KSB39-1-4M	8.0	3.0	3.4	4.8
KSB39-2-4M	6.0	3.0	1.0	3.3
KSB39-3M	5.0	2.0	1.0	2.7
KSB39-4-4M	6.5	3.0	1.0	3.5
KSB42-2-2M	7.5	3.0	3.0	4.5
KSB43-2M	6.5	2.0	1.0	3.2
KSB46-2M	6.0	3.0	1.0	3.3
KSB47-1-2M	5.5	1.0	1.0	2.5
KSB47-2-2M	4.0	2.0	1.0	2.3
KSB47-2M	8.0	1.0	1.0	3.3
KSB52-2M	6.0	2.0	1.0	3.0
Checks				
Samantha	6.0	2.5	5.5	4.7
Teresa	5.5	1.0	4.3	4.3
Mean	5.6	1.1	2.5	3.1
LSD $_{0.05Gen}$	3.6	3.3	0.6	1.6
LSD $_{0.05Loc}$				0.5
LSD $_{0.05GenXLoc}$				2.8
CV (%)	31.4	13.6	22.2	15.3

LSD= least significant difference, CV= coefficient of variation, Disease severity scale, 1 to 3= resistant, 4 to 6= intermediate resistance, 7 to 9= susceptible (van Schoonhoven and Pastor-Corrales, 1987)

The commercial check varieties on the other hand showed intermediate resistance to rust in all sites. Rust severity among the check varieties ranged from 5.5 to 6 at Kabete, 1 to 2.5 at Embu and 4.3 to 5.5 at Mwea. Teresa (4.3) appeared to be more resistant to rust than Samantha (4.7) (Table 5.9).

In general, 19 lines were outstanding in the sense that they showed more resistance to rust as compared to the check varieties. Sixteen new lines were resistant to rust in the three sites. KSB12-143-3-1M and KSB30-1-2M were more resistant to rust in the three sites. The new lines reduced rust severity by 25.8%. This means that the test lines may have inherited rust resistance genes from their parents.

5.3.3.4.2 Anthracnose

There were indications of disease prevalence in Kabete and Embu whereas there were no disease signs at Mwea. This implies that climatic conditions in Mwea limited the development and growth of anthracnose pathogens. However, disease pressure was low at Kabete and Embu.

Location effects played a key role in the variations in genotypic reaction to anthracnose in the three sites (Table 5.5; Appendix 13). Anthracnose infection ranged from 1 to 4 at Kabete and 1 to 6 at Embu. Twenty one new bush lines were resistant to anthracnose 16% of which had complete resistance (Table 5.10). Out of the four test lines that were resistant to anthracnose at Kabete KSB33-3-1M was resistant at Embu while KSB47-2-2M, KSB30-3-1-2M and KSB27-143-2-1M showed intermediate resistance. At Embu and 48% out of 21 lines showed complete resistance (score of 1). KSB27-143-2-1M was the most affected by anthracnose at Embu (Table 5.10). Disease severity ranged from resistance to intermediate resistance in both sites. No cases of susceptibility to anthracnose were recorded both sites.

The check varieties showed resistance in Kabete and Embu and intermediate resistance at Mwea (Table 5.10). Teresa was most affected by anthracnose at Mwea (4.5) compared to Samantha (3.5).

Table 5. 10 Anthracnose severity scores on bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Genotypic Anthracnose severity scores			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	2.0	1.0	1.0	1.3
KSB04-1-1M	1.5	1.0	1.0	1.2
KSB06-1-1-2M	2.0	1.0	1.0	1.3
KSB08-3-4M	2.5	4.5	1.0	2.7
KSB12-143-3-1M	1.5	1.5	1.0	1.3
KSB13-1-1-1M	1.5	2.5	1.0	1.7
KSB22-3-1T	2.5	3.0	1.0	2.2
KSB23-143-1-1M	3.5	4.0	1.0	2.8
KSB27-143-2-1M	1.0	6.0	1.0	2.7
KSB30-3-1-2M	1.0	4.0	1.0	2.0
KSB33-1-2M	2.0	4.0	1.0	2.3
KSB33-3-1M	1.0	3.0	1.0	1.7
KSB36-1-5M	2.5	1.0	1.0	1.5
KSB39-1-1M	3.0	1.0	1.0	1.7
KSB39-1-4M	4.0	1.0	1.0	2.0
KSB39-2-4M	3.5	1.0	1.0	1.8
KSB39-3M	1.5	1.0	1.0	1.2
KSB39-4-4M	2.0	1.0	1.0	1.3
KSB42-2-2M	3.0	3.5	1.0	2.5
KSB43-2M	1.5	2.0	1.0	1.5
KSB46-2M	2.0	3.0	1.0	2.0
KSB47-1-2M	1.5	1.0	1.0	1.2
KSB47-2-2M	1.0	3.5	1.0	1.8
KSB47-2M	2.5	1.0	1.0	1.5
KSB52-2M	3.5	1.0	1.0	1.8
Checks				
Samantha	2.5	1.0	3.5	2.3
Teresa	3.0	3.0	4.5	3.5
Mean	2.2	1.5	2.4	2.1
LSD $_{0.05Gen}$	2.5	3.5	0.9	1.2
LSD $_{0.05Loc}$				0.5
LSD $_{0.05GenXLoc}$				2.1
CV (%)	10.9	15.3	7.0	10.5

LSD= least significant difference, CV= coefficient of variation, Disease severity scale, 1 to 3= resistant, 4 to 6= intermediate resistance, 7 to 9= susceptible (van Schoonhoven and Pastor-Corrales, 1987)

The test lines were more resistant to anthracnose in all sites compared to the check varieties. Reaction to anthracnose infection ranged from 1.2 to 2.8 in the three sites with a mean of 1.8. The

new snap bean lines reduced anthracnose severity by 37.9%. On average, all the test lines were resistant to anthracnose in the three sites.

5.3.3.4.3 Angular leaf spot

Angular leaf spot was prevalent at the three sites but was more severe at Embu. Angular leaf spot pressure was low at Kabete and Mwea (Table 5.5; Appendix 13). The disease infection ranged from 1 to 4.5 at Kabete, 1 to 7 at Embu and 1 to 3 at Mwea. The mean disease severity was 2.2 at Kabete, 2.4 at Embu and 1.2 at Mwea (Table 5.11).

Location effects significantly contributed to the variations in angular leaf spot infection among the test lines (Table 5.5; Appendix 13). Angular leaf spot was more pronounced at Embu whereas the disease pressure was low at Kabete and Mwea. (Table 5.11). Nineteen test lines were resistant to angular leaf spot at Kabete, seven of which had score of 1. All these lines were resistant to angular leaf spot at Mwea and Embu except KSB27-143-2M which showed intermediate resistance at Embu. KSB39-1-1M and KSB39-1-4M were most affected by angular leaf spot at Kabete (4.5). At Embu, disease severity ranged from 1 to7. Out of twenty resistant test lines, twelve had a score of 1 indicating complete resistance. KSB39-2-1-2M and KSB46-2M were susceptible to angular leaf spot at Embu. All the test lines were resistant to angular leaf spot at Mwea with disease severity ranging from 1 to 3 and a mean of 1.22 (Table 5.11).

The check varieties revealed intermediate resistance to angular leaf spot at Kabete and Mwea. However, Samantha proved to be resistant to angular leaf spot at Embu. In general, the test lines were more resistant to angular leaf spot at the three trial sites. Two lines, KSB30-3-1-2M and KSB47-2M were outstanding with complete resistance (score of 1) at all the trial sites. Twenty three new bush lines were resistant to angular leaf spot while only KSB39-2-1-2M and KSB46-2M showed intermediate resistance. The test lines reduced angular leaf spot severity by 51.3%.

Table 5. 11 Angular leaf spot severity scores on bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Genotype angular leaf spot severity scores			
Genotype	**Kabete**	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	2.0	6.5	2.0	3.5
KSB04-1-1M	3.0	2.0	1.0	2.0
KSB06-1-1-2M	1.0	3.0	2.0	2.0
KSB08-3-4M	2.0	3.0	1.0	2.0
KSB12-143-3-1M	1.5	1.0	1.0	1.2
KSB13-1-1-1M	2.5	2.0	1.0	1.8
KSB22-3-1T	3.5	2.5	1.0	2.3
KSB23-143-1-1M	2.0	5.0	1.0	2.7
KSB27-143-2-1M	1.0	5.5	1.0	2.5
KSB30-3-1-2M	1.0	1.0	1.0	1.0
KSB33-1-2M	2.5	1.0	1.0	1.5
KSB33-3-1M	1.0	3.0	1.0	1.7
KSB36-1-5M	2.0	1.0	1.0	1.3
KSB39-1-1M	4.5	1.0	1.0	2.2
KSB39-1-4M	4.5	1.0	1.0	2.2
KSB39-2-4M	4.0	1.0	1.0	2.0
KSB39-3M	3.5	1.0	1.0	1.8
KSB39-4-4M	1.0	2.0	3.0	2.0
KSB42-2-2M	2.5	4.0	1.0	2.5
KSB43-2M	1.5	1.0	1.0	1.2
KSB46-2M	3.5	7.0	1.5	4.0
KSB47-1-2M	1.5	1.0	1.0	1.2
KSB47-2-2M	2.5	2.0	1.0	1.8
KSB47-2M	1.0	1.0	1.0	1.0
KSB52-2M	1.0	1.0	2.0	1.3
Checks				
Samantha	4.5	1.5	4.5	3.5
Teresa	3.5	4.0	6.0	4.5
Mean	2.4	2.4	1.5	2.1
LSD $_{0.05Gen}$	2.7	2.3	1.8	1.3
LSD $_{0.05Loc}$				0.4
LSD $_{0.05GenXLoc}$				02.2
CV (%)	11.2	9.4	11.9	10.7

LSD= least significant difference, CV= coefficient of variation, Disease severity scale, 1 to 3= resistant, 4 to 6= intermediate resistance, 7 to 9= susceptible (van Schoonhoven and Pastor-Corrales, 1987)

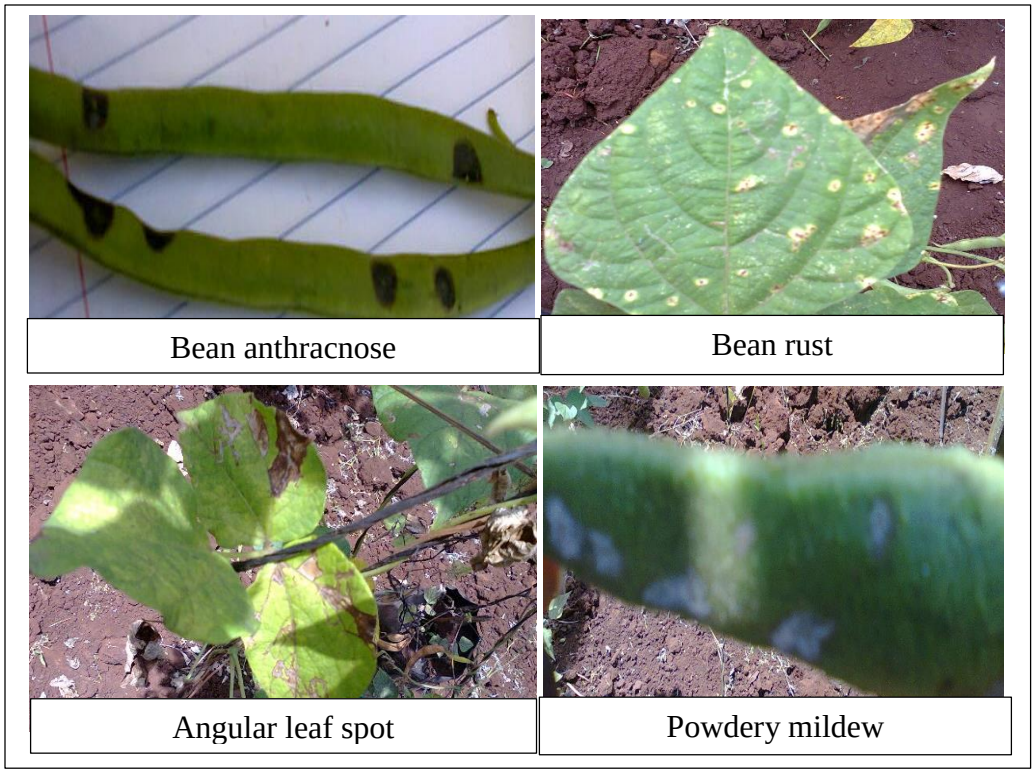


Figure 5. 2 Snap bean diseases in Embu

5.3.3.5 Pods per plant

Location effects were significant for number of pods per plant among genotypes at the three trial sites (Table 5.5). The test lines produced more pods per plant in Kabete (37.1) compared to Embu (27.1) and Mwea (25.5). Number of pods per plant ranged from 20.8 to 54.4 at Kabete, 14.3 to 44.6 at Embu and 11.3 to 41.7 at Mwea (Table 5.12). Two test lines, KSB39-3M and KSB33-3-1M, yielded less that the lowest yielding check variety (22.8) while 17 new lines yielded more than the best check variety (29.0) at Kabete. Twenty one new lines yielded more than the mean yield of the check varieties at Kabete. At Embu, 17 test lines had smaller number of pods per plant than the lowest yielding check while 5 yielded more number of pods than the best check variety. KSB30-3-1-2M and KSB39-2-1-2M were notably the worst with a mean of 14.7 pods per plant. There were generally low number of pods per plant at Mwea.

In general, the number of pods per plant in the three sites ranged from 19.4 to 41.7 with a mean of 29.4. This indicates that the new bush lines had more pods per plant in comparison to the check varieties (27.8) (Table 5.12). Thirteen test lines had more number of pods than the average number of pods per plant among the check varieties. KSB-47-2-2M and KSB23-143-1-1M were notably

outstanding with >399 pods per plant in the three sites. The new lines yielded more pods per plant than the check varieties by 6%.

Grade distribution

The test lines produced more extra-fine pods than the check varieties at the three trial sites. KB33-1-2M at Kabete; and KSB22-3-1T, KSB47-1-2M, KSB46-2M, KSB47-2M and KSB42-2-2M at Embu and Mwea produced more than 50% of the extra-fine pods. KSB23-143-1-1M had the highest proportion of extra-fine pods at Kabete (41 %), while KSB42-2-2M yielded the highest number of extra-fine pods in Embu (57.6 %) and Mwea (60 %) (Table 5.12). Twenty one (21) test lines had more than 50% of fine pods at Kabete compared to 1 (KSB06-1-1-2M) at Embu and Mwea. The line KSB06-1-1-2M consistently produced more than 50% of fine pods at the three sites. More bobby pods were produced at Embu by KSB42-2-2M as the highest yielder, whereas at Embu and Mwea, KSB39-4-4M had the highest percentage of bobby pods.

The percentage of extra-fine pods among the check varieties ranged from 31.7 to 37% with an average of 34.8%. This was less by 4.1% than the percentage proportions of the new bush lines' extra-fine pods. Although the check varieties (45.6%) and the new lines (46.3%) had almost the same proportions of fine pods, the total pod yield of premium grades among the new lines was higher since the new lines had more number of pods compared to the checks. The check varieties however had the lowest proportions of bobby pods compared to the test lines (Table 5.12).

The production of premium pods (extra fine and fine pods) amongst the test lines ranged from 83.2 to 99.1% at Kabete, 65.4 to 92.8% at Embu, and 62.4 to 93.7% at Mwea. The percentage of the premium pods was high at Kabete (96%) in comparison to Embu (80.2%) and Mwea (79.3%). These percentage proportions were higher than those of the check varieties by 3.4% at Kabete, 5.1% at Embu and 5.9% at Mwea.

In Kabete, 24 test lines produced a minimum of 94.3% premium pods. The highest yielders of premium pods were KSB39-4-4M at Kabete, and KSB 47-1-2M at Embu and Mwea. However, some of the test lines such as KSB06-1-1-2M at Kabete, and KSB39-4-4M in Embu and Mwea produced more bobby pods although there were low percentages of bobby pods at the three sites. On the other hand, Samantha was the best producer of premium pods at Kabete (96.2%) whereas Teresa was the highest producer of premium pods in Embu and Mwea trial sites (80.8%).

Table 5. 12 Pods plant^{-1} among bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

Genotype	Number of pods plant^{-1}			
	Kabete	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	38.2	15.1	12.2	21.8
KSB04-1-1M	30.5	23.8	20.9	25.1
KSB06-1-1-2M	26.9	25.9	23.0	25.2
KSB08-3-4M	35.7	27.9	25.0	29.6
KSB12-143-3-1M	27.4	44.6	41.7	37.9
KSB13-1-1-1M	25.2	27.8	24.9	25.9
KSB22-3-1T	39.1	32.6	29.7	33.8
KSB23-143-1-1M	54.4	36.8	33.8	41.7
KSB27-143-2-1M	42.6	24.0	21.1	29.2
KSB30-3-1-2M	32.7	14.3	11.3	19.4
KSB33-1-2M	35.1	26.6	23.7	28.5
KSB33-3-1M	20.8	25.8	22.9	23.2
KSB36-1-5M	28.4	23.7	20.8	24.3
KSB39-1-1M	39.3	23.1	20.2	27.5
KSB39-1-4M	39.3	33.6	30.7	34.5
KSB39-2-4M	38.2	27.7	24.8	30.2
KSB39-3M	22.7	25.9	23.0	23.9
KSB39-4-4M	54.2	26.0	23.0	34.4
KSB42-2-2M	25.2	31.2	28.3	28.2
KSB43-2M	53.8	31.3	28.4	37.9
KSB46-2M	52.3	18.9	16.0	29.1
KSB47-1-2M	44.3	22.0	19.1	28.5
KSB47-2-2M	43.4	38.8	35.8	39.3
KSB47-2M	50.7	22.3	19.4	30.8
KSB52-2M	27.4	26.9	24.0	26.1
Checks				
Samantha	22.8	28.4	25.5	25.6
Teresa	29.0	31.9	29.0	30.0
Mean	36.3	27.3	24.4	29.3
LSD $_{0.05Gen}$	26.5	17.5	17.5	14.3
LSD $_{0.05Loc}$				4.8
LSD $_{0.05GenxLoc}$				24.7
CV (%)	10.7	9.4	12.6	13.3

LSD= least significant difference, CV= coefficient of variation.

The proportion of premium pods ranged from 75.5% to 94.9% in the three sites. The lowest yielder of the premium pods was KSB39-4-4M, whereas KSB47-1-2M produced the highest percentage of premium pods in all the trial sites. The total mean production of premium pods in the three sites was 85.2% for the new bush lines against the check varieties' 80.3%. Six test lines which include KSB42-2-2M, KSB43-2M, KSB46-2M, KSB47-1-2M, KSB47-2M and KSB22-3-1T were found to be the highest yielders of premium pods with an average of 92.8% (Table 5.13). As seen from the table, KSB23-143-1-1M, KSB47-2-2M, KSB39-4-4M, KSB39-1-4M and KSB12-143-3-1M had the highest number of pods per plant and more than average percentages of premium pods.

Table 5. 13 Pods plant^{-1} and % proportions distribution per market class for bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Kabete				Embu				Mwea			
		%				%				%		
Genotype	Pods plant^{-1}	Extra Fine	Fine	Bobby	Pods plant^{-1}	Extra Fine	Fine	Bobby	Pods plant^{-1}	Extra Fine	Fine	Bobby
KSB 39-2-1-2M	38.2	36	59.5	4.5	15.1	38.1	44	17.9	12.2	40.6	41.4	18
KSB04-1-1M	30.5	34.6	57.5	8	23.8	24.6	45.8	29.6	20.9	23	44.7	32.3
KSB06-1-1-2M	26.9	26	57.2	16.8	25.9	34.4	50	15.6	23.0	33.8	50	16.2
KSB08-3-4M	35.7	26	72.2	1.8	27.9	39	29.9	31.1	25.0	39.5	25.8	34.7
KSB12-143-3-1M	27.4	37.1	62	0.9	44.6	31	40.6	28.4	41.7	30.6	39.9	29.5
KSB13-1-1-1M	25.2	48.1	48.7	3.3	27.8	29.1	44.4	26.5	24.9	28.5	43.5	28
KSB22-3-1T	39.1	41.6	52.1	6.3	32.6	50.5	38.3	11.2	29.7	52.2	36.8	11
KSB23-143-1-1M	54.4	41	56.7	2.3	36.8	37.8	42.8	19.4	33.8	38	42.1	20
KSB27-143-2-1M	42.6	30.5	67.6	1.9	24.0	40.8	41.4	17.8	21.1	42.7	39.2	18.1
KSB30-3-1-2M	32.7	30.4	67.4	2.3	14.3	26.6	49.3	24	11.3	24.9	47.8	27.4
KSB33-1-2M	35.1	50	44.4	5.7	26.6	40.6	37	22.4	23.7	41.4	35	23.6
KSB33-3-1M	20.8	37.5	58.3	4.2	25.8	36.7	42.3	21	22.9	37.2	41	21.8
KSB36-1-5M	28.4	31.7	65.7	2.6	23.7	32.8	43.4	23.8	20.8	32.5	42.2	25.2
KSB39-1-1M	39.3	38.7	53.6	7.8	23.1	36.5	40.8	22.7	20.2	36.1	38	25.9
KSB39-1-4M	39.3	48	46.5	5.5	33.6	38.9	37	24.2	30.7	39.4	35.4	25.2
KSB39-2-4M	38.2	41.7	55.3	3	27.7	42.1	36.1	21.8	24.8	43.2	34.1	22.8
KSB39-3M	22.7	40.2	54.1	5.7	25.9	36.2	39.5	24.3	23.0	36.5	38	25.5
KSB39-4-4M	54.2	38.9	60.4	0.7	26.0	24.8	40.6	34.7	23.0	23.4	38.9	37.7
KSB42-2-2M	25.2	46.7	42.3	11	31.2	57.6	33.5	8.9	28.3	60	31.6	8.4
KSB43-2M	53.8	43	56.5	0.5	31.3	45.3	43.6	11.1	28.4	46.7	42.4	10.9
KSB46-2M	52.3	34.4	65.1	0.5	18.9	52.1	39.1	8.9	16.0	56.4	35.8	7.8
KSB47-1-2M	44.3	33	65.2	1.9	22.0	51.7	41	7.3	19.1	54.4	39.3	6.3
KSB47-2-2M	43.4	39.6	60	0.4	38.8	38.6	45.6	15.9	35.8	39.1	44.8	16.1
KSB47-2M	50.7	36.4	63	0.6	22.3	53.2	37.9	8.9	19.4	56	35.7	8.3
KSB52-2M	27.4	29.2	67.8	3	26.9	40.7	42.2	17.1	24.0	41.4	40.9	17.7
Checks												
Samantha	22.8	58.1	38.2	3.7	28.4	28.4	44.5	27.1	25.5	27	43.4	29.6
Teresa	29.0	23.2	65.6	11.2	31.9	35.8	41.5	22.7	29.0	36	40.3	23.7
Mean	36.3	37.8	57.9	4.3	27.3	38.7	41.2	20.1	24.4	39.3	39.5	21.2
LSD 0.05Gen	26.5	20.3	21.6	7.6	17.5	14.3	13.1	16.4	17.5	17.6	15.4	19.5
CV (%)	10.7	26.1	18.1	32.7	9.4	18	15.5	39.6	12.6	21.8	19	44.8

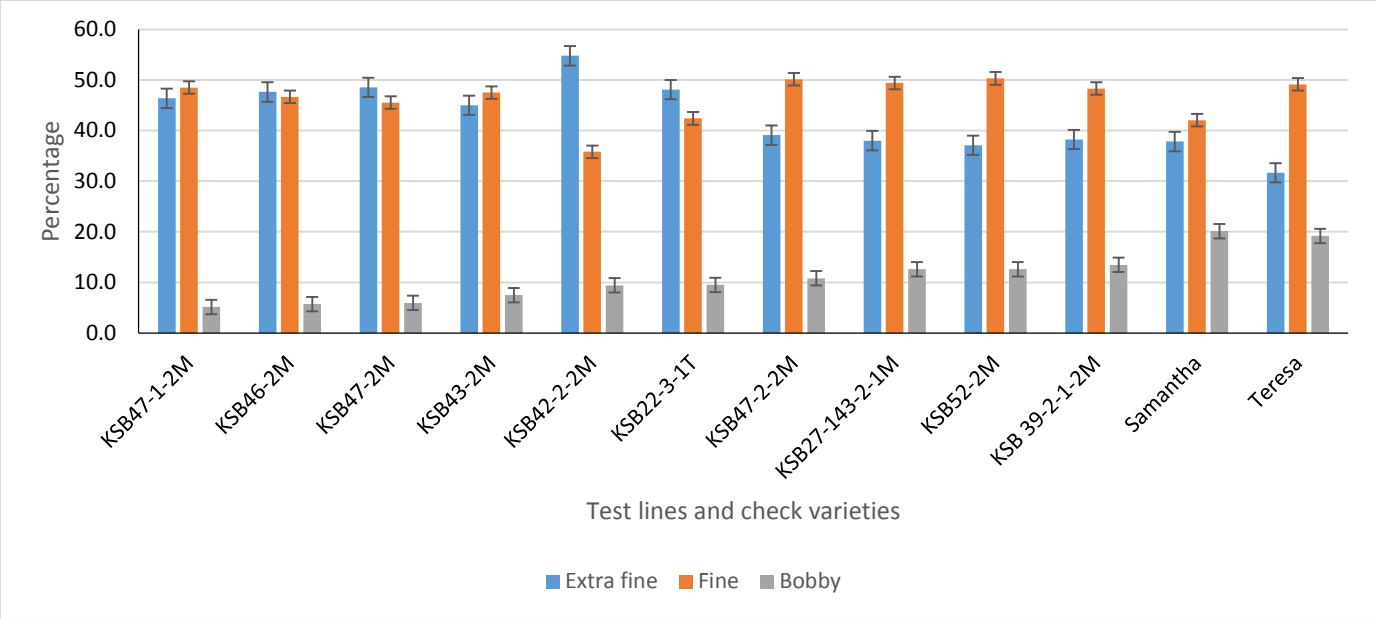


Figure 5. 3 Mean grade distribution among selected test lines and the checks at Kabete, Embu and Mwea

5.3.3.6 Pod length

Location had a statistically significant (P≤ 0.05) effect in the expression of pod length among genotypes in the three trial sites (Table 5.5). Pod lengths among genotypes varied significantly. Genotype x location interactions significantly influenced the expression of pod lengths in the three trial sites (Figure 5.4). Genotypes formed longer pods at Embu (9.4cm) and Kabete (9.1cm) compared to and Mwea (7.2cm). In each site, the check varieties formed longer pods than the test lines. For instance, the mean pod length of the check varieties was10.6cm at Kabete, 10.9cm at Embu and 9.3cm at Mwea.

Pod length ranged from 4.4 to 12.2cm at Kabete. Six test lines including KSB39-2-1-2M, KSB33-1-2M, KSB22-3-1T, KSB36-1-5M, KSB39-1-1M and KSB12-143-3-1M attained the recommended HCDA pod lengths. Two lines exceeded the average pod length of the check varieties (Table 5.14). At Embu, pod length among genotypes ranged from 5.6 to 11.6cm. Eleven test lines met the recommended pod length of ≥ 10cm while four exceeded the average length of the check varieties (Table 5.14). At Mwea, genotypic pod length ranged from 1.7 to 12.1cm. Four test lines formed longer pods than the average length of the check varieties. These lines were; KSB39-4-4M, KSB30-3-1-2M, KSB47-1-2M and KSB22-3-1T. KSB47-1-2M and KSB22-3-1T formed the longest pods at Mwea (mean 11.6cm).

The pod lengths ranged from 6.3 to 10.9cm with a mean of 8.6cm among the test lines at the three trial sites. The test lines had shorter pods than the check varieties except KSB22-3-1T which consistently formed longer pods at the three sites. Only KSB39-1-1M and KSB22-3-1T met the recommended pod length at the three sites (Table 5.14).

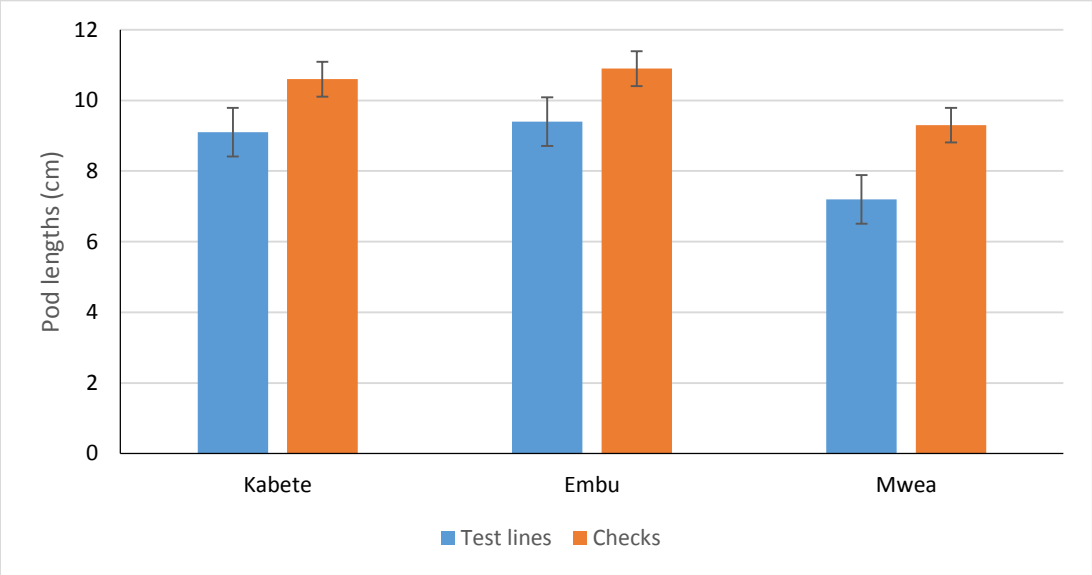


Figure 5. 4 Mean pod lengths (cm) of the test lines and the checks across locations

Table 5. 14 Mean pod lengths (cm) of advanced bush snap bean lines at Kabete, Embu and Mwea in 2013 and 2014

	Genotypic pod lengths (cm) per market grade											
	Kabete				Embu				Mwea			
Genotype	Extra Fine	Fine	Bobby	Mean	Extra Fine	Fine	Bobby	Mean	Extra Fine	Fine	Bobby	Mean
KSB 39-2-1-2M	12.0	16.6	1.9	10.1	9.0	11.3	7.6	9.3	3.0	4.7	6.9	4.9
KSB04-1-1M	7.8	8.1	10.5	8.8	8.2	11.4	9.4	9.7	5.0	6.7	6.3	6.0
KSB06-1-1-2M	6.8	8.7	8.0	7.8	10.9	12.3	7.1	10.1	6.7	7.9	10.5	8.4
KSB08-3-4M	8.2	11.4	0.8	6.8	9.4	12.9	11.3	11.2	6.8	8.7	10.3	8.6
KSB12-143-3-1M	11.5	13.9	11.0	12.2	8.2	9.4	7.9	8.5	7.8	8.1	10.5	8.8
KSB13-1-1-1M	10.9	15.1	3.4	9.8	10.6	13.2	11.1	11.6	3.7	4.6	5.2	4.5
KSB22-3-1T	11.5	15.7	3.9	10.4	9.6	11.0	9.6	10.1	11.2	12.7	12.5	12.1
KSB23-143-1-1M	4.5	10.6	10.6	8.6	8.1	9.8	8.7	8.9	7.0	5.4	6.3	6.2
KSB27-143-2-1M	10.6	13.4	0.9	8.3	8.6	8.2	5.6	7.4	5.0	6.8	7.5	6.4
KSB30-3-1-2M	5.3	6.9	1.1	4.4	4.6	7.2	4.9	5.6	7.0	11.6	10.6	9.8
KSB33-1-2M	12.2	16.1	2.7	10.3	10.7	10.8	9.7	10.4	2.9	4.6	6.7	4.8
KSB33-3-1M	9.7	12.6	1.1	7.8	10.0	12.7	9.9	10.8	6.6	7.8	8.0	7.5
KSB36-1-5M	10.6	18.2	2.5	10.5	10.2	12.4	8.4	10.3	4.5	5.1	7.9	5.8
KSB39-1-1M	12.8	16.7	6.8	12.1	9.8	10.5	9.7	10.0	6.9	7.5	9.9	8.1
KSB39-1-4M	9.0	14.6	2.3	8.7	12.4	12.5	10.0	11.6	5.5	8.3	9.0	7.6
KSB39-2-4M	13.0	15.2	1.2	9.8	10.7	12.3	11.2	11.4	6.0	5.1	10.5	7.2
KSB39-3M	12.6	14.4	0.8	9.3	10.0	12.0	8.0	10.0	5.3	7.5	10.0	7.6
KSB39-4-4M	12.0	14.4	3.2	9.9	9.2	8.3	9.9	9.2	7.3	9.7	12.0	9.7
KSB42-2-2M	7.0	9.8	2.2	6.3	9.4	11.9	3.3	8.2	3.3	4.0	6.0	4.4
KSB43-2M	11.7	15.1	1.8	9.5	9.9	10.9	4.5	8.4	8.4	7.5	7.3	7.7
KSB46-2M	12.6	15.6	0.0	9.4	9.6	10.8	3.2	7.9	7.2	5.9	9.9	7.7
KSB47-1-2M	10.7	15.1	1.1	9.0	9.4	10.1	4.3	7.9	8.5	11.8	13.0	11.1
KSB47-2-2M	12.0	15.4	1.7	9.7	9.4	11.4	8.1	9.7	1.0	1.2	2.8	1.7
KSB47-2M	10.8	15.5	1.0	9.1	9.3	10.8	2.6	7.6	4.4	6.0	8.9	6.4
KSB52-2M	11.7	15.7	2.2	9.9	9.5	10.6	6.7	8.9	5.8	5.0	9.4	6.7
Checks												
Samantha	6.8	4.5	1.9	4.4	6.5	7.4	7.9	7.3	1.8	3.4	7.7	4.3
Teresa	6.0	11.8	2.9	6.9	9.0	9.3	10.5	9.6	4.3	8.2	8.4	7.0
Mean	10.0	13.4	3.2		9.3	10.8	7.8		5.7	6.9	8.7	
Lsd $_{0.05\ Gen}$	3.4	3.2	3.4		2.6	3.0	3.6		3.4	3.6	4.1	
Lsd $_{0.05\ Harv}$	1.8	1.7	1.9		1.4	1.6	2.0		1.8	1.9	2.3	
Lsd $_{0.05\ GenXHarv}$	9.5	9.0	9.7		7.4	8.5	10.4		9.6	10.1	11.7	
CV (%)	34.8	34.1	17.5		30.4	39.8	13.6		16.8	14.7	15.6	

5.3.3.7 Pod yield

Location effects significantly affected yields of the test lines and the check varieties at the three trial sites (Table 5.5). The G x E effects were significant in the expression of pod yield per hectare (Table 5.5). Therefore variations that existed among the test lines and the check varieties were not attributed to the genotype but also to the trial site and the G x E interactions. The test lines had high yields in Kabete (12, 544.6 kg ha^{-1}) compared to Embu (7, 193.9 kg ha^{-1}) and Mwea (9, 090.3 kg ha^{-1}). Pod yield ranged from 5341 to 18, 997.0 kg ha^{-1} at Kabete, 2315.0 to 10, 522.0 kg ha^{-1} at Embu and 2, 009.0 to 18, 535.0 kg ha^{-1} at Mwea (Table 5.15). KSB39-2-1-2M and KSB06-1-1-2M yielded less that the lowest yielding check (7, 090.0 kg ha^{-1}) while 18 new bush lines yielded more than the best check (10, 306.0 kg ha^{-1}) at Kabete (Table 5.15). Nineteen new lines yielded more than the mean yield of the checks (8, 698.0 kg ha^{-1}) at Kabete. Eight test lines had lower yields than the lowest yielding check whereas 7 had more yields than the best check variety at Embu. KSB46-2M was the highest yielding test line and the only one which exceeded 10, 000 kg ha^{-1} at Embu. At Mwea, The test lines performed better than the check varieties by 49%. Ten lines yielded more than 10,000.0 kg $ha^{-1}$with an average of 13, 234.0 kg ha^{-1}. KSB12-143-3-1M and KSB30-3-1-2M were the best yielders (18, 270.0 kg ha^{-1}) at Mwea.

In general, pod yield ranged from 5, 819.0 to 12, 220.7 with a mean of 9, 609.6 kg ha^{-1} in the three sites. The check varieties had lower yields (7, 402.3 kg ha^{-1}) than the test lines (9, 609.6 kg ha^{-1}). This points out that the bush test lines were better yielders compared to the check varieties (Table 5.15). Ten new bush lines had yields >10, 000 kg ha^{-1} and only one (KSB39-2-1-2M) line had lower yields than the average yield of the check varieties (Table 5.15). KSB22-3-1T had the highest yield in the three sites. The new bush lines out yielded the check varieties by 29.8%.

Grade distribution

The test lines had higher proportions of extra-fine pods than the check varieties at the three trial sites. The mean percentage proportions of extra-fine pods were 31.2% at Kabete, 47.4% at Embu and 31.8% at Mwea (Table 5.16). The check varieties had 38% of the extra-fine pods which was less than 36.8% of the test lines' pods. The yield of extra-fine pods ranged from 1, 785 to 5, 896.0 kg ha^{-1} at Kabete, 1, 279.0 to 5, 468.0 kg ha^{-1} at Embu and 156.0 to 8, 878 kg ha^{-1} at Mwea (Table 5.16). More Extra fine pod yields were realized at Kabete (3, 746.8 kg ha^{-1}) compared to Embu (3, 319.2 kg ha^{-1}) and Mwea (3, 213.8 kg ha^{-1}).

At Kabete, the checks had a mean yield of 24.6% extra-fine pods. Only KSB30-3-1-2M produced smaller proportions of extra-fine pods compared to the lowest yielding check variety (21.8%). Five test lines yielded higher proportions of extra-fine pods (36%). These lines were KSB33-1-2M, KSB 39-3M, KSB39-1-4M, KSB47-2M and KSB43-2M. KSB33-1-2M was the highest yielder (38.9%) of extra-fine pods at Kabete (Table 5.16). Table 5.16 shows that six test lines yielded more extra-fine pods (37.4%) than the average yield of check varieties (3, 756.0 kg ha^{-1}) at Embu. Thirteen new lines had lower proportions of extra-fine pod yields compared to the lowest yielding check variety whereas only two lines out yielded the best check by 25.6%. The best lines at Embu were KSB43-2M and KSB47-2-2M. The test lines produced higher proportions of extra-fine pods at Mwea compared to the check varieties. Although 6 out of 25 new lines had lower proportions of extra-fine pods compared to the lowest yielding check, 10 lines yielded higher proportions of extra-fine pods compared to the best check variety. Three test lines were outstanding at Mwea since they produced the highest proportions of extra fine pods (49.2%). They include KSB22-3-1T, KSB30-3-1-2M and KSB12143-3-1M (Table 5.16).

In general, the new line had higher proportions of extra-fine pods compared to the checks at the three trial sites. The proportion of extra-fine pods ranged from 2399.7 to 5515.0 kg ha^{-1} with a mean of 3426.6 kg ha^{-1} compared to the checks' 2415.0 to 2958.3 kg ha^{-1} (2686.7). The new bush lines out yielded the check varieties in extra-fine pods by 27.5%. Six test lines were outstanding in the three sites with an average of >4000 kg ha^{-1} of extra-fine pods. These lines were; KSB39-1-1M, KSB39-1-4M, KSB39-3M, KSB43-2M, KSB12-143-3-1M and KSB22-3-1T (Table 5.16).

More fine pods were produced in Kabete (8266.5 kg ha^{-1}) compared to Embu (2308.0 kg ha^{-1}) and Mwea (2423.6 kg ha^{-1}) (Table 5.16). The check varieties produced more fine pods than the test lines at Mwea. The proportions of fine pods ranged from 34.7 to 81.9% at Kabete, 16.9 to 62.6% at Embu and 1 to 59.4% at Mwea. KSB06-1-1-2M had lower yields of fine pods compared to the lowest yielding check variety (Teresa) while 22 new lines had high proportions (65.6%) of fine pods compared to the highest yielding check (36%) at Kabete (Table 5.6). The yields of fine pods in twenty three bush lines was two times the average yield of the check varieties. The line KSB39-2-1-2M, KSB08-3-4M, KSB39-3M, KSB47-2M, KSB46-2M and KSB27-143-2-1M produced the highest proportions (66.8%) of fine pods at Kabete (Table 5.16). At Embu, the average proportion of fine pods was 30.6% among the test lines and 24.5% for the check varieties. Three test lines had

lower yields than the lowest yielding check variety while six test lines yielded more than the best check variety by 22.6%. KSB46-2M was considered the best producer of fine pods at Embu (62.6%). The test lines produced an average of 23.6% of fine pods compared to the check varieties (45.6) at Mwea. Ten test lines had an average of 11.9% yields of fine pods which was lower than the lowest yielding check variety (24.5%). Five test lines produced an average of 42.8% fine pods which was higher than the best check variety (66.7%). Ten lines yielded more than the average yield of the check varieties (Table 5.16). KSB30-3-1-2M, KSB13-1-1-1M, KSB36-1-5M and KSB39-3M were the highest yielders (mean of 47.3%) of fine pods at Mwea. In general, fine pod yield ranged from 1474.0 to 6997.0 kg ha^{-1} with a mean of 4332.7 kg ha^{-1} at the three sites. The yield of the check varieties ranged from 2785.0 to 3088.3 kg ha^{-1} with a mean of 2936.7 kg ha^{-1}. The new lines yielded more fine pods than the check varieties by 47.5%. KSB22-3-1T, KSB36-1-5M, KSB27-143-2-1M, KSB46-2M, KSB08-3-4M, KSB47-2M and KSB39-3M were the most outstanding lines in the production of fine pods since they had an average of 5907.0 kg ha^{-1}.

Although the test lines produced higher yields of bobby pods in comparison to the check varieties, the proportions of the bobby pods among them (4.4%) were lower than those of the check varieties (8.5%) at Kabete. KSB04-1-1M and KSB06-1-1-2M had the highest proportions (13.2%) of bobby pods at Kabete whereas KSB39-1-1M, KSB39-3M and KSB22-3-1T were the highest yielders of bobby pods with an average of 6.9%. Nineteen lines yielded less bobby pods than the average yield of the check varieties (3.1%). Six lines had <1% of bobby pods. KSB47-1-2M, KSB06-1-1-2M and KSB47-2-2M had the lowest yield of bobby pods. KSB47-2-2M and KSB39-3M had the lowest proportions (0.4%) of bobby pods at Kabete (Table 5.16). The range of bobby pods at Embu was 5.3 to 39% with an average of 22% whereas that of the check varieties was 20.8 to 27.3% with a mean of 24.1%. Fifteen lines had lower proportions of bobby pods (16.8%) compared to the lowest yielding check varieties while ten had higher proportions 29.9%) of bobby pods in relation to the highest yielding check variety. KSB46-2M and KSB42-2-2M had the lowest proportion (7.2%) of bobby pods at Embu. The proportion of bobby pods at Mwea ranged from 9.8 to 86.6% while those of the check varieties ranged from 9.1 to 24%. This shows that the test lines (42.6%) had higher proportions of bobby pods in comparison to the check varieties (16.6%). All the test lines had a higher proportion of bobby pods in comparison to the lowest check that yielded 9.1%

bobby pods. While KSB47-1-2M had the highest proportion of bobby pods, KSB47-2M was the highest yielder of bobby pods (48.4%).

Premium Pods

The test lines produced higher proportions of premium pods compared to the check varieties at Kabete and Embu trial sites. In Mwea, however, the check varieties (83.5%) had higher proportions of premium pods than the test lines (55.4%). Higher proportions of premium pods were realized in Kabete (95.6%) as compared to Embu (77.9%) and Mwea (55.4%). All the test line had higher proportions of premium pods than the check varieties (74.2%) at Kabete. However, at Embu only 14 test lines exceeded the average proportion of the checks' premium pods while at Mwea, only KSB36-1-5M was considered the best since it had the highest proportions of premium pods that exceeded the average yield of the premium pods of the check varieties. The new lines KSB12-143-3-1M, KSB23-143-1-1M, KSB46-2M, KSB08-3-4M, KSB39-3M, KSB30-3-1-2M and KSB36-1-5M were considered the best since they had the highest proportions of premium pods (Figure 5.3).

Table 5. 15 Pod yield among bush snap beans at Kabete, Embu and Mwea in 2013 and 2014

	Pod yield (kg ha^{-1})			
Genotype	Kabete	**Embu**	**Mwea**	**Mean**
KSB 39-2-1-2M	6616	4797	6044	5819
KSB04-1-1M	10556	5736	2972	6421.3
KSB06-1-1-2M	5341	7101	7317	6586.3
KSB08-3-4M	13845	7361	8632	9946
KSB12-143-3-1M	8618	9057	18005	11893.3
KSB13-1-1-1M	8628	7313	12297	9412.7
KSB22-3-1T	13665	8618	14379	12220.7
KSB23-143-1-1M	11793	8517	6747	9019
KSB27-143-2-1M	17471	5185	7536	10064
KSB30-3-1-2M	8207	2315	18535	9685.7
KSB33-1-2M	14984	6087	7757	9609.3
KSB33-3-1M	8796	7118	9899	8604.3
KSB36-1-5M	10615	7110	10895	9540
KSB39-1-1M	14667	6204	12783	11218
KSB39-1-4M	14926	8778	10028	11244
KSB39-2-4M	12995	7592	7250	9279
KSB39-3M	7971	7326	13756	9684.3
KSB39-4-4M	13130	7669	8729	9842.7
KSB42-2-2M	16369	8262	8258	10963
KSB43-2M	14395	9129	6661	10061.7
KSB46-2M	17667	10522	2972	10387
KSB47-1-2M	18997	5733	10700	11810
KSB47-2-2M	13586	9817	2134	8512.3
KSB47-2M	17648	5355	10962	11321.7
KSB52-2M	12129	7145	2009	7094.3
Checks				
Samantha	7090	6356	5623	6356.3
Teresa	10306	8463	6576	8448.3
Mean	12260	7210	8886	9446
LSD $_{0.05Gen}$	7107.6	5524.3	8121	4309.2
LSD $_{0.05Loc}$				1436.4
LSD $_{0.05GenXLoc}$				7463.8
CV (%)	28.2	37.3	44.6	39.7

LSD= least significant difference, CV= coefficient of variation.

Table 5. 16 Pod yield (kg ha^{-1}) of bush snap bean lines at Kabete, Embu and Mwea in 2013 and 2014

	Extra-fine				Fine				Bobby			
		%				%				%		
Genotype	Pod yield (kg ha^{-1})	Kabete	Embu	Mwea	Pod yield (kg ha^{-1})	Kabete	Embu	Mwea	Pod yield (kg ha^{-1})	Kabete	Embu	Mwea
KSB 39-2-1-2M	2554.7	42	49	56.9	1474.0	37.4	24.1	8	2085.5	0.7	18.7	64.4
KSB04-1-1M	2399.7	32.2	49.7	30.5	4640.7	42.5	29.9	15	1875.0	15.6	21.1	28.1
KSB06-1-1-2M	3026.7	61.9	57.3	27.6	5045.7	62.3	41.5	20.4	1960.2	10.7	14.4	10.7
KSB08-3-4M	2960.7	16.5	38.4	34.1	4172.0	60.5	20.6	40.6	1704.8	4.3	29.2	30
KSB12-143-3-1M	5212.7	32.8	47.9	49.3	6031.0	69.3	49.4	34.1	2096.9	0.8	8.7	48.4
KSB13-1-1-1M	3536.0	35.2	50.2	10.8	6807.7	61.4	24.7	57.9	2480.5	0.4	30	22.4
KSB22-3-1T	5215.0	27	44.2	46.3	3649.0	71.8	28.8	5.9	1011.4	3.9	20.3	50.6
KSB23-143-1-1M	3365.7	30.6	49.4	35.2	4331.0	56.8	28.5	20.5	2846.4	5.7	28.8	46
KSB27-143-2-1M	2765.0	23.5	47.9	23.5	4016.0	62.9	22.4	25	2664.4	4.3	29.7	25.7
KSB30-3-1-2M	3814.7	21.8	55.4	45.1	3260.3	67.4	46.9	22	1161.7	7.6	9	45.2
KSB33-1-2M	3345.0	38.9	46	12.4	4505.3	60.2	26.7	26.1	2712.1	9.8	25.5	41.6
KSB33-3-1M	3130.7	29.5	50.9	26.8	4138.3	76.3	22.5	31.2	1732.2	1.9	22.1	23.8
KSB36-1-5M	3131.3	20.9	50.7	30.8	4233.3	52.6	27.8	35.4	2030.7	8.5	26.1	43.9
KSB39-1-1M	4001.0	29.9	47.8	32.3	4216.3	63.7	33	10.3	1561.6	0.9	12.9	47
KSB39-1-4M	4066.7	37.5	42.7	33.5	6997.0	71.6	62.6	17	709.3	0.7	5.3	52.5
KSB39-2-4M	3069.3	31.6	44.2	26.8	3921.0	65.3	29.5	31.1	1732.0	4.1	21.2	33.7
KSB39-3M	4071.0	38.3	45.2	19.7	2666.3	63	42.2	6	2025.3	7.2	9.2	58.2
KSB39-4-4M	3597.0	30.8	42.7	38.2	3695.3	67.6	17.4	9	2550.0	1.6	39.9	52.8
KSB42-2-2M	3290.0	25	44.1	32.9	5337.3	76	22.8	59.4	1071.7	3.1	26.5	9.8
KSB43-2M	4284.0	35.4	54.1	42.6	4226.0	73.5	29.2	1	1209.2	0.4	16.3	86.6
KSB46-2M	2681.0	27.7	32.1	30.5	5679.0	81.9	29.2	42.6	1306.7	1.6	32.4	23.3
KSB47-1-2M	3443.3	29.7	48.5	35.8	3833.7	63.2	28.2	13.7	2375.8	5.1	27.7	59.5
KSB47-2-2M	3077.0	26.1	54.5	12.5	5451.7	74.2	32	24.3	1847.6	2.3	20.1	52.2
KSB47-2M	3194.0	29.9	42	17.5	3313.3	67.8	27.1	17.4	2160.7	2.7	22	55.9
KSB52-2M	2433.7	24.3	50.9	43.5	2676.3	62.1	16.9	17	1345.6	5.7	33.4	52.5
Checks												
Samantha	2415.0	36	53.7	24.3	2785.0	45.5	19.1	66.7	822.6	4.4	27.3	9.1
Teresa	2958.3	13.1	49.3	51.5	3088.3	50.1	29.9	24.5	1568.4	12.5	20.8	24
Mean	37.5	31.4	64.8	4.8	40.1	47.7	30.1	22.2	22.7	32.2	25.3	40.7
LSD $_{0.05Gen}$	16.6	29.7	42.8	9.6	19.4	20.6	21	18.5	15.4	39	36.2	43.4
LSD $_{0.05Loc}$	5.5				6.5				5.1			
LSD $_{0.05GenXLoc}$	28.8				33.7				26.7			
CV (%)	38.6	46	32.1	39.3	42.2	21	33.9	40.5	28.1	58.8	29.5	24.9

LSD= least significant difference, CV= coefficient of variation.

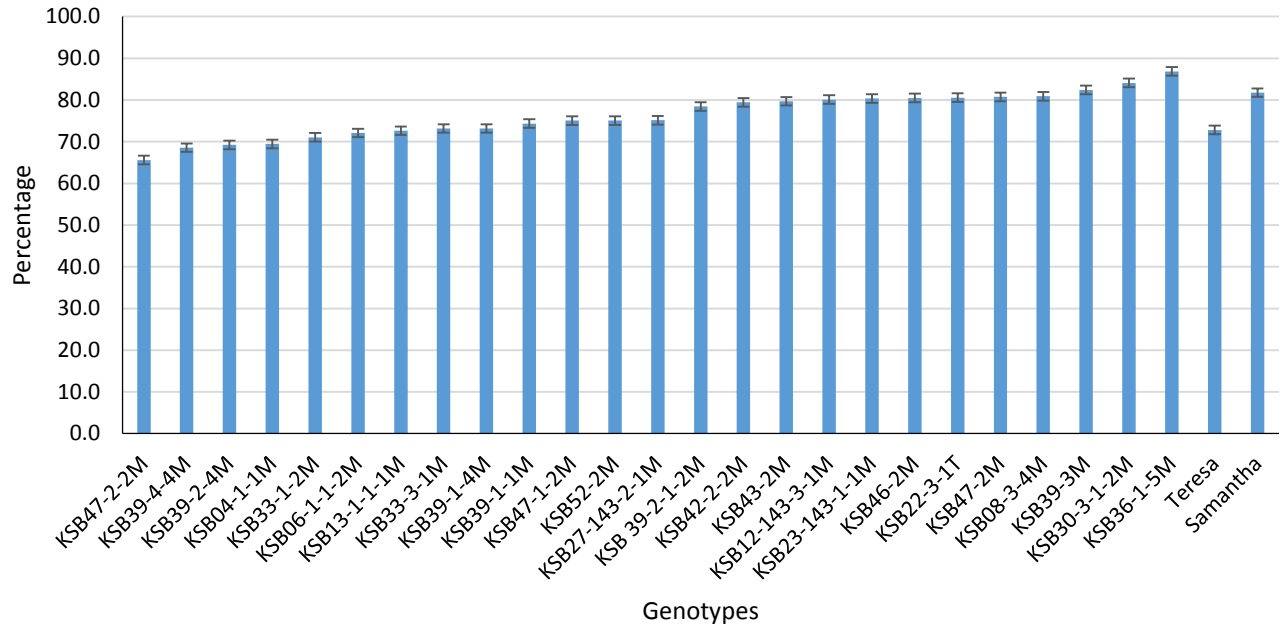


Figure 5. 5 Proportion of premium pods among advanced bush snap bean and the check varieties at Kabete, Embu and Mwea.

5.3.4 Promising advanced bush snap bean lines

Out of the 25 advanced bush snap bean lines evaluated in AYT, the best sixteen lines were identified based on multiple disease resistance to rust, anthracnose and angular leaf spot; pod quality (pod length, pod shape, pod curvature and pod colour), and pod yield (% premium pods and total pod yield) (Table 5.17). The selection was done on the basis of the mean performance of the lines at the three sites for all studied traits. The promising lines had good to excellent plant vigour (1-3) and flowered between 37 to 43 days. All the promising test lines exhibited multiple disease resistance to rust, anthracnose and angular leaf spot with scores of 1-3. Ten of 16 of the promising lines attained the HCDA (2009) recommended pod length, pod diameter and average pod length of 10.6cm. The promising lines had an average of 395 pods per plant, 75% of which were premium grade (Table 5.17).

The total pod yield of the promising lines ranged from 8,134.7 to 13,359.7 kg ha^{-1} with a mean of 10,470.9 kg ha^{-1}. The promising lines out yielded the checks by 41.5% in all the three sites. The selected lines also had market preferred pod quality attributes including round shape, pod curvature and pod colour. All had straight, round and green pods (Table 5.17).

Table 5. 17 The promising advanced bush snap bean lines selected from preliminary and advanced yield trials based on disease resistance, pod quality and pod yield (kg ha^{-1})

	Agronomic traits			Disease severity scores				Pod length (cm)			Pods plant^{-1}		Pod Yield (kg ha^{-1})		Pod Quality		
Genotype	Plant Vigour	Days to 50% flowering	Days to first picking	Rust	Anthracnose	Angular leaf spot	Mean	Extra fine	Fine	Mean premium pods	% Premium pods plant^{-1}	Mean podsplant^{-1}	%Premium pod yield	Total yield (kgha^{-1})	Pod Curvature	Pod Colour	Pod Shape
KSB08-3-4M	2.0	40.0	51.0	3.2	2.7	2.0	2.6	8.1	11.0	9.6	77.5	29.6	86.9	9946.0	Green	Straight	Round
KSB12-143-3-1M	2.8	37.8	46.7	1.2	1.3	1.2	1.2	9.2	10.5	9.8	80.4	37.9	77.6	11893.3	Green	Straight	Round
KSB13-1-1-1M	2.3	40.8	51.5	4.0	1.7	1.8	2.5	8.4	11.0	9.7	80.8	25.9	81.9	9412.7	Green	Straight	Round
KSB22-3-1T	1.3	38.0	49.3	3.9	2.2	2.3	2.8	10.8	13.1	12.0	90.5	33.8	84.0	12220.7	Green	Straight	Round
KSB27-143-2-1M	3.7	42.3	51.0	2.3	2.7	2.5	2.5	8.1	9.5	8.8	87.4	29.2	81.6	10064.0	Green	Straight	Round
KSB33-1-2M	3.0	40.0	49.3	3.3	2.3	1.5	2.4	8.6	10.5	9.6	82.8	28.5	78.9	9609.3	Green	Straight	Round
KSB36-1-5M	1.3	39.8	50.8	3.3	1.5	1.3	2.0	8.4	11.9	10.2	82.8	24.3	88.8	9540.0	Green	Straight	Round
KSB39-1-1M	1.7	39.3	50.5	4.9	1.7	2.2	2.9	9.8	11.6	10.7	81.2	27.5	75.8	11218.0	Green	Slightly curved	Round
KSB39-1-4M	1.7	38.5	48.5	4.8	2.0	2.2	3.0	9.0	11.8	10.4	81.7	34.5	74.7	11244.0	Green	Straight	Round
KSB39-2-4M	2.0	41.0	49.0	3.3	1.8	2.0	2.4	9.9	10.9	10.4	84.2	30.2	74.4	9279.0	Green	Straight	Round
KSB39-3M	2.0	40.5	50.2	2.7	1.2	1.8	1.9	9.3	11.3	10.3	81.5	23.9	81.4	13359.7	Green	Straight	Round
KSB39-4-4M	1.7	40.2	49.7	3.5	1.3	2.0	2.3	9.5	10.8	10.2	75.7	34.4	74.1	9842.7	Green	Straight	Round
KSB43-2M	1.3	41.2	50.3	3.2	1.5	1.2	2.0	10.0	11.2	10.6	92.5	37.9	84.5	10061.7	Green	Straight	Round
KSB46-2M	4.3	42.2	51.3	3.3	2.0	4.0	3.1	9.8	10.8	10.3	94.3	29.1	93.2	10387.0	Green	Straight	Round
KSB47-1-2M	1.7	43.3	51.3	2.5	1.2	1.2	1.6	9.5	12.3	10.9	94.9	28.5	75.1	8134.7	Green	Straight	Round
KSB47-2M	1.7	42.7	51.0	3.3	1.5	1.0	1.9	8.2	10.8	9.5	94.1	30.8	81.5	11321.7	Green	Straight	Round

5.4 DISCUSSION

5.4.1 Agronomic traits

Plant vigour was generally good in all sites and variations were due to location effects. The variations in locations were attributed to differences in altitudes, climatic conditions and soil types in the trial sites. Vadez *et al*. (2011) found that climatic conditions affect the adaptation of legumes. Good plant vigour implies that the three trial sites are suitable for the cultivation of snap beans under similar climatic conditions. The variations observed in the floral development and anthesis were as a result of environmental and genotypic variations. According to Raffi and Nath (2004), environmental effects have significant influence on the phenotypic characteristics in dry beans. The performance of the genotypes in the trial sites was influenced by both the genotype, environment and interaction between the genotype and the environment. It is therefore important to ascertain the amount of genotypic effects responsible for the expression of these traits among the genotypes (Silva *et al*., 2004).

The test lines and the check varieties were early flowering in Mwea compared to Kabete and Embu. This is attributed to the fact that lower altitude zones are warmer and hence the warm conditions facilitate early flowering as indicated by Bishop *et al*. (2016) who found that warm conditions enhanced early flowering of Faba beans. High temperatures experienced at Mwea enhanced earliness among the snap bean test lines and the checks. However, snap bean test lines were low yielding at Mwea compared to the high altitude zones of Kabete and Embu. High temperatures just before flowering affect pod setting in snap bean (Bishop *et al*., 2016). The early flowering in Mwea could also be attributed to water deficits which limited the crops' water use efficiency (WUE). This is because despite the availability of supplementary irrigation, the rate of evaporation was high leading to low soil moisture. Trials in Kabete performed better than those of Mwea and Embu due to the long rain season. Kabete and Embu are high altitude zones with relatively low temperatures. Therefore the test lines flowered later in Embu and Kabete compared to Mwea. This confirms the reports of Al-Suhaibani (2009) and Bishop *et al*. (2016) who found that insufficient availability of water leads to early flowering in faba beans. Days to first picking on the other hand were directly proportional to the number of days to 50% flowering as expected. This implies that the snap bean plants that flowered earlier were first picked earlier and vice versa.

5.4.2 Disease Reaction

The results showed significant genotypic variation as well as location effects in rust, anthracnose and angular leaf spot in the three trial sites. However, disease pressure was low in Mwea and Embu but high in Kabete. Of the three diseases, rust was the most prevalent and severe at the three sites. Rust was prevalent and severe at Kabete compared to Embu and Mwea. In Embu however, rust infections were not severe hence the 86% resistance. Low rust scores in Mwea were as a result of drier conditions, associated with low altitude zones and the high temperatures experienced during the experimental period, which did not favor the growth of pathogens (Laine and Barres, 2013). Highly humid conditions experienced in Embu and Kabete favored the development of disease pathogens. Sprinkler irrigation that was utilized in Embu and Kabete led to the widespread of disease pathogens. This explains why there was high disease pressure at Embu and Kabete. Despite the prevalence of diseases at Mwea, Embu and Kabete, five test lines (KSB22-3-1T, KSB43-2M and KSB36-1-5M, KSB39-3M and KSB46-2M emerged the best in all the traits tested.

At Embu and Mwea, genotypes showed resistance to intermediate resistance but the same genotypes were either susceptible or showed intermediate resistance resulting in only 16% of genotypic resistance to rust in Kabete. This implies that there could different races of rust in Kabete compared to those in Embu and Mwea (Arunga *et al*., 2012). Anthracnose symptoms were only evident in Kabete and Embu where humid conditions favoured disease development. Generally, disease variations that were observed are attributed to genotypic, location and interaction effects as well as agronomic activities. Kabete and Embu which are more humid experienced higher disease infections as compared to Mwea. Mersha and Hau, (2008) indicated that humidity coupled with cool temperatures of 16 to 28°C promote the development of rust, angular leaf spot and anthracnose causing pathogens. This was also confirmed by Wahome *et al*. (2011) and Mulanya (2016). Wet conditions that resulted from overhead irrigation in Embu and Kabete accounted for widespread of the disease pathogens resulting to low resistance of the test lines to rust, angular leaf spot and anthracnose compared to Mwea. The check varieties showed intermediate resistance as expected. Teresa was more resistant to rust compared to Samantha.

Test lines that exhibited resistance to rust, angular leaf spot and anthracnose may have inherited resistance genes from the various sources used in population development which include *ur* genes which confer resistance to rust, genes resistant to angular leaf spot from Mex 54 and *Co* genes for resistance to anthracnose from G2333. This confirms the results obtained by Wahome *et al*. (2011)

and Mulanya (2016). Resistance to rust (64%), angular leaf spot (100%) and anthracnose (92%) was reported among the test lines at the three trial sites

5.4.3 Pod traits and Pod yield

The results indicated that the variations observed on market grades and the number of pods per plant were as a result of location effects. Eighty four percent (84%) of the test lines produced more extra-fine pods in Kabete compared to Mwea and Embu. Additionally, in Kabete, genotypes produced 96% of premium pods compared to Embu (80.2%) and Mwea (79.3%). On the other hand, pod lengths varied significantly due to genotypic effects. These variations were highly influenced by location, genotype and their interactions. A higher percentage of extra fine pods attained the HCDA (2011), required pod length in Kabete. Conversely, more genotypes formed longer pods at Embu. However, it was noted that the minimum pod length of 10cm was achieved when pods were at their fine stage. KSB22-3-1T and KSB43-2M consistently formed longer pods at the three trial sites. This implies that despite the variations in climatic conditions that affect pod length these lines inherited good pod quality genes from their respective commercial varieties that are well adapted and have good pod quality. For instance, KSB22-3-1T was a cross between Morgan and Awash 1 where Morgan is well adapted and has good pod quality. These variations that result from locations is attributed to the variations in the climatic conditions (Irmak, 2014).

Yield variations were as a result of location effects. Therefore higher yields were realized in Kabete compared to Embu and Mwea. This indicates that the climatic conditions were favorable and the test lines were tolerant since high disease pressure and rust prevalence was reported in Kabete. Generally, the test lines out-yielded the checks' premium pods by 4.9%. The average yield of the test lines out yielded the check varieties indicating that the advanced test lines are better than the check varieties (Mulanya, 2016).

5.5 CONCLUSION AND RECOMMENDATIONS

The objective of this study was to establish whether there are variation in pod quality, pod yield and multiple disease resistance between the advanced bush snap bean lines and the check varieties. It was found that the test lines had 1-4 plant vigour scores as compared to 3-7 in checks as observed in all the three sites. The flowering dates of the test lines were not significantly different from the check varieties although some flowered earlier. Additionally, the test lines reduced disease severity by 25.8% (rust), 37.9% (anthracnose) and 51.3% (angular leaf spot). Out of the 25 test lines, the sixteen selected advanced lines exhibited multiple disease resistance to rust, anthracnose and angular leaf spot; pod quality; and high yields hence they can be validated in national performance trials and made available to farmers. These genotypes can also be exploited in breeding programs for the development of high yielding disease resistant bush snap bean varieties with excellent pod qualities.

CHAPTER SIX

GENERAL DISCUSSION, CONCLUSIONS AND RECOMMENDATIONS

6.1 Introduction

Snap bean production in Kenya is gaining importance due to the export market as well as the domestic market. However, smallholder farmers are limited by challenges such as disease constraints leading to overdependence on fungicides; increased costs of production; post-harvest losses and often stringent market regulations at the export destination. The smallholder farmers further depend on the bush snap beans which are often susceptible to major diseases like rust, anthracnose, angular leaf spot, BCMV and root rots among others. Besides, cultivars that confer resistance to these diseases have not been formally released and made available for smallholder farmers. Although Wahome (2011) selected climbing beans which showed multiple disease resistance, they were not the highest yielders and had poor pod qualities. This study was therefore advanced with the objective of: (1) establishing the mode of inheritance for climbing capacity and pod yield in snap beans; (2) evaluating and selecting for pod quality, pod yield and multiple disease resistance in advanced climbing snap bean populations; and (3) carrying out advanced yield trials through evaluation and selection for pod quality, pod yield and multiple disease resistance among advanced bush snap bean populations. The genetic information generated here is highly significant for breeders and snap bean breeding programs. Besides, the new climbing and bush snap beans with multiple disease resistance, high yields and good pod qualities will enhance stallholder output with increased returns.

The first objective was achieved by carrying out crosses between climbing snap bean with multiple disease resistance and susceptible commercial check varieties in order to establish gene action, heritability, heterosis and correlation amongst traits. The six climbing snap bean lines had been developed from crosses between climbing and bush snap beans (Progeny I nursery) followed by subsequent selection for growth habit and multiple disease resistance by Wahome (2011). The second and the third objectives were accomplished through the progression of advanced climbing and bush snap bean (Progeny I) populations in preliminary and advanced yield trials, evaluation and selection for agronomic traits, multiple disease resistance, pod quality and pod yield.

The progeny I nursery was developed from crosses between sources of disease resistance and susceptible commercial varieties. Sources of resistance to rust (Beldakmi, Belmineb, and

Beltgrade lines), anthracnose (G2333), angular leaf spot (Mex 54 and L227-10) and root rots (L227-10 were used in the crosses while the susceptible commercial varieties included Morelli, Amy, Paulista, Foskelly, Morgan, Julia, Teresa, Alexandria, Kutuless and Vernandon (Kimani, 2006). Some of the disease resistant varieties were of type IV growth habit for example G2333 (Checa and Blair, 2012). The F_1 progenies that resulted from these crosses were advanced through bulk population method to F_5 generation and/or backcrossed to their recurrent commercial parents (Kimani, 2006). Wahome (2011) evaluated 674 (F_6, $F_{7.9}$ and F_8) lines for growth habit and multiple disease resistance. These lines were artificially inoculated with rust, angular leaf spot and anthracnose isolates and advanced as Progeny I and II nurseries at Mwea and Thika in 2009 and 2010. Wahome *et al.* (2011) realized that six climbing lines were more resistant to rust, anthracnose and angular leaf spot than the check varieties and the advanced bush lines. However, these lines were not the highest yielders and had poor pod quality.

In this study, the first trial used the six climbing snap bean lines for genetic analysis with particular emphasis on climbing capacity and pod yield. Climbing capacity has been associated with high yields in common beans (Checa *et al.*, 2006). In the second trial, 53 advanced climbing snap beans (selected from Progeny I nursery) were evaluated in preliminary yield trials at Mwea during the long rain seasons (2013). Twenty lines that showered multiple resistance to disease, good pod qualities and high pod yield were selected and evaluated in advanced yield trials during the 2013 short rain seasons at Mwea and Embu. In the final trial, 59 advanced bush lines selected from progeny I nursery were evaluated for agronomic traits, multiple disease resistance, pod quality and pod yield in preliminary yield trials at Mwea during the long rain seasons of 2013. Twenty five lines were selected based on multiple disease resistance and good pod quality and evaluated in advanced yield trials at Mwea and Embu during the 2013 short rain season and at Kabete during the 2014 long rain season.

6.2 Genetic analysis for climbing capacity and pod yield

The University of Nairobi's Bean Program was centered in the selection for growth habit and multiple disease resistance in snap beans. The success of the program was realized by classifying snap beans as having type I, II, III or IV growth habit and identification of lines that showed multiple disease resistance. In this study, the mode of inherence of quantitative traits was established with a lot of emphasis on climbing capacity and pod yield among bush and climbing

snap bean crosses. The climbing lines were HAV 130, HAV 131, HAV 132, HAV 133, HAV 134 and HAV 135 while the bush lines included Paulista, Morgan, Samantha, Morelli, Serengeti, Star 2053, Teresa and Vernadon. The six climbing snap beans showed disease resistance to rust, anthracnose and angular leaf spot in comparison to the bush varieties which were susceptible to diseases leading to up to 100% yield losses in snap beans (Wahome *et al*., 2011). Six generations (P_1, P_2, F_1, F_2, BC_1P_1 and BC_1P_2) were generated from these crosses and evaluated for days to 50% flowering, plant height, internode length, number of pods per plant and pod length in 2014 at Kabete Field Station. The emphasis on climbing capacity and pod yield was informed by Checa *et al*. (2006) where climbing capacity was found to positively influence yields in common beans. Climbing capacity was measured quantitatively by measuring the plant height and internode length using a calibrated ruler while pod yield was measured in terms of number of pods per plant (Araujo, 2012; Chung and Goulden, 1971). The pod length was measured in centimetres using a calibrated ruler.

The results of this study indicated that there were significant genotypic differences ($P \leq 0.05$) in days to 50% flowering, plant height, internode length, number of pods per plant and pod lengths in all crosses. Tukey's multiple comparisons showed that the parental lines sharply contrasted in all the traits thus qualifying them for genetic analysis using generation means analysis. This further indicated that there is a great genetic gain within the parental lines with a possibility for exploitation of genetic variability and selection for climbing capacity and pod yield among the snap bean crosses (Hinkossa *et al*., 2013). Bush parents were early flowering; had shorter internodes, shorter plants and had fewer pods per plant while climbing parental plants flowered later (with longer internode lengths. The climbing parents were taller and had more number of pods per plant. However, P_1 plants formed longer pods (12.0cm) compared to P_2 plants (9.0cm). Diverse parents are a prerequisite for any breeding program and hence the parental lines utilized in the present study were appropriate (Breseghello and Coelho, 2013; Checa *et al*., 2006). F_1 progenies were within the parental ranges in days to 50% flowering, plant height, internode length and number of pods per plant. Pod lengths of F_1 plants were within the parental range except in Paulista x HAV 133 and Morgan x HAV 130 crosses where F_1 pods were longer that the pods of both parents. In most crosses, F_1 plants were early flowering, and outperformed the F_2 plants in all other traits. BC_1P_1 and BC_1P_2 were close to their recurrent parents in all traits and in all crosses (Checa *et al*., 2006).

The joint scaling tests indicated that the additive model was inadequate in the expression of the traits under study due to the significance of either A, B or C values in the t-test. Joint scaling tests therefore showed the presence on non-allelic interactions meaning that the Hayman's (1958) 6-parameter model was appropriate for all the traits studied.

Additive gene effects (m+a) were important for days to 50% flowering, internode lengths and number of pods per plant in most crosses while additive, dominance and epistatic gene effects accounted for plant height in all crosses and pod lengths in most crosses. All traits had high additive genetic variance in all crosses indicating that trait expression was as a result genetic effects and least influenced by the environment. This implies that these traits can easily be selected for in order to improve snap bean yields.Duplicate epistasis was responsible for days to 50% flowering, plant height and internode lengths in most crosses while complimentary epistasis was observed for number of pods per plant and pod lengths in most crosses. Morelli x HAV 130 and Serengeti x HAV 132 showed duplicate epistasis in all traits as compared to the other crosses. Ashwini *et al*. (2015) found that duplicate epistasis was responsible for number of pods per plant and pod length. Due to the presence of both fixable and non-fixable genes playing a role in the control of the traits under study, selection methods such as pedigree or single seed decent can be employed in selection for plant height, days to 50% flowering, internode length number of pods per plant and pod length in snap bean breeding program.

Plant height had high broad (65.6-91.7%) and narrow (57.9-83.3%) sense heritability in all crosses while days to 50% flowering in Star 2053 x HAV 131 cross had the highest broad sense (72.64%) and narrow sense (71.47%) heritability. Oluwayotin and Omolara (2014) found that the broad sense heritability of days to 50% flowering was high (98.9%) among soybean populations. However, they found that plant height had low broad sense heritability (3.92%) among the same populations. The high heritability in plant height and days to 50% flowering in Star 2053 x HAV 131 cross indicates that the inheritance of these traits is attributed to the genetic effects. On the other hand low heritabilities (both broad and narrow sense <30%) of internode length, number of pods per plant and pod length in all crosses indicated that there was high environmental effects in the expression of these traits. The selection for these traits should therefore be postponed to later generations when genes are fixed or such methods as intermating between segregrants can be employed to allow the build-up of favourable alleles for the improvement of plant height in these crosses (Hinkossa *et al*., 2013).

It was also found that snap bean hybrids can easily be developed due to the positive heterosis realised in various crosses. Heterosis was high for days to 50% flowering (Morgan x HAV 130, 70.2%; Star 2053 x HAV 131, 76.9%); plant height (Samantha x HAV 131, 60.1%; Serengeti x HAV 132, 80.9%; internode length (Samantha x HAV 131, 84.0%; and Serengeti x HAV 132, 93.5%); and number of pods per plant in (Star 2053 x HAV 131, 80.6%; Teresa x HAV 131, 88.1). The high positive heterosis is an evidence of the superior performance of F_1 hybrids relative to the mid-parental value and that these parents can be utilized in hybrid breeding due to the hybrid vigour. Negative hybrid vigour is equally important since it points out that selections can be done based on alternative traits.

The results further revealed that there were positive ($P \leq 0.05$) correlations between days to 50% flowering and plant height (Morelli x HAV 130, r = 0.9271**, Paulista x HAV 133, r = 0.9776**, Samantha x HAV 132, r = 0.9507** and Morgan x HAV 130, r=0.9688**); internode length (Teresa x HAV 131, r = 0.9737**); and number of pods per plant (Morelli x HAV 133, r = 0.9386**). Alemu *et al*. (2017) found contrasting results where number of pods per plant was negatively associated with days to 50% flowering. Sadeghi *et al*. (2011) also found that there was no significant correlation between dates to 50% flowering and plant height and internode length. However, they found that days to 50% flowering had negative significant correlation with number of pods per plant (-0.418**) and pod length (-0.308**). Plant height and internode length had a high significant positive correlation in Morgan x HAV 130 (r = 0.9974**), Samantha x HAV 132 (r = 0.9292**), Star 2053 x HAV 135 (r = 0.9731**) and Star 2053 x HAV 131 (r = 0.9482**). Plant height showed a positively significant association with number of pods per plant in Morelli x HAV 133 (r = 0.9951**) and Teresa x HAV 131 (r = 0.9662**) while internode lengths were positively associated with the number of pods per plant in Star 2053 x HAV 131 cross (r = 0.9039**). Positive correlation among the studied traits also pointed out that these traits can be exploited in the improvement of snap bean yields and pod quality (Mohammad *et al*., 2008). Pod length was significantly and negatively correlated days to 50% flowering, plant height, internode lengths and number of pods per plant. Araujo *et al*. (2012) found similar results where there was a negative significant correlation between number of pods per plant and pod lengths (-0.46**). This indicates that as the number of pods increases the pod lengths decrease due to competition.

6.3 Performance of new climbing snap bean lines

Climbing commercial snap bean varieties are not formally available for farmers in East and Central Africa. The available climbing beans that are locally developed have poor pod qualities despite the fact that they exhibit multiple disease resistance. Checa *et al*. (2006), found that climbing beans have higher yield compared to the bush types. Therefore selection for high pod yield, multiple disease resistance and good pod traits among the advanced climbing snap beans was the rationale for this study.

The results showed significant genotypic variation ($P \leq 0.05$) in snap bean agronomic traits (50% days to flowering, days to first picking), reaction to disease (rust, angular leaf spot and anthracnose) pod quality (pod length, market grades) and pod yield. The test lines were highly vigorous (3.1) compared to the check varieties (4.1) though growth vigour was not statistically significant. More than 70% of the test lines flowered in the 45^{th} day compared to the check varieties which flowered in 36 days. Days to 50% flowering contributed to differences in days to first picking which occurred in 55 days in comparison to the check varieties' 44 days after planting. Rust, anthracnose and angular leaf spot were severe at Embu where sprinkler irrigation was used. The test lines were highly resistant to rust (1.2), anthracnose (1.3) and angular leaf spot (1.2) compared to the check varieties respectively which had intermediate resistance (rust= 5.4, anthracnose= 3.6 and angular leaf spot= 3.9). The check varieties formed longer pods (10.0cm) compared to the test lines (7.7cm). The average pod yield was 9,831.55 kg ha^{-1} among the test lines compared to the check varieties (1858.6 kg ha^{-1}). Four test lines were found to be outstanding among the climbing snap beans. KSV27-145-1-1M produced 71.2% premium pods while KSV13-1-2-3M produced three times the average yield of the premium pods of the check varieties. KSV04-2-2M met all the market preferred pod characteristics among the test lines. KSV42-2M was also outstanding except that they had shorter pods. The new climbing snap bean lines out-yielded commercial bush varieties four fold. The new lines produced an average of 54% premium grades. The results of this study indicate that new climbing snap bean varieties with market preferred pod characteristics, high yield potential and resistance to major diseases can be developed from the selected lines. Exploitation of the longer harvest period of climbing beans can contribute to higher yields and better returns to investment especially for smallholder farmers, and to the overall competitiveness of the snap bean sub-sector. There is a possibility of improving snap bean yields for smallholder farmers in East Africa. Due to the multiple disease resistance exhibited by the

climbing snap beans, production costs are likely to be reduced (Kimani *et al*., 2006; Chemining'wa *et al.*, 2012). Local production of high yielding quality seed that has multiple disease resistance to major snap bean diseases and good pod traits would enhance snap bean production and competitiveness by enabling smallholder farmers to access the seed affordably. Further, the availability of the seed will enhance reduced costs of production since the farmers will not rely more on expensive fungicides. This will be economical to smallholder farmers who are highly constrained by diseases, high cost of pesticides and stringent export regulations. Fifteen high yielding climbing snap beans exhibiting multiple disease resistance and good pod quality were selected. This implies that locally adapted climbing snap beans with good pod quality can be developed for tropical conditions leading to improved productivity.

6.4 Performance of New bush Snap bean lines

The absence of high yielding bush snap beans with good pod traits and multiple disease resistance was the rationale of this study. Fifty three (F_6, $F_{7.9}$ and F_8) single plants in Progeny I were evaluated for plant vigour, days to 50% flowering, reaction to disease (rust, anthracnose and angular leaf spot), pod quality, and pod yield in preliminary yield trials. Twenty five (25) lines were selected and evaluated in advanced yield trials at Kabete (2014) and Embu and Mwea (2013).

The results revealed that location effects as well as genotypic and interaction effects between genotypes and locations contributed to the significant ($P \leq 0.05$) variations among genotypes in almost all traits. The new bush lines had a growth vigour of 2.3 like the check varieties. The test lines flowered three days earlier than the check varieties and were earlier picked 8 days later than the checks. Further, the test lines showed multiple disease resistance (2.4) compared to the check varieties which had intermediate resistance (3.8). While angular leaf spot was more severe among the three diseases, Wahome *et al*. (2011) found that rust was more limiting compared to the angular leaf spot and anthracnose. The test lines reduced disease severity by up to 36.8%. The test lines had 6% increase in number of pods per plant in comparison to the check varieties. Although the test lines formed shorter pods (8.6cm) than the check varieties, KSB22-3-1T and KSB39-1-1M met the recommended HCDA pod length. The results further revealed that the new bush lines had 80.6% premium pods compared to the check varieties which had 77.3%. The yields of the test lines exceeded those of the check varieties by 29.8%. KSB12-143-3-1M was the earliest flowering (37.8) with the strongest multiple disease resistance (1.2) and had the highest number of podsplant^{-}

[1] while KSB22-3-1T was the most vigorous (1.3) and formed the longest pods (12.0cm). KSB39-3M had the highest yields (13, 359.7 kg ha^{-1}) and KSB46-2 had the highest percentage of premium pods per plant (93.2%). The four lines had straight, round and green pods.

The advanced bush snap bean lines evaluated for yield and multiple disease resistance are promising and are recommended for snap bean improvement. The high yielding bush snap bean cultivars resistant to multiple diseases can be developed and made available to smallholder farmers who are often faced with the challenge of low yielding and highly susceptible commercial varieties (Wahome *et al*., 2013). While improved yields increases' the farmers' output, multiple disease resistance greatly reduces the production costs in terms of reduced overdependence on pesticides, cheap locally available seeds and non-limiting market restrictions in terms of MRLs (Odong, 2012). Further, this enhances improved food security and economic development through exports and creation of employment opportunities.

6.5 Conclusions

The objectives of this study were to: (i) establishing the mode of inheritance for climbing capacity and pod yield in snap beans; (ii) evaluating and selecting for pod quality, pod yield and multiple disease resistance in advanced climbing snap bean populations; and (iii) carrying out advanced yield trials through evaluation and selection for pod quality, pod yield and multiple disease resistance among advanced bush snap bean populations. The results obtained from genetic inheritance of climbing capacity and pod yield indicate that the parental lines used varied genetically. All the traits under study were quantitatively inherited since they exhibited continuous variation. The six parameter model showed that the traits under study are highly heritable and can easily be selected for in a breeding program. The additive and dominance genes that accounted for most traits suggest that selection procedures such as single seed decent and pedigree can be employed for an effective breeding program in snap beans. The high additive genetic variance that was observed denote that all traits under study are easily inheritable. High heritability presents high genetic gain in plant height and days to 50% flowering in snap beans. The positive correlation among the studied characters indicates that improvement of snap bean yield is achievable if these traits are utilized in a breeding program.

Additionally, the selected high yielding advanced climbing and bush snap beans showed multiple disease resistance (to rust, anthracnose and angular leaf spot) as well as good pod quality. Although

the advanced climbing lines flowered later than the bush and check varieties, they had higher yields accredited to longer harvest periods. Therefore the genotypes can be validated in national performance trials and made available to farmers for improved productivity. These genotypes can also be utilized in breeding programs for the development of high yielding disease resistant snap bean varieties with excellent pod qualities for increased food production and economic development.

6.6 Recommendations

Based on the results of this study, it is suggested that:

(i) The genetic information on gene action, genetic variability, and heritability of climbing capacity and pod yield in snap beans should be exploited in snap bean improvement breeding programs.

(ii) Information on correlation among traits should be exploited in the selection of quantitative traits for snap bean improvement. Much emphasis should be given to the strength and direction of trait associations.

(iii) Molecular techniques should be employed in the validation of genes responsible for climbing capacity and pod yield in snap bean.

(iv) The crosses between HAV131 and Samantha, Star 2053 and Teresa were outstanding hence molecular techniques should be applied to validate the genes.

(v) The segregating populations of snap bean crosses evaluated through generation mean analysis should be advanced and selected using single seed descent and/ or pedigree selection methods in order to identify the best performers for breeding programs.

(vi) The selected advanced climbing and bush snap bean lines should be evaluated for pod quality, multiple disease resistance and pod yield in the national performance trials preferably using molecular techniques and artificial disease inoculation for optimal results.

(vii) KSV04-2-2M, KSV13-1-2-3M, KSV27-145-1-1M and KSV25-1-1T should be considered in further selection for climbing capacity, pod yield and pod quality in climbing beans.

(viii) Among the advanced bush snap bean lines, KSB12-143-3-1M, KSB22-3-1T, KSB39-3M and KSB46-2M should be considered for validation in national performance trials (NPT).

(ix) Early flowering genotypes should be exploited for breeding early maturing snap bean genotypes.

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APPENDICES

Appendix 1: Climatic conditions at Kabete in 2014

Kabete Weather data for 2014					
Month	Maximum Temp (°C)	Minimum Temp (°C)	Mean Temp (°C)	Percentage Humidity	Total monthly rainfall (mm)
January	27.9	11.5	19.7	69.9	4.1
February	28.7	13.6	21.2	69.6	90.4
March	29.0	13.4	21.2	69.7	58.1
April	27.8	12.6	20.2	75.8	72.7
May	26.7	13.5	20.1	80.9	108.4
June	25.6	13.3	19.5	81.5	163.7
July	25.4	12.5	18.9	77.4	69.7
August	26.1	14.0	20.0	73.4	60.9
September	26.5	14.2	20.4	70.1	67.7
October	27.4	14.7	21.1	69.7	57.4
November	27.0	13.0	20.0	76.6	50.6
December	26.7	11.5	19.1	77.1	39.0

Appendix 2: ANOVA table of Plant height, 50% days to flowering, Internode length and number of pods per plant in eleven snap bean crosses evaluated at Kabete

CROSS	Analysis of variance for six generations of 11 crosses										
	PLANT HEIGHT					50% DAYS TO FLOWERING					
Paulista x HAV 133	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	35.01	35.01	0.87		Replication stratum	1	0.6	0.6	0.06	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	759626.4	151925.3	3771.65	<.001	Pop	5	1321.02	264.2	25.35	<.001
	Residual	129	5196.23	40.28			Residual	129	1344.49	10.42		
	Total	135	764857.6				Total	135	2666.11			
Morgan x HAV 130	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	30.12	30.12	0.63		Replication stratum	1	7.07	7.07	0.4	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	587883.8	117576.8	2476.81	<.001	Pop	5	2983.33	596.67	33.72	<.001
	Residual	129	6123.77	47.47			Residual	129	2282.54	17.69		
	Total	135	594037.7				Total	135	5272.93			
Samatha x HAV 132	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	6.18	6.18	0.18		Replication stratum	1	3.89	3.89	0.76	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	534678.5	106935.7	3096.41	<.001	Pop	5	2299.786	459.957	89.77	<.001
	Residual	129	4455.07	34.54			Residual	129	660.964	5.124		
	Total	135	539139.8				Total	135	2964.64			
Morelli x HAV130	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	26.47	26.47	0.61		Replication stratum	1	2.12	2.12	0.1	
	Replication.*Units* stratum						Replication.*Units* stratum					

	Pop	5	550966.3	110193.3	2547.83	<.001	Pop	5	910.18	182.04	8.65	<.001
	Residual	129	5579.22	43.25			Residual	129	2715.1	21.05		
	Total	135	556572				Total	135	3627.4			
Samantha x HAV 131	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	55.65	55.65	1.05		Replication stratum	1	67.76	67.76	6.29	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	432294.9	86458.99	1636.2	<.001	Pop	5	1309.47	261.89	24.3	<.001
	Residual	129	6816.53	52.84			Residual	129	1390.38	10.78		
	Total	135	439167.1				Total	135	2767.62			
Serengeti x HAV 132	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	333.6	333.6	7.88		Replication stratum	1	44.735	44.735	5.36	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	453383.4	90676.68	2141.06	<.001	Pop	5	1568.83	313.766	37.58	<.001
	Residual	129	5463.33	42.35			Residual	129	1076.994	8.349		
	Total	135	459180.4				Total	135	2690.559			
Star 2053 x HAV 135	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	2.38	2.38	0.06		Replication stratum	1	3.243	3.243	0.73	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	563415.6	112683.1	2623.77	<.001	Pop	5	2337.998	467.6	105.38	<.001
	Residual	129	5540.18	42.95			Residual	129	572.399	4.437		
	Total	135	568958.1				Total	135	2913.64			
Star 2053 x HAV 131	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	7.53	7.53	0.17		Replication stratum	1	1.44	1.44	0.05	
	Replication.*Units* stratum						Replication.*Units* stratum					
	Pop	5	409582.8	81916.55	1828.93	<.001	Pop	5	772178.6	154435.7	5877.01	<.001
	Residual	129	5777.83	44.79			Residual	129	3389.85	26.28		
	Total	135	415368.1				Total	135	775569.9			

Teresa x HAV 134

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	288.26	288.26	6.05	
Replication.*Units* stratum					
Pop	5	586281	117256.2	2460.28	<.001
Residual	129	6148.09	47.66		
Total	135	592717.4			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	26.47	26.47	1.69	
Replication.*Units* stratum					
Pop	5	1415.95	283.19	18.03	<.001
Residual	129	2026.53	15.71		
Total	135	3468.94			

Teresa x HAV 131

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	5.76	5.76	0.11	
Replication.*Units* stratum					
Pop	5	259672	51934.39	1024.37	<.001
Residual	129	6540.15	50.7		
Total	135	266217.9			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	18.38	18.38	1.31	
Replication.*Units* stratum					
Pop	5	2591	518.2	36.8	<.001
Residual	129	1816.59	14.08		
Total	135	4425.97			

Vernadon x HAV 134

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	11.76	11.76	0.24	
Replication.*Units* stratum					
Pop	5	427835.4	85567.09	1768.67	<.001
Residual	129	6240.93	48.38		
Total	135	434088.1			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	16.243	16.243	1.91	
Replication.*Units* stratum					
Pop	5	2112.18	422.436	49.7	<.001
Residual	129	1096.512	8.5		
Total	135	3224.934			

Paulista x HAV 133

INTRNODE LENGTH

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Replication stratum	1	33.701	33.701	5.53	
Replication.*Units* stratum					
Pop	5	1159.918	231.984	38.05	<.001
Residual	129	786.478	6.097		
Total	135	1980.096			

NUMBER OF PODS PER PLANT

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	39.18	39.18	3.21	
Rep.*Units* stratum					
Population	5	3742.74	748.55	61.34	<.001
Residual	129	1574.19	12.2		
Total	135	5356.11			

Morgan x HAV 130

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

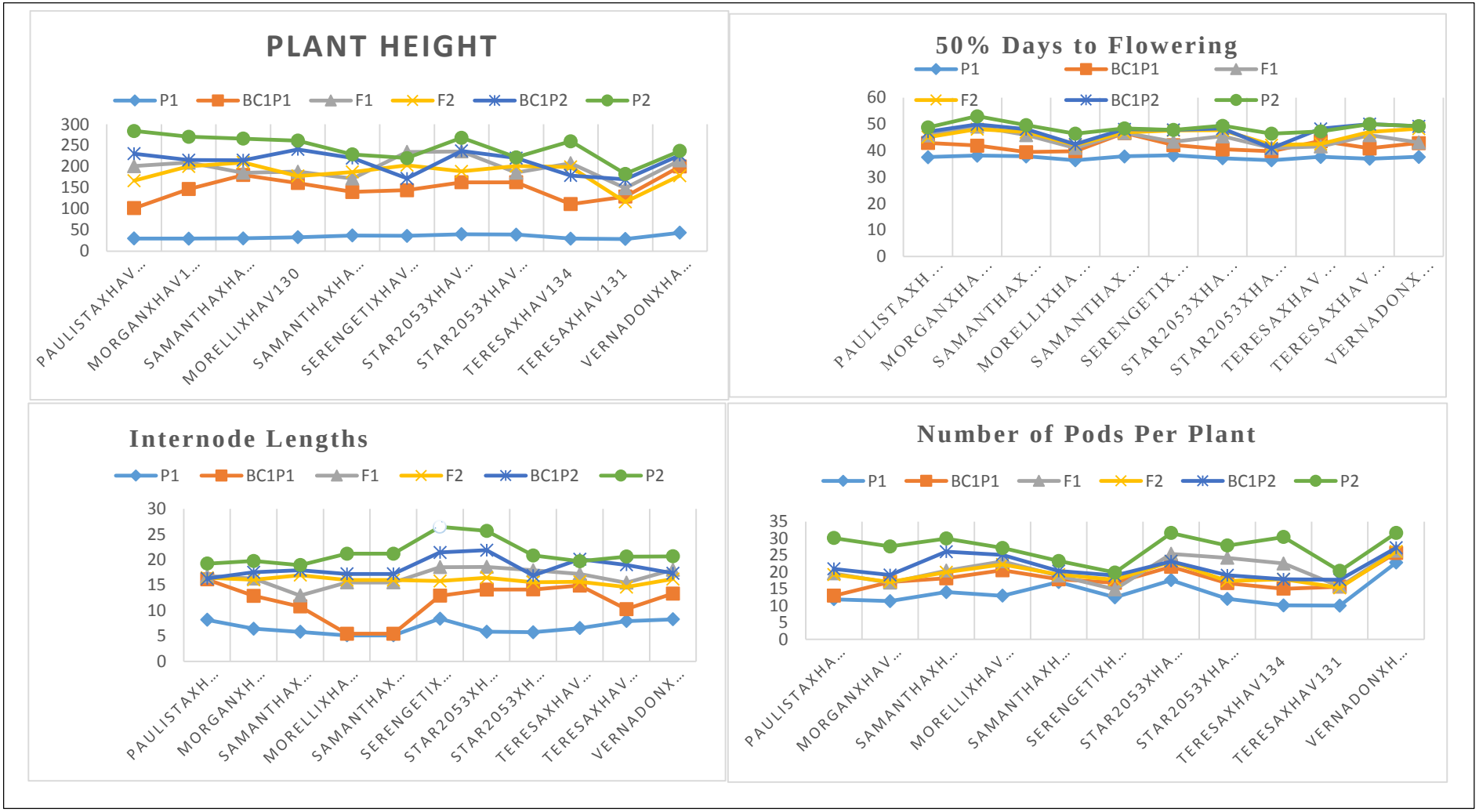
Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

	Replication stratum	1	0.381	0.381	0.1		Rep stratum	1	15.559	15.559	1.96	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	1872.005	374.401	96.1	<.001	Population	5	2289.487	457.897	57.63	<.001
	Residual	129	502.559	3.896			Residual	129	1024.925	7.945		
	Total	135	2374.945				Total	135	3329.971			
Samatha x HAV 132	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	15.289	15.289	2.23		Rep stratum	1	10.62	10.62	0.91	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	2253.95	450.79	65.86	<.001	Population	5	2918.53	583.71	49.76	<.001
	Residual	129	883.016	6.845			Residual	129	1513.32	11.73		
	Total	135	3152.255				Total	135	4442.47			
Morelli x HAV130	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	20.577	20.577	3.88		Rep stratum	1	6.618	6.618	0.7	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	4283.36	856.672	161.67	<.001	Population	5	2036.571	407.314	43.27	<.001
	Residual	129	683.557	5.299			Residual	129	1214.341	9.413		
	Total	135	4987.493				Total	135	3257.529			
Samantha x HAV 131	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	21.521	21.521	2.73		Rep stratum	1	0.596	0.596	0.07	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	1239.394	247.879	31.45	<.001	Population	5	413.1	82.62	9.09	<.001
	Residual	129	1016.842	7.882			Residual	129	1172.65	9.09		
	Total	135	2277.756				Total	135	1586.346			
Serengeti x HAV 132	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	2.796	2.796	0.42		Rep stratum	1	2.125	2.125	0.3	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	3579.911	715.982	108.78	<.001	Population	5	644.949	128.99	18.23	<.001

	Residual	129	849.053	6.582		Residual	129	912.683	7.075		
	Total	135	4431.759			Total	135	1559.757			
Star 2053 x HAV 135	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	10.562	10.562	2.09		Rep stratum	1	0.01	0.01	0	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	4023.59	804.718	159.4	<.001	Population	5	1764.39	352.88	34.24	<.001
	Residual	129	651.229	5.048			Residual	129	1329.6	10.31		
	Total	135	4685.38				Total	135	3093.99			
Star 2053 x HAV 131	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	6.795	6.795	1.12		Rep stratum	1	0.18	0.18	0.02	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	2157.028	431.406	71.29	<.001	Population	5	2703.08	540.62	53.41	<.001
	Residual	129	780.634	6.051			Residual	129	1305.67	10.12		
	Total	135	2944.458				Total	135	4008.93			
Teresa x HAV 134	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	1.167	1.167	0.15		Rep stratum	1	38.12	38.12	3.08	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	2105.565	421.113	55.04	<.001	Population	5	3971.54	794.31	64.19	<.001
	Residual	129	986.918	7.651			Residual	129	1596.34	12.37		
	Total	135	3093.65				Total	135	5606			
Teresa x HAV 131	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	25.596	25.596	5.68		Rep stratum	1	7.529	7.529	0.87	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	2215.45	443.09	98.29	<.001	Population	5	957.362	191.472	22.1	<.001
	Residual	129	581.509	4.508			Residual	129	1117.55	8.663		
	Total	135	2822.554				Total	135	2082.441			

Vernadon x HAV 134	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	6.618	6.618	1.2		Rep stratum	1	12.36	12.36	1.56	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Pop	5	1570.614	314.123	57.11	<.001	Population	5	671.48	134.296	16.98	<.001
	Residual	129	709.498	5.5			Residual	129	1020.094	7.908		
	Total	135	2286.729				Total	135	1703.934			

Appendix 3: Means of plant height, 50% days to flowering, internode length and number of pods per plant for all populations of eleven crosses



Appendix 4: Regression analysis for plant height, 50% days to flowering, internode length and number of pods per plant in eleven snap bean crosses evaluated in Kabete based on the 6-parameter model

Cross	Regression analysis											
	Terms Fitted: Constant + A + D + AA + AD + DD											
	Plant Height						Days to 50% Flowering					
Paulista x HAV 133	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	83982.41	16796.48	20441.97	<.001	Regression	5	157.9515	31.5903	811.74	<.001
	Residual	6	4.93	0.8217			Residual	6	0.2335	0.03892		
	Total	11	83987.34	7635.213			Total	11	158.185	14.38045		
Morgan x HAV130	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	68870.35	13774.07	4968.1	<.001	Regression	5	307.81	61.5621	240.61	<.001
	Residual	6	16.64	2.773			Residual	6	1.535	0.2559		
	Total	11	68886.99	6262.454			Total	11	309.345	28.1223		
Samantha x HAV132	Source	d.f.	s.s.	m.s.			Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	64036.83	12807.37			Regression	5	253.498	50.6995	107.18	<.001
	Residual	6	2.195	0.3658			Residual	6	2.838	0.473		
	Total	11	64039.03	5821.73			Total	11	256.336	23.3032		
Morelli x HAV130	Source	d.f.	s.s.	m.s.			Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	64725.94	12945.19			Regression	5	108.488	21.6975	24.45	<.001
	Residual	6	3.85	0.6417			Residual	6	5.325	0.8875		
	Total	11	64729.79	5884.526			Total	11	113.813	10.3466		
Samantha x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	76721.62	15344.32	2799.63	<.001	Regression	5	156.419	31.284	23.51	<.001
	Residual	6	32.89	5.481			Residual	6	7.984	1.331		
	Total	11	76754.5	6977.682			Total	11	164.403	14.946		

Serengeti x HAV132	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	52775.47	10555.09	1175.4	<.001	Regression	5	156.052	31.2105	51.41	<.001
	Residual	6	53.88	8.98			Residual	6	3.642	0.6071		
	Total	11	52829.35	4802.668			Total	11	159.695	14.5177		
Star 2053 x HAV135	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	67463.67	13492.74	2700.8	<.001	Regression	5	239.107	47.8214	97.3	<.001
	Residual	6	29.97	4.996			Residual	6	2.949	0.4915		
	Total	11	67493.65	6135.786			Total	11	242.056	22.0051		
Star 2053 x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	47153.27	9430.654	2230.35	<.001	Regression	5	45864.52	9172.904	20285.06	<.001
	Residual	6	25.37	4.228			Residual	6	2.713	0.4522		
	Total	11	47178.64	4288.967			Total	11	45867.23	4169.748		
Teresa x HAV134	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	66908.65	13381.73	2546.07	<.001	Regression	5	148.81	29.763	11.11	0.01
	Residual	6	31.54	5.256			Residual	6	16.07	2.679		
	Total	11	66940.19	6085.472			Total	11	164.89	14.99		
Teresa x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	30337.74	6067.55	405.72	<.001	Regression	5	273.331	54.6662	78.35	<.001
	Residual	6	89.73	14.95			Residual	6	4.186	0.6977		
	Total	11	30427.47	2766.13			Total	11	277.517	25.2289		
Vernadon x HAV134	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	51368.8	10273.76	3960.33	<.001	Regression	5	218.076	43.615	33.89	<.001
	Residual	6	15.57	2.594			Residual	6	7.722	1.287		
	Total	11	51384.37	4671.306			Total	11	225.798	20.527		

	Internode Length	**Number of pods per plant**

Paulista x HAV 133	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	142.34	28.468	27.9	<.001	Regression	5	427.732	85.546	73.23	<.001
	Residual	6	6.122	1.02			Residual	6	7.009	1.168		
	Total	11	148.462	13.497			Total	11	434.741	39.522		
Morgan x HAV130	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	227.774	45.5547	177.58	<.001	Regression	5	281.084	56.2169	57.58	<.001
	Residual	6	1.539	0.2565			Residual	6	5.858	0.9763		
	Total	11	229.313	20.8466			Total	11	286.942	26.0857		
Samantha x HAV132	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	253.498	50.6995	107.18	<.001	Regression	5	326.371	65.2741	265.82	<.001
	Residual	6	2.838	0.473			Residual	6	1.473	0.2456		
	Total	11	256.336	23.3032			Total	11	327.844	29.804		
Morelli x HAV130	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	437.758	87.5515	224.45	<.001	Regression	5	242.325	48.4651	126.93	<.001
	Residual	6	2.34	0.3901			Residual	6	2.291	0.3818		
	Total	11	440.098	40.0089			Total	11	244.616	22.2378		
Samantha x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	150.286	30.0572	59.02	<.001	Regression	5	48.281	9.6563	19.09	0
	Residual	6	3.056	0.5093			Residual	6	3.035	0.5058		
	Total	11	153.342	13.9402			Total	11	51.316	4.6651		
Serengeti x HAV132	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	406.143	81.2285	96.49	<.001	Regression	5	74.758	14.9515	18.05	0
	Residual	6	5.051	0.8419			Residual	6	4.97	0.8283		
	Total	11	411.194	37.3813			Total	11	79.727	7.2479		
Star 2053 x HAV135	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.

	Regression	5	469.984	93.9968	318.62	<.001	Regression	5	215.599	43.1198	231.29	<.001
	Residual	6	1.77	0.295			Residual	6	1.119	0.1864		
	Total	11	471.754	42.8867			Total	11	216.718	19.7016		
Star 2053 x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	265.353	53.071	38.21	<.001	Regression	5	321.02	64.203	38.34	<.001
	Residual	6	8.334	1.389			Residual	6	10.05	1.674		
	Total	11	273.687	24.881			Total	11	331.06	30.096		
Teresa x HAV134	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	244.05	48.809	24.04	<.001	Regression	5	480.263	96.053	84.06	<.001
	Residual	6	12.18	2.03			Residual	6	6.856	1.143		
	Total	11	256.23	23.293			Total	11	487.118	44.283		
Teresa x HAV131	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	238.978	47.7955	79.43	<.001	Regression	5	115.381	23.0763	61.58	<.001
	Residual	6	3.611	0.6018			Residual	6	2.249	0.3748		
	Total	11	242.588	22.0535			Total	11	117.63	10.6936		
Vernadon x HAV134	Source	d.f.	s.s.	m.s.	v.r.	F pr.	Source	d.f.	s.s.	m.s.	v.r.	F pr.
	Regression	5	187.246	37.4492	179.08	<.001	Regression	5	82.048	16.4097	22.64	<.001
	Residual	6	1.255	0.2091			Residual	6	4.349	0.7249		
	Total	11	188.501	17.1364			Total	11	86.397	7.8543		

Appendix 5: Climbing snap bean genotypes evaluated in preliminary yield trials at Mwea during the 2013 long rain season.

	Performance Test Lines and Checks in the Preliminary Yield Trials								
Test line/Check	Vigour	Pod length	Rust	Anthracnose	Angular Leaf Spot	Total Pod Yield	Pod Colour	Pod Curvature	Pod Shape
KSV01-1M	2.0	9.1	1.0	1.0	1.0	9955.0	Green	Straight	Round
KSV01-2M	0.5	7.2	0.5	0.5	0.5	352.0	Light Green	Slightly curved	Flat
KSV04-1-2M	1.5	10.2	1.0	1.0	1.0	12240.0	Green	Straight	Round
KSV04-2-2M	2.0	8.1	1.0	1.0	1.0	9943.0	Green	Straight	Round
KSV06-1-1-1M	3.0	8.9	1.0	1.0	1.0	1120.0	Green	Straight	Round
KSV08-2-2-1T	3.0	9.2	1.0	1.0	1.0	6447.0	Green	Straight	Round
KSV08-304-1-1M	2.0	7.8	1.0	1.0	1.0	973.0	Green	Straight	Flat
KSV08-3M	3.0	7.6	1.0	1.0	1.0	645.0	Green	Slightly curved	Round
KSV13-1-2-3M	2.0	8.3	1.0	1.0	1.0	13689.0	Green	Straight	Round
KSV13-147-3-2M	1.5	5.6	0.5	0.5	0.5	549.0	Light Green	Straight	Flat
KSV14-1-4M	1.5	7.8	1.0	1.0	1.0	8190.0	Green	Straight	Round
KSV17-1-1T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV17-145-1-1M	2.0	8.4	1.0	1.0	1.0	8739.0	Green	Straight	Round
KSV17-2-1-1T	1.0	9.2	1.0	1.0	1.0	7243.0	Green	Straight	Round
KSV19-1-2M	2.0	6.7	1.0	1.0	1.0	5494.0	Green	Straight	Round
KSV19-1M	2.0	5.1	1.0	1.0	1.0	613.0	Light Green	Curved	Round
KSV19-2-2T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV19-3M	1.5	6.8	1.0	1.0	1.0	837.0	Green	Curved	Round
KSV21-1-1-1T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV21-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV22-148-2-1T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV23-1M	1.5	9.8	1.0	1.0	1.0	1379.0	Green	Slightly curved	Flat
KSV23-1-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV23-66-3-1-2M	2.0	4.7	1.0	1.0	1.0	681.0	Green	Straight	Flat
KSV23-66-3-1-3M	2.5	9.5	1.0	1.0	1.0	1114.0	Light Green	Straight	Flat
KSV25-1-1T	3.0	11.8	1.0	1.0	1.0	6213.0	Green	Straight	Round
KSV27-145-1-1M	2.0	9.1	1.0	1.0	1.0	8702.0	Green	Straight	Round
KSV27-69-4-1-2T	2.0	8.9	1.0	1.0	1.0	7508.0	Green	Straight	Round
KSV27-69-4-2-1T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV29-2M	1.0	8.3	1.0	1.0	1.0	9934.0	Light Green	Straight	Round
KSV30-1-1-1M	2.5	4.8	1.0	1.0	1.0	776.0	Purple	Straight	Round
KSV36-1-1-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV37-3M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV41-1-1M	3.0	6.4	1.0	1.0	1.0	617.0	Purple	Curved	Round
KSV41-1-2-3M	1.0	8.3	1.0	1.0	1.0	9718.0	Green	Straight	Round
KSV41-1-2M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV41-1-2T	3.0	9.5	1.0	1.0	1.0	9132.0	Green	Straight	Round
KSV41-1-3M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV41-2-1-1M	1.0	6.7	1.0	1.0	1.0	7689.0	Green	Straight	Round

KSV41-2-1T	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV42-1-1M	2.5	4.6	1.0	1.0	1.0	971.0	Purple	Straight	Round
KSV42-2M	1.5	9.8	1.0	1.0	1.0	11737.0	Green	Straight	Round
KSV43-1T	1.5	8.5	1.0	1.0	1.0	8574.0	Green	Straight	Round
KSV44-1M	2.0	9.9	1.0	1.0	1.0	10056.0	Green	Straight	Round
KSV45-2M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV45-5-1T	2.5	4.9	1.0	1.0	1.0	310.0	Purple	Curved	Round
KSV46-2M	1.0	7.9	1.0	1.0	1.0	7654.0	Green	Straight	Round
KSV47-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSV49-1M	1.5	3.9	1.0	1.0	1.0	234.0	Light Green	Straight	Flat
KSV49-1T	3.0	5.8	1.0	1.0	1.0	1819.0	Light Green	Curved	Round
KSV49-2-1-2M	3.0	6.7	1.0	1.0	1.0	622.0	Purple	Slightly curved	Round
KSV49-2-2T	2.5	7.3	1.0	1.0	1.0	624.0	Green	Straight	Flat
KSV54-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
Checks									
Morelli	4.3	10.8	7.0	3.5	3.0	2513.9	Purple	Straight	Round
Morgan	3.8	11.4	5.3	3.3	4.3	2641.5	Green	Straight	Round
Samantha	4.5	11.7	5.0	2.5	5.0	2907.9	Light Green	Straight	Flat
Star 2053	4.5	10.9	5.0	4.0	3.5	3020.8	Green	Straight	Round
Teresa	3.5	11.3	4.8	4.8	3.5	3610.6	Light Green	Straight	Round
Grand Mean	1.4	7.8	0.7	0.7	0.7	3643.0			
$LSD_{0.05}$	1.2	2.6	0.2	0.2	0.2	1744.5			
CV (%)	46.6	15.9	19.3	19.3	19.3	27.6			

Appendix 6: Climatic conditions in Embu and Mwea, 2013

	Embu				Mwea			
	Maximum Temp (°C)	Minimum Temp (°C)	Mean Temp (°C)	Total monthly rainfall (mm)	Maximum Temp (°C)	Minimum Temp (°C)	Mean Temp (°C)	Total monthly rainfall (mm)
January	29.0	10.0	19.5	27.1	32.0	11.0	21.5	13.0
February	30.0	10.0	20.0	26.0	34.0	12.0	23.0	24.0
March	32.0	11.0	21.5	113.8	37.0	12.0	24.5	72.0
April	31.0	10.0	20.5	278.2	34.0	12.0	23.0	294.0
May	29.0	10.0	19.5	164.4	34.0	11.0	22.5	139.0
June	27.0	9.0	18.0	32.1	32.0	10.0	21.0	23.0
July	26.0	9.0	17.5	29.0	31.0	10.0	20.5	7.0
August	26.0	9.0	17.5	38.7	31.0	10.0	20.5	11.0
September	29.0	10.0	19.5	40.9	34.0	11.0	22.5	12.0
October	30.0	10.0	20.0	171.8	36.0	11.0	23.5	108.0
November	29.0	10.0	19.5	234.3	33.0	11.0	22.0	158.0
December	28.0	9.0	18.5	52.7	32.0	10.0	21.0	59.0

Appendix 7: Analysis of Variance of all traits studied in the selection of Advance climbing snap beans in two locations

Trait	Analysis of variance											
	Mwea						Embu					
Vigor	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.38	3.38	1.33		Rep stratum	1	89.78	89.78	9.3	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	96.08	4.003	1.57	0.137	Genotype	24	137.88	5.745	0.6	0.895
	Residual	24	61.12	2.547			Residual	24	231.72	9.655		
	Total	49	160.58				Total	49	459.38			
50% Days to Flowering	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.98	0.98	0.17		Rep stratum	1	18	18	1.18	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	322	13.417	2.31	0.023	Genotype	24	1333.88	55.58	3.63	0.001
	Residual	24	139.52	5.813			Residual	24	367	15.29		
	Total	49	462.5				Total	49	1718.88			
Days_to_1st_Picking	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	4.5	4.5	1.07		Rep stratum	1	403.3	403.3	2.21	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	979.48	40.812	9.7	<.001	Genotype	24	5018	209.1	1.14	0.372
	Residual	24	101	4.208			Residual	24	4386.7	182.8		
	Total	49	1084.98				Total	49	9808			
	Reaction to diseases											
Rust	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.92	3.92	3.61		Rep stratum	1	0.32	0.32	0.49	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	91.28	3.803	3.5	0.002	Genotype	24	278	11.5833	17.73	<.001

	Residual	24	26.08		1.087			Residual	24	15.68	0.6533		
	Total	49	121.28					Total	49	294			
Anthracnose	Source of variation	d.f.	s.s.	m.s.		v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.5		0.5	0.39		Rep stratum	1	0	0	0	
	Rep.*Units* stratum							Rep.*Units* stratum					
	Genotype	24	42.12		1.755	1.36	0.229	Genotype	24	100.72	4.197	1.68	0.106
	Residual	24	31		1.292			Residual	24	60	2.5		
	Total	49	73.62					Total	49	160.72			
Angula Leaf Spot	Source of variation	d.f.	(m.v.)	s.s.		m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1			0.781	0.781	0.64		Rep stratum	1	0.98	0.98	0.72	
	Rep.*Units* stratum								Rep.*Units* stratum					
	Genotype	24			61.469	2.561	2.09		Genotype	24	97.72	4.072	3	0.005
	Residual	23	-1		28.25	1.228			Residual	24	32.52	1.355		
	Total	48	-1		89.551				Total	49	131.22			
								Pod Length					
Extra Fine	Source of variation	d.f.	s.s.	m.s.		v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	25.28		25.28	1.38		Rep stratum	1	85.761	85.761	12.49	
	Replication.*Units* stratum							Rep.*Units* stratum					
	Genotype	24	879.93		36.66	2	0.048	Genotype	24	224.886	9.37	1.36	0.226
	Residual	24	440.59		18.36			Residual	24	164.788	6.866		
	Total	49	1345.79					Total	49	475.435			
Fine	Source of variation	d.f.	s.s.	m.s.		v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	0.2		0.2	0.01		Rep stratum	1	142.84	142.84	12.48	
	Replication.*Units* stratum							Rep.*Units* stratum					
	Genotype	24	385.9		16.08	0.95	0.549	Genotype	24	204.08	8.5	0.74	0.764
	Residual	24	405.82		16.91			Residual	24	274.65	11.44		

	Total	49	791.93				Total	49	621.57			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Replication stratum	1	7.42	7.42	0.28		Rep stratum	1	137.098	137.098	14.42	
	Replication.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	888.12	37.01	1.39	0.212	Genotype	24	576.462	24.019	2.53	0.014
	Residual	24	637.96	26.58			Residual	24	228.149	9.506		
	Total	49	1533.5				Total	49	941.71			

Pod Yield

Extra fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	6.63E+03	6.63E+03	0.02		Rep stratum	1	788520	788520	0.85	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	2.85E+08	1.19E+07	28.54	<.001	Genotype	24	98022815	4084284	4.41	<.001
	Residual	624	2.59E+08	4.16E+05			Residual	624	577879820	926089		
	Total	649	5.44E+08				Total	649	676691155			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	8.56E+06	8.56E+06	1.81		Rep stratum	1	2.45E+07	2.45E+07	1.5	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	1.36E+09	5.65E+07	11.91	<.001	Genotype	24	4.63E+09	1.93E+08	11.84	<.001
	Residual	624	2.96E+09	4.74E+06			Residual	624	1.02E+10	1.63E+07		
	Total	649	4.32E+09				Total	649	1.48E+10			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.
	Rep stratum	1	1.82E+05	1.82E+05	0.01		Rep stratum	1		1.59E+04	1.59E+04	0.01
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	6.26E+09	2.61E+08	9.71	<.001	Genotype	24		7.83E+08	3.26E+07	10.91
	Residual	624	1.68E+10	2.69E+07			Residual	623	-1.00E+00	1.86E+09	2.99E+06	
	Total	649	2.30E+10				Total	648	-1.00E+00	2.64E+09		

Total Pod Yield	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	1.21E+07	1.21E+07	0.38		Rep stratum	1	2.86E+07	2.86E+07	1.44	
	Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	24	8.18E+09	3.41E+08	10.88	<.001	Genotype	24	9.75E+09	4.06E+08	20.49	<.001
	Residual	624	1.96E+10	3.13E+07			Residual	624	1.24E+10	1.98E+07		
	Total	649	2.77E+10				Total	649	2.22E+10			

Appendix 8: Combined Analysis of Variance for all traits studied in the selection of advance climbing snap beans in Mwea and Embu

Trait	Combined Analysis of Variance					
Vigour	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	64	64	9.74	
	Rep.*Units* stratum					
	Genotype	24	96.5	4.021	0.61	0.903
	Location	1	27.04	27.04	4.11	0.048
	Genotype.Location	24	137.46	5.728	0.87	0.634
	Residual	49	322	6.571		
	Total	99	647			
50% Days to flowering	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	5.29	5.29	0.5	
	Rep.*Units* stratum					
	Genotype	24	1397.94	58.25	5.49	<.001
	Location	1	670.81	670.81	63.19	<.001
	Genotype.Location	24	257.94	10.75	1.01	0.47
	Residual	49	520.21	10.62		
	Total	99	2852.19			
Days_to_1st_Picking_C	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	246.49	246.49	2.6	
	Rep.*Units* stratum					
	Genotype	24	3686.64	153.61	1.62	0.076
	Location	1	8.41	8.41	0.09	0.767
	Genotype.Location	24	2310.84	96.29	1.01	0.467
	Residual	49	4649.01	94.88		
	Total	99	10901.39			
Rust	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.24	3.24	3.71	
	Rep.*Units* stratum					

	Genotype	24	304.84	12.7017	14.56	<.001
	Location	1	2.56	2.56	2.93	0.093
	Genotype.Location	24	64.44	2.685	3.08	<.001
	Residual	49	42.76	0.8727		
	Total	99	417.84			
Anthracnose	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.25	0.25	0.13	
	Rep.*Units* stratum					
	Genotype	24	112.34	4.681	2.51	0.003
	Location	1	0.25	0.25	0.13	0.716
	Genotype.Location	24	30.5	1.271	0.68	0.844
	Residual	49	91.25	1.862		
	Total	99	234.59			
Angular Leaf spot	Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.
	Rep stratum	1		0.01	0.01	0.01
	Rep.*Units* stratum					
	Genotype	24		132.612	5.525	4.24
	Location	1		0.091	0.091	0.07
	Genotype.Location	24		26.159	1.09	0.84
	Residual	48	-1	62.49	1.302	
	Total	98	-1	220.909		

	Pod Length				
Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	102.08	102.08	8.14	
	Rep.*Units* stratum					
	Genotype	24	680.02	28.33	2.26	0.008
	Location	1	0.37	0.37	0.03	0.864
	Genotype.Location	24	424.8	17.7	1.41	0.152
	Residual	49	614.34	12.54		

	Total	99	1821.6			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	66.11	66.11	4.28	
	Rep.*Units* stratum					
	Genotype	24	359.07	14.96	0.97	0.52
	Location	1	38.04	38.04	2.46	0.123
	Genotype.Location	24	230.92	9.62	0.62	0.895
	Residual	49	757.4	15.46		
	Total	99	1451.54			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	40.36	40.36	2.04	
	Rep.*Units* stratum					
	Genotype	24	1045.89	43.58	2.2	0.01
	Location	1	145.51	145.51	7.35	0.009
	Genotype.Location	24	418.7	17.45	0.88	0.623
	Residual	49	970.27	19.8		
	Total	99	2620.73			

Pod Yield

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.25E+05	3.25E+05	0.48	
	Rep.*Units* stratum					
	Genotype	24	2.23E+08	9.31E+06	13.88	<.001
	Location	1	2.82E+07	2.82E+07	42.05	<.001
	Genotype.Location	24	1.59E+08	6.64E+06	9.9	<.001
	Residual	1249	8.38E+08	6.71E+05		
	Total	1299	1.25E+09			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.10E+07	3.10E+07	2.95	

	Rep.*Units* stratum					
	Genotype	24	5.48E+09	2.29E+08	21.74	<.001
	Location	1	1.13E+09	1.13E+09	107.23	<.001
	Genotype.Location	24	5.00E+08	2.08E+07	1.98	0.003
	Residual	1249	1.31E+10	1.05E+07		
	Total	1299	2.03E+10			
Bobby	Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.
	Rep stratum	1		1.53E+05	1.53E+05	0.01
	Rep.*Units* stratum					
	Genotype	24		5.73E+09	2.39E+08	16
	Location	1		3.86E+09	3.86E+09	258.81
	Genotype.Location	24		1.31E+09	5.45E+07	3.65
	Residual	1248	-1	1.86E+10	1.49E+07	
	Total	1298	-1	2.95E+10		
Total Pod Yield	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.89E+07	3.89E+07	1.52	
	Rep.*Units* stratum					
	Genotype	24	1.70E+10	7.07E+08	27.68	<.001
	Location	1	7.20E+08	7.20E+08	28.16	<.001
	Genotype.Location	24	9.53E+08	3.97E+07	1.55	0.043
	Residual	1249	3.19E+10	2.56E+07		
	Total	1299	5.06E+10			

Appendix 9: Climatic conditions in Kabete (2014), Embu and Mwea in (2013)

Weather data for Kabet, Embu and Mwea						
	Kabete		Embu		Mwea	
Month	Temperature (°C)	Total monthly rainfall (mm)	Temperature (°C)	Total monthly rainfall (mm)	Temperature (°C)	Total monthly rainfall (mm)
January	19.7	4.1	19.5	27.1	21.5	13.0
February	21.2	90.4	20.0	26.0	23.0	24.0
March	21.2	58.1	21.5	113.8	24.5	72.0
April	20.2	72.7	20.5	278.2	23.0	294.0
May	20.1	108.4	19.5	164.4	22.5	139.0
June	19.5	163.7	18.0	32.1	21.0	23.0
July	18.9	69.7	17.5	29.0	20.5	7.0
August	20.0	60.9	17.5	38.7	20.5	11.0
September	20.4	67.7	19.5	40.9	22.5	12.0
October	21.1	57.4	20.0	171.8	23.5	108.0
November	20.0	50.6	19.5	234.3	22.0	158.0
December	19.1	39	18.5	52.7	21.0	59.0

Appendix 10: Advanced bush snap bean genotypes evaluated in preliminary yield trials at Mwea and Embu during the 2013 long rain season and Kabete during the long rain season, 2014

Genotype	Plant Vigour	50%Days to Flowering	Rust	Anthracnose	Angular leaf spot	Pod yield (kg ha^{-1})	Pod colour	Pod Curvature	Pod Shape
KSB 39-2-1-2M	2.0	35.0	2.0	1.0	2.0	10408.0	Green	Straight	Round
KSB04-1-1M	2.0	37.0	3.0	2.0	1.0	11763.0	Light Green	Straight	Round
KSB06-1-1-2M	3.0	38.5	5.0	1.0	1.0	13125.0	Green	Straight	Round
KSB06-1-1-4M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB06-1-2/1-1M	8.0	42.0	7.0	3.0	4.0	5319.0	Green	Slightly curved	Flat
KSB07-3-1-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB08-3-4M	1.0	37.0	4.0	3.0	1.0	12613.0	Light Green	Straight	Round
KSB10-152-1-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB12-143-3-1M	3.0	33.0	3.0	3.0	2.0	11243.0	Green	Straight	Round
KSB13-1-1-1M	3.0	39.5	5.0	4.0	2.0	11088.0	Green	Straight	Round
KSB13-1-2-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB13-1-2-2M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB13-147-3-2M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB14-1-2M	7.0	37.0	7.0	3.0	3.0	5981.0	Green	Slightly curved	Flat
KSB17-2-1-2M	9.0	36.0	3.0	2.0	3.0	4914.0	Light Green	Straight	Flat
KSB17-2-2T	6.0	44.0	1.0	1.0	1.0	3102.0	Green	Straight	Round
KSB18-2M	9.0	42.5	5.0	8.0	3.0	7101.0	Light Green	Straight	Round
KSB19-6M	5.0	41.5	5.0	4.0	2.0	3665.0	Light Green	Slightly curved	Round
KSB21-1-1-3M	8.0	37.5	3.0	4.0	9.0	7366.0	Purple	Straight	Round
KSB21-2M	9.0	39.5	8.0	3.0	6.0	7462.0	Green	Straight	Round
KSB22-3-1T	2.0	39.0	3.0	1.0	2.0	9169.0	Green	Straight	Round
KSB23-143-3-1M	0.5	26.3	2.0	1.0	1.0	8664.0	Green	Straight	Round
KSB23-66-1-2-1M	7.0	41.0	1.0	1.0	2.0	7544.0	Green	Straight	Round
KSB25-3-1-1M	5.0	40.5	6.0	4.0	4.0	7830.0	Green	Slightly curved	Round
KSB27-143-2-1M	3.0	38.0	3.0	1.0	1.0	8183.0	Green	Straight	Round
KSB27-169-1-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-

KSB27-69-4-2-1T	9.0	35.0	3.0	2.0	6.0	8214.0	Green	Slightly curved	Flat
KSB30-3-1-2M	3.0	38.0	3.0	1.0	3.0	10235.0	Green	Straight	Round
KSB30-3-1-3M	5.0	38.5	3.0	3.0	8.0	3302.0	Green	Straight	Round
KSB33-1-2M	3.0	42.0	2.0	1.0	3.0	7917.0	Green	Straight	Round
KSB33-3-1M	2.0	39.5	6.0	3.0	2.0	6294.0	Green	Straight	Round
KSB36-1-5M	2.0	41.0	5.0	6.0	4.0	7213.0	Green	Straight	Round
KSB39-1-1M	1.0	43.5	4.0	4.0	4.0	9245.0	Green	Straight	Round
KSB39-1-2M	4.0	40.0	3.0	1.0	3.0	5101.0	Light Green	Straight	Round
KSB39-1-4M	2.0	37.5	2.0	1.0	1.0	8215.0	Green	Straight	Round
KSB39-1-5M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB39-2-1-1M	5.0	36.0	2.0	1.0	1.0	5366.0	Green	Straight	Flat
KSB39-2-4M	3.0	43.0	2.0	3.0	2.0	8764.0	Green	Straight	Round
KSB39-3-1M	4.0	35.5	3.0	1.0	7.0	5462.0	Light Green	Straight	Round
KSB39-3M	1.0	39.0	3.0	1.0	3.0	11419.0	Green	Straight	Round
KSB39-4-4M	3.0	41.5	3.0	4.0	2.0	11428.0	Green	Slightly curved	Round
KSB42-1-2-2M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB42-1-2M	9.0	38.5	4.0	2.0	9.0	5544.0	Green	Straight	Round
KSB42-2-1-4M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
KSB42-2-2M	4.0	40.0	2.0	3.0	3.0	11964.0	Green	Straight	Round
KSB42-2M	6.0	39.0	6.0	3.0	8.0	5830.0	Purple	Straight	Round
KSB42-3M	9.0	34.5	6.0	3.0	9.0	6214.0	Green	Straight	Round
KSB43-2M	5.0	38.5	2.0	4.0	2.0	10847.0	Green	Straight	Round
KSB44-1-4M	4.0	42.0	4.0	2.0	3.0	2542.0	Green	Straight	Round
KSB45-1M	1.0	37.5	4.0	4.0	7.0	2988.0	Green	Slightly curved	Round
KSB45-3M	7.0	34.0	1.0	1.0	6.0	6664.0	Light Green	Straight	Round
KSB46-2M	3.0	44.0	3.0	4.0	7.0	11465.0	Green	Straight	Round
KSB47-1-2M	1.0	39.0	3.0	5.0	2.0	13603.0	Green	Straight	Round
KSB47-2-2M	1.0	42.0	3.0	6.0	4.0	10464.0	Green	Straight	Round
KSB47-2M	1.0	36.5	3.0	2.0	1.0	11017.0	Green	Straight	Round
KSB47-5M	7.0	42.5	4.0	1.0	2.0	3221.0	Light Green	Straight	Round
KSB52-2M	3.0	33.0	2.0	1.0	4.0	12621.0	Green	Straight	Round

KSB66-25-1-2-1M	0.0	0.0	0.0	0.0	0.0	0.0	-	-	-
Checks									
Samantha	3.0	39.0	5.0	3.0	1.0	5384.0	Light Green	Straight	Flat
Star 2053	1.0	37.5	6.0	1.0	5.0	4149.0	Green	Straight	Round
Teresa	5.0	38.0	2.0	5.0	3.0	6074.0	Green	Straight	Round
Grand Mean	3.4	31.3	2.9	2.2	2.8	6429.0			
LSD	1.3	8.9	3.0	2.8	2.0	2818.4			
CV	22.4	16.4	58.0	75.9	39.9	25.3			

Appendix 11: Analysis of variance for preliminary yield trials of advanced climbing snap beans in Mwea and Embu

Analysis of variance

Plant Vigour

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	1.1613	1.1613	2.01	
Rep.*Units* stratum					
Genotype	60	1032.419	17.207	29.77	<.001
Residual	62	35.8387	0.578		
Total	123	1069.419			

Days to 50% Flowering

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	0.65	0.65	0.02	
Rep.*Units* stratum					
Genotype	60	28494.69	474.91	18.09	<.001
Residual	62	1628.1	26.26		
Total	123	30123.44			

Reaction to rust

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	0	0	0	
Rep.*Units* stratum					
Genotype	60	507.484	8.458	2.91	<.001
Residual	62	180	2.903		
Total	123	687.484			

Reaction to anthracnose

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	5.452	5.452	2.05	
Rep.*Units* stratum					
Genotype	60	391.387	6.523	2.46	<.001
Residual	62	164.548	2.654		
Total	123	561.387			

Reaction to angular leaf spot

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	0.29	0.29	0.23	
Rep.*Units* stratum					
Genotype	60	801.097	13.352	10.52	<.001
Residual	62	78.71	1.27		
Total	123	880.097			

Total pod yield (kg ha^{-1})

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	1.84E+05	1.84E+05	0.05	
Rep.*Units* stratum					
Genotype	60	4.21E+09	7.02E+07	18.68	<.001
Residual	62	2.33E+08	3.76E+06		
Total	123	4.45E+09			

Appendix 12: Analysis of Variance of all traits studied in the selection of Advance bush snap beans

Trait	Analysis of variance														
	Kabete					Embu					Mwea				
Agronomic Traits															
Vigour	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	2.667	2.667	0.74		Rep stratum	1	0.019	0.01852	1		Rep stratum	1	2.667	2.667	1.3	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	207.704	7.989	2.23	0.02	Genotype	26	19	0.73077	39.46	<.001	Genotype	26	64.593	2.484	1.21	0.31
	Residual	26	93.333	3.59			Residual	26	0.481	0.01852			Residual	26	53.333	2.051		
	Total	53	303.704				Total	53	19.5				Total	53	120.593			
50% Days to flowering	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.667	0.667	0.29		Rep stratum	1	10.67	10.67	0.92		Rep stratum	1	14.519	14.519	4.22	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	528.704	20.335	8.76	<.001	Genotype	26	508.9	19.57	1.68	0.1	Genotype	26	164.148	6.313	1.83	0.06
	Residual	26	60.333	2.321			Residual	26	302.3	11.63			Residual	26	89.481	3.442		
	Total	53	589.704				Total	53	821.9				Total	53	268.148			
Days to First picking	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	6	6	2.52		Rep stratum	1	0.167	0.167	0.02		Rep stratum	1	3.13	3.13	2.77	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	657.037	25.271	10.6	<.001	Genotype	26	529.8	20.377	2.5	0.01	Genotype	26	170.333	6.551	5.8	<.001
	Residual	26	62	2.385			Residual	26	212.3	8.167			Residual	26	29.37	1.13		
	Total	53	725.037				Total	53	742.3				Total	53	202.833			
Reaction to diseases															

Rust	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.074	0.074	0.02		Rep stratum	1	0.167	0.16667	1.86		Rep stratum	1	0.296	0.296	0.12	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	249.259	9.587	2.9	0	Genotype	26	83.81	3.22365	35.92	<.001	Genotype	26	73.481	2.826	1.12	0.39
	Residual	26	85.926	3.305			Residual	26	2.333	0.08974			Residual	26	65.704	2.527		
	Total	53	335.259				Total	53	86.31				Total	53	139.481			
Angular Leaf Spot	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	2.667	2.667	1.56		Rep stratum	1	0.074	0.0741	0.09		Rep stratum	1	1.185	1.185	0.94	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	75.593	2.907	1.71	0.09	Genotype	26	74.48	2.8647	3.56	<.001	Genotype	26	171.037	6.578	5.21	<.001
	Residual	26	44.333	1.705			Residual	26	20.93	0.8048			Residual	26	32.815	1.262		
	Total	53	122.593				Total	53	95.48				Total	53	205.037			
Anthracnose	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	1.852	1.852	1.3		Rep stratum	1	0.296	0.2963	1.64		Rep stratum	1	4.167	4.167	1.42	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	39.148	1.506	1.05	0.45	Genotype	26	34.33	1.3205	7.3	<.001	Genotype	26	109.37	4.207	1.43	0.18
	Residual	26	37.148	1.429			Residual	26	4.704	0.1809			Residual	26	76.333	2.936		
	Total	53	78.148				Total	53	39.33				Total	53	189.87			
							Number of pods per plant											
Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	32905	32905	8.28		Rep stratum	1	66220	66220	31.86		Rep stratum	1	66220	66220	31.9	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	201727	7759	1.95	0.05	Genotype	26	99895	3842	1.85	0.06	Genotype	26	99895	3842	1.85	0.06

	Residual	26	103299	3973			Residual	26	54041	2079			Residual	26	54041	2079		
	Total	53	337931				Total	53	2.00E+05				Total	53	220157			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	82056	82056	6.08		Rep stratum	1	51646	51646	23.12		Rep stratum	1	51646	51646	23.1	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	433973	16691	1.24	0.3	Genotype	26	64481	2480	1.11	0.4	Genotype	26	64481	2480	1.11	0.4
	Residual	26	350976	13499			Residual	26	58086	2234			Residual	26	58086	2234		
	Total	53	867005				Total	53	2.00E+05				Total	53	174213			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0	0	0		Rep stratum	1	7397	7397	4.95		Rep stratum	1	7397	7397	4.95	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	10220	393.1	2.14	0.03	Genotype	26	58048	2233	1.49	0.16	Genotype	26	58048	2233	1.49	0.16
	Residual	26	4772	183.5			Residual	26	38860	1495			Residual	26	38860	1495		
	Total	53	14992				Total	53	1.00E+05				Total	53	104305			
							Percentage Proportions of the number of pods per plant											
Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	7.78	7.78	0.08		Rep stratum	1	111.4	111.43	2.31		Rep stratum	1	107.93	107.93	1.48	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	3375.9	129.84	1.33	0.24	Genotype	26	3990	153.46	3.18	0	Genotype	26	5340.91	205.42	2.81	0.01
	Residual	26	2540.14	97.7			Residual	26	1253	48.19			Residual	26	1898.61	73.02		
	Total	53	5923.82				Total	53	5354				Total	53	7347.45			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	91	91	0.83		Rep stratum	1	3.32	3.32	0.08		Rep stratum	1	0.84	0.84	0.01	

	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	3754.5	144.4	1.31	0.25	Genotype	26	1008	38.78	0.95	0.55	Genotype	26	1304.94	50.19	0.89	0.62
	Residual	26	2867.8	110.3			Residual	26	1061	40.82			Residual	26	1467.71	56.45		
	Total	53	6713.3				Total	53	2073				Total	53	2773.49			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	45.57	45.57	3.34		Rep stratum	1	76.29	76.29	1.2		Rep stratum	1	127.78	127.78	1.42	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	800.23	30.78	2.26	0.02	Genotype	26	2856	109.87	1.73	0.08	Genotype	26	3830.68	147.33	1.64	0.11
	Residual	26	354.46	13.63			Residual	26	1649	63.44			Residual	26	2336.39	89.86		
	Total	53	1200.26				Total	53	4582				Total	53	6294.84			
Total number of pods per plant	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	218886	218886	7.82		Rep stratum	1	3.00E+05	325579	26.68		Rep stratum	1	325579	325579	26.7	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	971771	37376	1.34	0.23	Genotype	26	4.00E+05	14929	1.22	0.31	Genotype	26	388151	14929	1.22	0.31
	Residual	26	727643	27986			Residual	26	3.00E+05	12204			Residual	26	317316	12204		
	Total	53	1918300				Total	53	1.00E+06				Total	53	1031046			
	Pod Lengths (cm)																	
Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	61.43	61.43	2.28		Rep stratum	1	10.26	10.26	0.61		Rep stratum	1	121.67	121.67	5.73	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	2677.5	102.98	3.83	<.001	Genotype	26	878.6	33.79	2.02	0	Genotype	26	2094.35	80.55	3.79	<.001
	Residual	404	10867.3	26.9			Residual	404	6762	16.74			Residual	404	8583.33	21.25		
	Total	431	13606.22				Total	431	7650				Total	431	10799.35			

Fine

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	141.9	141.9	6.92	
Rep.*Units* stratum					
Genotype	26	4647.6	178.75	8.72	<.001
Residual	404	8286.29	20.51		
Total	431	13075.78			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	96.06	96.06	3.86	
Rep.*Units* stratum					
Genotype	26	1138	43.75	1.76	0.01
Residual	404	10047	24.87		
Total	431	11281			

Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.	F pr.
Rep stratum	1		281.67	282	9.77	
Rep.*Units* stratum						
Genotype	26		2913.07	112	3.88	<.001
Residual	403	-1	11623.2	28.8		
Total	430	-1	14811.1			

Bobby

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	0.17	0.17	0.01	
Rep.*Units* stratum					
Genotype	26	4244.61	163.25	5.51	<.001
Residual	404	11967.75	29.62		
Total	431	16212.53			

Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.	F pr.
Rep stratum	1		9.86	9.86	0.29	
Rep.*Units* stratum						
Genotype	26		2818.71	108.4	3.23	<.001
Residual	403	-1	13511.7	33.53		
Total	430	-1	16336.3			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	212.75	212.75	6.29	
Rep.*Units* stratum					
Genotype	26	2293.04	88.19	2.61	<.001
Residual	404	13663.1	33.82		
Total	431	16168.9			

Pod Yield (kg ha^{-1})

Extra Fine

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	7834525	7834525	5.83	
Rep.*Units* stratum					
Genotype	26	75396206	2899854	2.16	0.03
Residual	26	34930771	1343491		
Total	53	1.18E+08			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	5.00E+07	4.80E+07	42.53	
Rep.*Units* stratum					
Genotype	26	4.00E+07	1429464	1.26	0.28
Residual	26	3.00E+07	1134395		
Total	53	1.00E+08			

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	23958921	2.40E+07	4.97	
Rep.*Units* stratum					
Genotype	26	2.66E+08	1.00E+07	2.12	0.03
Residual	26	1.25E+08	4823742		
Total	53	4.15E+08			

Fine

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	8012186	8012186	1.15	
Rep.*Units* stratum					

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	9.00E+06	8647360	2.67	
Rep.*Units* stratum					

Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
Rep stratum	1	1.36E+06	1.36E+06	0.36	
Rep.*Units* stratum					

	Genotype	26	4.60E+08	17675879	2.53	0.01	Genotype	26	9.00E+07	3465539	1.07	0.43	Genotype	26	2.01E+08	7.73E+06	2.04	0.04
	Residual	26	1.82E+08	6991154			Residual	26	8.00E+07	3237237			Residual	26	9.86E+07	3.79E+06		
	Total	53	6.49E+08				Total	53	2.00E+08				Total	53	3.01E+08			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	5.24E+04	5.24E+04	0.25		Rep stratum	1	9.00E+06	8590803	11.38		Rep stratum	1	22192768	2.20E+07	4.13	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	1.19E+07	4.57E+05	2.18	0.03	Genotype	26	3.00E+07	984641	1.3	0.25	Genotype	26	1.23E+08	4737514	0.88	0.63
	Residual	26	5.45E+06	2.10E+05			Residual	26	2.00E+07	754656			Residual	26	1.40E+08	5378847		
	Total	53	1.74E+07				Total	53	5.00E+07				Total	53	2.85E+08			
Total Pod	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	5.14E+07	5.14E+07	4.3		Rep stratum	1	2.00E+08	1.60E+08	22.75		Rep stratum	1	7.12E+07	7.12E+07	4.56	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	7.39E+08	2.84E+07	2.38	0.02	Genotype	26	2.00E+08	6062482	0.84	0.67	Genotype	26	9.52E+08	3.66E+07	2.35	0.02
	Residual	26	3.11E+08	1.20E+07			Residual	26	2.00E+08	7222871			Residual	26	4.06E+08	1.56E+07		
	Total	53	1.10E+09				Total	53	5.00E+08				Total	53	1.43E+09			

Percentage (%) Proportions per Market class

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	47	47	0.23		Rep stratum	1	22.4	22.4	0.22		Rep stratum	1	409.2	409.2	1.14	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	5586.1	214.8	1.03	0.47	Genotype	26	1559	60	0.6	0.9	Genotype	26	7565.8	291	0.81	0.7
	Residual	26	5419.2	208.4			Residual	26	2610	100.4			Residual	26	9344	359.4		
	Total	53	11052.3				Total	53	4192				Total	53	17319			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.

	Rep stratum	1	178.1	178.1	0.41		Rep stratum	1	0.4	0.4	0		Rep stratum	1	701.2	701.2	2.26	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	5617.7	216.1	0.5	0.96	Genotype	26	5637	216.8	2.08	0.03	Genotype	26	14692.5	565.1	1.82	0.07
	Residual	26	11266.3	433.3			Residual	26	2714	104.4			Residual	26	8082.8	310.9		
	Total	53	17062.1				Total	53	8352				Total	53	23476.5			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	57.12	57.12	2.61		Rep stratum	1	16.77	16.77	0.21		Rep stratum	1	390.7	390.7	0.88	
	Rep.*Units* stratum						Rep.*Units* stratum						Rep.*Units* stratum					
	Genotype	26	892.55	34.33	1.57	0.13	Genotype	26	3745	144.03	1.79	0.07	Genotype	26	17933.1	689.7	1.55	0.14
	Residual	26	568.75	21.88			Residual	26	2095	80.59			Residual	26	11570.1	445		
	Total	53	1518.42				Total	53	5857				Total	53	29893.9			

Appendix 13: Combined analysis of variance of all studied traits for advanced bush snap beans in Kabete (2014) and Embu and Mwea in 2013

Trait	Combined Analysis of variance				
	Agronomic Traits				
Plant Vigour	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.006	0.006	0	
	Rep.*Units* stratum					
	Genotype	26	105.864	4.072	2.14	0.005
	Location	2	107.568	53.784	28.22	<.001
	Genotype.Location	52	185.432	3.566	1.87	0.006
	Residual	80	152.494	1.906		
	Total	161	551.364			
50% Days to Flowering	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	20.765	20.765	3.63	
	Rep.*Units* stratum					
	Genotype	26	536.086	20.619	3.61	<.001
	Location	2	267.309	133.654	23.38	<.001
	Genotype.Location	52	665.691	12.802	2.24	<.001
	Residual	80	457.235	5.715		
	Total	161	1947.086			
Days to first picking	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	4.84	4.84	1.26	
	Rep.*Units* stratum					
	Genotype	26	903.827	34.763	9.02	<.001
	Location	2	254.309	127.154	33.01	<.001
	Genotype.Location	52	453.358	8.718	2.26	<.001
	Residual	80	308.16	3.852		
	Total	161	1924.494			
	Reaction to Diseases					
Rust	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.006	0.006	0	
	Rep.*Units* stratum					
	Genotype	26	88.901	3.419	1.77	0.028
	Location	2	548.012	274.006	141.89	<.001
	Genotype.Location	52	317.654	6.109	3.16	<.001
	Residual	80	154.494	1.931		
	Total	161	1109.068			
Angular Leaf Spot	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.222	0.222	0.17	
	Rep.*Units* stratum					
	Genotype	26	126.086	4.849	3.81	<.001
	Location	2	27.309	13.654	10.73	<.001

	Genotype.Location	52	195.025	3.75	2.95	<.001
	Residual	80	101.778	1.272		
	Total	161	450.42			

Anthracnose	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	0.5	0.5	0.32	
	Rep.*Units* stratum					
	Genotype	26	53.938	2.075	1.34	0.163
	Location	2	35.42	17.71	11.43	<.001
	Genotype.Location	52	128.914	2.479	1.6	0.029
	Residual	80	124	1.55		
	Total	161	342.772			

Number of pods per plant

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	37022	37022	8.72	
	Rep.*Units* stratum					
	Genotype	26	258834	9955	2.34	0.002
	Location	2	73265	36633	8.63	<.001
	Genotype.Location	52	142683	2744	0.65	0.953
	Residual	80	339705	4246		
	Total	161	851510			

Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	9415	9415	1.17	
	Rep.*Units* stratum					
	Genotype	26	208573	8022	1	0.481
	Location	2	764417	382208	47.55	<.001
	Genotype.Location	52	354361	6815	0.85	0.736
	Residual	80	643082	8039		
	Total	161	1979848			

Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	9862	9862	9.02	
	Rep.*Units* stratum					
	Genotype	26	79245	3048	2.79	<.001
	Location	2	100040	50020	45.77	<.001
	Genotype.Location	52	47072	905	0.83	0.765
	Residual	80	87424	1093		
	Total	161	323643			

Percentage Proportions of number of pods per plant per market class

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	187.79	187.79	2.62	
	Rep.*Units* stratum					
	Genotype	26	7435.48	285.98	3.99	<.001
	Location	2	57.79	28.89	0.4	0.669
	Genotype.Location	52	5271.27	101.37	1.42	0.08

	Residual	80	5731.13	71.64		
	Total	161	18683.45			

Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	36.38	36.38	0.53	
	Rep.*Units* stratum					
	Genotype	26	2924.66	112.49	1.65	0.047
	Location	2	11111.67	5555.83	81.47	<.001
	Genotype.Location	52	3143.06	60.44	0.89	0.676
	Residual	80	5455.59	68.19		
	Total	161	22671.36			

Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	58.85	58.85	1.04	
	Rep.*Units* stratum					
	Genotype	26	4615.6	177.52	3.13	<.001
	Location	2	9666.12	4833.06	85.33	<.001
	Genotype.Location	52	2871.8	55.23	0.98	0.533
	Residual	80	4531.09	56.64		
	Total	161	21743.46			

Total no of pods	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	151128	151128	5.81	
	Rep.*Units* stratum					
	Genotype	26	810505	31173	1.2	0.266
	Location	2	703213	351606	13.52	<.001
	Genotype.Location	52	937568	18030	0.69	0.921
	Residual	80	2081190	26015		
	Total	161	4683604			

Pod Length (cm)

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	13.64	13.64	0.66	
	Rep.*Units* stratum					
	Genotype	26	2503.27	96.28	4.66	<.001
	Harvest	7	1379.65	197.09	9.54	<.001
	Location	2	4741.38	2370.69	114.74	<.001
	Genotype.Harvest	182	3434.88	18.87	0.91	0.769
	Genotype.Location	52	3147.15	60.52	2.93	<.001
	Harvest.Location	14	1446.98	103.36	5	<.001
	Genotype.Harvest.Location	364	6762.43	18.58	0.9	0.871
	Residual	647	13367.99	20.66		
	Total	1295	36797.37			

Fine	Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1		69.27	69.27	3.09	
	Rep.*Units* stratum						

	Genotype	26		3079.81	118.45	5.29	<.001
	Harvest	7		3781.64	540.23	24.11	<.001
	Location	2		9166.21	4583.1	204.54	<.001
	Genotype.Harvest	182		3726.13	20.47	0.91	0.768
	Genotype.Location	52		5600.91	107.71	4.81	<.001
	Harvest.Location	14		2113.19	150.94	6.74	<.001
	Genotype.Harvest.Location	364		6329.42	17.39	0.78	0.996
	Residual	646	-1	14474.64	22.41		
	Total	1294	-1	48340.66			

Bobby	Source of variation	d.f.	(m.v.)	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1		106.89	106.89	3.65	
	Rep.*Units* stratum						
	Genotype	26		3508.22	134.93	4.61	<.001
	Harvest	7		762.58	108.94	3.72	<.001
	Location	2		7365.25	3682.63	125.75	<.001
	Genotype.Harvest	182		6261.88	34.41	1.17	0.081
	Genotype.Location	52		5869.92	112.88	3.85	<.001
	Harvest.Location	14		3802.19	271.58	9.27	<.001
	Genotype.Harvest.Location	364		9532.69	26.19	0.89	0.883
	Residual	646	-1	18919.02	29.29		
	Total	1294	-1	56064.7			

Pod Yield in kg ha^{-1}

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	27249516	27249516	8.98	
	Rep.*Units* stratum					
	Genotype	26	85857512	3302212	1.09	0.374
	Location	2	5844634	2922317	0.96	0.386
	Genotype.Location	52	2.92E+08	5620611	1.85	0.006
	Residual	80	2.43E+08	3032867		
	Total	161	6.54E+08			

Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	3.73E+05	3.73E+05	0.08	
	Rep.*Units* stratum					
	Genotype	26	2.51E+08	9.66E+06	2.02	0.009
	Location	2	1.13E+09	5.66E+08	118.37	<.001
	Genotype.Location	52	5.00E+08	9.61E+06	2.01	0.002
	Residual	80	3.82E+08	4.78E+06		
	Total	161	2.26E+09			

Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	20650156	20650156	9.43	
	Rep.*Units* stratum					
	Genotype	26	54614063	2100541	0.96	0.529
	Location	2	2.05E+08	1.02E+08	46.75	<.001
	Genotype.Location	52	1.06E+08	2039538	0.93	0.603

	Residual	80	1.75E+08	2188853		
	Total	161	5.61E+08			

Percentage Yield proportions per market Class

Extra Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	169.3	169.3	0.81	
	Rep.*Units* stratum					
	Genotype	26	4102.4	157.8	0.75	0.79
	Location	2	8558.6	4279.3	20.43	<.001
	Genotype.Location	52	10304.6	198.2	0.95	0.58
	Residual	80	16756.8	209.5		
	Total	161	39891.6			
Fine	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	63.3	63.3	0.22	
	Rep.*Units* stratum					
	Genotype	26	8896.8	342.2	1.2	0.267
	Location	2	50280.6	25140.3	87.9	<.001
	Genotype.Location	52	17050.3	327.9	1.15	0.287
	Residual	80	22879.9	286		
	Total	161	99170.8			
Bobby	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	120.4	120.4	0.67	
	Rep.*Units* stratum					
	Genotype	26	4857.9	186.8	1.04	0.43
	Location	2	35969.4	17984.7	100.06	<.001
	Genotype.Location	52	16706.7	321.3	1.79	0.01
	Residual	80	14379.8	179.7		
	Total	161	72034.1			
Total pod yield	Source of variation	d.f.	s.s.	m.s.	v.r.	F pr.
	Rep stratum	1	6.61E+07	6.61E+07	4.7	
	Rep.*Units* stratum					
	Genotype	26	4.87E+08	1.87E+07	1.33	0.167
	Location	2	7.16E+08	3.58E+08	25.43	<.001
	Genotype.Location	52	1.36E+09	2.62E+07	1.86	0.006
	Residual	80	1.13E+09	1.41E+07		
	Total	161	3.76E+09			